APCCMI2025
BANGKOK

The 20th Asia Pacific Congress of
Clinical Microbiology and Infection

2-4 November 2025
ICONSIAM, Bangkok, Thailand

Abstract Book

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CAS-002: Dolutegravir plus Lopinavir/ritonavir as a Second-Line Two-Drug Regimen in PLHIV – A Case Series of Clinical Success

Barbara Cariza Buenafe, Mark Kristoffer Pasayan

Research Institute for Tropical Medicine

Introduction
The 2021 WHO guidelines recommend Dolutegravir (DTG) combined with a nucleoside reverse transcriptase inhibitor (NRTI) backbone as the preferred second-line regimen following first-line antiretroviral therapy failure. However, this approach may not adequately address prior drug-related toxicities or insufficient immunologic response.

Case Presentation
We present six PLHIV cases transitioned to a Dolutegravir (DTG) plus ritonavir-boosted Lopinavir (LPV/r) regimen. Three males (ages 34, 24, 36) developed transfusion-refractory anemia on Zidovudine. Two others (42/F, 60/M) had NRTI resistance and Tenofovir-induced renal impairment. One (52/F) experienced persistent CD4 depletion and recurrent opportunistic infections (OIs), including lepromatous leprosy, despite two prior ART regimens.

Within 24 weeks on DTG + LPV/r, all patients achieved viral suppression and CD4 counts >400 cells/mm³, with resolution of OIs and correction of anemia and nephrotoxicity.

The D2EFT study showed that an INSTI plus ritonavir-boosted PI regimen achieves robust CD4 recovery and viral suppression without NRTIs, with a CD4 gain of 56 cells/mm³ and 84.7% suppression at 48 weeks. Our case series showed similar outcomes within 24 weeks. DTG + LPV/r proved cost-effective and well-tolerated, with no gastrointestinal side effects reported, highlighting its safety, high resistance barrier, and efficacy in treatment-experienced patients with complex clinical backgrounds.

Conclusion
In our setting, DTG + LPV/r is the available regimen, and our experience demonstrated favorable virologic and immunologic outcomes while also addressing adverse drug reactions. Although large-scale data are still limited, these results indicate promising clinical outcomes with DTG + LPV/r. This NRTI-sparing two-drug regimen may be considered for patients failing first-line ART.

Patient	Sex/Age	Reason for Switching Regimen	Previous Issues	Outcomes after 24 Weeks		
				CD4	VIRAL LOAD	CLINICAL OUTCOME
1	M/34	Transfusion-refractory anemia following Zidovudine regimen	Anemia	439	20	Anemia resolved
2	M/24	Transfusion-refractory anemia following Zidovudine regimen	Anemia	408	UNDETECTABLE	Anemia resolved
3	M/36	Transfusion-refractory anemia following Zidovudine regimen	Anemia	501	UNDETECTABLE	Anemia resolved
4	F/42	NRTI resistance, Tenofovir-induced renal impairment	Nephrotoxicity, NRTI resistance	435	<40	AKI resolved
5	M/60	NRTI resistance, Tenofovir-induced renal impairment	Nephrotoxicity, NRTI resistance	692	<40	AKI resolved
6	F/52	Persistent CD4 depletion, recurrent OI (including leprosy)	Low CD4, recurrent OIs (lepromatous leprosy)	499	20	Regression of lesions of leprosy

Table 1. Clinical outcomes of patients switched to Dolutegravir plus Lopinavir/ritonavir as second-line regimen after 24 weeks

CAS-003: Calvarial Tuberculosis in a Patient with Disseminated Multidrug-Resistant Tuberculosis and Advanced HIV Disease: A Rare Case Report

Don Michael Bernardino, Aileen Gascon

Research Institute for Tropical Medicine

Introduction

A total of 1.3 million people died from Tuberculosis (TB) in 2022. Multidrug-resistant Tuberculosis (MDR-TB) remains a public health crisis and a health security threat. Only about 2 in 5 people with drug resistant TB accessed treatment in 2022. Calvarial tuberculosis is a rare manifestation of TB, characterized by lytic lesions in the skull. When associated with multidrug-resistant tuberculosis (MDR-TB) coinfected with HIV, the condition poses diagnostic and therapeutic challenges. This report details a case of calvarial TB in a 41-year-old male with advanced HIV disease and disseminated MDR-TB, highlighting its rarity and clinical significance.

Case Presentation

The patient, diagnosed with HIV in 2015, had been treated for a psoas abscess drug-susceptible TB but lost to follow-up after starting antiretroviral therapy. He presented with fever, cough, and dyspnea. Examination revealed two soft, non-tender skull masses. A cranial computed tomography (CT) scan showed lytic lesions in the left frontal and right high posterior parietal bones. Sputum, Cerebrospinal fluid (CS) and parietal mass aspirate revealed rifampicin-resistant Mycobacterium tuberculosis.

Additional tests indicated resistance to first line TB drugs, confirming disseminated MDR-TB involving the calvaria, central nervous system (CNS), and lungs. He began an 18-month regimen with Levofloxacin, Bedaquiline, Linezolid, and Cycloserine, and was referred for surgical intervention.

Conclusion

This case emphasizes the rarity and clinical significance of calvarial TB in disseminated MDR-TB and advanced HIV. Early diagnosis and comprehensive management, including surgical and medical interventions, are crucial. Multidisciplinary care and individualized treatment regimens are essential for managing MDR-TB in immunocompromised patients.

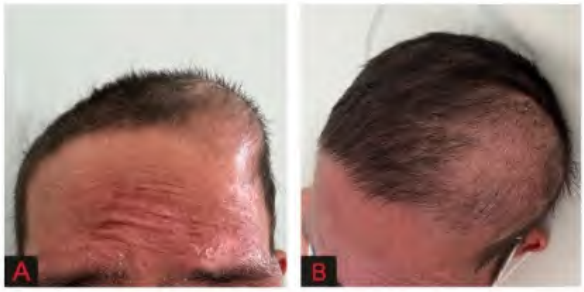


Fig. 1 (**A, B**) Image showing 5 x 5 x 2 cm soft, fluctuant, non-tender mass, frontal area slightly left from the midline.

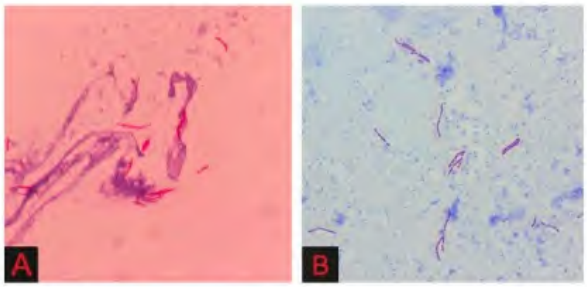


Fig 2. (**A, B**) Ziehl-Neelsen staining of the parietal mass aspirate showed positive for acid-fast bacilli.

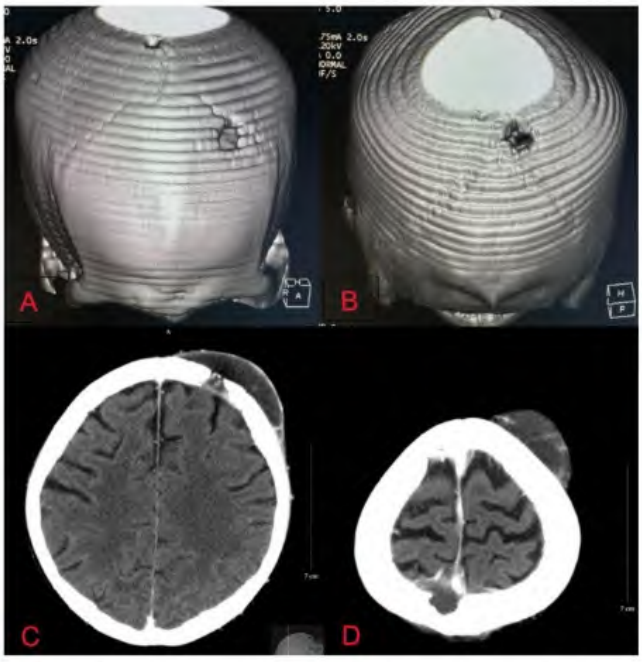


Fig. 3 (A, B) Cranial CT with reconstruction showing lytic lesions on the external board of the left frontal (A) and right high posterior parietal (B) region. **(C, D)** Contrast-enhanced axial cranial CT scan showing lytic lesions in the inner and outer tables of the left frontal and right high posterior parietal bones with subgaleal soft tissue swellings exhibiting subtle rim enhancement. The lesions measured approximately 6.97 x 2.07 cm (W x AP) in the left frontal region and 3.8 x 1.6 cm in the right high posterior parietal region

CAS-004: Erythema Nodosum Leprosum in an HIV patient with Poor CD4 Cell Recovery: A True Co-Infection

Barbara Cariza Buenafe, Jemelyn Garcia

Research Institute for Tropical Medicine

Introduction

As of 2021, leprosy remains endemic in the Philippines, with over 1,000 cases annually. Increasing numbers of people living with HIV (PLHIV) have led to more HIV-leprosy co-infections, typically presenting as tuberculoid leprosy with IRIS, while lepromatous forms rarely occur in severe immunosuppression with poor CD4 recovery.

Case Presentation

We report a 51-year-old female with rectal adenocarcinoma and advanced HIV on Lamivudine + Zidovudine + Dolutegravir for three months, presenting with multiple erythematous tender papules with central umbilication on the upper extremities, chest, and face. This was accompanied by bipedal edema, facial swelling, and violaceous nodules on the anterior leg. Skin punch biopsy showed foamy histiocytes and multinucleated giant cells consistent with Hansen's Disease. She was treated as Lepromatous Leprosy with Erythema Nodosum Leprosum and started on a 12-month MDT regimen and tapering prednisone. On follow-up, the lesions flattened, and edema and joint pains resolved.

Lepra reactions are immunologically mediated episodes of acute inflammation. In HIV patients, they are triggered by an unstable immune system. Most leprosy cases in HIV are linked to IRIS after HAART initiation. Our patient's CD4 count dropped to 36 cells/mm³ from 68 despite three months of HAART, likely due to ongoing HIV-1 and leprosy co-infection. Untreated co-infections and conditions like malignancy are known contributors to CD4 lymphopenia.

Conclusion

In HIV-leprosy co-infection, it appears that the patient's cell-mediated immunity, not HIV itself, alters the clinico-immunopathological spectrum of leprosy. No treatment modification is needed in HIV-leprosy cases. However, potential interactions between anti–M. leprae and anti-HIV drugs should be considered.

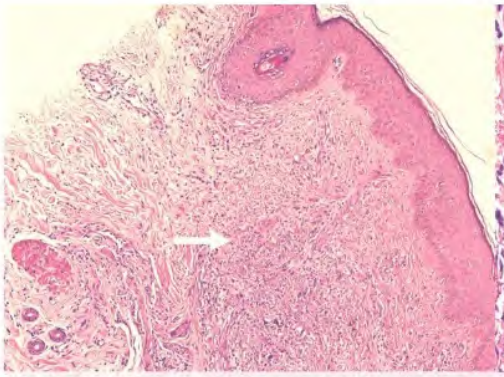


Fig 1. Multinucleated giant cells (white arrow) on LPO view

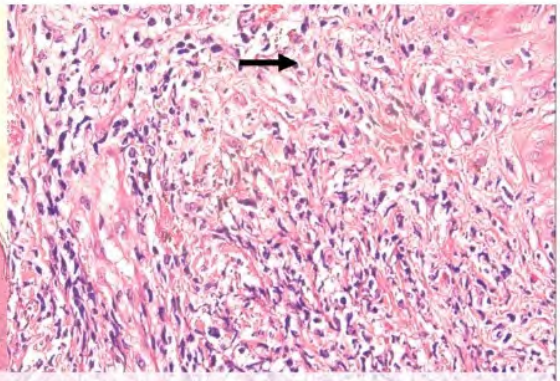


Fig 2. Foamy histiocytes typical of Hansen's Disease (black arrow) on HPO view

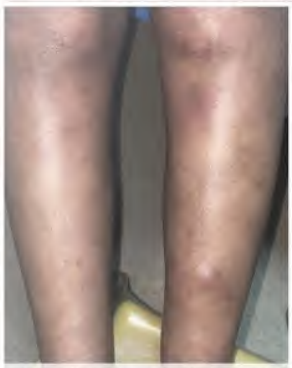


Fig 3. Erythematous nodules on both legs typical of Erythema Nodosum Leprosum

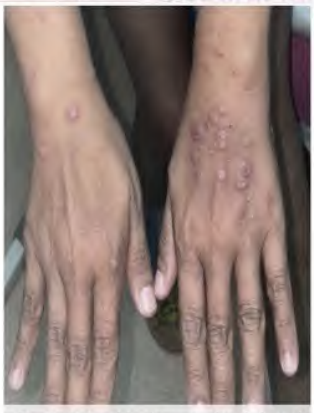


Fig 4. Raised lesions on both hands

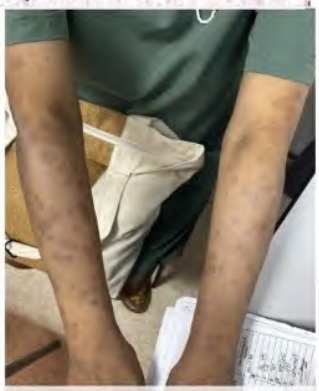


Fig 5. Flattened lesions on both hands after 6th week of MDT

CAS-006: Insights into Candida haemulonii Bloodstream Infection: A Case Series from Tertiary Hospital in Quezon City, Philippines

Lordieliza Melendrez, Armin Masbang

St. Luke's Medical Center - Quezon City

Introduction
Candida haemulonii is an emerging, multidrug-resistant non-albicans Candida species recognized as a cause of invasive candidiasis, including bloodstream infections (BSI). This case series describes four patients with C. haemulonii BSI, highlighting diagnostic and therapeutic challenges.

A retrospective review was conducted on four patients with confirmed C. haemulonii bloodstream infections from 2024 to 2025 at St. Luke's Medical Center – Quezon City. Clinical data, including demographics, comorbidities, risk factors, microbiologic findings, treatment, and outcomes were analyzed.

Case Presentation
All patients were male, aged 53 to 73 years, with significant comorbidities including diabetes mellitus, cardiovascular disease, and advanced malignancy. Two patients had recent hospitalizations, and two had central venous catheters at the time of infection. All patients had prior exposure to broad-spectrum antibiotics. C. haemulonii was isolated from blood cultures and identified using MALDI-TOF MS. In two cases, the infection was catheter-related, while in the other two, no clear source was identified. All patients received echinocandin-based treatment: three with anidulafungin and one with micafungin; one patient also received voriconazole. All strains were resistant to azoles and amphotericin B. The duration of antifungal therapy was 14 days, either from blood culture clearance or treatment initiation. All four patients survived to discharge, with hospital stays ranging from 30 to 95 days.

Conclusion
C. haemulonii bloodstream infection is a challenging pathogen, particularly in patients with underlying comorbidities and prior broad-spectrum antibiotic exposure. These factors may increase susceptibility to opportunistic infections. Timely identification, antifungal susceptibility-guided therapy, and antimicrobial stewardship are critical in managing such infections, especially in high-risk patients.

CAS-007: A Case of Erythema Induratum of Bazin: Uncovering the Link to Tuberculosis

Elham Jaji, Ayen Gianan-Gascon

Research Institute for Tropical Medicine

Introduction
Erythema Induratum of Bazin (EIB) is a hypersensitivity reaction to Mycobacterium tuberculosis, it can occur with both active and latent TB infection.

Case Presentation
A 21-year-old immunocompetent Filipino woman presented to the RITM Dermatology Clinic with a one-month history of painful erythematous nodules on the posterior aspect of both legs, without any constitutional symptoms of tuberculosis. She denied exposure to an active tuberculosis patient. A skin biopsy and relevant workup were performed, including ASO titer, hepatitis profile, chest X-ray, tissue culture, and tissue PCR for tuberculosis, all of which were negative. However, IGRA was positive, and histopathology revealed mild spongiosis of the epidermis with dense inflammatory infiltrates composed of lymphocytes, histiocytes, neutrophils, and multinucleated giant cells with vasculitis. These findings supported a diagnosis of lobular panniculitis consistent with EIB, leading to her referral to the Tuberculosis Clinic for evaluation.

Further workup for active tuberculosis and other immunologic and infectious causes of nodular vasculitis was unremarkable. However, a high-resolution chest CT scan revealed a tree-in-bud pattern in the right upper lobe, indicative of active pulmonary tuberculosis. As a result, anti-TB medications were initiated, and she was treated for active pulmonary TB disease.

Conclusion
Identifying an active source of tuberculosis before initiating anti-TB medications for EIB is crucial for optimizing treatment outcomes and preventing unnecessary drug exposure. Since EIB is a tuberculid, it represents a hypersensitivity reaction to Mycobacterium tuberculosis, often linked to latent or active TB. Detecting an active source ensures targeted treatment, reducing the risk of drug resistance and relapse.

CAS-008: Uncommon Source, Severe Consequence: Tetanus from a Malignant Breast Mass

Lordieliza Melendrez, Jelly Gozun

St. Luke's Medical Center - Quezon City

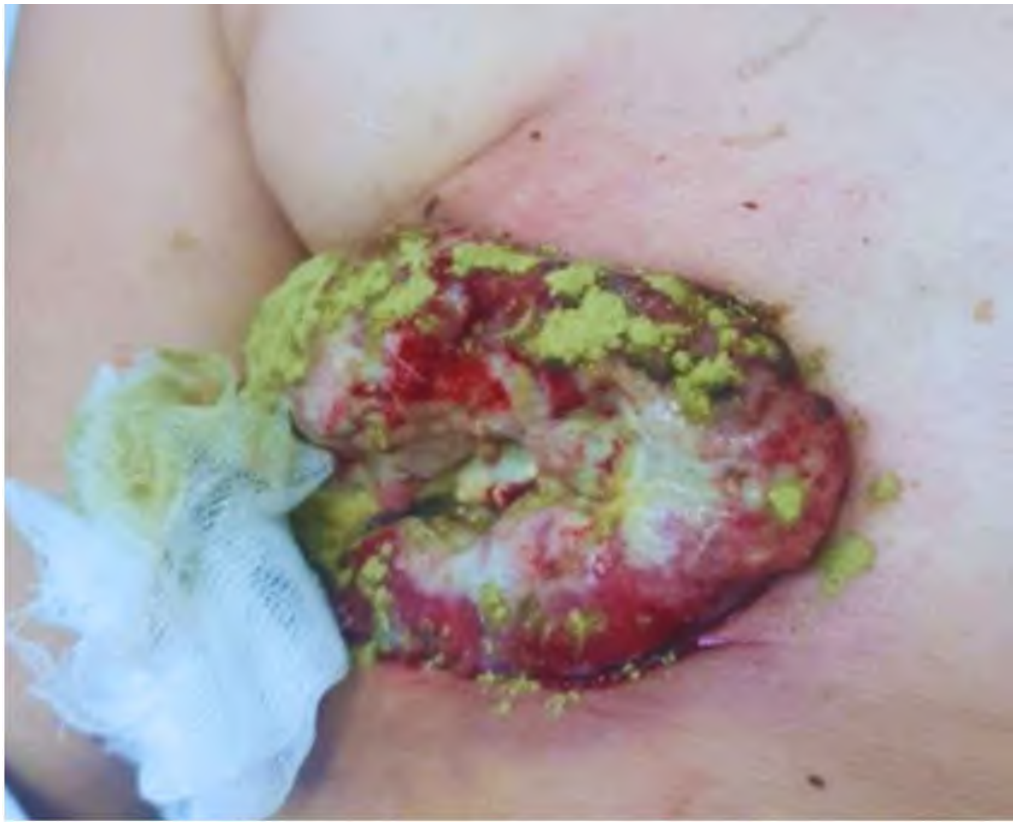
Introduction
Tetanus, a life-threatening disease caused by Clostridium tetani, remains a concern in areas with low immunization coverage. Spores typically enter through wounds, burns, or trauma. We report only the third case in global literature of tetanus arising from a necrotic breast tumor—and the first in our country.

Case Presentation
A 44-year-old Filipino woman presented with a four-day history of worsening jaw pain, dysphagia, trismus, and spontaneous neck and abdominal spasms. Her vaccination status was unknown. Additionally, she presented with a 10x10 cm necrotic breast mass with a foul-smelling greenish discharge, covered with leaves, dung, and unidentified medication. Based on her presentation, she was managed as a case of tetanus infection.

She received 500 IU human anti-tetanus immunoglobulin, 0.5 mL tetanus toxoid, and was started on intravenous metronidazole and ceftriaxone. Diazepam was administered for spasm control. Although symptoms improved, she declined further evaluation for her breast mass and was discharged against medical advice.

Conclusion
Tetanus is marked by severe neurological, cardiovascular, and respiratory complications, along with physical and psychological effects. It manifests as trismus, dysphagia, and muscle spasms. Common sources include chronic wounds and contaminated injuries. There are no known data on tetanus in breast cancer patients. In this case, traditional applications on the necrotic mass may have introduced C. tetani spores. The tumor's anaerobic environment likely facilitated toxin production.

This case underscores the importance of timely tetanus prevention through vaccination, early wound care, and patient education, especially in underserved areas where traditional remedies are common and access to healthcare is limited.



CAS-009: Fatal Mycobacterium abscessus Pneumonia in a Patient with Bronchiectasis and Autoimmune Necrotizing Myopathy

Lordieliza Melendrez, Armin Masbang

St. Luke's Medical Center - Quezon City

Introduction
Mycobacterium abscessus is an emerging non-tuberculous mycobacterium (NTM) causing pulmonary infections, particularly in patients with underlying structural lung disease and immunosuppression. Management is difficult due to its intrinsic resistance and the toxicity of prolonged multidrug regimens.

Case Presentation
A 71-year-old male with a history of chronic bronchiectasis and autoimmune necrotizing myopathy presented with worsening cough, dyspnea, and intermittent low-grade fever. Chest imaging revealed multifocal infiltrates with areas of cavitation, suggestive of nonresolving pneumonia. Despite multiple courses of empiric antibiotics, symptoms persisted and patient remained ventilated. Bronchoscopy with bronchoalveolar lavage (BAL) was performed, and acid-fast bacilli were detected on staining. Culture later identified Mycobacterium abscessus subsp. abscessus. The patient was started on a combination regimen of intravenous amikacin, oral clarithromycin, and linezolid. Although initial clinical stabilization was noted, he developed worsening metabolic acidosis and elevated lactate levels by the 4th week of therapy. Despite intensive care support, he eventually expired due to refractory lactic acidosis, likely secondary to linezolid-associated mitochondrial toxicity.

Conclusion
This case underscores the diagnostic challenge of NTM infections in patients with chronic lung disease, where symptoms may overlap with recurrent bacterial infections. M. abscessus is particularly difficult to manage due to its multidrug resistance and the need for prolonged, toxic regimens. Linezolid, though effective against resistant organisms, poses a significant risk for hematologic and metabolic complications in elderly patients. Early recognition of drug toxicity and judicious use of therapy are crucial in managing such infections.

CAS-010: Uncharted Waters: Aeromonas hydrophila Causing Pleural Infection in an Immunocompromised Patient

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[1]St. Luke's Medical Center - Quezon City

Introduction
Aeromonas hydrophila is a gram-negative bacillus typically found in aquatic environments. It can cause gastroenteritis, soft tissue infections, and sepsis, but pleural involvement is rare. We present an unusual case of acute bacterial empyema due to A. hydrophila in an immunocompromised patient.

Case Presentation
A 60-year-old Filipino male with stage IV pancreaticobiliary carcinoma and malignant pleural effusion presented with acute dyspnea. He had recurrent episodes of spontaneous bacterial peritonitis treated with various antibiotics. On arrival, purulent drainage was noted from his chest pigtail catheter, and empyema thoracis was diagnosed. Empiric broad-spectrum antibiotics were started. Culture of the pleural fluid grew A. hydrophila, pansensitive to tested antibiotics. The patient responded well to continued antibiotic therapy and was discharged.

Conclusion
A. hydrophila is a facultatively anaerobic gram-negative rod often associated with freshwater exposure. Extra-intestinal manifestations, such as bacteremia and pneumonia, are uncommon. Empyema thoracis is particularly rare. Reported cases often involve patients with underlying hepatobiliary disease or malignancy.

Although the connection between Aeromonas infections and liver cirrhosis is not fully understood, it seems that Aeromonas spp. may exhibit heightened virulence in cirrhotic patients. The antibiotic susceptibility pattern of the isolate aligns with previous reports, showing broad susceptibility. However, patients with A. hydrophila empyema often face high mortality rates, up to 50%, likely due to their immunocompromised states.

This case underscores a rare presentation of A. hydrophila empyema in an immunocompromised patient. As extra-intestinal infections become more frequently recognized in Southeast Asia, further investigation into the pathogenesis and optimal management of Aeromonas infections is warranted.

CAS-013: Case Report: Helminthiasis With Endoscopic Image of Duodenal Polyp, Gastric Bleeding, and Severe Active Ulcerative Colitis

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Introduction

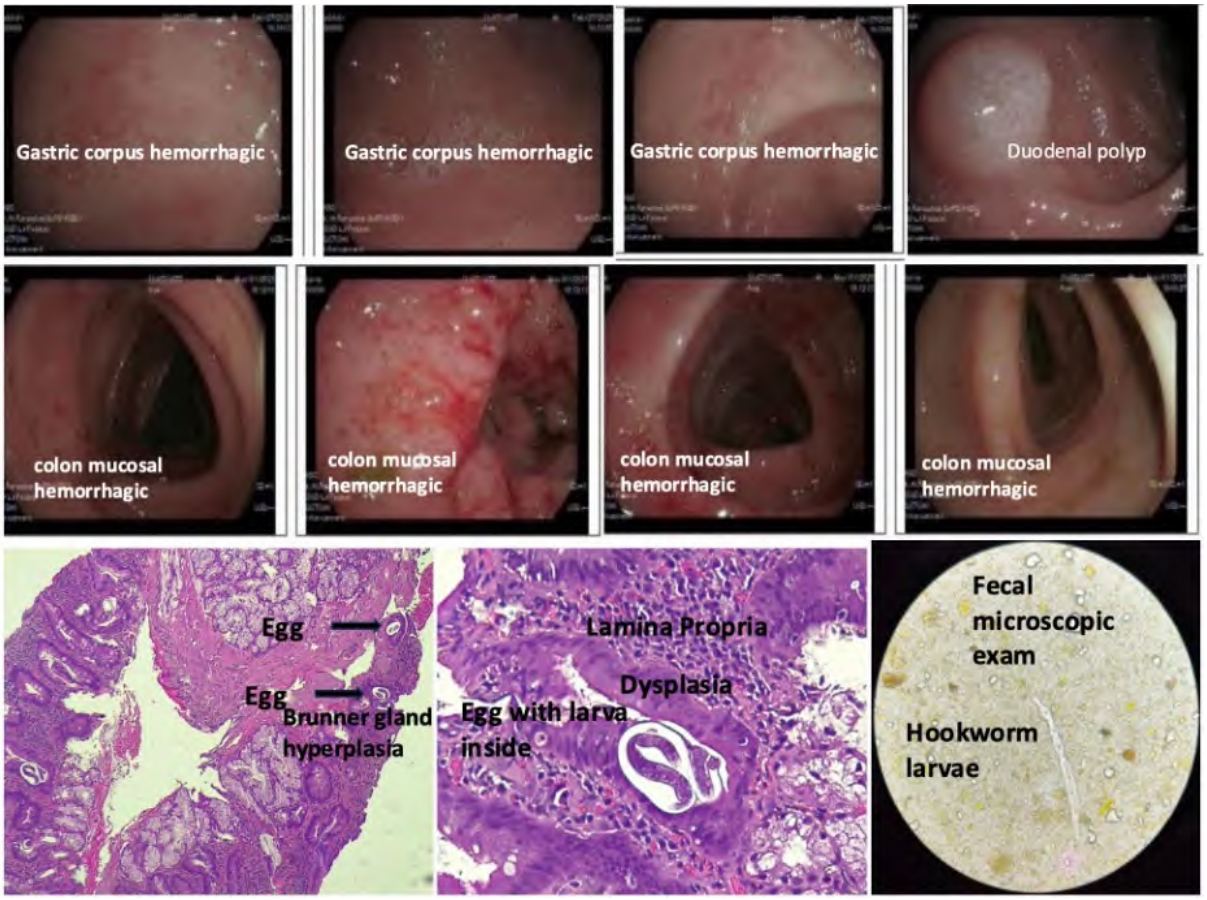
Soil Transmitted Helminth (STH) infections are the most common infections worldwide, with an estimated 1.5 billion people infected, or 24% of the global population. In Southeast Asia, more than 69% of infections are caused by nematode species, and 25% of the studied population in Asia is infected with at least one species. This remains a problem in Indonesia, with a prevalence of 30% of the population. Poor sanitation is the etiology. Gastrointestinal manifestations are often found to be related to both upper and lower gastrointestinal symptoms. Endoscopic examination of the gastrointestinal tract followed by histopathological examination through biopsy is one of the accurate diagnostic approaches.

Case Presentation

A 43-year-old man with clinical manifestations of abdominal pain, anorexia, and weight loss. From physical examination, appeared lethargic, pale conjunctiva, epigastric, and paraumbilical tenderness. Anemia was found with hemoglobin (Hb): 10.4 g/dl. Endoscopic examination found grade 3 hemorrhagic gastritis corpus, sessile polyp of duodenal bulb accompanied by active severe ulcerative pancolitis (UCEIS-3; MES-3). Histopathology results showed inflammatory polyps, mild dysplasia accompanied by helminthic ovum. Microscopic stool samples found hookworm larvae (fig.1).

Conclusion

Helminthiasis can manifest as inflammation of the gastrointestinal tract to bleeding. Several case reports of gastrointestinal polyps due to worm infection. When clinical manifestations are found in endemic areas, screening should be done. Treatment with corticosteroids and immunosuppressants can cause hyperinfection. We have reported a case report of a 45-year-old man diagnosed with helminthiasis with endoscopic images of duodenal polyps accompanied by inflammation and bleeding of the gastrointestinal tract.



CAS-014: Streptococcus pyogenes pyelonephritis: Two Cases Seen within Weeks of Each Other

Lei Wei[1], Stewart Retnam[1], Suma Sathyanarayana Rao[1], Pooja Rao[2], Timothy Barkham[2], Yu Kit Chan[1]

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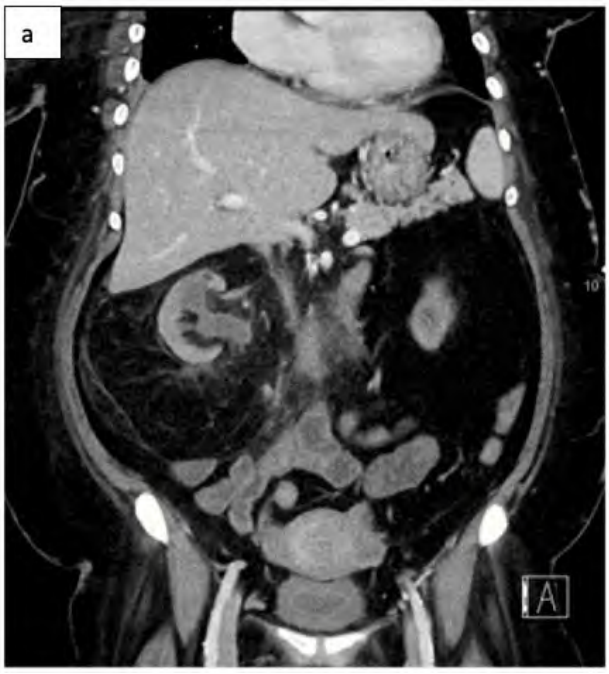
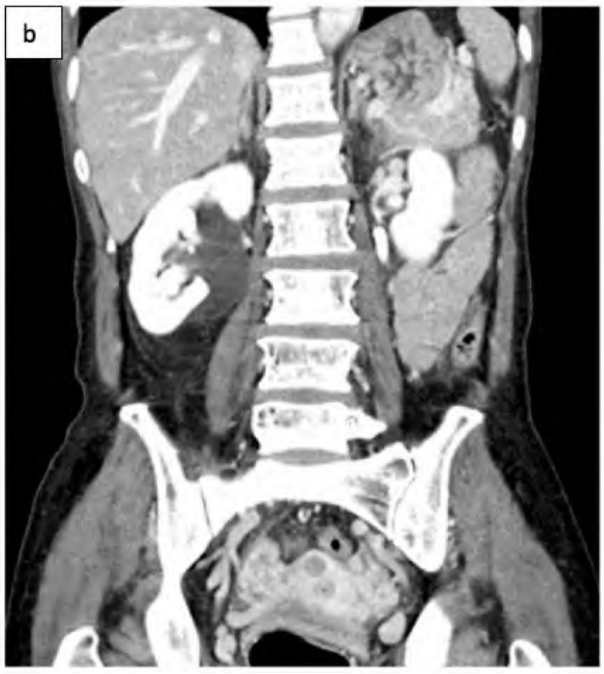
Introduction
Streptococcus pyogenes (Group A Streptococcus-GAS) is a very unusual uropathogen. We describe the clinical, radiological and typing findings in two cases of invasive GAS urosepsis.

Case Presentation
Case 1: a 53-year-old female on hemodialysis presented with fever, lower abdominal pain, nausea, and vomiting. Computed tomography (CT) showed right pyelonephritis, with features suggestive of right pyonephrosis and mild cystitis but no obstructing lesion (Figure a). Turbid urine was aspirated via percutaneous nephrostomy. GAS was isolated from both the urine and blood cultures.

Case 2: a 63-year-old female with metastatic colon adenocarcinoma complained of abdominal discomfort and urinary frequency at a routine clinic visit. Urine culture grew GAS. She did not receive antibiotics until one week later when she was hospitalized with fever, right abdominal pain, and a positive right renal punch. A CT scan showed right hydroureteronephrosis secondary to mass effect from retroperitoneal metastases (Figure b). Blood cultures grew GAS. The urine culture was sterile, but it had been collected 12 hours after the initiation of antibiotics. Typing showed emm 49 in case 1 and emm 89 in case 2. Both patients were allergic to penicillin and were treated with cefazolin with good clinical response.

Conclusion
The occurrence of two cases of rare GAS urosepsis within a few weeks of each other prompted concern that they were due to cross infection; typing reassured us that they were not. Ready availability of typing can dissipate anxiety and restore calm.





CAS-015: Mycetoma with Superimposed Bacterial Co-infection

Jelena Louise Arreza, Mishelle Vonnabie Bala

VSMMC

Introduction
Mycetoma is a localized chronic, suppurative, and deforming granulomatous infection of the skin, subcutaneous tissue, skin and bones, affecting mainly the feet. It is often seen in tropical and subtropical areas.

Case Presentation
We reported a case of a 38-year-old male presenting with infected wound right foot with 3 years history of swelling with pus discharge localized in his right medial dorsal foot associated with painful ambulation. He was initially diagnosed with bacterial osteomyelitis with wound tissue culture of Escherichia coli and given Cefuroxime IV. The aggressive course and progression of the disease affected the short bones of the involved foot thus radical resection of the soft tissue right foot with excision off 1st metatarsal foot right was done. He was then diagnosed as a case of maduramycosis based on the biopsy result and was started on Voriconazole however because of drug unavailability it was later replaced with Itraconazole taken for 6 weeks. He was then discharged and advised to follow-up after 2 weeks. During the follow up, the wound was found to improving and he was advised to continue Itraconazole for another 4 weeks as part of the treatment.

Conclusion
An approach that involves early diagnosis, use of systemic antibiotics or antifungal agents, and surgical removal of lesions are the basis for the treatment of this disease. Early recognition of mycetoma in a chronic skin and bone infection of the extremities is very important since it will avoid potential complications that will lead to functional and aesthetical impairment.

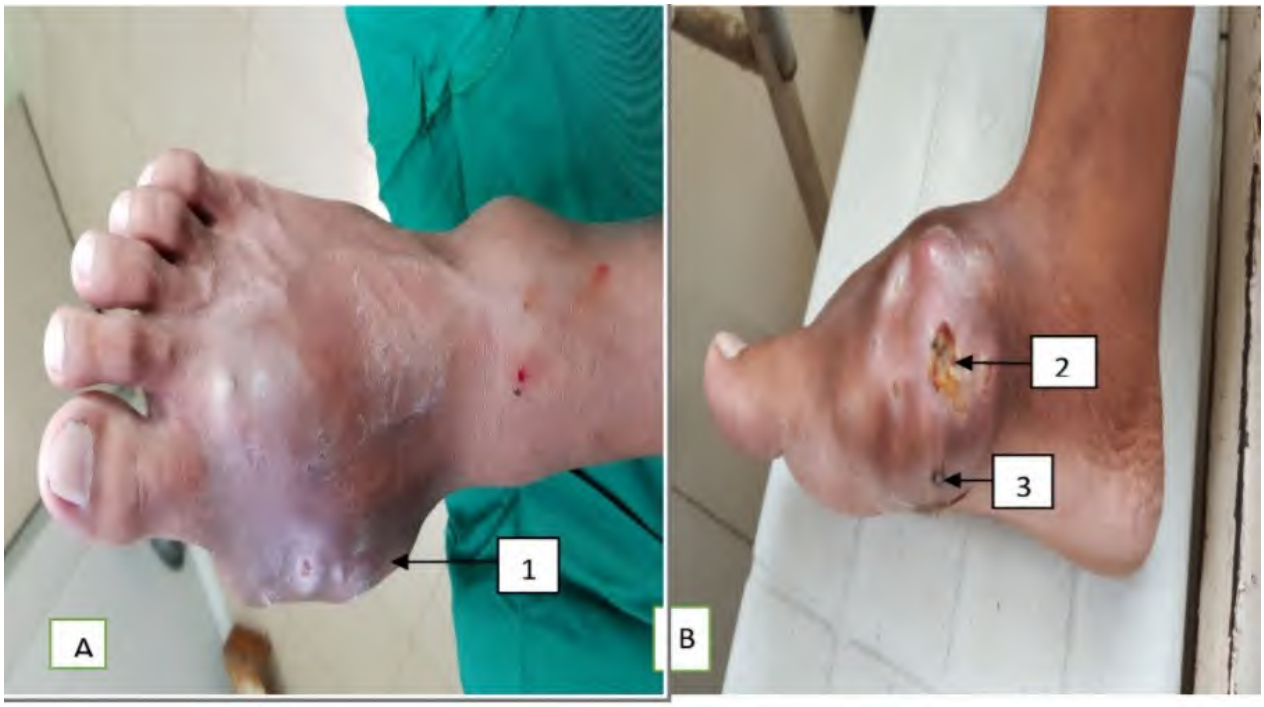


Figure 1. A, B Eumycetoma triad: 1) subcutaneous mass, 2) sinus tracts, and 3) grain discharge.

CAS-016: Candida tropicalis Native-Valve Endocarditis initially presenting as persistent Candida orthopsilosis Fungemia after short-term Total Parenteral Nutrition in a Stage IIB Colon Cancer patient: A Case Report

Dianne Roce Belarmino, Ruth Doligon, Vinhcent Sandoval

VRP Medical Center

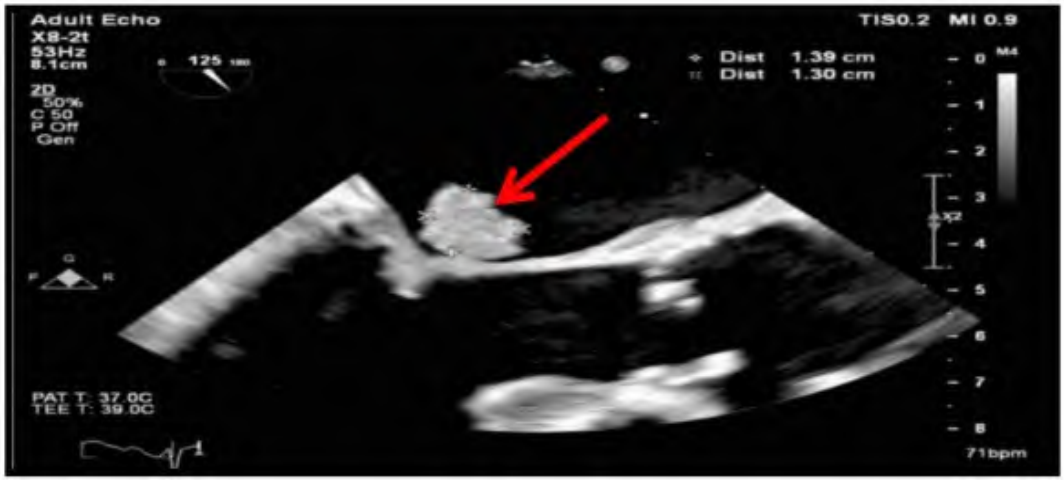
Introduction
Fungal infective endocarditis (IE) is a rare debilitating opportunistic infection with high mortality and difficulty in diagnosing. It frequently affects prosthetic valves and is associated with long-term total parenteral nutrition (TPN). This case is an immunocompromised elderly who developed persistent candidemia after short-term TPN and eventually fungal IE despite multiple antifungal medications.

Case Presentation
A 67-year-old male with pre-operative mitral regurgitation was admitted for hemicolectomy for Stage IIB colon cancer. He was placed on TPN and developed a fever three days after. Patient was given Piperacillin-Tazobactam but was shifted to Micafungin after positive blood culture (BC) to Candida spp. TPN was discontinued but fever persisted. Repeat BC revealed Candida orthopsilosis.

Patient was discharged with Fluconazole. Repeat BC every two weeks showed persistent candidemia. One month post-hemicolectomy, the patient was readmitted for myocardial infarction. He was febrile with no cardiac murmurs. Patient underwent a coronary angiogram revealing a thrombus leading to angioplasty. Fever and candidemia persisted post-angioplasty. Transesophageal echocardiography confirmed the presence of vegetation on the mitral valve indicative of valvular replacement.

Prior to cardiothoracic surgery, Amphotericin B was started for suspected fungal brain abscess after focal seizures. Mitral valve tissue culture revealed a different species, Candida tropicalis. Patient was discharged with Fluconazole after a repeat BC showing eradication of candidemia after successful mitral valve replacement surgery.

Conclusion
Suspicion of fungal infective endocarditis should always be considered in the setting of persistent candidemia. Repeat 2D echocardiography along with blood culture is recommended for earlier diagnosis to prevent embolic events especially among high risk.



CAS-019: A Rare Case of Tuberculous Meningitis with Concurrent HHV-7 Encephalitis in an Immunocompetent Host: Radiological Clues to a Diagnostic Challenge

Nuratiqah Izzah Sharidon[1], Wan Nurliyana Wan Ramli[1], Subashini Gunasegaran[1], Ainur Elliana Sohaimi[1], Mohd Aiman Saiful Suhardi[1], Farah Hazwani Musatafa[2], Wan Irfan W Mustapha[1], Radhiana Hassan[1], Mohd Ghaddafi Wahab[1], Sulaila Basiam[2], Nur Munirah Ibrahim[2], Noorlina Noordin[2], Dzawani Mohamad[2]

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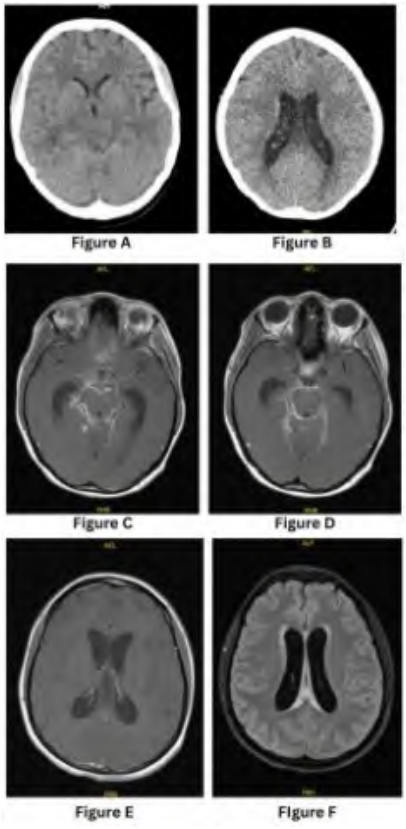
[2]Medical Department, Hospital Tengku Ampuan Afzan, Pahang, Malaysia

Introduction
Human herpesvirus 7 (HHV-7) encephalitis is rare in immunocompetent individuals and may clinically mimic tuberculous meningitis (TBM). Magnetic resonance imaging (MRI) plays a vital role in differentiating central nervous system (CNS) infections, particularly when patients fail to respond to standard empirical therapy.

Case Presentation
A 21-year-old immunocompetent female presented with a two-week history of fever, headache, vomiting, and altered mental status. Examination revealed meningeal irritation signs with a Glasgow Coma Scale score of 13/15. Initial investigations showed leukocytosis, elevated ESR, and cerebrospinal fluid (CSF) features consistent with meningitis. She was empirically started on intravenous ceftriaxone and acyclovir, later escalated to meropenem. Repeat CSF analysis revealed elevated opening pressure, high protein, and a low CSF:serum glucose ratio. Due to persistent fever and lymphocytic pleocytosis, empirical antituberculous therapy was initiated on day 7. Serial contrast-enhanced CT scans demonstrated progression from cerebritis to obstructive hydrocephalus, necessitating Omaya shunt insertion and intravenous dexamethasone. Despite therapy, her neurological symptoms persisted. CSF viral PCR was subsequently positive for HHV-7, and MRI brain showed leptomeningeal enhancement involving the basal cisterns, midbrain, and bilateral frontal and temporal lobes, with periventricular T2/FLAIR hyperintensities. IV ganciclovir was initiated on day 11, leading to significant clinical improvement at day 5 of therapy. She completed 14 days of antimicrobial therapy and continued anti-TB treatment for six months.

Conclusion
This case highlights the diagnostic complexity of overlapping CNS infections. MRI played a pivotal role in identifying atypical radiological features suggestive of viral encephalitis, supporting the diagnosis of HHV-7 infection and enabling timely, targeted antiviral therapy.



CAS-020: Tuberculosis Active Case-Finding at Workplace in a Country with Low Tuberculosis Incidence Rate

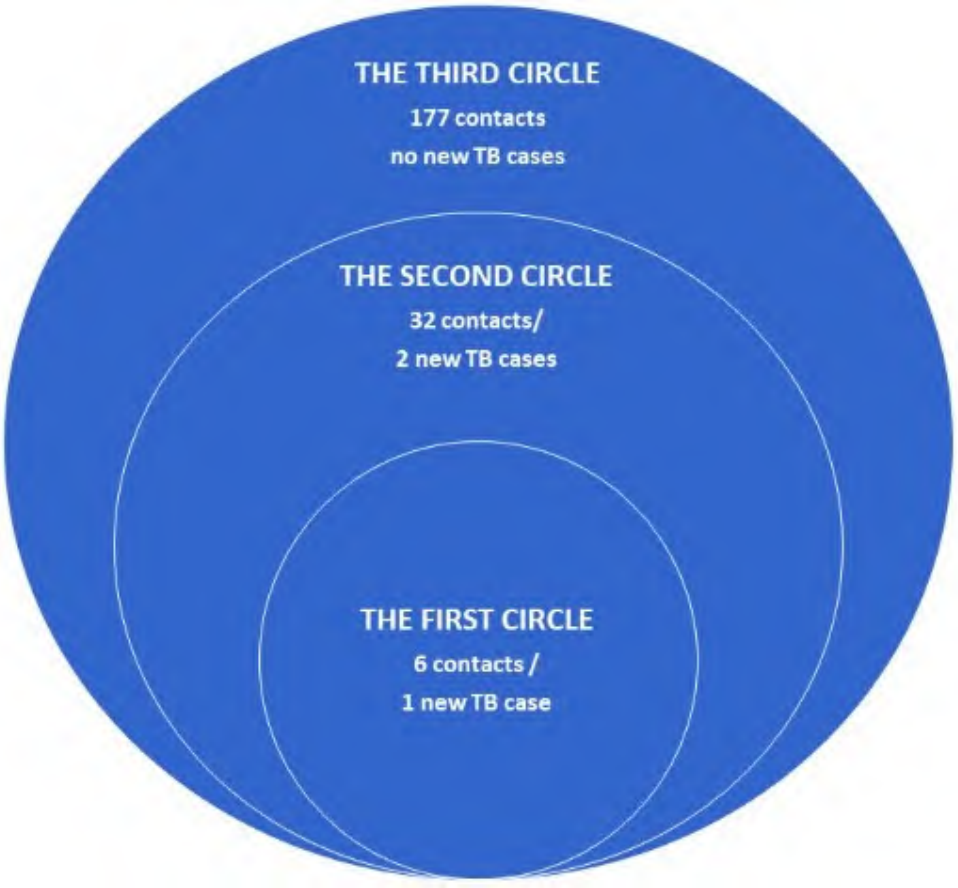
Anamarija Jurcev Savicevic[2], Zrinka Puharic[1]

[1]Faculty of Dental Medicine and Health Osijek, Croatia
[2]School of Medicine, University of Split, Faculty of Health Sciences University of Split, Teaching Public Health Institute of Split and Dalmatia County

Introduction
Tuberculosis (TB) contact tracing is an important public health measure to control the spread of TB in low-burden settings.

Case Presentation
Here we present extensive contact tracing at workplace of smear-positive index patient in Croatia, European country with TB low incidence rate, and detected outbreak. Contact tracing was performed mostly in concentric circles. It involved TB education, interviewing, TST, chest X-ray and additional tests as needed. Contact investigation included 227 persons. Initially TST was done in 223 people, 20 of them not returned for the reading; 48% had negative result, more of 14 mm was recorded in 7% and more than 20 mm in one tested contacts. CXR was refused or CXR results were not delivered in 55 workers. Consultation of pulmologist was requested for 29 tested workers. Three new TB patients were identified; with TST results 17 mm, 8 mm and negative (the patient with diabetes on insulin therapy), all with CXR suggestive of TB. In two of them TB was bacteriologically confirmed. Isolated strains were genotyped and all three bacteriologically confirmed cases (the index case and two secondary cases) had same code. The follow-up was done after the window period with no detected new cases.

Conclusion
Two of three new TB patients, who were not close contacts of the index patients, were rapidly detected by spreading the contact investigation. Isolated genotype is not common in Croatia. That points to TB transmission as a result of late detection of the disease, due to the patients and/or health system delay.



CAS-021: When Cryptococcus neoformans Hides in Plain Sight: A Case of Pelvic Abscess and Osteomyelitis

Anati Binti Zulkifli

Changi General Hospital

Introduction
Cryptococcus neoformans, a fungal pathogen commonly linked to pulmonary and central nervous system infections in immunocompromised individuals, can occasionally cause osteomyelitis and abscesses, even in those without significant immunosuppression. Such presentations, however, are rare.

Case Presentation
A 72-year-old man presented with fever, left groin swelling and pain. His medical history included Type 2 Diabetes Mellitus, chronic venous insufficiency with recurrent lower limb cellulitis, and prostate carcinoma previously treated with surgery and chemoradiotherapy. Months prior, he had received prolonged antibiotics for pyelonephritis and osteomyelitis of the pubic symphysis and left superior pubic ramus. He had no neurological and respiratory symptoms.

Imaging done revealed a rim-enhancing collection in the left proximal gracilis/adductor muscles and chronic, non-healed fractures with erosions in the pubic bones. Pus drained from the left thigh grew Proteus mirabilis and Morganella morganii.

A subsequent culture grew Cryptococcus neoformans complex after prolonged incubation, and a pubic bone biopsy also confirmed Cryptococcus species. Serum cryptococcal antigen was positive at a titre of 1:80. He was started on a course of oral Fluconazole.

Conclusion
This case highlights that Cryptococcus neoformans can infect atypical sites, such as bones, mimicking bacterial infections. Prolonged culture incubation and targeted biopsy are essential for identifying fungal pathogens in chronic, refractory infections while serum cryptococcal antigen testing is a valuable diagnostic tool, even in the absence of pulmonary or neurological involvement. Effective treatment requires a multidisciplinary approach, including anti-fungal therapy and surgical intervention.

CAS-022: Severe Leptospirosis Complicated by Weil's Syndrome, Acute Pancreatitis, and Aseptic Meningoencephalitis: A Case Report and Literature Review

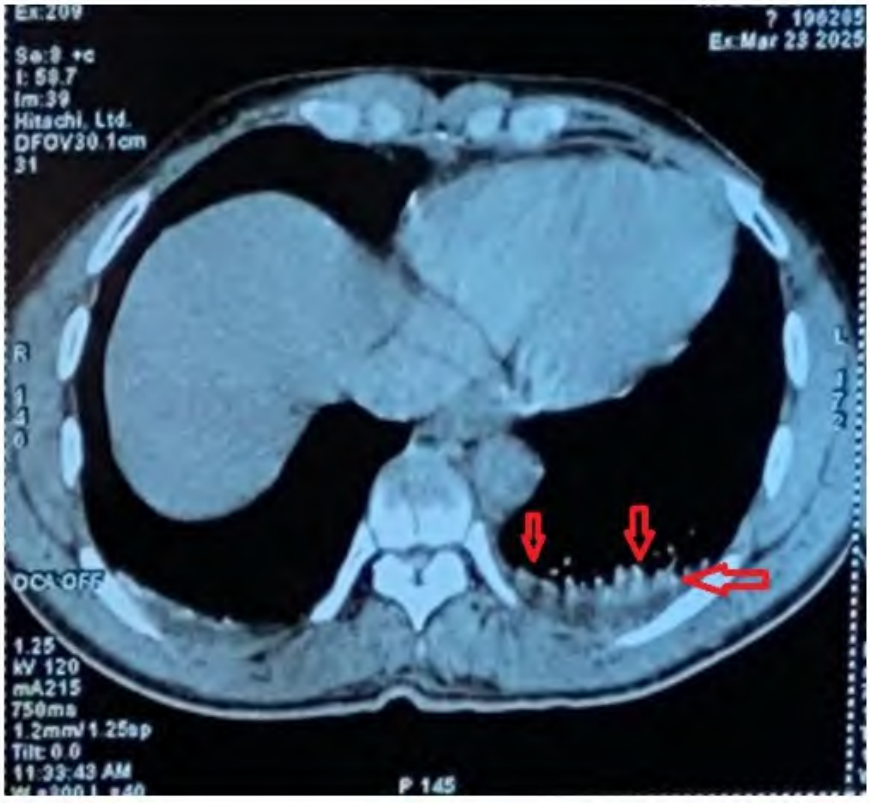
Hassan Kamena Mwana-yile Mwana-yile, Sanaa Jebbar, Sara El Ansari, Mustapha Sodqi, Kamal El Filali Marhoum

Ibn Rochd University Hospital, Faculty of Medicine and Pharmacy, Hassan II University, Casablanca, Morocco

Introduction
Leptospirosis is a neglected and re-emerging zoonotic disease that can lead to rare complications, including aseptic meningitis, acute pancreatitis, and Weil's syndrome. The aim is to report a clinical case of severe leptospirosis complicated by Weil's syndrome, acute pancreatitis, and aseptic meningitis, admitted to the Infectious Diseases department of Ibn Rochd Hospital in Casablanca, Morocco.

Case Presentation
Patient AN, a 48-year-old slaughterhouse worker with a high-risk occupation, was admitted with severe symptoms including bright orange conjunctival and skin jaundice, accompanied by a hemorrhagic syndrome characterised by hematemesis (vomiting blood), gingivorrhagia (bleeding gums), hematuria (blood in urine), and renal failure. His lab results showed a creatinine level of 51.2 mg/dL and a glomerular filtration rate of 16 mL/minute, with oligoanuria (urine output of only 200 mL in 24 hours), consistent with Weil's syndrome. He required four sessions of hemodialysis.Lumbar puncture was performed for suspected meningoencephalitis. The cytobacteriological examination revealed lymphocytic aseptic meningitis with a pleocytosis of 32 elements, elevated protein levels (1.09 g/l), and normal glucose levels (0.9 g/l).The persistent bright orange jaundice, along with the onset of abdominal pain and vomiting, was associated with elevated lipemia levels of 492 IU/l and an increase in CRP to 132.1 mg/l. This prompted the need for an abdomino-pelvic CT scan, which revealed necrotic pancreatitis (mCTSI 10). Leptospirosis serology, conducted on the tenth day of cephalosporin therapy, came back positive. Unfortunately, the patient passed away on the twentieth day of hospitalisation.

Conclusion
The rare complications of severe leptospirosis may occur concomitantly.



CAS-023: Herpes Simplex Virus Infection Presenting as Umbilicated Crusted Papules in an AIDS Patient

Kirk Llew Quijote, Emmerson Gale Vista, Joland San Juan

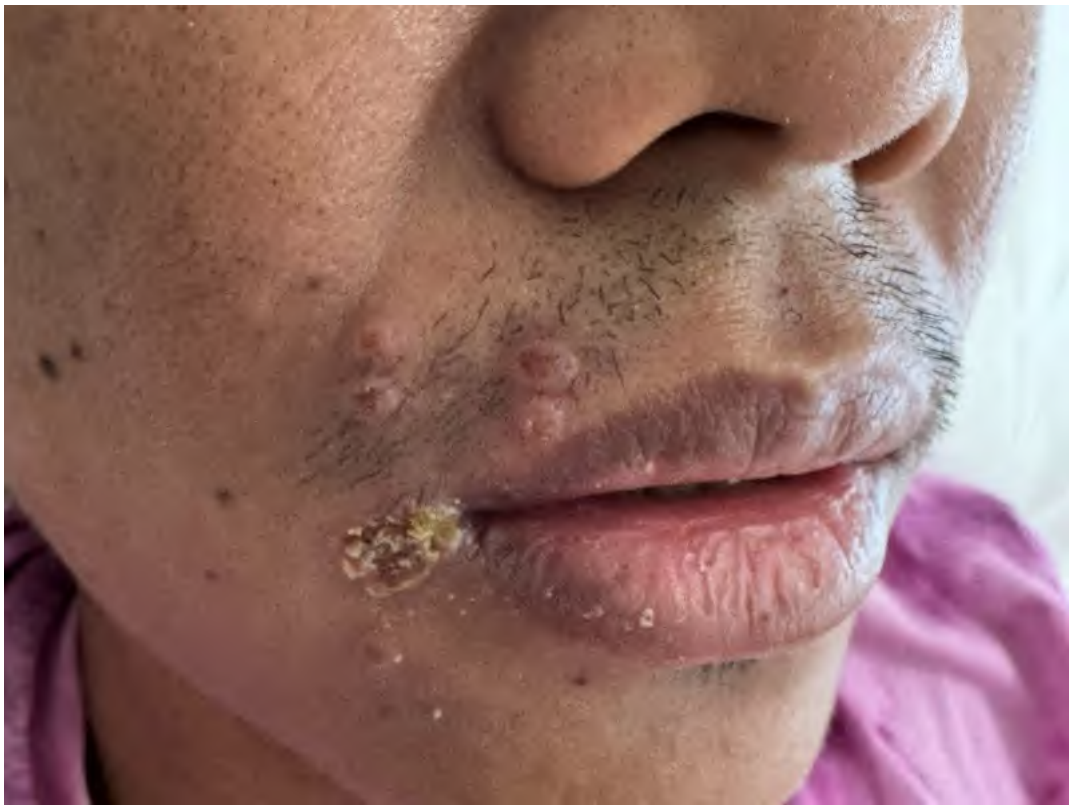
Research Institute for Tropical Medicine

Introduction
Herpes simplex virus (HSV) typically presents with painful vesicular eruptions. However, in immunocompromised individuals, particularly those with advanced human immunodeficiency virus (HIV) infection, clinical manifestations may be atypical and mimic other dermatologic or systemic conditions, leading to diagnostic challenges.

Case Presentation
We report the case of a 26-year-old Filipino male with an eight-year history of HIV infection, maintained on a once-daily regimen of lamivudine, tenofovir disoproxil fumarate, and efavirenz. He presented with an eight-day history of asymptomatic, umbilicated, skin-colored papules with yellowish crusts localized to the right perioral area. Review of systems revealed low-grade fever and weight loss. His most recent CD4 count was 94 cells/μL. Differential diagnoses included monkeypox, molluscum contagiosum, and systemic fungal infections.

Histopathologic examination of a skin biopsy confirmed HSV infection, showing ballooning degeneration of keratinocytes, multinucleated giant cells with eosinophilic intranuclear inclusions (Cowdry type A bodies), and overlying scale crust. Periodic acid-Schiff and Gomori methenamine silver staining, fungal cultures, and cryptococcal antigen tests were negative. The diagnosis was herpes labialis with secondary bacterial infection. Treatment with oral acyclovir and topical mupirocin resulted in resolution of the lesions.

Conclusion
This case highlights the importance of recognizing atypical HSV presentations in patients with advanced HIV, where immune dysregulation allows for unusual morphologies thereby mimicking other etiologies. Molluscum-like papules may obscure the diagnosis, particularly in resource-limited settings or when co-infections are suspected. Early biopsy and appropriate histopathologic evaluation are essential for accurate diagnosis and timely antiviral therapy, preventing complications such as chronic or disseminated infection.



CAS-025: Invasive Fungal Rhinosinusitis in a Patient Undergoing Hemodialysis

Keita Kano

Osaka Dental University/Uji Takeda Hospital

Introduction
Invasive fungal rhinosinusitis is a rare but potentially life-threatening infection caused by the inhalation of fungal spores. It primarily affects the mucosa of the nasal cavity and sinuses, leading to inflammation, necrosis, and tissue loss. The condition typically occurs in immunocompromised individuals. Here, we present a case of invasive fungal rhinosinusitis diagnosed based on oral findings in a patient undergoing hemodialysis.

Presentation
A 75-year-old man was referred to our department because of swelling and pain in the right maxillary gingiva. Oral examination revealed a well-defined mass in the gingiva of the maxillary molar. CT imaging revealed opacification of the entire right maxillary sinus with internal calcification and bone defects in the anterior and suborbital walls. Biopsy revealed no obvious neoplastic lesions or malignant findings. A clinical diagnosis of maxillary fungal rhinosinusitis was suspected, and the patient underwent removal of fungal colonies from the maxillary sinus. Histopathological findings showed Y-shaped, branching filamentous fungi, suggestive of Aspergillus, leading to a diagnosis of invasive fungal rhinosinusitis. No recurrence was observed during the 33-month postoperative follow-up.

Conclusion
Invasive fungal rhinosinusitis is a potentially harmful disease, particularly in immunocompromised patients. Fungal infection should be considered in such individuals presenting with bony erosion or necrosis. Early diagnosis is key to the successful management of invasive fungal rhinosinusitis.

CAS-028: Non-Typhoidal Salmonella in Urine Culture: A Harbinger of Systemic Complications?

Yee Ting Nicole Yim[3], Alicia Xin Yu Ang[1], Ray Junhao Lin[1], Stephanie Sutjipto[2]

[1]Department of Infectious Diseases, Woodlands Health, Singapore
[2]National Centre for Infectious Diseases, Singapore
[3]Tan Tock Seng Hospital, Singapore

Background
Urinary tract infections (UTIs) caused by non-typhoidal Salmonella (NTS) serovars are uncommon and usually asymptomatic. NTS is typically transmitted through the faecal-oral route and most commonly presents as self-limiting symptoms of gastroenteritis, where antibiotic treatment is not required in immunocompetent patients. Serious complications such as endovascular infections may occur with bacteraemia, usually in immunocompromised patients.

Method
We reviewed the medical records of 2 patients admitted to Woodlands Health between October 2024 and February 2025 with NTS bacteriuria.

Results
Both patients were male and presented with non-specific acute febrile illness with no vomiting nor diarrhoea. Urine cultures grew pan-sensitive NTS, while multiple sets of blood cultures were negative. Both patients were found to have systemic complications on computed tomography (CT) scans. The first, an 87-year-old nursing home resident who had a persistent fever, was diagnosed with an aortic arch penetrating atherosclerotic ulcer. The second, an immunocompromised patient on high-dose steroids for IgA nephropathy, was diagnosed with an acute perforated descending colon diverticulitis after presenting with fever and abdominal pain. Both patients were treated with a six-week course of antibiotics with clinical resolution.

Conclusions
Primary UTIs caused by Salmonella are uncommon. Presence of Salmonella in urine cultures should not be ignored as insignificant, as it may signal a more serious systemic infection. Even without bacteraemia, Salmonella bacteriuria in certain clinical scenarios warrants further clinical evaluation for occult foci and metastatic complications. Early recognition and appropriate imaging can be critical in identifying deep-seated infections and guiding effective treatment.

CAS-030: Not Just Back Pain: Candida Spondylodiscitis in an Elderly Patient

Lei Wei, Sahota Amandip Singh, Monica Chan, Pei Hua Lee

Tan Tock Seng Hospital

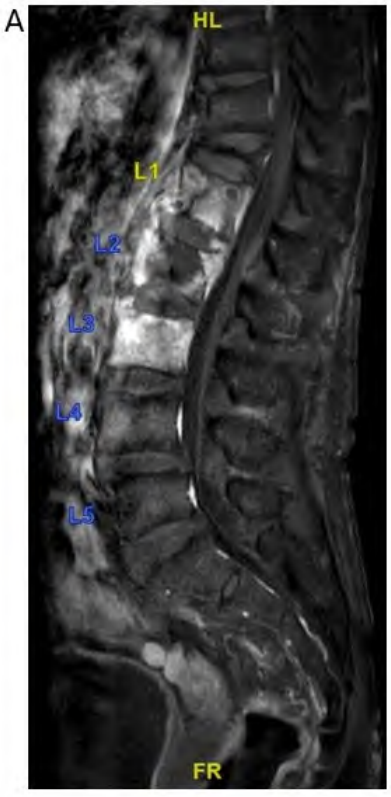
Introduction
Candida is a rare cause of spondylodiscitis. Its indolent course and nonspecific clinical features often delay diagnosis, particularly in elderly patients with multiple comorbidities.

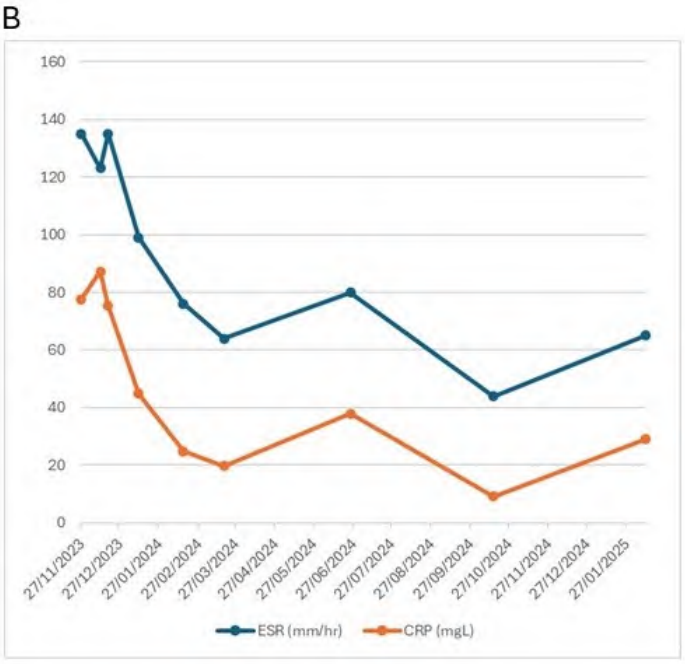
Case Presentation
An 88-year-old woman presented with progressive lower back pain and immobility over several months. Her medical history included hypertension, hyperlipidemia, type 2 diabetes mellitus, Grave's disease, osteoporosis, chronic kidney disease, and previously treated rectal adenocarcinoma. She was afebrile and hemodynamically stable. Examination revealed lumbar spine tenderness. Inflammatory markers (ESR, CRP) were elevated without leukocytosis; blood cultures were negative. Magnetic resonance imaging (MRI) of the thoracolumbar spine demonstrated spondylodiscitis involving L1–L3, with intraosseous involvement, paravertebral extension, and bilateral psoas abscesses (Fig. 1A).

An initial computed tomography-guided biopsy was non-diagnostic. She was empirically treated with cefazolin and ciprofloxacin, later escalated to piperacillin-tazobactam, without improvement. A repeat biopsy two months later yielded Candida albicans from paravertebral fluid, susceptible to fluconazole. Retrospective review revealed a prior episode of Candida albicans fungemia following gastrointestinal ulceration 10 months earlier, treated with a 2-week course of fluconazole. No metastatic complications such as endocarditis or endophthalmitis were identified.

Given her age and multiple comorbidities, conservative management was pursued. She received oral fluconazole for 18 months, with improvement in inflammatory markers and serum (1-3)-β-d-glucan (Fig. 1B). Serial MRI demonstrated resolution of bilateral psoas abscesses with stable spondylodiscitis and paravertebral collection.

Conclusion
This case highlights the diagnostic challenge of Candida spondylodiscitis, particularly with negative blood cultures and inconclusive initial biopsy. Prior candidemia warrants high suspicion, and early repeat biopsy is key for diagnosis and targeted therapy.





	08/12/2023	25/06/2024	15/10/2024	11/02/2025
(1-3)-β-d-glucan (pg/mL)	>500	268	248	109

CAS-031: An Uncommon Pathogen: Dyella spp. in Blood Cultures from Hemodialysis

Kwanchon Jearakitiwanich

Lerdsin General Hospital, Thailand

Introduction
Dyella spp. are Gram-negative bacteria commonly found in the environmental source worldwide and are rarely associated with human infections. Their clinical significance remains poorly understood. Identification using conventional laboratory methods, such as biochemical testing is challenging. Although, MALDI-TOF MS has improved diagnostics capabilities. Its accuracy is limited to available databases. This report presents a case of Dyella spp. bacteremia in a hemodialysis patient.

Case Presentation
A 35-year-old Thai woman with end-stage renal disease (ESRD) on chronic hemodialysis presented with acute fever and chills during dialysis. Physical examination showed temperature 38°C, respiratory rate 22/min, heart rate 80/min, and blood pressure 130/60 mmHg. All blood cultures from both central and peripheral lines show Gram-negative rods. Identification methods including MALDI-TOF MS and automated biochemical tests failed to achieve reliable results, with some suggesting unrelated organisms. Further confirmed used 16S rRNA gene sequencing was performed and confirmed Dyella spp. The patient was treated empirically with piperacillin-tazobactam and recovered without complications. No other source of infection or contamination was identified.

Conclusion
This case demonstrates that Dyella spp. an uncommon bloodstream infection. Hemodialysis patients are at high risk of infection. When routine conventional identification methods failed, 16S rRNA gene sequencing proved essential for accurate diagnosis. The patient responded good to empirical treatment with piperacillin-tazobactam, supporting its potential effectiveness against such rare pathogens. Early recognition and appropriate intervention are essential to improving outcomes in high-risk clinical settings.

CAS-032: Case Report: A Cluster of Zika Virus Disease in General Hospital, Chonburi, Thailand

Supanun Wongsermsin , Jetapong Insawang, Juntana Malai

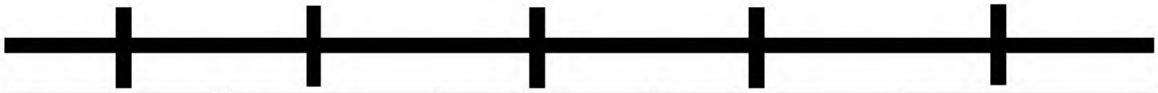
Queen Savang Vadhana Memorial Hospital, Thai Red Cross Society

Introduction
The Zika virus, a Flavivirus spread by Aedes mosquitoes, usually has mild symptoms, such as low-grade fever, conjunctivitis, arthralgia, myalgia, and maculopapular rash. Guillain-Barré syndrome occurs in a small percentage of individuals, approximately 1.23%. Vertical transmission can cause Congenital Zika syndrome. This syndrome is marked by severe birth defects, including microcephaly.

Case Presentation
We report a cluster of Zika virus infection in one 35-year-old female presenting with fever, arthralgia, non-purulent conjunctivitis, and maculopapular rash, and her 65-year-old mother also presented with the same complaints. The patient has no history of traveling. She reported multiple mosquito bites; her residence is near the forest. The infection with Zika virus was confirmed by RT-PCR in urine. The results were reported in July 2024. After receiving the results, the office of disease prevention and control region 6 conducted a field investigation at the patient's residence and workplace. Residents in the surveillance zone were provided with health education, including information about diseases and symptoms that require medical attention, as well as strategies for eliminating mosquito breeding sites. The survey found no pregnant women or additional symptomatic cases within the area. The infectious control unit was under surveillance, and prevention and control measures for the notifiable disease were maintained for 28 days without the emergence of new cases.

Conclusion
The mosquito-borne Zika virus remains an important public health problem. Although most cases present mild symptoms, pregnant women are able to experience serious consequences. Understanding local epidemiological patterns allows communities to immediately begin surveillance, vector control, resource allocation, and health education.

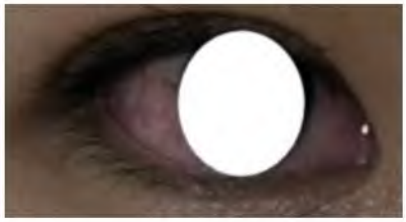
Figure1 Timeline of Symptoms in a Patient Diagnosed with Zika Virus Infection

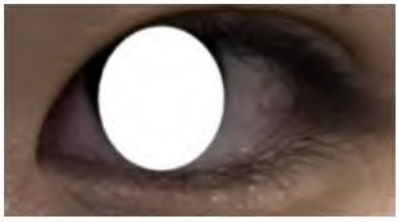


28 June	30 June	1 July	2 July	4 July
Fever Joint pain Fatigue	Erythematous rash at chest wall, arms, and legs, conjunctivitis, myalgia	Fever Joint pain Fatigue	Low grade fever, joint pain (worsen), Sore throats, rash, Urine RT-PCR positive for Zika virus	conjunctivitis (improved), no rash, myalgia(improved)

Figure2 demonstrates the characteristic maculopapular rash on bilateral upper extremities.

Figure3 demonstrates the characteristics of non-purulent conjunctivitis in both eyes.





CAS-033: A Case of Leptospirosis with Few Typical Symptoms and Signs

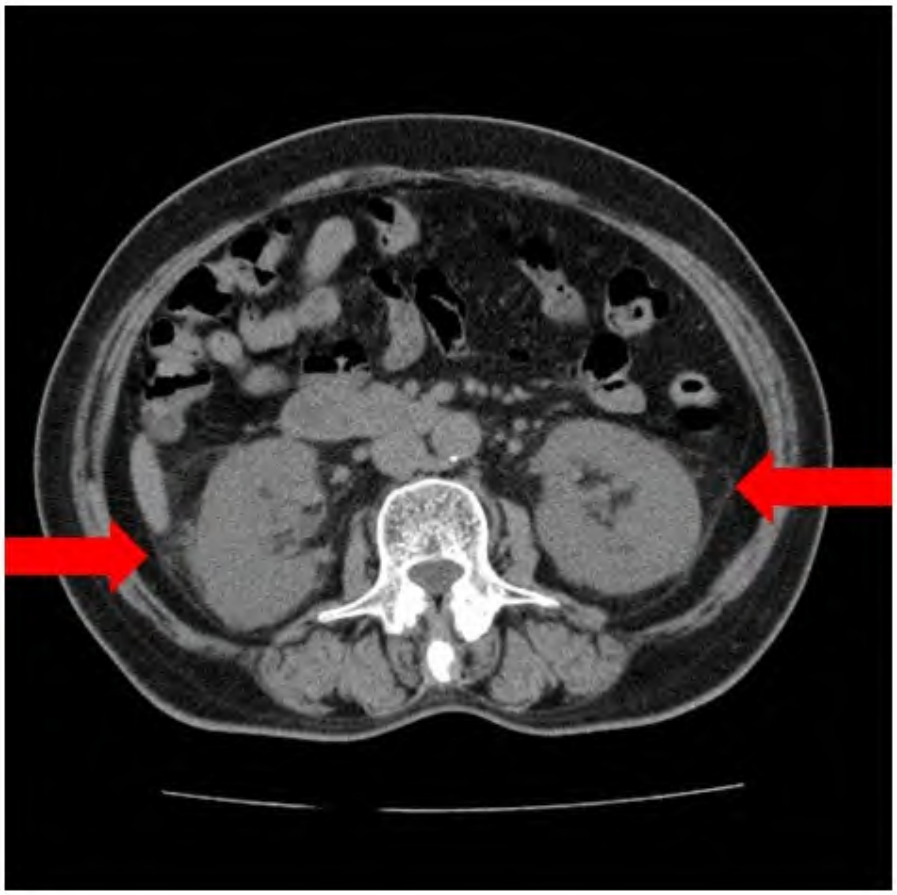
Ko Iida, Michinori Shirano, Tetsushi Goto

Osaka City General Hospital

Introduction
The diagnosis and treatment of tropical disease leading to a few typical symptoms and signs are challenging, especially in endemic settings. We present here a case of mild to moderate leptospirosis and discuss how to optimize clinical management.

Case Presentation
An 81-year-old female presented with progressively worsening fever and fatigue. 11 days to 19 days before admission, she traveled to Panama with walking through marshland for bird watching. She had a history of hypertension. Her first impression was relatively sick. Blood tests were unremarkable except for increase of C-reactive protein (22.89 mg/dL, normal value<0.3 mg/dL) and thrombocytopenia and slightly kidney dysfunction. Urinalysis revealed mild proteinuria and pyuria. Plain CT on the abdomen revealed a misty mesentery around kidneys (Figure 1). Initially, she was treated with ceftriaxone and then transitioned to levofloxacin, suspected of Typhoid Fever or Urinary Tract Infection. Her symptoms continued to do well. After discharge, she was diagnosed with leptospirosis by microscopic agglutination test.

Conclusion
We present a case of mild to moderate leptospirosis without known typical symptoms and signs. Leptospirosis might be overlooked among undiagnosed tropical diseases with successful progression due to antibiotics.



CAS-034: First Human Case of Calidifontibacter indicus Peritonitis in a Patient Undergoing CAPD: A Case Report in Malaysia

Yii Ling Liow[2], Habib Abdul Hakim Bin Esa[3], Annie Maxwell[2], Su Ying Ng[1]

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[2]Hospital Sultanah Aminah Johor Bahru (HSAJB), Ministry of Health Malaysia
[3]Infectious Disease Research Center, Institute of Medical Research, National Institutes of Health (NIH), Ministry of Health Malaysia

Introduction

Peritoneal dialysis (PD)-related peritonitis is a serious complication in patients on continuous ambulatory peritoneal dialysis (CAPD). While most cases are caused by common Gram-positive or Gram-negative organisms, rare pathogens may occasionally be implicated. Calidifontibacter indicus, an environmental actinobacterium, has not previously been reported as a human pathogen. We describe the first known case of C. indicus isolated from peritoneal fluid of a patient undergoing CAPD in Malaysia.

Case Presentation

A 72-year-old man with end-stage renal failure on CAPD presented with abdominal discomfort and cloudy PD fluid. PD effluent showed a WBC count of 370/µL (81% polymorphs), and Gram stain revealed Gram-positive bacilli. Culture yielded small whitish colonies, but Matrix-assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOF MS) failed to identify the organism. Molecular analysis at a national reference laboratory confirmed C. indicus. The patient was empirically treated with intraperitoneal ceftazidime and cefazolin, followed by vancomycin due to unresolved symptoms. Oral fluconazole was added empirically for fungal coverage. The patient's clinical condition improved, with decreasing PD fluid turbidity and WBC counts, and he was discharged in stable condition.

Conclusion

This is the first documented human infection caused by Calidifontibacter indicus. This case highlights the diagnostic challenge posed by rare actinobacteria pathogen in PD-related infections and the importance of molecular tools in pathogen identification when conventional methods fail. Early empirical treatment contributed to a favorable outcome. Clinicians should remain vigilant for unusual organisms in CAPD-related peritonitis and consider integrating molecular tools into routine diagnostics to improve pathogen identification and guide management strategies.

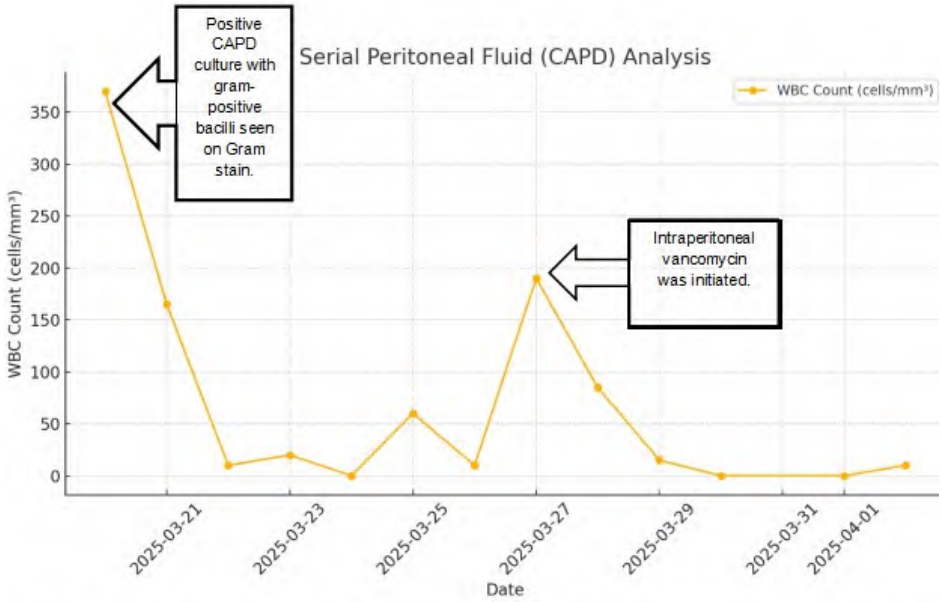


Fig 2: The graph shows the trend of WBC counts in serial Continuous ambulatory peritoneal dialysis (CAPD) fluid samples over time. It illustrates a clear downward trajectory from 370 to under 10 cells/mm³, aligning with clinical improvement.

CAS-035: Clinal Course of Pythium Insidiosum Antibody Positive in Asymptomatic Thai Thalssemic Patient: A Case Report

Parinya Noppakao

Amnatcharoen Hospital

Introduction
Human pythiosis is an infectious disease with high mortality and disability rates. Most reported cases are from Thailand and India. Patients in the at-risk group are those with thalassemia, and the disease is often found in a stage with obvious symptoms. Diagnosis is made through tissue biopsy, immunological testing, and molecular testing. The detection of antibodies against the pathogen while the patient is still asymptomatic for human pythiosis has not been previously reported.

Case Presentation
The patient is a 64-year-old Thai female farmer with a history of Beta thalassemia-hemoglobin E disease who is transfusion-dependent. She has extramedullary hematopoiesis and iron overload, with a serum ferritin of 5283 ng/ml. A Pythium antibody test by immunochromatography in April 2024 was positive, and a second test also yielded a positive result with a titer of 1:800. Serum (1->3)-Beta-D-Glucan concentration was positive at 85.7 pg/ml. The patient has no symptoms of human pythiosis and no claudication. A physical examination revealed mild abnormal dorsalis pedis and posterior tibial artery pulse. The patient refused further radiologic investigation. The patient has been followed up to the present and has not yet shown any symptoms of human pythiosis.

Conclusion
The detection of Pythium antibodies along with abnormal biomarker in a patient at risk for human pythiosis may represent an early stage of the disease, which is a new clinical syndrome.

CAS-036: Hypervirulent Klebsiella pneumoniae Osteomyelitis Mimicking Osteosarcoma in a Previously Healthy Patient with Newly Diagnosed Diabetes Mellitus

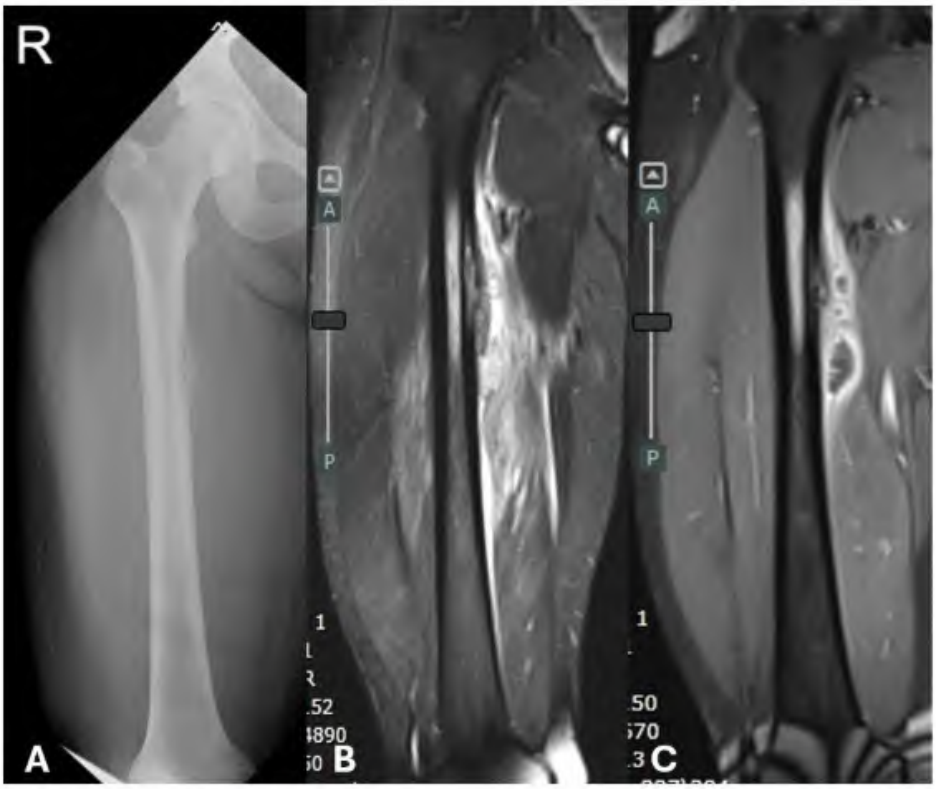
Nattapat Sangkakul, Sarunyou Chusri

Infectious Disease Unit, Division of Internal Medicine, Faculty of Medicine, Prince of Songkla University, Hat Yai, Songkhla, Thailand

Introduction
Hypervirulent Klebsiella pneumoniae (hvKP) is well known for causing invasive infections, including liver abscess, endophthalmitis, and bacteremia, often in patients with diabetes mellitus. Bone involvement is uncommon and can mimic malignancy, leading to delayed diagnosis and unnecessary intervention.

Case Presentation
A 27-year-old previously healthy man who works as a farmer presented with pain and swelling of the right proximal femur for 4 weeks without fever or a history of trauma. Magnetic resonance imaging (MRI) revealed an abnormal infiltrative intramedullary lesion at proximal shaft of the right femur with intracortical lesion and cortical destruction suspicious for periosteal osteosarcoma. Histopathological report from bone biopsy revealed chronic inflammation without malignant cells. Blood cultures and bone tissue grew K. pneumoniae. Genomic sequencing confirmed K1 capsular serotype as hypervirulent strain (positive for wzi-1 gene). The patient was newly diagnosed with type 2 diabetes mellitus during hospitalization. He was treated with six weeks of intravenous ceftriaxone followed by oral ciprofloxacin. Clinical symptoms are resolved with radiographic improvement and no metastatic foci on abdominal and chest imaging.

Conclusion
Hypervirulent Klebsiella pneumoniae (hvKP) osteomyelitis can closely mimic bone malignancy both clinically and radiographically, particularly in individuals with diabetes mellitus. This case highlights the importance of considering hvKP in the differential diagnosis of aggressive skeletal lesions, especially in endemic regions and populations at risk. Failure to recognize may lead to delayed diagnosis and inappropriate management with unnecessary surgery or oncologic intervention.



(A) Plain film of the femur showing medial cortical osteolytic lesion with periosteal reaction. **(B,C)** T2 and T1-weight with gadolinium (MRI)showing intramedullary lesion with cortical destruction at medial cortex.

CAS-038: Measles Complicated by Myelitis

Raïssa Bongungu

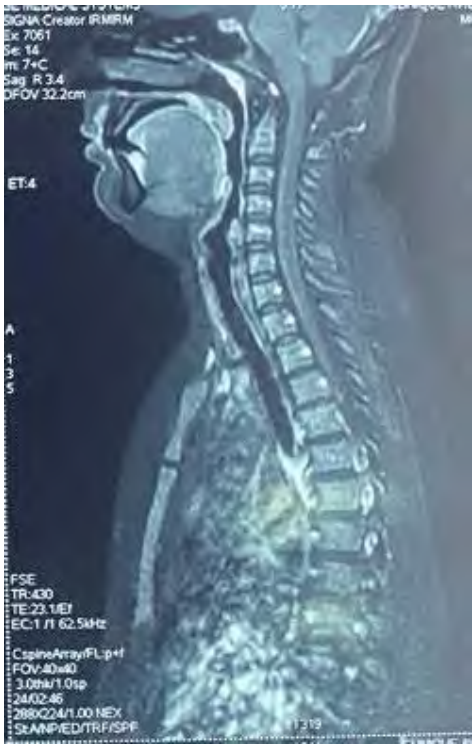
Chu Ibn Rochd Casablanca

Introduction
Measles is a highly contagious and immunizing viral infectious disease caused by a virus called paramyxovirus, which occurs worldwide and is responsible for the most dreadful complications, including myelitis, which is the most unusual, with a favorable outcome under treatment.

Objectives: To report a case of measles with spinal cord involvement in a patient at the Casablanca Infectious Diseases Department, Chu Ibn Rochd.

Case Presentation
This was a 37-year-old female patient, previously treated for measles, was admitted for paresthesia of both lower limbs with vesico-sphincter disorders that appeared 8 days after treatment. Neurological examination revealed hypotonia of both lower limbs with superficial hypoesthesia. Spinal cord MRI showed a nodular lesion of the C7 vertebral body with T2 iso signal, T2 hypersignal and STIR, suggesting a vertebral angioma associated with myelitis. Measles serology was positive. Functional recovery was partial under corticosteroid therapy, requiring rehabilitation sessions for full recovery of motor

Conclusion
Despite the advent of vaccination, measles remains a pathology with a high morbidity and mortality rate. This also implies the occurrence of formidable complications, including myelitis, a complication that evolves favorably with treatment and functional rehabilitation. Diagnosis is based on spinal cord MRI.



CAS-039: Laysan Fever: A Case Series of a Rare and Emerging Disease

Robert Partridge

Warren Alpert Medical School of Brown University

Introduction
Laysan Fever (LF), first described in the 1990's, is a rare disease that has received limited scientific study. Caused by an unknown virus suspected to be transmitted through the bite of the seabird tick Omithodoros capensis, LF occurs in humans who enter seabird colonies in the remote Northwestern Hawaiian Islands (NWHI), 1300km west of Oahu. This abstract describes suspected LF cases in 3 out of 4 healthy seasonal ecological workers on one atoll in NWHI in spring/summer 2023. Symptoms/timeline were compared with the published case definition: to receive an LF diagnosis a patient must have at least 3 of 7 primary symptoms (feverishness, fatigue, headache, nausea, anorexia, myalgia/arthralgia) while residing in NWHI, or within 14 days of departure, without other etiology of illness.

Case Presentation
Case1. 24-year-old female noted 6-9 tick bites 3 days before symptom onset. Symptoms included headache, otalgia, fatigue, nausea, abdominal cramping, and chills, resolving day 13.

Case2. 29-year-old female noted 7 tick bites 4-5 days before symptom onset. Developed fatigue, myalgias, headache, lightheadedness, nausea, and cervical lymphadenopathy, resolving day 10.

Case3. 25-year-old female exposed to seabird ticks with no noted bites. Initially had fatigue, followed by abdominal cramps, nausea/vomiting, headache, and anorexia, resolving day 9.
(See Table.)

Conclusion
While typically self-limited, LF causes significant illness and can interfere with activities of daily living. LF cases in NWHI are likely underreported, as healthcare access and disease surveillance is limited. Further research is necessary to determine the etiologic agent of LF, transmission mode/frequency, and possible diagnostic testing, treatment, and prevention.

Table: Symptom complex by day of illness

	Case 1	Case 2	Case 3
Day 1	Headache, bilateral otalgia, fatigue	Fatigue, exacerbated by activity/sun exposure	Lethargy, fatigue, abdominal cramps, nausea, vomiting
Day 2	Headache, bilateral otalgia, fatigue	Fatigue, exacerbated by activity/sun exposure	Lethargy, fatigue, abdominal cramps, headache
Day 3	Headache, bilateral otalgia, fatigue	Fatigue, exacerbated by activity/sun exposure	Lethargy, fatigue, abdominal cramps; severe headache; anorexia
Day 4	Headache, bilateral otalgia, fatigue	Fatigue, exacerbated by activity/sun exposure; myalgias	Lethargy, fatigue, abdominal cramps, severe headache, anorexia
Day 5	Nausea, upper abdominal cramping	Fatigue, exacerbated by activity/sun exposure; myalgias; nausea; severe headache, lightheadedness; cervical lymphadenopathy	Lethargy, fatigue, abdominal cramps, severe headache, anorexia. Improving, but worse with sun exposure.
Day 6	Nausea, upper abdominal cramping	Fatigue, exacerbated by activity/sun exposure; myalgias; nausea; severe headache, lightheadedness; cervical lymphadenopathy	Headache and abdominal pain improved. Appetite returned.
Day 7	Nausea, upper abdominal cramping	Fatigue, exacerbated by activity/sun exposure; abdominal cramping; nausea	Fatigue
Day 8	Nausea, upper abdominal cramping	Fatigue, exacerbated by activity/sun exposure; abdominal cramping; nausea	Fatigue
Day 9	Nausea, upper abdominal cramping	Symptom improvement	All symptoms resolved
Day 10	Nausea, upper abdominal cramping	All symptoms resolved	
Day 11	Lower abdominal cramping, non-bloody diarrhea		
Day 12	Abdominal pain, fatigue, chills		
Day 13	All symptoms resolved		

CAS-040: Plasmid Carrying Tandem Amplification of blaKPC-2 Mediates Carbapenem Resistance with Minimal Fitness Cost in Hypervirulent Klebsiella pneumoniae

Yanyan Lu[2], Jianping Jiang[1], Jianfeng Zhang[1]

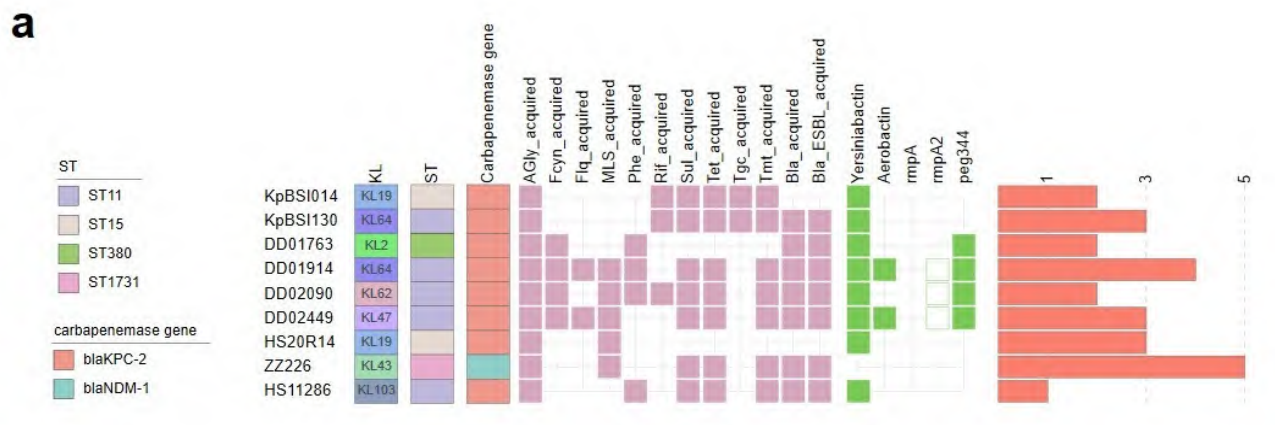
[1]Huashan Hospital
[2]Institute of Antibiotics

Background
Carbapenem-resistant hypervirulent Klebsiella pneumoniae (CR-hvKP) usually remains susceptible to carbapenems or exhibits loss of hypervirulence due to the substantial fitness burden. While the tandem gene amplification (TGA) of blaKPC-2 can confer meropenem resistance in CR-hvKP. This study aims to investigate the dissemination and formation of blaKPC-2 TGA, and its impact on meropenem resistance and pathogenicity in CR-hvKP.

Method
Eight CRKP isolates carrying tandem carbapenemase genes, ST11 CRKP HS11286, ST23 hvKP RJF999, and ST374 hvKP RJF293, and Escherichia coli C600 were used for microbiological experiments. 939 KPC plasmids retrieved from GenBank were analyzed to investigate molecular epidemiology and genomic features. Whole-genome sequencing (WGS) was used to detect the gene mutation events. ddPCR, and qPCR were employed to detect the TGA. Phenotypic characterization was assessed through conjugation assays, minimal inhibitory concentration (MIC) determination, capsule quantification and related experiments.

Results
Eight CRKP isolates harboring tandem-amplified carbapenemase genes exhibited meropenem heteroresistance. Plasmids carrying blaKPC-2 TGA were transferable and can confer changeable meropenem resistance in hvKP. This blaKPC-2 TGA-mediated resistance incurred rare reductions in capsule production. Isolates harboring a blaKPC-2 TGA plasmid maintained hypervirulence with meropenem resistance, resulting in poorer treatment outcomes in murine infection models compared to KPC plasmid with one copy of blaKPC-2. blaKPC-2 TGA requires an IS26-blaKPC-2-IS26 structure. In silico analysis revealed 42.0% (394/939) of KPC plasmids in GenBank, including 57.1% (8/14) from ST23 CR-hvKP isolates, contained IS26- blaKPC-2-IS26-like structures.

Conclusions
blaKPC-2 TGA confers adjustable meropenem resistance in CR-hvKP, enabling convergence of hypervirulence and high-level meropenem resistance, posing a significant threat to clinical therapy.



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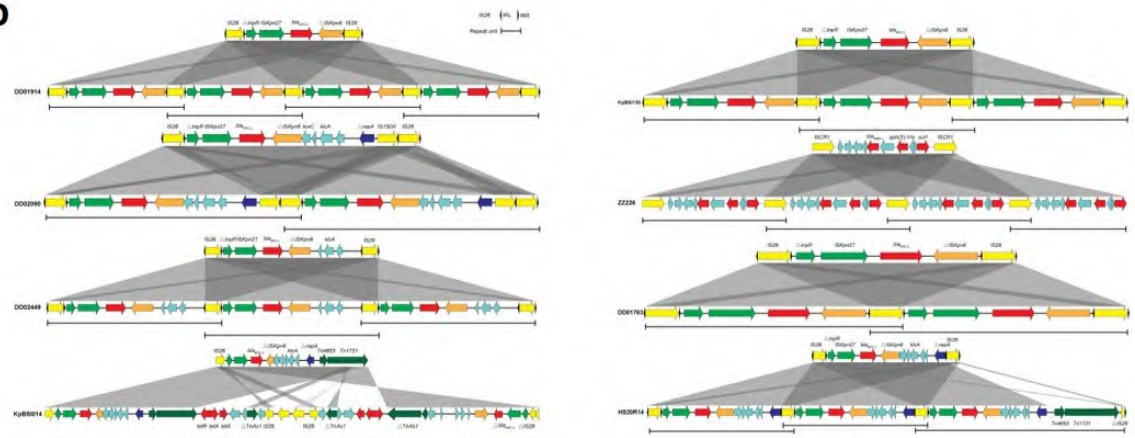

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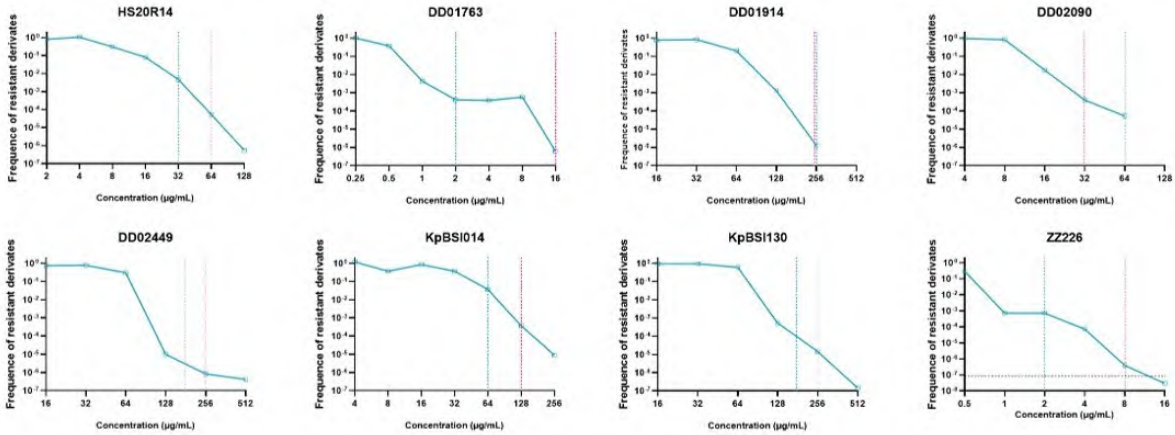

HS20R14
DD01763
DD01914
DD02090
DD02449
KpBSI014
KpBSI130
ZZ226
Frequence of resistant derivates
Concentration (µg/mL)

CAS-041: Salmonella from a Neck Abscess of a Patient Recently Diagnosed with Nasopharyngeal Cancer: A Case Report

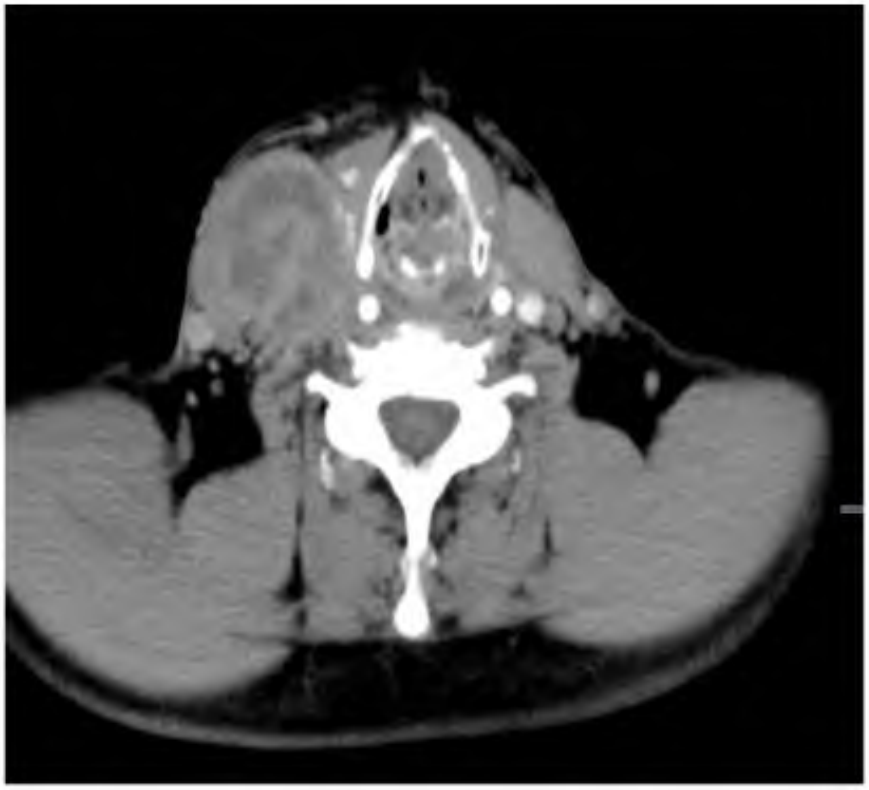
Albert Abunaga, Ma Tarcela Gler

Makati Medical Center

Introduction
Salmonella is an Enteroinvasive bacterium that can lead to a variety of clinical diseases. The most common presentation is gastroenteritis, but extraintestinal manifestations can also occur. While neck abscesses have multiple bacterial causes, Salmonella is a relatively rare culprit.

Case Presentation
In this paper, we report a 61-year old male presenting with 1-month history of enlarging right anterolateral neck mass and fever without diarrhea, abdominal pain, or vomiting. Patient sought consult with an ENT wherein CT scan of the neck revealed 4 x 3.9 x 6.6 cm heterogeneously enhancing soft tissue mass with some areas of necrosis in the right anterolateral neck. Patient was advised admission for Incision and Drainage of Right Lateral Neck Abscess and Incisional Biopsy of Right Lateral Neck Node Mass with Neck Exploration. Specimens were obtained wherein Klebsiella pneumonia and Salmonella Paratyphi C were isolated from the abscess. Routine Histopathology of the neck mass showed soft tissue with poorly differentiated carcinoma. Further immunohistochemistry revealed a Non Keratinizing Squamous Cell Nasopharyngeal Carcinoma. Patient was given Levofloxacin 750mg tablet once daily for total of 10 days and noted resolution of abscess.

Conclusion
Although uncommon, Salmonella should be included in the differential diagnosis of neck abscesses, particularly in patients with underlying immunocompromising conditions such as malignancy. Having an immunocompromised condition increases the likelihood of severe and disseminated Salmonella infections. Effective management includes high index of suspicion, radiologic tests, prompt surgical intervention, and accurate microbiological identification.



CAS-042: Toxigenic Corynebacterium diphtheriae in Two Patients with Divergent Outcomes: Evidence of Nosocomial Transmission

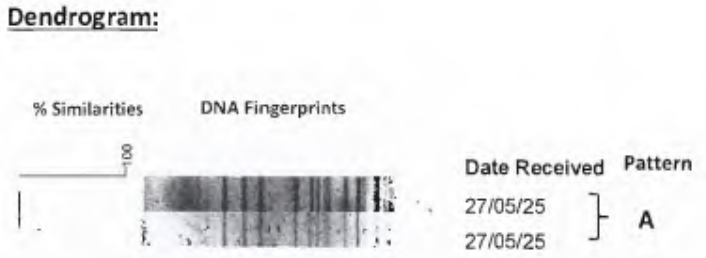
Nurazian Binti Abdul Raof[1], Yii Ling Liow[1], Su Ying Ng[2], Nurulyumni Faraha Binti Md Sharizam[5], Shabhina A/P Baghauan[5], Yaminie Nair A/P A Mahdavan[5], Nuraida Binti Khalid[4], Marlene Ing Yin Zin[3], Siti Fatimah Zahara Binti Nor Rosli[3]

[1]Hospital Sultan Ismail (Pathology Department), Johor Bahru
[2]Hospital Sultanah Aminah (Clinical Research Centre), Johor Bahru
[3]Hospital Sultanah Aminah (Emergency and Trauma Department), Johor Bahru
[4]Hospital Sultanah Aminah (Forensic Department), Johor Bahru
[5]Hospital Sultanah Aminah (Pathology Department), Johor Bahru

Introduction
Diphtheria, caused by toxigenic Corynebacterium diphtheriae, remains a concern among unvaccinated populations. Although the incidence in Malaysia is low due to successful immunization programs, sporadic cases still occur. Nosocomial transmission is infrequently reported but can have severe consequences. This report describes two temporally linked diphtheria cases at a tertiary hospital with differing outcomes, raising the possibility of hospital-acquired transmission.

Case Presentation
The first case involved a 4-month-old Rohingya refugee with respiratory distress, fever, and poor feeding. The patient was intubated and admitted to the paediatric intensive care unit, where he recovered following administration of diphtheria antitoxin and appropriate antibiotic therapy. The second case, reported one day earlier, concerned a 44-year-old detainee who was unresponsive upon arrival and succumbed shortly after. Post-mortem revealed diphtheritic pseudomembranes. In both cases, Corynebacterium diphtheriae was isolated from clinical specimens, confirmed to be toxigenic by Elek test and PCR. Pulsed-field gel electrophoresis (PFGE) revealed identical strain profiles. Both patients had overlapping exposure to the same healthcare personnel and setting, raising suspicion of nosocomial transmission.

Conclusion
This report highlights a probable case of diphtheria transmission within a healthcare setting, emphasizing the need for heightened clinical awareness and strict infection control, especially during aerosol-generating procedures. It also marks the vulnerability of unvaccinated groups, including refugees and detainees. Continued molecular surveillance and prompt public health response are essential, even in low-incidence settings, to prevent similar occurrences.



CAS-044: Challenges in Tuberculous Meningitis Diagnosis: A Case Report of Progressive Headache in an Adult

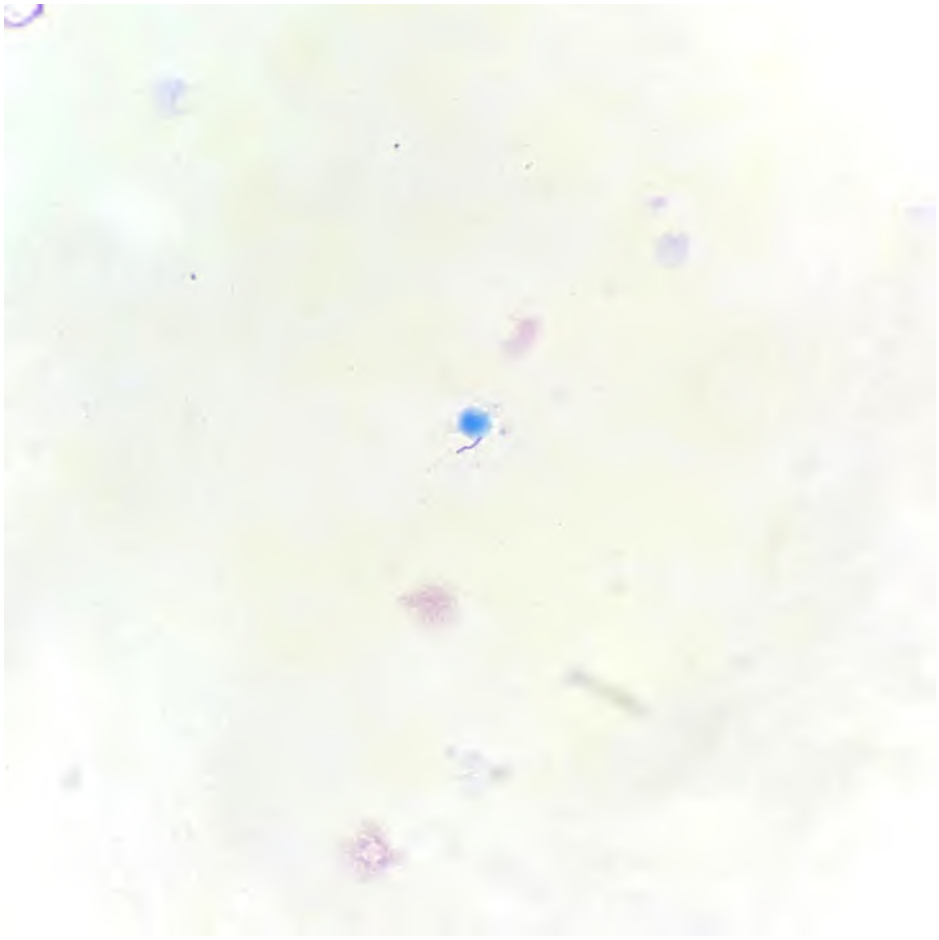
Irmadianti Pramana Putri, Wilda Mahdani, Zinatul Hayati, Endang Mutiawati Rahayuningsih, Asyriva Yossadania, Endah Cahya Sufiany, Idham Idham

Syiah Kuala University

Introduction
Tuberculous meningitis is a progressive and severe central nervous system infection from Mycobacterium tuberculosis. It has a high morbidity and mortality rate due to a delay in diagnosis, often due to nonspecific initial symptoms.

Case Presentation
A 34-year-old woman presented with a severe headache for three days that continued to worsen, with nausea and fever. Physical examination revealed a negative pathological reflex and no sign of meningeal stimulation. Initial examination showed normal routine blood test results, blood culture showed no bacterial growth, Human Immunodeficiency Virus (HIV) antibody testing yielded non-reactive results, thorax image showed an impression of interstitial pneumonia, and CT scan of the head without contrast showed no infarction, hemorrhage, or signs of intracranial enhancement. The patient received antipyretic therapy and antibiotics, but showed no significant clinical improvement. Ziehl-Neelsen (ZN) staining of a cerebrospinal fluid (CSF) specimen revealed the presence of acid-fast bacilli (AFB), suggesting a diagnosis of tuberculous meningitis. However, the patient passed away before anti-tuberculosis therapy could be initiated.

Conclusion
Tuberculous meningitis often goes undiagnosed early due to symptoms resembling other infections. Early diagnosis of tuberculous meningitis is crucial to prevent severe complications and death.



CAS-045: India Ink as a Lifeline: Early Diagnosis of Cryptococcal Meningitis in an Immunocompetent Host in a Resource-Limited Setting

Endah Cahya Sufiany, Wilda Mahdani, Zinatul Hayati, Teuku Yasir, Asyriva Yossadania, Irmadianti Pramana Putri, Idham Idham

Syiah Kuala University

Introduction

Cryptococcal meningitis (CM) is a life-threatening fungal infection mainly affecting immunocompromised individuals, but increasingly seen in immunocompetent patients. Limited access to advanced diagnostics in resource-limited hospitals delays timely treatment. India ink remains a practical, rapid tool that enables early detection and guides life-saving intervention.

Case Presentation

A 58-year-old immunocompetent male from Aceh, Indonesia, presented with high fever, severe headache, vomiting, decreased consciousness, and positive nuchal rigidity. HIV serology was negative, and there was no history of diabetes mellitus or immunosuppressive therapy. A non-contrast brain computed tomography (CT) scan revealed cerebral edema. Cerebrospinal fluid (CSF) analysis showed elevated opening pressure (390 mmH_2O), increased white blood cell count with mononuclear predominance, and positive India ink staining for encapsulated yeast. Despite repeated CSF cultures consistently revealing Staphylococcus epidermidis, clinical features and laboratory evidence confirmed cryptococcal meningitis. The patient was initially treated with high-dose fluconazole 1200 mg/day for two weeks as induction therapy. This was followed by consolidation therapy with fluconazole 800 mg/day according to the Infectious Diseases Society of America (IDSA) guidelines. Concurrent bacterial infections were managed with targeted antibiotics, levofloxacin, and vancomycin. The patient showed clinical improvement, with normal intracranial pressure and resolution of neurological symptoms.

Conclusion

This case highlights that India ink remains a valuable diagnostic tool in hospitals lacking advanced testing. Timely identification of cryptococcal meningitis in an immunocompetent host allowed prompt antifungal therapy, intracranial pressure control, and co-infection treatment with appropriate antibiotics, contributing to successful management.

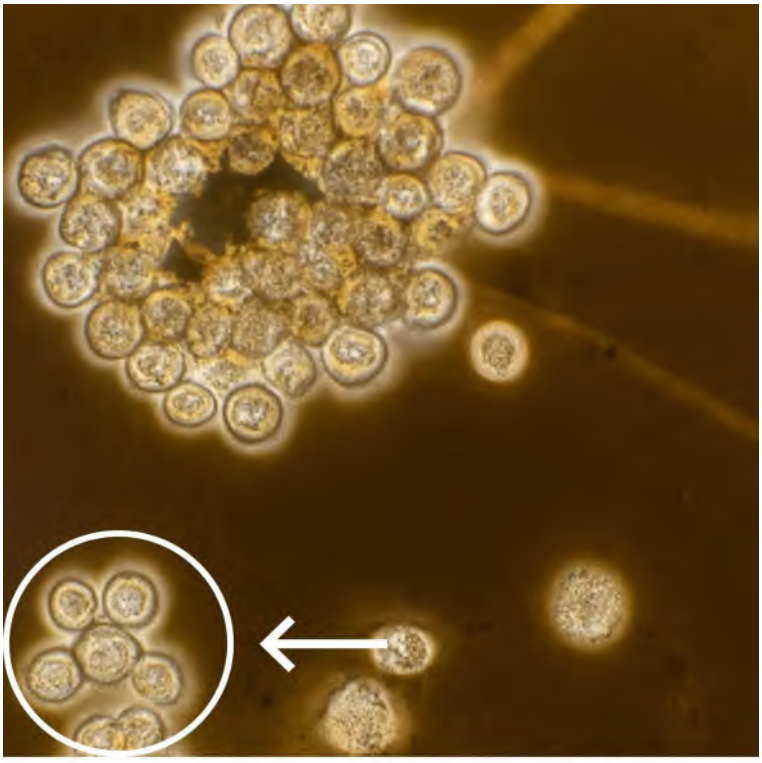


Figure: India ink staining of centrifuged CSF, encapsulated yeast-like cells of *Cryptococcus sp*. characterized by a clear halo indicating the polysaccharide capsule.

CAS-046: Severe Leptospirosis Complicated by Weil's Syndrome, Necrotising Pancreatitis, and Aseptic Meningoencephalitis: A Case Report and Literature Review

Hassan Kamena Mwana-yile Mwana-yile, Mustapha Sodqi, Sanaa Jebbar, Sara El Ansari, Latifa Marih, Kamal El Filali Marhoum

Ibn Rochd University Hospital, Faculty of Medicine and Pharmacy, Hassan II University, Morocco

Introduction
Leptospirosis is a neglected and re-emerging zoonotic disease that can lead to rare complications, including septic meningitis, acute pancreatitis, and Weil's syndrome. This case report aims to describe a case of severe leptospirosis complicated by Weil syndrome, necrotising pancreatitis, and aseptic meningitis, admitted to the Infectious Diseases Department of Ibn Rochd Hospital in Casablanca,

Case Presentation
We present a 48-year-old patient, called AN, who worked in a poultry slaughterhouse and was admitted for hemorrhagic icteric leptospirosis, complicated by several rare manifestations. These included Weil syndrome, characterized by conjugated icterus, renal failure (oligoanuria with diuresis of 300cc/24 h associated with creatinine 45.5 mg/L, GFR at 15 ml/min) as well as hemorrhages; lymphocytic aseptic meningitis, which presented with pleocytosis with 32 cells/mm3, elevated protein levels (1.09 g/L) and normal blood glucose levels (0.9 g/L); and necrotizing pancreatitis, confirmed on clinical (abdominal pain and vomiting), biological (lipasemia at 492 IU/l and CRP at 132.1 mg/l) and radiological (large acute necrotizing collection replacing a large part of the pancreas, in favor of necrotizing pancreatitis mCTSI 10) grounds. Leptospirosis serology was positive for IgM antibodies. The patient was initially treated with a third-generation cephalosporin for ten days, then with a quinolone from day eleven.

Conclusion
The rare complications of leptospirosis can overlap, making treatment management challenging.

CAS-047: Management of Empyema in a Patient with Super Super Obesity: A Case Report

Genta Kinoshita, Makoto Gotouda, Atsusi Yamakawa, Akari Nakabayashi, Katsuki Nomura, Manami Fujinaga, Natsuki Moriya, Atsuya Hane, Takanori Yamaguti, Kei Suzuki

Advanced Emergency and Intensive Care Center, Mie University Hospital

Introduction
Super super obesity (SSO; BMI ≥60 kg/m²) significantly complicates the management of critical infections such as empyema. Challenges include technical difficulties in ventilation and drainage. We report a case of empyema with SSO, emphasizing the multidisciplinary approach required.

Case Presentation
A 44-year-old man with SSO (height 170 cm, estimated weight 220 kg, BMI 76 kg/m²) presented with fever and dyspnea. Imaging revealed a large right-sided empyema. The patient developed respiratory failure requiring mechanical ventilation, which was complicated by poor compliance and difficulty achieving adequate ventilation without high airway pressures. Standard care with antibiotics and drainage was initiated, but chest tube management was technically difficult due to a thick chest wall. Prone positioning and ECMO were considered but unfeasible due to extreme body habitus and safety concerns. A structured rehabilitation and nutritional support program were introduced early during ICU stay. Progressive weight reduction improved respiratory mechanics. On day 27, successful extubation was achieved without further complications.

Conclusion
This case illustrates the unique challenges of managing empyema in SSO, particularly regarding ventilation and drainage. A multidisciplinary strategy—including tailored respiratory management, early rehabilitation, and intensive nutritional support—was essential for successful extubation and recovery. Weight reduction should be prioritized in a severe respiratory infection patient with SSO to improve respiratory function and clinical outcomes.

CAS-048: Two Cases of Pharyngeal Syphilis with Characteristic Findings: An Important Differential Diagnosis for Refractory Pharyngitis

Atsuya Hane, Atsushi Yamakawa, Makoto Gotouda, Katsuki Nomura, Akari Nakabayashi, Genta Kinoshita, Manami Fujinaga, Natsuki Moriya, Takanori Yamaguchi, Kei Suzuki

Mie University Hospital

Introduction
The differential diagnosis of refractory pharyngitis is diverse. We report two cases of syphilitic pharyngitis with characteristic findings, highlighting their educational value in clinical practice.

Case Presentation
1） A man in his 30s presented with prolonged pharyngeal symptoms. Despite receiving symptomatic treatment for possible viral pharyngitis at a local clinic, his condition did not improve, and he was referred to our hospital due to persistent low-grade fever and cervical lymphadenopathy.

2) A man in his 50s presented to a local clinic with a two-month history of sore throat. A mass-like lesion was observed involving the palatine tonsils and extending to the soft palate. A biopsy was performed; however, no definitive diagnosis was made, and the patient was referred to our hospital for further evaluation.

In both cases, pharyngeal inspection revealed the so-called “butterfly appearance” characterized by typical whitish mucosal patches along the soft palate, strongly suggestive of pharyngeal syphilis. Serologic testing confirmed the diagnosis, with both Treponema pallidum (TP) and rapid plasma reagin (RPR) tests returning positive. The patients were treated with benzylpenicillin, resulting in rapid clinical improvement. Detailed history-taking revealed a history of commercial sex work exposure, which was
considered the likely route of infection.

Conclusion
Syphilis has been increasing dramatically in recent years, making early diagnosis and treatment critically important. Although pharyngeal syphilis is rare, it presents with characteristic findings that can lead to an immediate diagnosis. We present these cases to highlight their clinical significance.

CAS-049: Cluck of the Draw: A Case of Streptococcus Gallinaceus Infective Endocarditis

Trevor Tan[1], Chen Seong Wong[1], Wilson Goh[2], Constance Chen[3]

[1]National Centre for Infectious Diseases
[2]National University Health System
[3]Tan Tock Seng Hospital

Introduction
Streptococcus gallinaceus was first isolated from broiler chickens in 2002 and is an opportunistic infection within the poultry industry. Infections in humans are rare and have only seen in abattoir workers or poultry farmers; just three cases of invasive infections have been reported thus far.

We report a case of Streptococcus gallinaceus bacteraemia and infective endocarditis in a relatively immunocompromised patient with systematic lupus erythematous (SLE). This was subsequently complicated by Libman-Sacks endocarditis and a left ventricular thrombus.

Case Presentation
The patient presented with a month's history of intermittent fevers and loss of appetite. She also reported right index and ring finger pain and discolouration over a week. Clinical examination yielded embolic features on her right 2nd and 4th digits. Two sets of blood cultures were positive for Streptococcus gallinaceus. The patient handled raw chickens when preparing food but there was otherwise no prolonged exposure.

Transthoracic echocardiography revealed a 4mm lesion on the anterior mitral leaflet and a 1cm lesion over the posterior mitral leaflet, which were confirmed on transoesophageal echocardiography. A 0.5 x 1cm left ventricular thrombus was also observed. There was trivial mitral regurgitation. She was successfully treated with a six-week course of ceftriaxone and discharged well.

Conclusion
Post-treatment transthoracic echocardiography showed worsening mitral regurgitation and a new 2mm aortic valve lesion. Repeat transoesophageal echocardiography was performed which confirmed Libman-Sacks endocarditis of the mitral and aortic valves. She was started on anticoagulation. Repeat blood cultures were negative for Streptococcus gallinaceus or other pathogenic organisms. She remains well and afebrile off antibiotics.

CAS-050: Successful Treatment with Isavuconazole and Liposomal Amphotericin B For Relapsed HIV-associated Cryptococcosis: A Case Report

Tomoyuki Fujii[2], Moeka Honda[2], Takeshi Kawaguch[2], Akiko Kitamura[2], Masatoshi Kimura[2], Yuki Rikitake[2], Chihiro Iwao[2], Ichiro Takajo[2], Yasutoshi Hirabara[1], Taiga Miyazaki[2]

[1]Department of Pharmacy, University of Miyazaki Hospital, Miyazaki, Japan
[2]Division of Respirology, Rheumatology, Infectious Diseases and Neurology, Department of Internal Medicine, Faculty of Medicine, University of Miyazaki, Miyazaki, Japan

Case Introduction
Disseminated cryptococcosis is a severe fungal infection. Standard treatment includes liposomal amphotericin B and flucytosine, followed by fluconazole. However, resistance to fluconazole is an increasing concern. Isavuconazole, a broad-spectrum triazole, has shown promise in clinical trials but remains off-label for cryptococcosis in the United States and Europe. We report a case of HIV-associated cryptococcal meningitis that relapsed as disseminated disease and was successfully treated with liposomal amphotericin B and isavuconazole.

Case Presentation
A Japanese man in his 20s was diagnosed with HIV-1 infection and cryptococcal meningitis. Due to intolerance to flucytosine, induction therapy with liposomal amphotericin B monotherapy was administered, followed by fluconazole (400 mg/day) for consolidation and 200 mg/day for maintenance. Four months into maintenance therapy, the patient developed fever and cough. Imaging and biopsies revealed disseminated cryptococcosis involving the lungs and cervical lymph nodes. Although reinduction with fluconazole and liposomal amphotericin B was ineffective, a combination of isavuconazole and liposomal amphotericin B led to clinical improvement, and maintenance with oral isavuconazole achieved sustained disease control. Blood levels of isavuconazole and liposomal amphotericin B were monitored for adequacy while treatment continued.

Conclusion
We report a relapsed case of HIV-associated disseminated cryptococcosis successfully treated with liposomal amphotericin B and isavuconazole. In general, MICs of isavuconazole against Cryptococcus neoformans are much lower than those of fluconazole. In addition, isavuconazole has excellent drug transferability to the central nervous system (CNS), representing a promising therapeutic option for cryptococcosis, including CNS infections.

CAS-051: Tuberculous Arthritis Complicating a Gout Flare: A Case Report

Shellany Luba, Gamaliel Garcia

Negros Oriental Provincial Hospital

Introduction
Concomitant infection of chronic gouty arthritis with Mycobacterium tuberculosis is uncommon. According to Philippine data, only a few cases have been reported. Patients with chronic joint inflammation are prone to concomitant infection, and in an area with a high tuberculosis burden, there should be a high index of suspicion for its occurrence.

Case Presentation
We report a case of a 45-year-old male with long-standing gouty arthritis admitted due to an acute flare. Pertinent to the patient's history was the non-resolving gouty attacks in the past two weeks, even with febuxostat and steroid use. He was also previously admitted in the past year due to severe infections: severe leptospirosis and lung abscess. On admission, chest x-ray showed pneumonia and a cavitary granulomatous infection with endobronchial spread on chest CT scan. Arthrocentesis was done on the involved joint, which revealed monosodium urate crystals and M. tuberculosis on Gene X-pert. A diagnosis of concurrent gouty arthritis with tuberculous arthritis was made. The patient was then started on isoniazid, rifampicin, pyrazinamide, and ethambutol drug regimen, but was later revised to HRE regimen on the 7th day of medication due to swelling of the left knee and hyperuricemia. Colchicine and febuxostat with a topical pain reliever were maximized. Daily or as-needed arthrocentesis was done until left knee joint swelling resolved.

Conclusion
This case report highlights the importance of prompt synovial aspiration and examination for prompt diagnosis of musculoskeletal TB as a concomitant infection in long-standing gouty arthritis in a flare.

Fig. 1. A. Left knee swelling with limited range of motion. B. Aspirated synovial fluid positive for MTB. C. chest Xray on admission, showed pneumonia.

CAS-053: A Rare Case of Hemophilus influenzae Septic Arthritis and Necrotizing Fasciitis in an Immunocompetent Adult

Dongdong Ren

Tan Tock Seng Hospital

Introduction
Hemophilus influenzae is an uncommon cause of septic arthritis or necrotising fasciitis in adults and it mostly occurs in immunocompromised hosts including those with prior splenectomy. Here, we report a rare case of H. influenza type b-associated septic arthritis with necrotising fasciitis in an immunocompetent adult.

Case Presentation
A 61-year-old previously healthy Chinese man presented with a 2-day history of fever and left lower limb pain. There was no history of trauma or water/animal exposure. He was febrile, with tense and tender posterior left thigh and calf. He deteriorated rapidly into septic shock, requiring intensive unit care. MRI scan revealed deep intermuscular fasciitis involving the posterior compartment of mid-distal thigh and leg. Surgical exploration demonstrated frank pus from left knee joint, tracking along fascial planes. H. influenza (Figure1) was isolated from pus and deep tissue cultures. The isolate was identified by MALDI-TOF and serotyped as type b by whole genome sequencing. β-lactamase was not detected. Phenotypic susceptibility testing was performed as per CLSI M100 and the isolate was susceptible to amoxicillin, levofloxacin and co-trimoxazole. Blood cultures, HIV screen, immunoglobulin and lymphocytes subset were all unremarkable.

The patient underwent multiple debridements, fasciectomy, vacuum-assisted closure and eventual skin grafting. He completed a 5-week antibiotics course and made a full recovery with preserved limb function and resolution of inflammation by 2months.

Conclusion
This case highlights the invasiveness of H. influenza, which can cause fulminant musculoskeletal infection even in immunocompetent host. Early surgical intervention with microbiology workup and targeted therapy is key to favorable outcome.

CAS-055: Opportunistic Polymicrobial Pneumonia in a Patient Receiving Ustekinumab Therapy: A Case Report and Review of the Literature

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Introduction
Biologic immunosuppressive agents increase opportunistic infection risk, with diagnosis complicated by atypical presentations. Ustekinumab, an IL-12/23 inhibitor for psoriasis, psoriatic arthritis, and inflammatory bowel disease, is though unlikely to cause serious infection compared to the conventionally used TNF-alpha inhibitors. However, emerging reports suggest an association with opportunistic infections.

Case Presentation
A 32-year-old male plumber receiving Ustekinumab for psoriasis presented with a 9-month history of chronic cough, breathlessness, and wheeze, improving when away from construction sites. Physical exam revealed inspiratory and expiratory wheeze. Chest CT demonstrated tree-in-bud consolidation in the right middle and superior lobes with bilateral lower lobe inflammatory changes. A bronchoalveolar lavage and tissue sample showed polymicrobial environmental pathogens: Nocardia cyriacigeorgica, Cryptococcus neoformans var grubii, 3 Aspergillus spp., as well as Pseudomonas aeruginosa and Candida albicans. Ustekinumab discontinuation together with targeted therapy for pulmonary nocardiosis and cryptococcosis resulted in radiological resolution and clinical recovery.

Conclusion
This represents the first reported instance of opportunistic polymicrobial lung infection in an Ustekinumab-treated patient. There are scant reports in the literature describing opportunistic infections with the use of Ustekinumab. These studies generally demonstrate favourable outcomes, with most patients achieving recovery following Ustekinumab discontinuation and targeted therapy. The underlying Ustekinumab driven immunological changes resulting in susceptibility to multiple environmental pathogens remain unclear and warrants further investigation. This case underscores the need for ongoing post marketing surveillance for infectious complications of monoclonal antibodies and small molecule targeted immunomodulators.

CAS-056: Acute Leukemia Presenting with Febrile Neutropenia, Candidemia, and Neutropenic Enterocolitis in an Adult with Probable Turner Syndrome: A Clinical Dilemma

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[3]Department of Medicine, Section of Infectious Diseases, Ilocos Training and Regional Medical Center, Philippines

Introduction
Neutropenic enterocolitis (NE) is a life-threatening condition typically occurring in immunocompromised individuals, particularly following chemotherapy. Its development in chemotherapy-naïve patients with leukemia is rare. Furthermore, candida-associated NE is exceptionally uncommon, and the coexistence of Turner syndrome in such cases is scarcely described.

Case Presentation
A 40-year-old Filipino female presented with physical features suspicious of Turner syndrome. These included a short stature, a broad chest, and primary amenorrhea. The patient was admitted because of recurrent gingival bleeding, dizziness, and fatigue. Laboratory findings revealed pancytopenia and an absolute neutrophil count of 440 cells/µL. Trephine biopsy confirmed an acute lymphoblastic leukemia. The patient subsequently developed febrile neutropenia, candidemia (Candida parapsilosis), and later, persistent diarrhea. Intra-abdominal imaging revealed bowel dilation and features of a gonadal dysgenesis. This finding supported the clinical diagnosis of a neutropenic enterocolitis and Turner syndrome, respectively. Unavailability of cytogenetic studies precluded further analysis of associated chromosomal abnormalities. Antimicrobial management with cefepime, meropenem, vancomycin, and fluconazole has significantly improved clinical outcomes. Despite recovery from the infection, the patient declined chemotherapy.

Conclusion
This case underscores the diagnostic and therapeutic challenges in managing neutropenic enterocolitis in a chemotherapy-naïve patient with leukemia and probable Turner syndrome. Candida parapsilosis as the causative organism highlights the importance of considering antifungals early in treating persistent febrile neutropenia. The potential link between Turner syndrome and hematologic malignancy remains an area for further investigation. Early recognition and multidisciplinary management are critical in improving outcomes in rare clinical scenarios.

CAS-057: A Rare Imported Case of Hepatic Hydatic Cyst in Singapore

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[2]Department of General Surgery, Tan Tock Seng Hospital, Singapore
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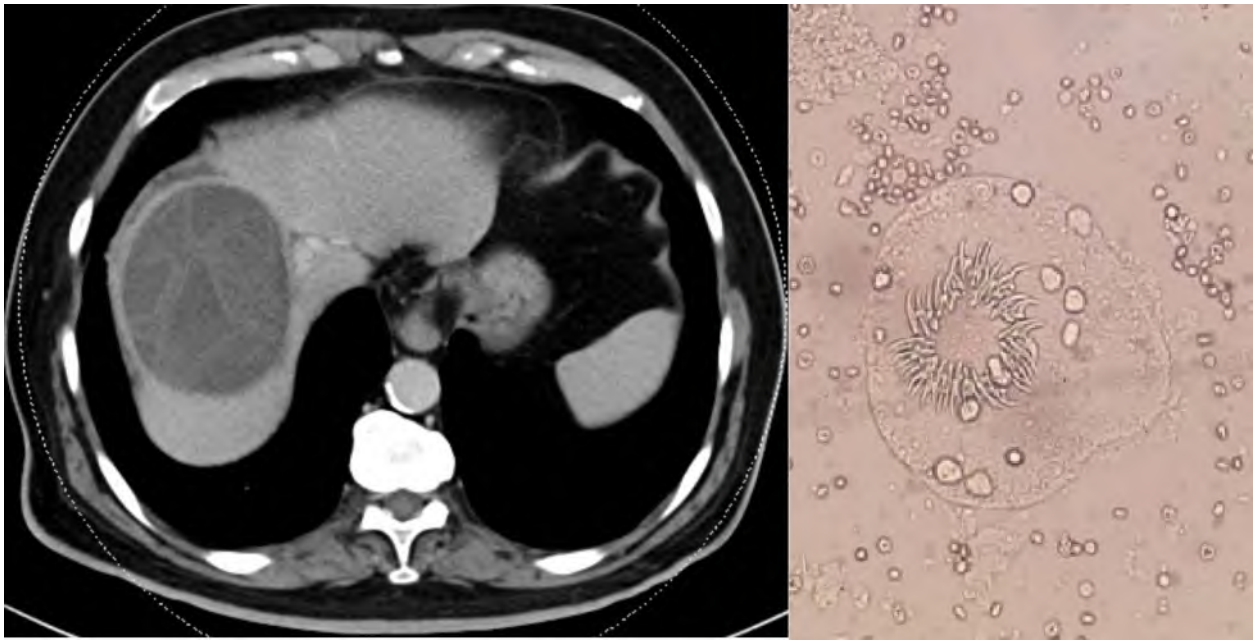
Introduction
Hydatid disease is a zoonosis caused by Echinococcus tapeworms. It is endemic in the Middle East, Central Asia and the Mediterranean, but rare in developed countries like Singapore. Canines are definitive hosts while livestock are intermediate hosts. Humans are accidental intermediate hosts infected by ingestion of eggs from environmental contamination by animal faeces.

Case Presentation
We report a rare case of hepatic hydatid disease in a 72-year-old Singaporean man with travel history to Saudi Arabia for Muslim religious pilgrimages. He avoided contact with canines for religious reasons and denied livestock exposure. In 2020, he was admitted for fever, during which an abdominal CT scan incidentally revealed two hepatic cysts with septations. The larger Segment 7 and 8 cyst contained detached membranes, with eventual development of a water-lily sign in a follow-up scan. A separate segment 6 cyst showed multiple daughter cysts within. These were monitored outpatient and remained stable. In November 2021, his fever recurred, likely due to chest infection. He was diagnosed with stage CE3b hepatic cystic echinococcosis, based on imaging findings and positive serum Echinococcus antibody. He was started on albendazole and underwent PAIR (puncture, aspiration, injection of scolicidal agent and re-aspiration) of Segment 6 in September 2022 as he declined surgery. Echinococcus species were identified in the cyst fluid. Albendazole was discontinued two months post-procedure, and he remains well.

Conclusion
This case highlights the importance of clinical vigilance for imported Echinococcus infections. Early recognition is essential to prevent complications including cyst rupture with anaphylaxis, biliary communication and super-imposed infection.



CAS-058: Two Isn't Better than One: A Case of Post-traumatic Polymicrobial Meningitis Involving Ralstonia pickettii & Psuedomonas stutzeri

Patrick Antonne Gonzalez, Jessica Marie Cuaderno, Mark Kristoffer Pasayan

Research Institute for Tropical Medicine

Introduction

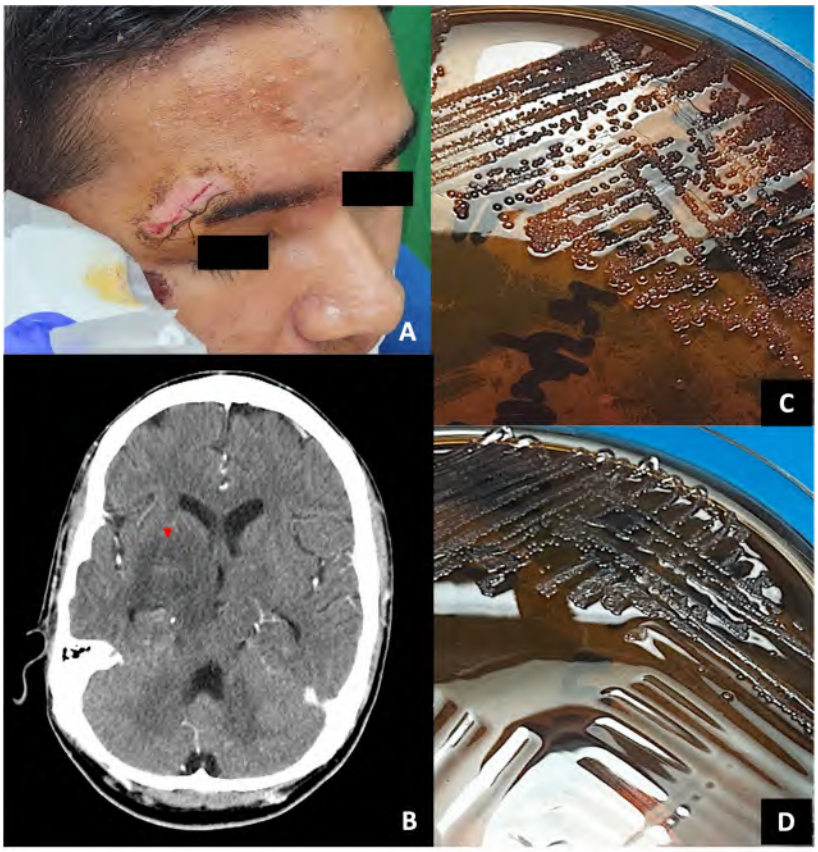
Polymicrobial bacterial meningitis is a rare entity usually associated with trauma or another infectious focus. Involved species are usually gram positives or anaerobes. While polymicrobial nervous system infections are common among immunocompromised individuals, involvement of multiple bacterial species remains unusual.

Case Presentation

A 24 year old male gay Filipino newly diagnosed with HIV was admitted at our institution last April 2025 following three months of progressive weight loss, tremors, left sided weakness and a scalp laceration following a fall. No history of fever or sensorial changes was elicited. Workup revealed HIV positivity, a CD4 count of 43 and multiple nonenhancing bilateral basal ganglia and thalamic lesions on contrast CT scan, attributed primarily to toxoplasmosis. No fractures nor masses were appreciated. He was started on co-trimoxazole and ceftriaxone and underwent lumbar tap after dexamethasone decompression. Elevated opening pressure (49cm H2O) and clear free flowing cerebrospinal fluid were appreciated. Workup was negative initially for bacterial or mycobacterial involvement. On subculture, Ralstonia pickettii and Pseudomonas stutzeri were isolated. Subsequent chest, whole abdominal CT scan and 2D echocardiography failed to reveal occult foci. Ceftriaxone was shifted to ceftazidime and the patient's condition significantly improved afterward. He was sent home on cotrimoxazole and antiretrovirals and advised regular follow-up following completion of ceftazidime.

Conclusion

To our knowledge, appears to be the first local case of polymicrobial bacterial meningitis on record. This also appears to be the first report of meningitic coinfection between Ralstonia pickettii and Pseudomonas stutzeri and highlights the remarkable possibility of unusual pathogens among the immunocompromised.



CAS-059: An Autopsy Case of Good's Syndrome Diagnosed Based on the Presence of Thymoma

Natsuki Moriya, Atsushi Yamakawa, Makoto Gotouda, Katsuki Nomura, Akari Nakabayashi, Genta Kinoshita, Manami Fujinaga, Atsuya Hane, Takanori Yamaguchi, Kei Suzuki

Advanced Emergency and Critical Care Center, Mie University Hospital

Introduction
Good's syndrome is a rare adult-onset immunodeficiency characterized by thymoma, hypogammaglobulinemia, B-cell depletion, and T-cell abnormalities. Due to its rarity, diagnosis is often delayed.

Case Presentation
A 73-year-old woman presented with persistent fever. Despite empirical antibiotic therapy, her symptoms did not improve. Imaging studies revealed ascites and pleural effusion, and she was referred to our hospital. The ascites was exudative, but cytological examination was negative, consistent with infectious ascites. She was diagnosed with refractory bacterial peritonitis, and diagnostic laparoscopy was performed. However, no gastrointestinal perforation or other definitive infectious source was identified. Multiple antimicrobial regimens were administered, but her condition showed little improvement. Her medical history included thymoma. Immunological testing showed severe hypogammaglobulinemia (IgG 186 mg/dL, IgA 20 mg/dL, IgM 3 mg/dL), and flow cytometry revealed a marked reduction of B cells, suggestive of Good's syndrome. Intravenous immunoglobulin (IVIG) therapy was initiated. However, her condition rapidly deteriorated, and she died on hospital day 19. Postmortem examination showed no specific infectious or neoplastic findings but demonstrated diffuse inflammatory changes. The clinical course was consistent with Good's syndrome.

Conclusion
Although rare, Good's syndrome should be considered in adult patients with unexplained persistent infections and a history of thymoma. Early recognition and prompt initiation of immunoglobulin replacement therapy may be essential to improve outcomes. It is also suggested that the degree of immunodeficiency may be more severe than the level of hypogammaglobulinemia alone would indicate, and further accumulation of case reports is warranted.

CAS-060: Sepsis Secondary to Rhizobium radiobacter in an Immunocompetent Adult with Ascending Cholangitis: A Case Report

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Negros Oriental Provincial Hospital

Introduction
Rhizobium radiobacter is a Gram-negative bacterium found in plants and agricultural soil. R. radiobacter infrequently affects humans, and most of infections develop in immunocompromised patients and those with indwelling catheters. Due to its low virulence and rarity in clinical settings, it is infrequently reported resulting in its low incidence globally. Based on the limited literature of R. radiobacter, acute cholangitis caused by this pathogen is rarely reported. Herein, we present a case of sepsis secondary to R. radiobacter in an immunocompetent adult with ascending cholangitis.

Case Presentation
We present a case of a 41-year-old Filipino male farmer from Mabinay, Negros Oriental, admitted for a 3-day history of right upper quadrant pain and jaundice. He had no known comorbidities and was managed as sepsis secondary to ascending cholangitis. Abdominal CT scan (Fig. 1) showed intrahepatic and extrahepatic biliary ductal dilatation without an enhancing mass. Blood cultures (Fig. 1) isolated Rhizobium radiobacter after 28 hours. Empiric treatment with Piperacillin/Tazobactam (4.5g IV q8h) was given, and the patient improved. Rhizobium radiobacter, formerly Agrobacterium, is a plant pathogen rarely infecting humans, usually affecting immunocompromised hosts or those with catheters. It is an uncommon cause of biliary infections. No standard treatment exists due to its rarity, though it is generally susceptible to aminoglycosides, fluoroquinolones, extended-spectrum beta-lactams, and carbapenems.

Conclusion
Rhizobium radiobacter is an uncommon but possible cause of biliary tract infections like ascending cholangitis, even in patients without known risk factors. This case highlights the need for clinicians to consider it in sepsis workups regardless of comorbidity status.

CAS-061: Amoeboma Masquerading as a Colorectal Malignancy in an Asymptomatic Patient: A Diagnostic Challenge in Non-Endemic Settings

Tiara Joy Foo, Jolene Oon

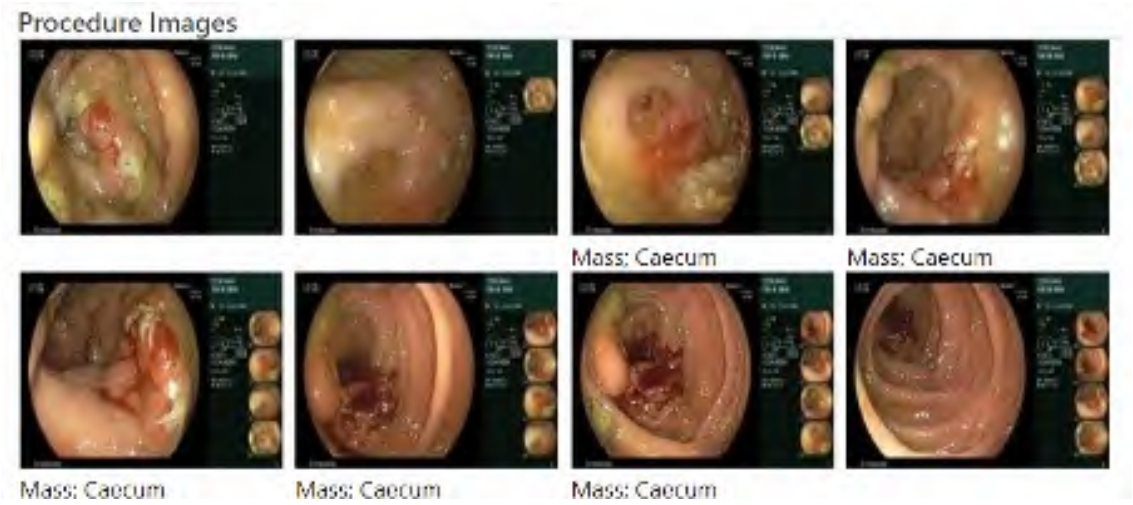
NUHS

Introduction
Amoeboma is a rare manifestation of Entamoeba histolytica (E. histolytica) infection, presenting as a tumour-like inflammatory mass composed of granulation tissue and trophozoites. It may mimic colorectal carcinoma radiologically and endoscopically. While typically linked to invasive colitis, it can occur in asymptomatic individuals, leading to diagnostic uncertainty in non-endemic regions.

Case Presentation
An 80-year-old male originally from Myanmar, residing in Singapore for two decades, was referred following a positive faecal occult blood test during routine screening. He had a background of hypertension, was not immunocompromised, and denied alcohol use. He was asymptomatic, with unremarkable physical examination and initial laboratory findings. Computed tomography imaging revealed a colonic mass suspicious for malignancy. Colonoscopic biopsy of the mass lesion demonstrated ulcerated granulation tissue with amoebic trophozoites, staining positive for periodic acid–Schiff (PAS). He was referred to Infectious Diseases for further management. E. histolytica serology was positive. Despite being asymptomatic, he was treated with oral metronidazole followed by paromomycin to prevent disease progression. Surgical intervention was avoided.

This case highlights the importance of considering infectious mimics of malignancy in asymptomatic patients. Amoeboma, though uncommon, may present long after prior exposure to endemic regions. Without careful clinical and pathologic correlation, such cases may result in unnecessary surgical resection. Diagnosis hinges on travel or residence history, characteristic histopathology, and supportive serology.

Conclusion
Amoeboma should be included in the differential diagnosis of colorectal masses. Early recognition enables curative medical therapy and avoids overtreatment of a rare, but entirely treatable, infection.



CAS-062: A Case Report of a Skin Infection Caused by Mycobacterium mageritense in a Healthy Patient in Japan

Poowadon Muenraya[1], Shinnosuke Fukushima[1], Jumpei Uchiyama[1], Hideharu Hagiya[2]

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[2]Department of Infectious Diseases, Okayama University Hospital, Okayama, Japan

Introduction
Mycobacterium mageritense (newly classified as Mycolicibacterium mageritense) is a rapidly growing nontuberculous mycobacterium that rarely causes infections in both immunocompromised and healthy individuals. Here, we report a case of skin infection caused by M. mageritense in a healthy adult patient, with the results of genomic characterization.

Case Presentation
A 48-year-old healthy man presented with a persistent skin infection on his right lower leg, accompanied by inguinal lymphadenitis. Bacterial cultures from both infected foci detected a mycobacterium, which was identified as M. mageritense using mass spectrometry. The abscess was surgically removed, and wound irrigations were repeatedly performed. Although various antimicrobial agents were administered throughout the clinical course, the patient mostly underwent a combinatory therapy of levofloxacin and minocycline. Gradual improvement was observed, and complete resolution was achieved after four months of therapy. Later, we performed whole-genome sequencing analysis to identify the bacterial species, detect antimicrobial resistance genes, and compare the phylogenetic relatedness between the present strain and those previously deposited in the database. The draft genome showed the highest similarity to a previously deposited M. mageritense isolate. Antimicrobial resistance genes were detected as follows (% identity): erm (40) (98.8%), aac (2')-Ib (84.2%), tet (V) (81.2%), and RbpA (97.3%).

Conclusion
This case highlights that M. mageritense can cause a clinically significant skin infection in a healthy patient. Further clinical and microbiological data are warranted to elucidate the disease burden that potentially poses to humans.

CAS-063: Multiple Klebsiella pneumoniae Liver Abscess Mimicking Malignant Liver Tumor

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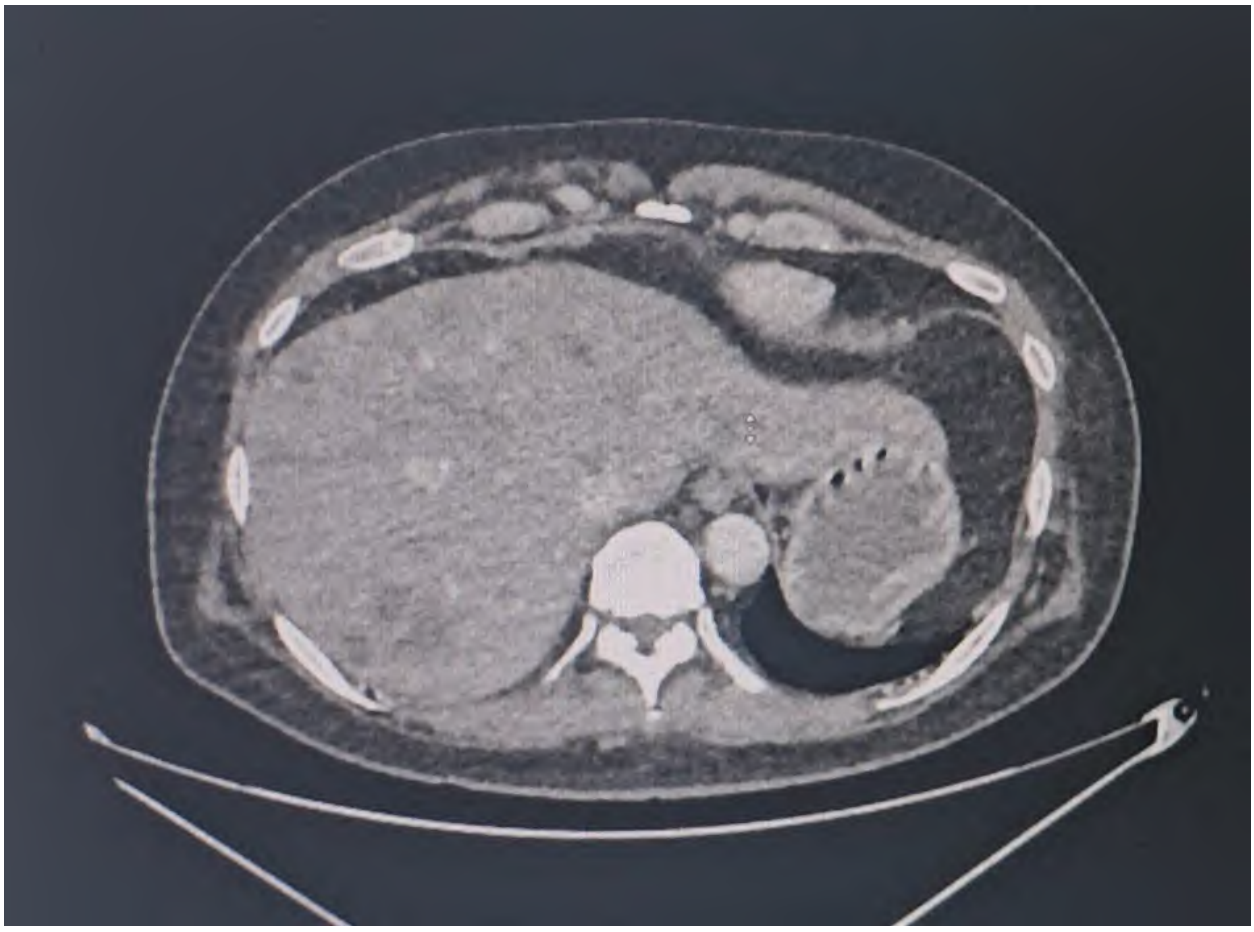
Division of Gastroenterohepatology, Department of Internal Medicine, Fatmawati General Hospital

Introduction
Klebsiella pneumoniae has been reported as the leading etiology of pyogenic liver abscess, especially in East and Southeast Asia. The infection predominantly occur in diabetic patients. Some Klebsiella pneumoniae liver abscess manifests as a single or multiple solid masses mimicking a malignant lesion which potentially can delay the diagnosis and management.

Case Presentation
A 50-year-old male, newly diagnosed with diabetes mellitus, presented with fever persisting for 8 days followed by decline in consciousness since one day before admission. There was no history of abdominal pain or bloody stools. Vital signs showed a temperature of 39°C, tachycardia, tachypnea with normal blood pressure. Neurological examination showed Glasgow Coma Scale score of 13 (E3V4M6). Hepatomegaly was observed. Laboratory examination showed neutrophil leukocytosis, thrombocytopenia, elevated procalcitonin, and acute kidney injury. Computed tomography of his abdomen showed a large solid nodule with smaller multiple nodules occupying the liver. Since Alpha-fetoprotein (AFP) and markers for hepatitis B and C viruses were negative and blood culture positive for Klebsiella pneumoniae, the liver nodule biopsy was performed. The biopsy revealed abundant inflammatory cells with necrotic debris, consistent with abscess. Patient was initially treated with meropenem and then de-escalated to ciprofloxacin based on susceptibility test. After two weeks of antibiotic therapy, the large nodule was liquified and aspiration of abscess was done. The patient progressed well and was discharged. After eight weeks of antibiotics, the ultrasound showed resolution of abscess.

Conclusion
Klebsiella pneumoniae liver abscess should be considered as a differential diagnosis when evaluating liver nodule in patients presenting with sepsis.



CAS-064: A Case of Severe HIV-Associated Psoriasis Successfully Treated with Glucocorticoids and Antiretroviral Therapy

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[1]Department of Dermatology, Ehime University Graduate School of Medicine
[2]Department of Hematology, Clinical Immunology and Infectious Diseases, Ehime University Graduate School of Medicine

Introduction
HIV-associated psoriasis can be atypical and refractory, sometimes prompting HIV diagnosis. We report a case of severe, topical therapy-refractory HIV-associated psoriasis, in which HIV had progressed to AIDS. Treatment with glucocorticoids and antiretroviral therapy (ART) led to clinical improvement.

Case Presentation
A 37-year-old man presented with erythema on the anterior chest that had persisted for seven months and was unresponsive to topical treatment. By the time of the initial visit, the rash had become generalized, and clinicopathological findings confirmed severe psoriasis vulgaris. He was a man who has sex with men, with a history of treated syphilis. He was diagnosed with HIV-1 infection through screening and confirmatory serological tests, with no evidence of an AIDS-defining illness. Initiation of ART was delayed while awaiting approval for disability-based assistance. He missed the scheduled ART initiation visit due to fever and returned two weeks later with mild dyspnea. He was diagnosed with pneumocystis pneumonia (PCP). Treatment with trimethoprim–sulfamethoxazole and prednisolone led to the prompt resolution of PCP and a parallel improvement in his psoriasis. ART was initiated after three weeks of hospitalization. A mild flare of psoriasis occurred during glucocorticoid tapering but responded well to continued ART and topical therapy. No immune reconstitution inflammatory syndrome (IRIS) developed, and he was discharged after five weeks. Prednisolone was gradually tapered off over five months, and psoriasis has remained in remission.

Conclusion
Immune restoration induced by ART has likely contributed to the control of psoriasis. Co-administration of glucocorticoids may have prevented IRIS-related flares and facilitated psoriasis control.

CAS-065: When B. cepacia Isn't: A Case of Invasive Melioidosis with Rare CNS and Vascular Involvement in a Diabetic Patient

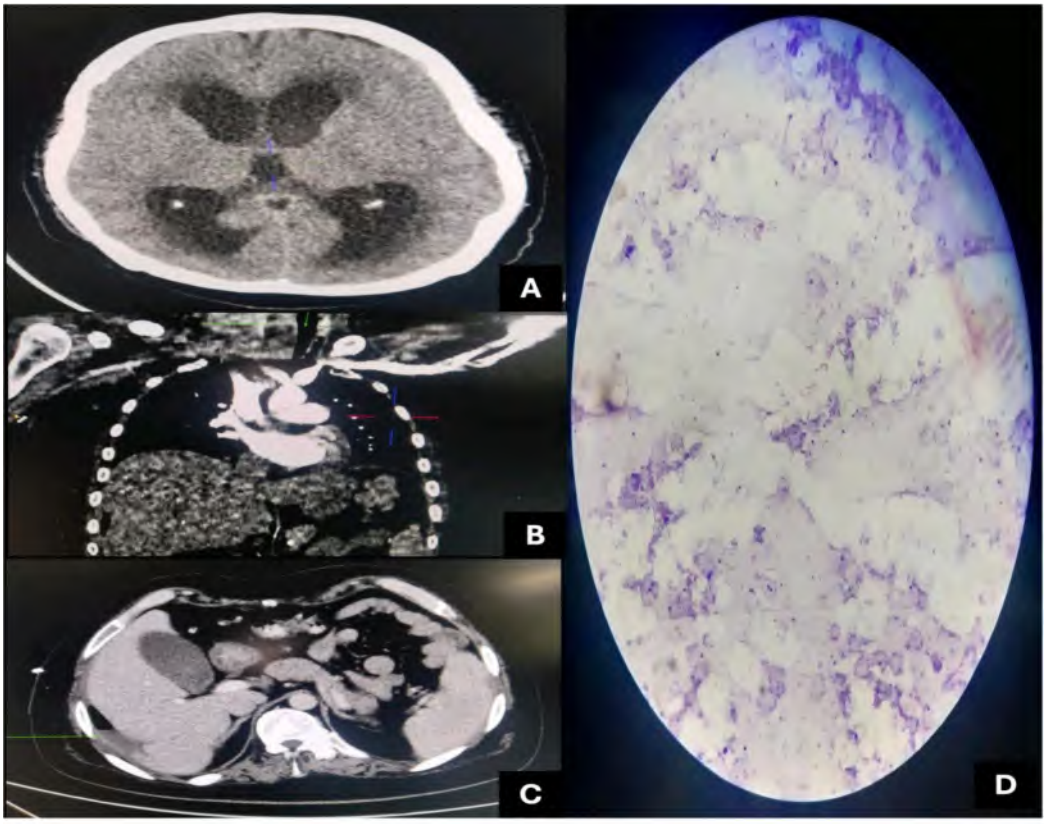
Jelena Louise Arreza, Raquel Victoria Ecarma

Philippine Heart Center

Introduction
Melioidosis is an emerging infectious disease in tropical regions caused by Burkholderia pseudomallei, an environmental Gram-negative bacillus. Its diverse clinical manifestations and frequent misidentification by conventional biochemical systems pose diagnostic challenges. While hepatic abscesses are common, neurological and vascular involvement are rare and often underrecognized. Early and accurate identification is critical to avoid relapse and improve outcomes.

Case Presentation
We report a case of a 29-year-old male with newly diagnosed type 2 diabetes mellitus presenting with fever, a pulsatile right neck mass, dizziness, and acute left-sided weakness. Imaging studies revealed a ruptured right common carotid artery pseudoaneurysm necessitating emergent surgical repair, concurrent acute watershed infarcts, hydrocephalus requiring ventriculoperitoneal shunting, and right hepatic lobe abscess managed with aspiration and drainage. Five months prior, he had been treated for hepatic abscess, with cultures reportedly demonstrating B. cepacia. During the current admission, blood cultures identified B. pseudomallei. Management was then directed toward multifocal invasive melioidosis with septicemia, CNS involvement, and vascular infection. Therapy commenced with intravenous meropenem, which was transitioned to intravenous ceftazidime. This regimen was de-escalated to six-month oral course of trimethoprim-sulfamethoxazole. He was discharged in stable condition, with close outpatient follow-up.

Conclusion
This case highlights the varied manifestations of melioidosis, including rare neurologic and vascular complications. It also underscores the potential for misidentification with Burkholderia cepacia, leading to delayed or suboptimal therapy. Clinicians in endemic areas should maintain a high index of suspicion for melioidosis in diabetic patients with recurrent abscesses or unusual systemic involvement, and consider confirmatory diagnostic methods to improve accuracy.



CAS-066: Successful Treatment of Simultaneous Intracranial Toxoplasmosis and Tuberculosis in Advanced Immunosuppression: A Case Report

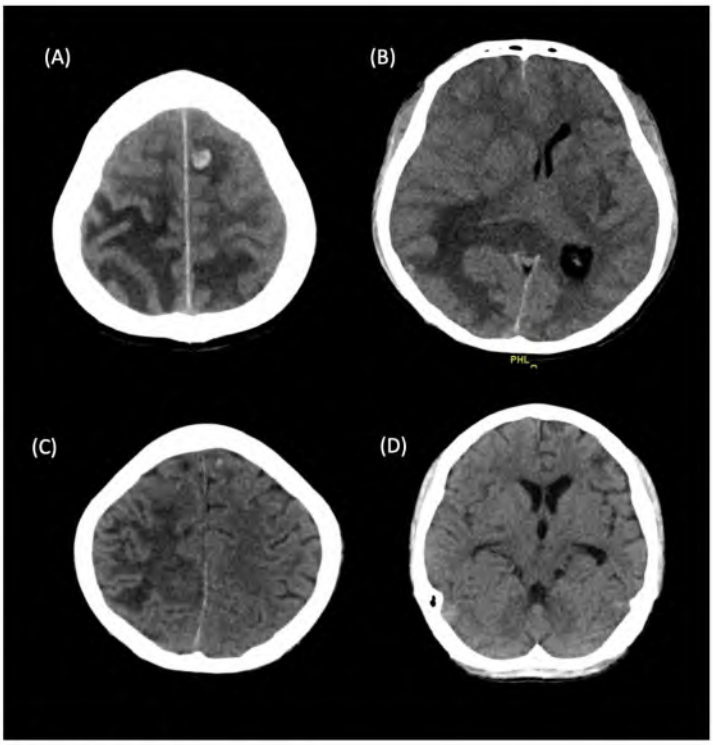
Fadia Fauzi[1], Nur Izati Mustapa[2]

[1]Medicine, Universiti Teknologi MARA
[2]Ministry of Health Malaysia

Introduction
Toxoplasmosis encephalitis and tuberculous meningitis are familiar central nervous system (CNS) infections causing high morbidity and mortality in HIV patients. However, concurrent infections are not common occurrence.

Case Presentation
A 28-year-old intravenous drug user presented with one week history of fever, headache, vomiting, and altered consciousness. He tested positive for HIV with CD4 <35 cells/μL. Radiological findings of leptomeningeal enhancement, cerebral edema, hydrocephalus and multiple intra-axial lesions involving bilateral basal ganglia, pons and cerebral hemispheres; raised suspicion of tuberculous meningitis and cerebral toxoplasmosis. Empiric treatment was initiated with clindamycin, pyrimethamine, and folinic acid for toxoplasmosis, along with corticosteroids and a 4-drug anti-TB regimen for tuberculous meningitis. Laboratory investigations revealing borderline toxoplasma IgM, strongly positive toxoplasma IgG level of over 400IU/mL, and positive Mycobacterium tuberculosis PCR from a burr hole drainage abscess supports the probable diagnosis of cerebral toxoplasmosis and confirmed the diagnosis of tuberculous meningitis. His treatment was later complicated by poor oral tolerance and hepatotoxicity, requiring multiple anti-TB regimen adjustments including temporary switch to intravenous agents. Reassessment of CT brain after 3 weeks showed smaller intra-axial lesion. Initiation of antiretroviral therapy was withheld for four weeks to reduce the risk of immune reconstitution inflammatory syndrome. He recovered well from the infection with concomitant residual weakness requiring rehabilitation.

Conclusion
This case highlights the complexity of managing multiple CNS infection in a newly diagnosed HIV patient with a rare presentation of concurrent infections. Essentially, it requires multidisciplinary approach, including early antimicrobial therapy and neurosurgical intervention which enhanced the patient's positive outcome.



(A)(B) CT Brain at presentation

(C)(D) Repeated CT brain after 3 weeks of treatment

CAS-068: An Unusual Case of Neuro-melioidosis

Alicia Xin Yu Ang, Nimrod Gabornes, Soon Keng Goh

Woodlands Health

Introduction
Melioidosis is caused by Burkholderia pseudomallei. Neuro-melioidosis is rare but potentially fatal.

Case Presentation
A 69-year-old male presented with fever, headache, and myalgia. His white blood cells were up to 35.4 x 109/L, C-reactive protein up to 285.4 mg/L and ferritin up to 1,162ug/L. Multiple blood cultures, Computed Tomography scans of this thorax, abdomen and pelvis and Positron Emission Tomography scans were unremarkable. Magnetic Resonance Imaging of the brain revealed an area of leptomeningeal enhancement in the right posterior temporal region, and dural enhancement along the falx, but cerebrospinal fluid analysis was unyielding. He refused a meningeal biopsy. He did not respond to Amoxicillin-Clavulanate nor Ceftriaxone. There was no laboratory nor clinical evidence of an auto-immune condition. Melioidosis serology was sent due to an occupational history with extensive soil contact and returned positive at 1:64. He was empirically treated with IV Meropenem then Ceftazidime for the 8 weeks of intensive phase treatment. Inflammatory markers improved and fever resolved within 2 weeks of intensive phase treatment. Post-intensive phase treatment, repeat melioidosis serology turned negative, dural enhancement on brain imaging resolved, and he remained asymptomatic. He completed his consolidation therapy with oral Trimethoprim-Sulfamethoxazole.

Conclusion
It is not standard to diagnose melioidosis using serology, nor rely on an improvement in serological titers to measure treatment response; however, without meningeal biopsy for cultures, these were crucial for managing this patient. Empiric melioidosis treatment resulted in resolution of symptoms and improvement in brain imaging and laboratory results, making this case clinically consistent with neuro-melioidosis.

CAS-069: Heed the Warning – Staphylococcus aureus in Urine Can Mean Something Serious!

Alicia Xin Yu Ang

Woodlands Health

Introduction
While majority of Staphylococcus aureus bacteriuria reflect colonization or uncomplicated urinary tract infection, it can represent haematogenous seeding from an occult infection. It is important to evaluate for bacteraemia in appropriate patients with Staphylococcus aureus bacteriuria, even without fever.

Case Presentation
A 75-year-old man presented with a fall while bending forward to wash his feet. Post-fall, he suffered neck, bilateral shoulder, bilateral hand and right knee pain. Full blood count on admission showed elevated white blood cell count of 18.4 x10^9/L. Inflammatory markers and urinalysis were sent to look for infective precipitants for the fall. C-reactive protein was >380 mg/L, procalcitonin was 3.84 ug/L and urine cultures returned positive for methicillin-susceptible Staphylococcus aureus (MSSA). There was no pyuria. Thus, multiple blood cultures were sent and grew MSSA. Further work-up revealed that he had right knee septic arthritis, infective endocarditis with a 0.35cm tubular mass attached to the mitral valve (on trans-oesophageal endocarditis), cervical and thoracic spondylodiscitis and a 3.3cm saccular aneurysm along the aortic arch that was not amenable to endovascular intervention. He underwent a right knee washout, and intra-operative cultures also grew MSSA. The patient was treated with 8-week course of intravenous Cefazolin with good biochemical and clinical response. Despite complicated MSSA bacteraemia with multiple metastatic sites of involvement, the patient remained afebrile throughout.

Conclusion
Staphylococcus aureus bacteriuria has been reported to be associated with Staphylococcus aureus bacteraemia in between 8-27% of patients. Early detection of Staphylococcus aureus bacteraemia in patients with SABU can guide targeted therapy.

CAS-070: Behind the Wheeze: A Case of Delayed Tuberculosis Diagnosis in an Adolescent with Underlying Bronchial Asthma

Rinusha Manogaran[1, 2], Hasni Mahayidin[2], Nur Hanani Ahmad[1], Idimaz Hajar Jabbari[1]

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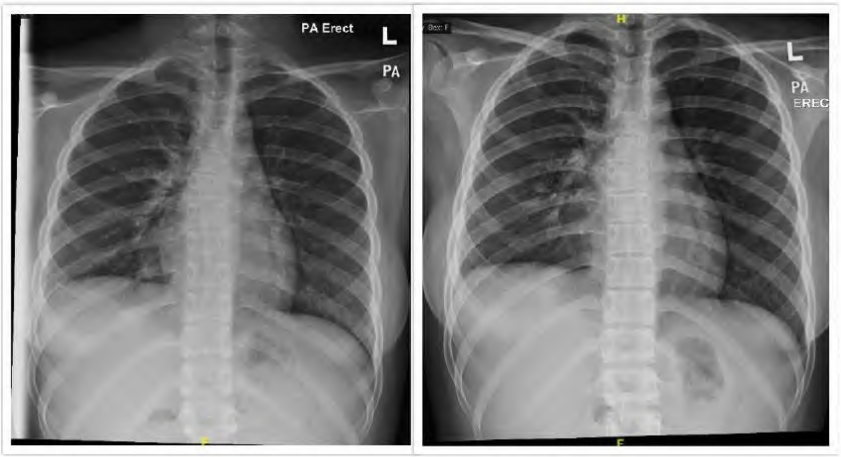
Introduction
Pulmonary tuberculosis (PTB) continues to pose a considerable threat to the adolescent population, particularly in those with underlying chronic conditions like bronchial asthma. This case highlights the diagnostic difficulties in adolescents with PTB complicated by underlying bronchial asthma, where persistent cough was initially thought to be an acute asthma exacerbation, thus delaying the actual diagnosis.

Case Presentation
A 13-year-old girl with a history of newly diagnosed bronchial asthma presented with a 4-month history of productive cough and shortness of breath. She visited the healthcare facility multiple times and was repeatedly treated for acute asthma exacerbation secondary to upper respiratory tract infection. However, worsening of symptoms despite proper use of bronchodilators and chest radiograph findings (Figure 1) prompted admission and workup for PTB, including sputum acid-fast bacilli smears, which were negative for Mycobacterium tuberculosis (MTB), followed by the MTB rapid PCR test (M10 MDR-TB) which was positive, confirming tuberculosis (TB) infection. She was then started on intensive phase of anti-TB regime and subsequently discharged well with follow-up appointment at the nearest health clinic.

Conclusion
This case underscores the value of considering PTB as the differential diagnosis in adolescents with underlying bronchial asthma. A high index of suspicion is needed in managing such patients, as the symptoms may overlap and can be easily attributed to exacerbations of bronchial asthma. Although adolescent PTB typically resembles adult-like disease, some cases may still present as paucibacillary PTB. Rapid molecular testing is crucial in diagnosing such smear-negative cases.

Figure 1



Chest radiographs showing subtle right perihilar haziness at initial presentation (a), with progression over six weeks to right mid and lower zone reticulonodular opacities, right pleural effusion, and elevated right hemidiaphragm (b).

Table I: Summary of Laboratory Investigations

Investigations	Results	Reference range
White blood cell	20.1 (N 70%, L 16%)	(4-10) x 10^9/L
Hemoglobin	11.6	12-15 g/dL
Platelet	510	(150-410) x 10^9/L
Urea	3.1	3.2-8.2 mmol/L
Creatinine	41	62-115 µmol/L
C-reactive protein	2.38	0.0-5.0 mg/dl
ESR	84	0-12 mm/hr
AFB smear x 3 (Sputum)	Negative	
M10 MDR-TB (Sputum)	MTB detected. Rifampicin and Isoniazid resistance not detected	

N = Neutrophil; ESR = Erythrocyte sedimentation rate; AFB = Acid-fast bacilli; MTB = *Mycobacterium tuberculosis*

CAS-071: More Than Just a Swollen Leg: The Silent Invasion of Community-Associated Methicillin-Resistant Staphylococcus aureus Infection

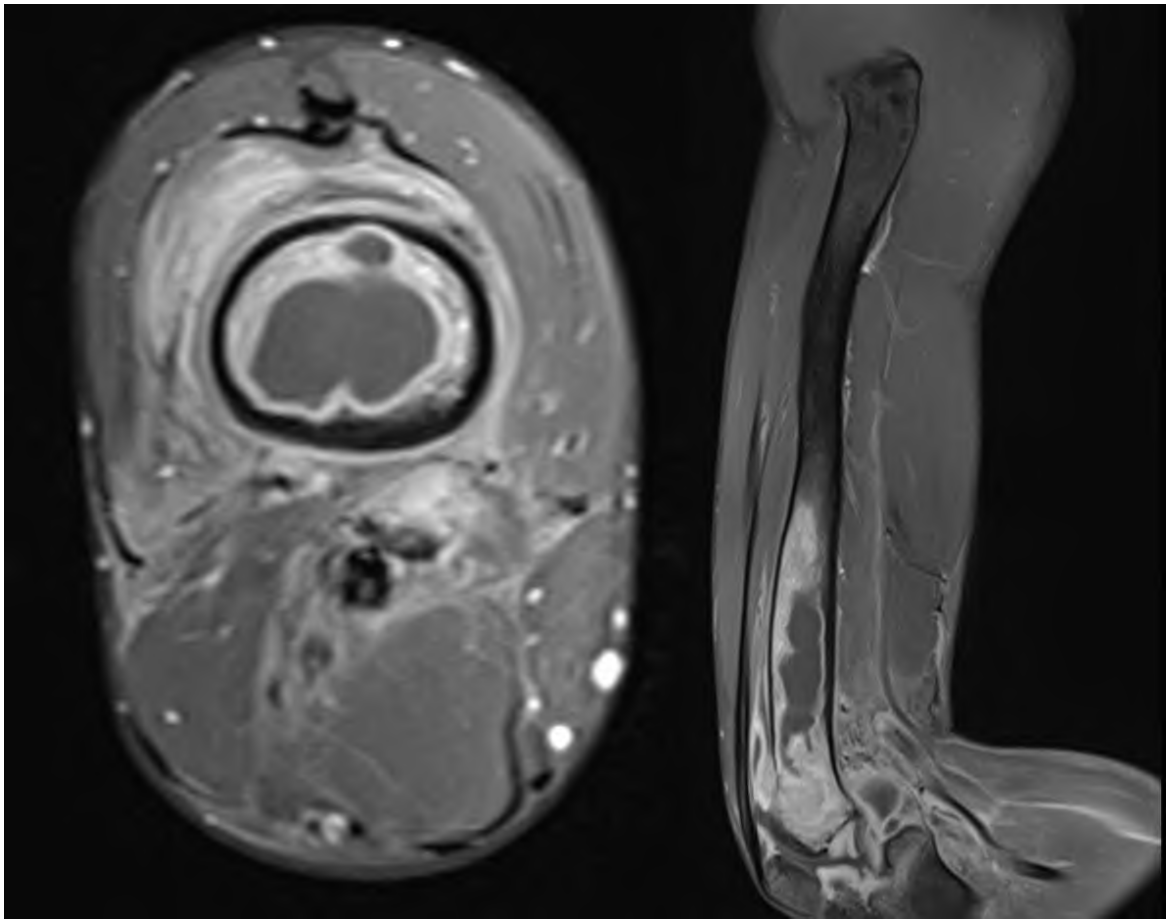
Krison Sum, Wilson Goh

MOHH

Introduction
Community-Associated Methicillin-Resistant Staphylococcus aureus (CA-MRSA) is an emerging global health concern, known to cause serious infections. Among patients with MRSA bloodstream infections, up to 85% had prior colonisation, which implies that 15% were not colonised or at least not detected prior to infection.

Case Presentation
A healthy 23-year-old male presented with five days of right leg pain and swelling. He denied trauma, insect bites, or wounds, despite working in construction. Examination revealed right calf tenderness, edema, and minimal erythema. Labs showed significant leucocytosis (35 × 109/L) normal 4.3-10 x 109/L) and elevated CRP (232 mg/L) (normal <5mg/L). Blood cultures and MRSA screening of nares and axillae were negative. MRI revealed a 20 × 6 × 2 cm rim-enhancing intramuscular collection between the medial gastrocnemius and soleus, communicating with the knee joint, and a 2 × 2.8 × 4.9 cm Brodie's abscess in the right distal femur (Figure 1). HIV screen and HbA1c were normal. Surgical management included knee arthrotomy with drainage, femoral corticotomy, debridement and drainage of the calf abscess. Cultures confirmed MRSA. He was treated with intravenous vancomycin, followed by oral trimethoprim-sulfamethoxazole with favorable response.

Conclusion
This case underscores that CA-MRSA can cause deep-seated musculoskeletal infections even in immunocompetent individuals without classic risk factors. Some may even have complicated infections without being a colonizer of MRSA. Early imaging, surgical intervention, and appropriate antibiotic therapy are critical for favorable outcomes. Clinicians should maintain a high index of suspicion for CA-MRSA in similar presentations, regardless of patient risk profile.



CAS-073: A Rare Disseminated Presentation of Melioidosis: Orbital Cellulitis, Superior Ophthalmic Vein Thrombosis, and Probable Subdural Abscess

Kittipong Suwanlert

Kham Thale So hospital

Introduction

Melioidosis is endemic in Southeast Asia. While pneumonia and bacteremia are common, orbital and intracranial complications are rare and often under-recognized. These manifestations pose diagnostic and therapeutic challenges, particularly in resource-limited settings.

Case Presentation

A 58-year-old man with poorly controlled diabetes, hypertension, and dyslipidemia presented with one week of fever, malaise, dry cough, and right eye swelling. He had direct ocular exposure to contaminated water five days before the onset of symptoms while working in a rice field. Initially diagnosed with pneumonia, he was treated with intravenous ceftriaxone and oral roxithromycin. During admission, his periorbital swelling and headache worsened. Blood cultures yielded Burkholderia pseudomallei. He was referred to a tertiary center for suspected central nervous system involvement. Brain and orbital computer tomography showed right orbital cellulitis with proptosis, enlargement of the superior ophthalmic vein (5.4 mm) with a filling defect, and a crescentic hypodense lesion over the right frontoparietal convexity, suggestive of early subdural abscess or hygroma. During admission there, he developed a generalized tonic-clonic seizure. He was treated with intravenous phenytoin, later switched to oral. He was transferred back to the rural hospital to complete a 28-day course of intravenous ceftazidime and received subcutaneous enoxaparin bridged to warfarin. He was discharged on oral trimethoprim-sulfamethoxazole for six months and continues INR monitoring. The patient responded well, with no further seizures, and remains under ophthalmologic follow-up.

Conclusion

This case illustrates rare presentations of melioidosis with orbital and intracranial complications. It highlights the importance of exposure history, early recognition, and prolonged therapy in endemic areas.

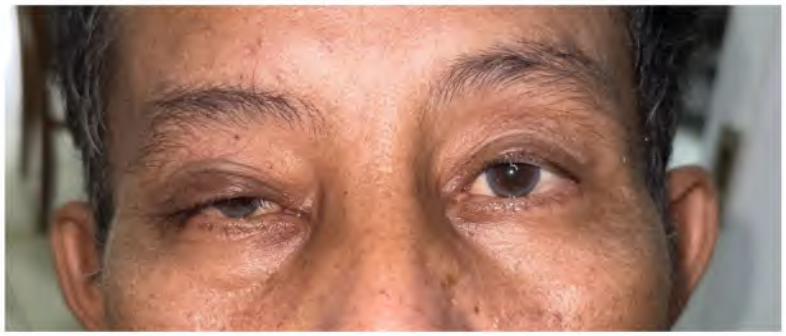
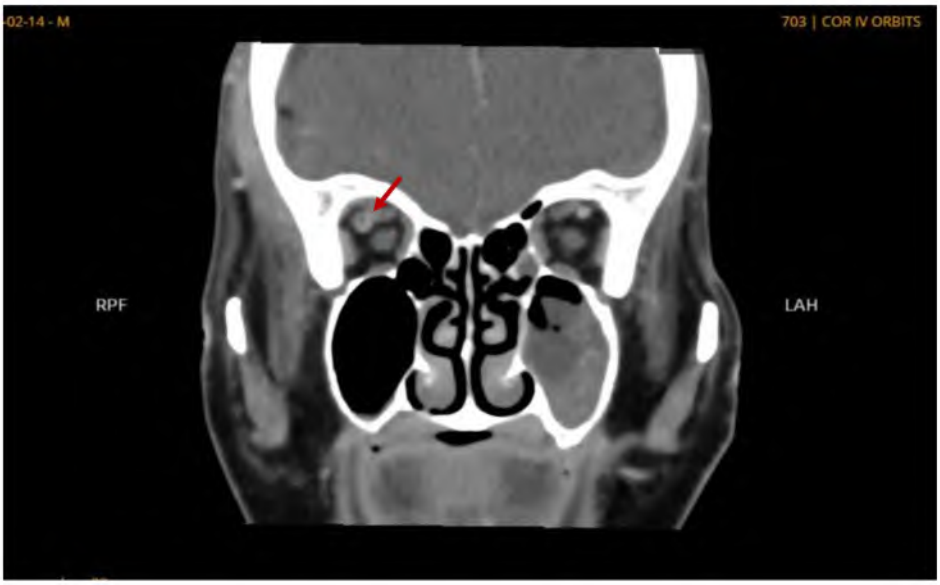


Figure 1. Clinical photograph showing right periorbital swelling and ptosis during follow-up.

(Informed consent was obtained from the patient.)



Figures 2. Coronal contrast-enhanced CT orbit showing enlargement of the right superior ophthalmic vein (red arrow) with an eccentric low-density filling defect, consistent with thrombosis.

CAS-074: Brucella at the Clinic: A Case of High-Risk Occupational Exposure in an Urban Veterinarian

Wilson Goh, Isaac Ng, Sai Meng Tham, Priscillia Lye

National University Health System

Introduction
Brucellosis is a globally significant zoonosis, though rare in developed urban settings such as Singapore. Among the four Brucella species pathogenic to humans, Brucella canis (B. canis) is less commonly reported but poses occupational risks to veterinarians. Diagnosis is challenging due to serological limitations, and the use of post-exposure prophylaxis (PEP) remains controversial. We present a rare case of high-risk B. canis exposure in a veterinarian, highlighting diagnostic challenges and the role of PEP.

Case Presentation
A 33-year-old male veterinarian presented following high-risk exposure during an orchiectomy on a local dog with orchitis. Canine scrotal fluid, later PCR-positive for B. canis, splashed onto his scrubs and a healing chest wound. The patient was asymptomatic and physical examination was unremarkable. Given the high-risk exposure and limited local diagnostics, a shared decision was made to initiate PEP with doxycycline and rifampicin for three weeks. Brucella serology (the only serology we have available in Singapore), processed by Mayo Clinic, was negative. At three-month follow-up, he remained well with no adverse drug effects.

Conclusion
This case underscores important considerations in managing B. canis exposure. With rising pet ownership in Singapore, veterinarians face increased occupational risk. Diagnosis is difficult, as B. canis lacks smooth lipopolysaccharide, rendering standard serology ineffective. Symptoms are non-specific, and definitive tests like rough lipopolysaccharide agglutination, PCR, or Karius testing are limited locally; cultures are slow and unreliable. Misdiagnosis may lead to inappropriate PEP. PEP may be justified after risk assessment. Greater clinician awareness and improved diagnostics are crucial for urban zoonotic preparedness.

CAS-075: The Paradox of Healing: Adult-Onset Still's Disease in the era of Human Immunodeficiency Virus Treatment

Nicholas Chan, Isaac Ng, Priscillia Lye, Sai Meng Tham

National University Health System

Introduction

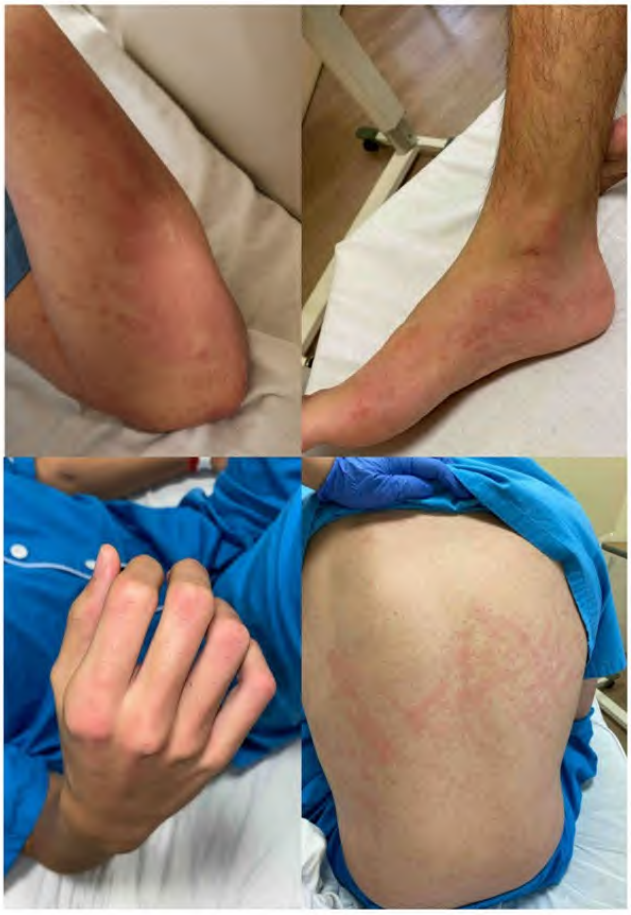
Adult-onset Still's disease (AOSD) is a rare systemic autoinflammatory disorder with unclear etiology, often presenting with fever, rash, and arthritis. Its pathogenesis may involve genetic, environmental, and infectious triggers. The role of immune dysregulation, particularly T-cell involvement, suggests a potential link with conditions such as Human Immunodeficiency Virus (HIV) infection.

Case Presentation

A 21-year-old Chinese male with recently diagnosed HIV presented with daily fevers for three months, accompanied by significant weight loss, migratory polyarthritis, and urticated plaques over the limbs and trunk (Figure 1). There were no focal infective symptoms, mucocutaneous ulcers, or recent exposures. He had no personal or family history of autoimmune disease or tuberculosis. Antiretroviral therapy (bictegravir, emtricitabine, tenofovir alafenamide) had been initiated six months earlier, resulting in an undetectable viral load and increased CD4 count (from 346 to 534 cells/μL) prior to symptom onset. Examination revealed urticated plaques and symmetric arthritis of large and small joints. Investigations showed neutrophilic leukocytosis, elevated inflammatory markers, transaminitis, and negative autoimmune and infectious screens. Imaging was unremarkable. AOSD was diagnosed based on Yamaguchi criteria and he responded well to corticosteroids and NSAIDs.

Conclusion

AOSD is a diagnosis of exclusion often associated with immune dysregulation. In this patient, symptom onset following immune recovery from antiretroviral therapy raises the possibility of immune reconstitution inflammatory syndrome (IRIS) unmasking AOSD. Increased T-cell activation post antiretroviral therapy may trigger autoinflammatory pathways. Clinicians should consider AOSD as a possible differential diagnosis in HIV patients presenting with fevers, joint pains and rashes after antiretroviral therapy initiation.



CAS-077: Catheter-Related Bloodstream Infection Caused by Chryseobacterium arthrosphaerae: The First Reported Case

Tomonori Takano[2], Shun Yamazawa[1], Hiroyuki Kunishima[2]

[1]St. Marianna University Hospital
[2]St. Marianna University School of Medicine

Introduction
Chryseobacterium species are non-fermenting, gram-negative bacilli commonly found in environmental sources. Although usually considered opportunistic pathogens, they have been increasingly implicated in healthcare-associated infections, particularly in immunocompromised patients or those with indwelling catheters. Here, we report the first documented case of catheter-related bloodstream infection (CRBSI) caused by Chryseobacterium arthrosphaerae.

Case Presentation
A woman in her 50s was admitted for pain management related to metastatic breast cancer. Her medical history included type 2 diabetes (HbA1c 6.1%) and neurogenic bladder secondary to spinal compression fractures from vertebral metastasis. On hospital day 11, she developed pyelonephritis and septic shock due to Escherichia coli, which was treated with meropenem for 10 days. On day 30, she experienced recurrent septic shock without an identifiable source. Since a peripherally inserted central catheter (PICC) had been in place for 21 days, CRBSI was suspected. Blood cultures and catheter tip cultures were obtained, and the PICC was removed. Chryseobacterium arthrosphaerae was isolated from the catheter tip and two aerobic blood cultures. TMP-SMX was initiated, later switched to piperacillin-tazobactam based on susceptibility results. After a 14-day course, the patient's condition improved, and she was discharged on day 61.

Conclusion
Reports of CRBSI due to Chryseobacterium species are rare, and this is the first case attributed to C. arthrosphaerae. Although some species have been associated with high mortality, susceptibility data are limited. This case highlights the need for further investigation into the pathogenic potential of rare Chryseobacterium species.

CAS-078: Atypical Co-Infection of Human Herpesvirus 7 Encephalitis in a Young Immunocompetent Female with Tuberculous Meningitis: A Diagnostic Challenge

Subashini Gunasegaran[1], Wan Nurliyana Wan Ramli[1], Nuratiqah Izzah Sharidon[1], Ainur Elliana Sohaimi[1], Mohd Aiman Saiful Suhardi[1], Mohd Noor Ismail[2], Muhammad Aiman Mohd Azhari[2], Radhiana Hassan[2], Mohd Ghaddafi Wahab[3], Sulaila Basiam[4], Nur Munirah Ibrahim[4], Dzawani Mohamad[4], Noorlina Noordin[4]

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Introduction

Human herpesvirus 7 (HHV-7) encephalitis is rare, particularly in immunocompetent individuals. While HHV-7 virus typically infects children and remains latent, reactivation in immunocompromised adults is more commonly reported. Its pathogenesis in central nervous system infections among immunocompetent hosts remains poorly understood.

Case Presentation

We report a case of a 21-year-old previously healthy female who presented with a two-weeks history of fever and symptoms suggestive of raised intracranial pressure, followed by acute behavioural changes. She exhibited signs of meningism with a positive Kernig's sign. Lumbar puncture revealed elevated opening pressure, lymphocytic pleocytosis, elevated protein, and a low serum:CSF glucose ratio. Empirical intravenous (IV) ceftriaxone and acyclovir were initiated, followed by escalation to IV meropenem due to persistent symptoms. Contrast-enhanced CT brain showed features of cerebritis. A positive Mantoux test and sustained fever led to empirical anti-tuberculosis therapy on day 7. Neuroimaging revealed non-communicating hydrocephalus, necessitating ventriculoperitoneal shunting and IV dexamethasone the next day. Despite treatment, the patient remained confused by day 9. MRI brain revealed bilateral temporal and frontal lobe hyperintensities with cerebral oedema and basal meningeal enhancement. CSF PCR was positive for HHV-7 and negative for Mycobacterium tuberculosis. A final diagnosis of HHV-7 encephalitis co-existing with tuberculous meningitis was made. The patient showed marked clinical improvement after five days of IV ganciclovir and completed a two-week antiviral course alongside planned six-month anti-TB therapy.

Conclusion

This case underscores the need to consider HHV-7 as a potential cause of refractory encephalitis, even in immunocompetent individuals, particularly when standard therapies fail.

CSF Summary	3 Feb 2025	6 Feb 2025	9 Feb 2025 (Omaya shunt)
Opening pressure	60cmH20	13cmH20	
Glucose	1.3	1.4	2.2
Protein	1.34	1.27	0.77
Albumin	659.7	700.3	397.4
Cell count	0	10	75
Neutrophil	0	10	10
Lymphocyte	0	0	65
C&S	No growth	No growth	-
Fungal C&S	No growth	-	-
MTB C&S	Negative	-	-
MTB PCR	-	Negative	-
AFB	Negative	-	-
Indian Ink	Negative	Negative	Negative
Cytology	No malignant cells		
PCR Panel			Human Herpes Virus 7 - Detected

CAS-079: A Case Report of Recurrent Steroid-Refractory Paradoxical Reactions in Tuberculosis in HIV-Negative Host: A Diagnostic and Therapeutic Challenge

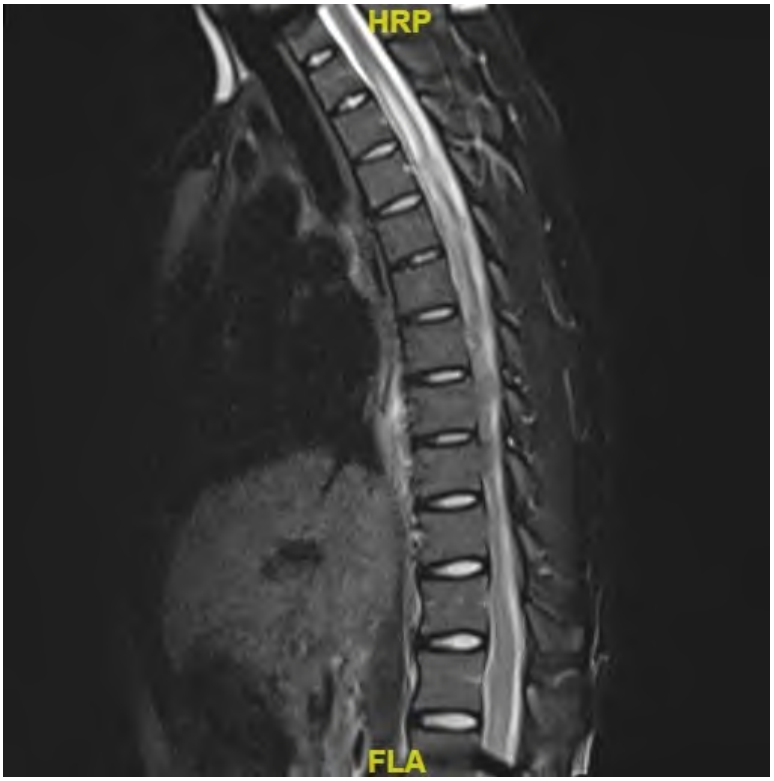
Lulu Nuari, Sofiati Dian, Sobaryati Sobaryati

Padjadjaran University

Introduction
Paradoxical reactions occur in 10–25% of HIV-negative tuberculosis (TB) patients, more frequently in extrapulmonary TB, particularly involving the central nervous system (CNS). They often present as new or worsening neurological deficits. While corticosteroids are typically effective, some cases are refractory. We report a recurrent, steroid-resistant paradoxical reaction, highlighting the need for alternative immunotherapy.

Case Presentation
A 25-year-old woman with HIV-negative pulmonary TB developed progressive bilateral lower limb weakness, urinary and fecal retention, and a thoracic sensory level two weeks after initiating anti-TB therapy, despite improvement of pulmonary symptoms. Neurological examination revealed nuchal rigidity, central cranial nerve palsies, and spastic paraplegia without sacral sparing. Cerebrospinal fluid showed pleocytosis and markedly elevated protein, with Marais score of 10, supporting TB meningitis. Spinal MRI demonstrated longitudinally extensive transverse myelitis from Th2–Th7 and arachnoiditis from Th2–Th12. Adequate anti-TB therapy and corticosteroids were continued, and intrathecal steroids were administered; however, spinal symptoms persisted, and severe central neuropathic pain developed one month post-discharge. A paradoxical reaction was suspected, prompting high-dose intravenous methylprednisolone, but no clinical improvement was observed. Although infliximab has shown promise in similar steroid-refractory cases, it was not pursued due to financial limitations and lack of insurance coverage.

Conclusion
This case highlights severe CNS paradoxical reactions in TB, where corticosteroids may fail to achieve optimal outcomes. Limited access to advanced immunotherapies remains a challenge in resource-limited settings. Clinical trials are needed to strengthen evidence and ensure broader therapeutic access within Indonesia's universal health coverage.



CAS-081: Secondary Central Nervous System Infection by Acinetobacter baumannii Following Intracranial Hematoma Evacuation: A Case Report and Diagnostic-Therapeutic Insights

Ling Chen, Wan Chen, Xiongfei He, Chao Luo, Huiyu Liao

Xindu District People's Hospital of Chengdu

Introduction

Central nervous system (CNS) infection after intracranial hematoma evacuation, especially those caused by multidrug-resistant organisms, is associated with poor prognosis and poses significant therapeutic challenges. Acinetobacter baumannii is a common nosocomial pathogen.

Case Presentation

A 41-year-old male with a history of hypertension was admitted due to sudden onset of impaired consciousness and urinary incontinence. Cranial CT revealed a large hematoma in the left frontal lobe and basal ganglia, with intraventricular and subarachnoid hemorrhage. Emergency hematoma evacuation, cranioplasty, and dural repair were performed, with prophylactic ceftriaxone administered postoperatively. On postoperative day 3, the patient developed high fever; blood and BALF cultures were negative. Pulmonary infection was later suspected and piperacillin-tazobactam was administered, with BALF cultures yielding Escherichia coli and Enterobacter cloacae. After pulmonary improvement, antibiotics were discontinued, but recurrent fever prompted a switch to meropenem. CSF analysis indicated CNS infection, and vancomycin was added. CSF TNGS identified A. baumannii, leading to cefoperazone-sulbactam combined with intravenous and intrathecal polymyxin B. The patient's temperature and CSF parameters improved. During treatment, electrolyte disturbances, coagulopathy, and hepatic and renal dysfunction occurred, managed with supportive care and CRRT. Antibiotics were discontinued after CSF normalization. The patient recovered and was discharged, currently able to live independently.

Conclusion

Rapid pathogen identification is crucial in complex CNS infections. When cultures are negative, TNGS can promptly guide targeted therapy. Vigilance for drug-related adverse effects and multidisciplinary collaboration are essential for optimizing outcomes.

	10-25	10-28	11-06	11-09	11-11	11-12	11-13	11-15	11-16	11-17	11-19	11-26	12-01	12-05
Body Temperature (°C)	39.4	38.4	36.7	38.9	39	38.2	39	38	37	36.8	36.6	38.5	36.4	37
CSF Nucleated Cell Count (106 /L)		911			15060		10974	10490	880	2200	540	310	84	22
CSF Neutrophil Percentage (%)		90			92		95	92	98	90	84	79	60	10
CSF Total Protein (mg/L)		10079.8			4382.16		4299.44	4710.4	7380	6196.61	4360.67	2947.67	3283.29	1392.73
CSF Glucose(mmol/L)		2			0.1		0.2	0.3	0.9	1.1	1.7	3.5	3.4	3.6
Blood White Cell Count (109/L)	8.11	10.5	10.96	17.83	15.1					7.46	7.85	12.3	10.45	9.45
C-Reactive Protein (mg/L)	251.21	308.27	12.58		157.3							166.15	102.5	23.3
Procalcitonin(ng/L)	0.15	0.22	0.05	0.09						0.09	0.1	0.45	0.24	0.09
CSF Targeted Next-Generation Sequencing (Sequence Count)						Acinetobacter baumannii (46)		Acinetobacter baumannii (20)					Acinetobacter baumannii (12)	Acinetobacter baumannii (1)
Blood Culture							Negative						Negative	Negative
CSF Culture												Negative	Negative	Negative
Bronchoalveolar Lavage Culture			Enterobacter cloacae and Escherichia coli											

CAS-082: Mpox in Patients Seen at the Research Institute for Tropical Medicine: A Case Series

L. Angelique Gene Duran, Adrian Kevin Agonoy, Christine Lyka Sayson, Lorrie Suzette Urbano-Cruz, Mark Kristoffer Pasayan, Marie Socouer Oblepias

Research Institute for Tropical Medicine

Introduction
WHO declared the mpox outbreak a public health emergency of international concern twice in 3 years, in July 2022 and August 2024. To date, the Philippines has reported 15 confirmed cases. We described the demographics, presentations, transmission risks, outcomes, and viral genetic clades of confirmed mpox cases seen in our institution.

Case Presentation
Data was obtained from cases seen and confirmed by RT-PCR at the Research Institute for Tropical Medicine's Special Pathogens Laboratory. Analyses were descriptive.

Six cases in this report were five cisgender men who have sex with men—three were known to be living with HIV with good virologic response to ART—and one cisgender female. The median age was 31 years old. Two were documented to have traveled internationally prior to symptoms.

The cases commonly presented with any rash (100%), fever (100%), malaise (100%), genital rash (67%), localized lymphadenopathy (16.67%), and headache (16.67%). All skin lesions were umbilicated, presenting as vesicles (100%), papules (83%), or pustules (50%).

Secondary bacterial skin infections were reported in two cases. Sequelae included post-inflammatory hyperpigmentation and scarring of previous lesions. There were no severe complications nor deaths. Genetic analysis identified all cases belonging to MPXV clade II.

Conclusion
This case series highlighted the disproportionate impact of mpox on young MSM and PLHIV, consistent with global trends. Most PLHIV experienced mild disease, emphasizing the protective effect of antiretroviral therapy. Despite the small sample size, the study emphasizes the need for ongoing surveillance, early diagnosis, and targeted public health interventions to reduce transmission in high-risk groups.

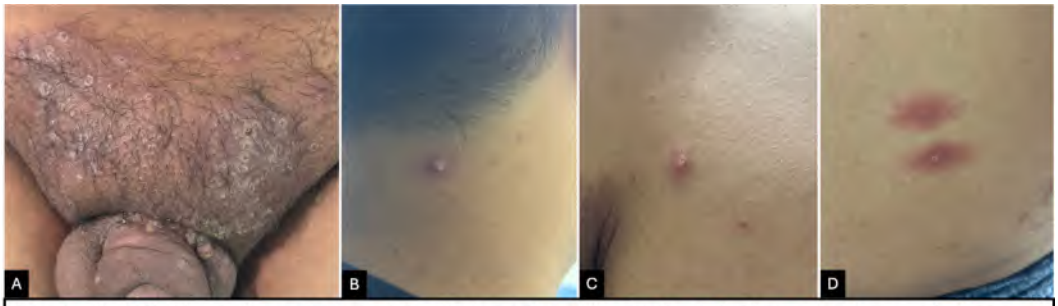


Figure 1. Multiple erythematous umbilicated papules with purulent discharge on the penile base (A). Erythematous umbilicated papules on the nape (B), upper trunk (C), and abdomen (D).

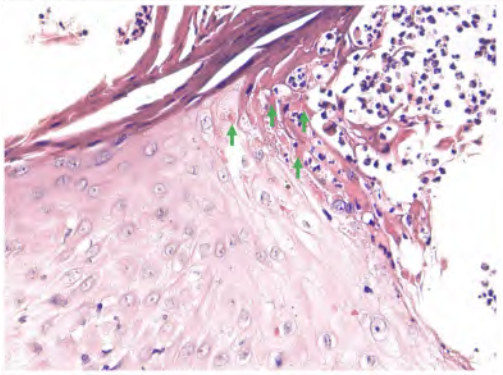


Figure 2. Guarnieri bodies (green arrows) (H&E, 40x)

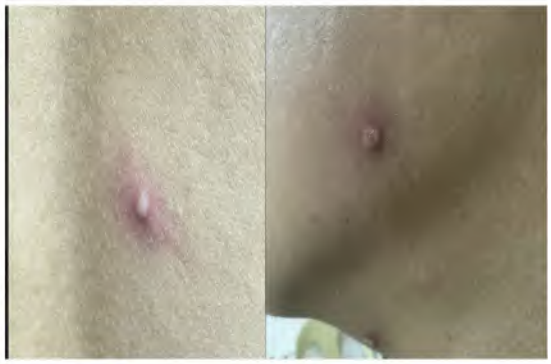


Figure 3. A solitary erythematous ulcer with purulent discharge on the penile base

CAS-083: A Giant Hepatic Abscess in an Immunocompetent Female: A Rare Presentation with an Unusual Pathogen

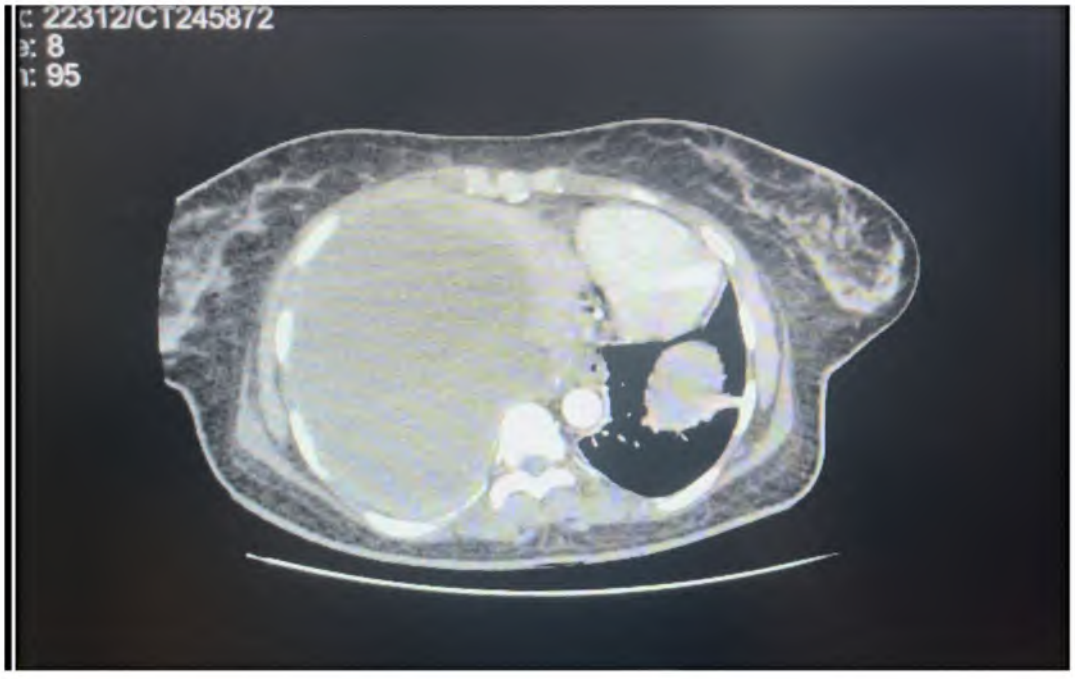
Essel Bangalando, Dehuel Cuyacot, Gamaliel Garcia

Negros Oriental Provincial Hospital

Introduction
Hepatic abscesses are rare in healthy individuals and may mimic thoracoabdominal conditions, delaying diagnosis. While most are polymicrobial and occur in high-risk hosts, this case describes a giant pyogenic liver abscess in a previously healthy female, with over two liters of purulent drainage—highlighting the need for clinical vigilance even in low-risk patients.

Case Presentation
A 41-year-old immunocompetent, non-smoking, non-alcoholic female presented with a two-week history of non-productive cough, malaise, and anorexia, progressing to fever, dyspnea, and right upper quadrant pain. She was tachycardic and tachypneic; hepatomegaly and decreased right breath sounds were noted. Laboratory workup showed leukocytosis and anemia. Chest radiograph revealed a right pleural effusion. Abdominal ultrasound detected a hepatic fluid collection; contrast-enhanced CT confirmed a ring-enhancing hepatic abscess (15×12×22 cm). Percutaneous drainage yielded 2,138 mL of thick pus. Despite limited access to prolonged targeted therapy, the patient improved and was discharged in stable condition. Culture revealed methicillin-resistant Staphylococcus haemolyticus, an uncommon hepatic abscess pathogen.

Conclusion
This is one of the largest reported hepatic abscesses in an immunocompetent adult. Timely imaging and drainage were critical to recovery. This case underscores that even in the absence of traditional risk factors, pyogenic liver abscesses may evolve into massive, life-threatening infections. It highlights the necessity of maintaining a high index of suspicion in patients with nonspecific thoracoabdominal symptoms and supports the critical role of early imaging and intervention. Prompt percutaneous drainage, even in resource-constrained settings, can significantly improve patient outcomes and should be considered a priority in the management algorithm.



CAS-086: Enterococcus and Tuberculous CNS Co-Infection in an Immunocompetent Female – A Case Report

L. Angelique Gene Duran, Aneriza Lim-Angeles, Lorrie Suzette Urbano-Cruz

Research Institute for Tropical Medicine

Introduction

Central Nervous System (CNS) co-infection with Mycobacterium Tuberculosis (MTB) and Enterococcus species is rare, especially among immunocompetent individuals. We report the first documented case of concurrent Enterococcus faecalis meningitis and tuberculous meningitis (TBM) in a healthy adult female with presumed ocular tuberculosis that was successfully managed with medical therapy alone without the need for surgical intervention.

Case Presentation

A 29-year-old Filipino female presented with subacute fever, behavioral changes, and progressive somnolence. On admission, she had nuchal rigidity and a decreased Glasgow Coma Scale (GCS), nuchal rigidity, and headache. Cerebrospinal fluid analysis revealed lymphocytic pleocytosis, hypoglycorrhachia, and elevated protein. Cefepime was initiated alongside anti-tuberculosis treatment (isoniazid, rifampicin, pyrazinamide, and ethambutol); however, the patient showed a suboptimal clinical response, with persistent nuchal rigidity and headache. GeneXpert MTB/RIF detected drug-susceptible Mycobacterium tuberculosis, while CSF culture grew Enterococcus faecalis through Brain Heart Infusion broth. Fundoscopic examination revealed a subretinal choroidal tubercle, suggestive of ocular tuberculosis and disseminated disease. Targeted therapy was initiated with intravenous ampicillin, which resulted in marked clinical improvement, including normalization of GCS and resolution of CNS symptoms.

Conclusion

Clinicians should maintain a high index of suspicion for CNS co-infections when patients have atypical presentations of meningitis, especially in TB-endemic settings. This case highlights the critical importance of microbiologic confirmation, timely shift to targeted therapy, and neurologic monitoring. Clinical recovery without surgical intervention and the patient's improved GCS following appropriate treatment emphasize the value of early recognition and organism-specific management.

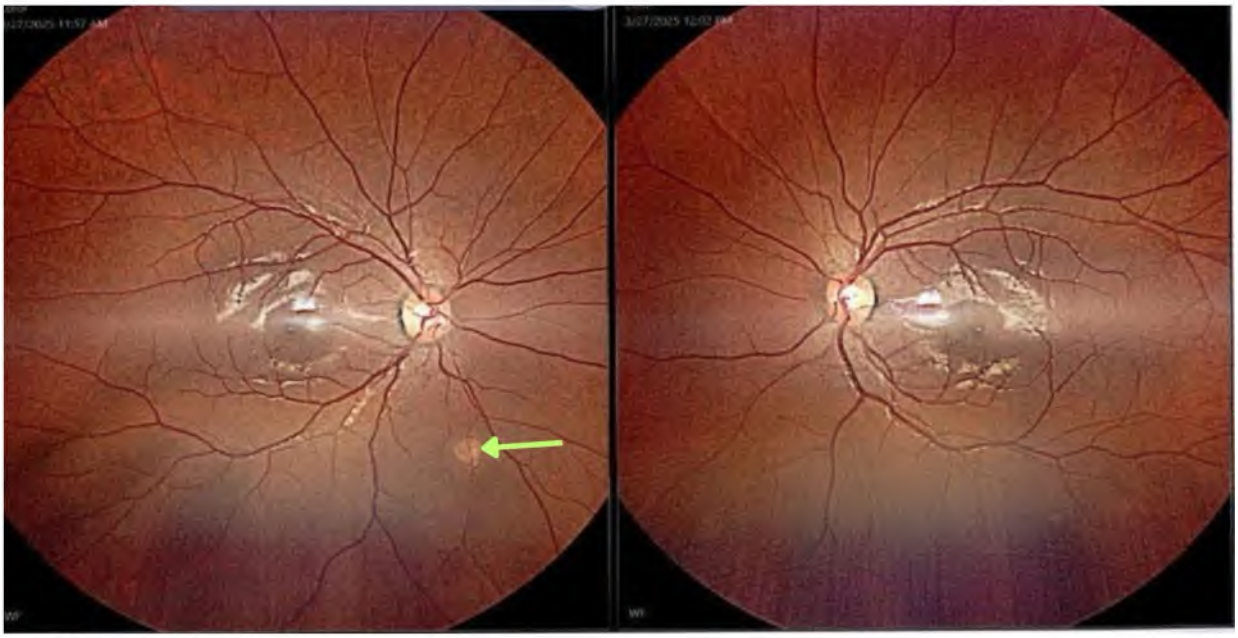


Figure 1.
Subretinal choroidal tubercle (arrow), identified on fundoscopic examination, consistent with ocular tuberculosis.

CAS-087: Analysis of Published Case Studies Evaluating Brincidofovir as a Potential Antiviral Treatment for Mpox Clade II Infections

Kevin Yeo[1], David Cassie[2]

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Introduction

Mpox is a systemic infection caused by the mpox virus (MPXV; formerly monkeypox) and is currently listed as a Public Health Emergency of International Concern (PHEIC) by the World Health Organization (WHO). To date, no antiviral has demonstrated efficacy in the treatment of mpox in humans. Brincidofovir (BCV) is a lipid-modified acyclic nucleotide with in vitro and in vivo activity against MPXV clades I and II. Intracellularly, BCV is phosphorylated to cidofovir-diphosphate, a viral DNA polymerase inhibitor. BCV is only licensed in the U.S. and Canada for the treatment of smallpox. It has been used under FDA-authorized emergency use for severe mpox patients in the U.S.

Presentation

Based on a pubmed search, we identified and reviewed 26 published clade II case reports from May 2022 – June 2025 and interpreted to assess future clinical evaluation of BCV in mpox. The use of BCV as either monotherapy, or in combination with cidofovir, Vaccinia Immunoglobulin Intravenous (VIGIV), or tecovirimat (TCV), in 16 patients resulted in healing and/or absence of new lesions, and improvements in clinical symptoms. Five patients that received BCV monotherapy had mpox recovered, with reduced pain, crusting lesions and absence of fever within 72 hours. Most patients (21/26) had HIV and were immunocompromised.

Conclusion

BCV has been reported to be synergistic with TCV in orthopoxviral infections, with future clinical evaluation being considered. BCV is being evaluated in a randomized, double-blind, placebo-controlled trial in the Democratic Republic of Congo (DRC), in adults and pediatrics with Clade I mpox (PACTR202405860723287).

Subject	Age	Mpox Lesions	Underlying Diagnosis	First Line Treatment	Other Treatment	BCV Doses, n	Complications	BCV Adverse Events	Outcome	Source (Location)
1	37	Necrotic confluent lesions of face, torso, digits	HIV/AIDS	TCV, BCV, VIGIV	ART	NR	NR	NR	Recovered	[1] (USA)
2	30-40	Face, scalp, trunk, limbs, palms, genitals	None	BCV	NR	1	Ulcerated inguinal lesion	Transaminitis	Recovered	[2] (United Kingdom)
3	30-40	Face, scalp, trunk, limbs, palms, soles, genitals	None	BCV	Broad spectrum antibiotics, drainage	2	Deep tissue abscess	Transaminitis	Recovered	
4	30-40	Face, trunks, hands, labia	None	BCV	Antibacterial eye drops	2	Subungual lesion, conjunctivitis	Transaminitis	Recovered	
5	30	Face, oral cavity, torso, extremities, genitals	Renal transplant	BCV	Acyclovir, piperacillin-tazobactam, doxycycline	2	Tonsillitis with airway compromise	NR	Recovered	[3] (Saudi Arabia)
6	25	Widespread vesicular rash	Renal transplant	BCV	Acyclovir, piperacillin-tazobactam, doxycycline	2	Proctitis	NR	Recovered	
7	50	Papulonecrotic plaques face, trunk, extremities, genital plaques	HIV/AIDS	TCV, VIGIV, CDV, BCV, intralesional CDV	NR	NR	NR	NR	Recovered	[4] (USA)
8	35	Ulcers nose, finger, soles, abdomen, anogenital	HIV/AIDS	TCV	ART, CDV, VIGIV, BCV	6	NR	NR	Recovered	[5] (USA)
9	33	Widespread coalescent necrotic skin lesions	HIV/AIDS	TCV	BCV, VIGIV, vancomycin, cefepime, linezolid, meropenem	2	Hand and eye swelling, pulmonary nodules, pleural effusion	NR	Death	[6] (USA)
10	51	Necrotic plaques face; pustules tongue, extremities, trunk, scrotum, perianal area; eschars hands	HIV/AIDS	TCV, VIGIV	ART, broad spectrum antibiotics, BCV	2	altered mental status, proctitis, rectal bleeding, respiratory failure, sepsis	Transaminitis (prior to BCV)	Death	[7] (USA)
11	27	Coalescent necrotic facial plaques; finger necrosis; lesions on back, perianal area, nose, extremities, nasal septum, tongue, pharynx	HIV/AIDS	TCV	ART, valacyclovir, VIGIV, BCV	1	Proctitis, rectal bleeding, perianal HSV, renal failure, seizure, respiratory failure, sepsis	NR	Death	
12	30s	Verrucous plaques palm, forearm, foot	HIV/AIDS	TCV	ART, oral antibiotics, debridement, BCV	2	NR	Transaminitis	Recovered	[8] (USA)

13	43	Hand, face, arm, leg and tongue lesions	HIV/AIDS	TCV	VIGIV, BCV	2	Pneumonia, pleural effusion	NR	Recovered	[9] (USA)
14	NR	NR	HIV/AIDS	TCV	BCV, VIGIV, CDV (IV, topical and intralesional)	4	NR	NR	NR	[10] (USA)
15	20s	Diffuse, necrotic skin and oropharyngeal lesions	HIV/AIDS	TCV	ART, VIGIV, BCV	2	Renal failure, sepsis	NR	Death	[11] (USA)
16	38	Necrotic facial and disseminated skin lesions; pulmonary nodules	HIV/AIDS	TCV, CDV, VIGIV, BCV	ART, broad spectrum antibiotics	NR	Syphilis	NR	Recovered	[12] (USA)
17	29	Disseminated skin lesions; pulmonary nodules	HIV/AIDS	TCV	CDV, VIGIV, BCV	NR	Syphilis	NR	Recovered	
18	28	Genital skin lesions	HIV/AIDS	TCV	ART, VIGIV, BCV, prednisone, broad spectrum antibiotics	1	Possible IRIS; encephalopathy, acute kidney injury, tenosynovitis	NR	Death	[13] (USA)
19	31	Entire body, genitalia	HIV/AIDS, diabetes mellitus	TCV	ART, CDV, VIGIV, BCV	1	Possible IRIS; scrotal infection, penile strictures, wrist swelling	NR	Recovered	
20	38 (26-63)	NR	HIV/AIDS	TCV	BCV	NR	NR	NR	NR	[14] (USA)
21		NR	HIV/AIDS	TCV	BCV	NR	NR	NR	NR	
22		NR	HIV/AIDS	TCV	BCV	NR	NR	NR	NR	
23		NR	HIV/AIDS	TCV	BCV	NR	NR	NR	NR	
24	35	Abdomen, finger, scrotum	HIV/AIDS	TCV	ART, CDV (IV, topical), VIGIV, BCV	1	Proctocolitis	NR	Recovered	[15] (USA)
25	38	Face, perianal, arms, legs, chest, truck and back lesions, diffuse vesicles, postules, crusted ulcerated papules with seroszanguinous drainage, and excoriations	HIV/AIDS	TCV	BCV	4	Syphilis	NR	Recovered	[16] (USA)

CAS-088: When a Sore Throat Takes a Sinister Turn

Krison Sum, Wilson Goh

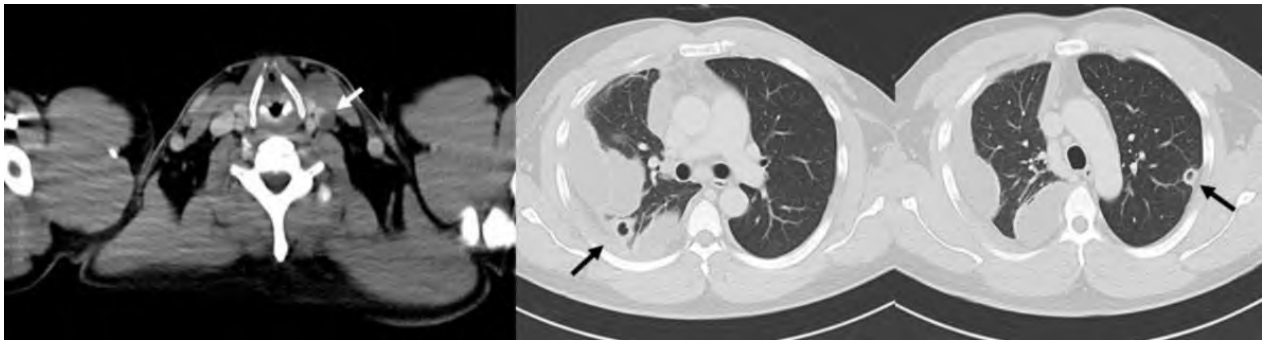
MOHH

Introduction
Lemierre's Syndrome is an uncommon but potentially life-threatening complication of oropharyngeal infections, most often affecting healthy young adults. It is characterized by septic thrombophlebitis of the internal jugular vein, typically caused by Fusobacterium necrophorum. Hematogenous spread may result in septic emboli, particularly in the lungs, and can also involve joints, bones, liver, or brain. Timely diagnosis and prompt initiation of treatment are crucial to reducing morbidity and mortality.

Case Presentation
A 38-year-old previously healthy man presented with a 4-day history of sore throat and fever. He was initially diagnosed with viral pharyngitis and treated symptomatically. His condition deteriorated, and he re-presented to the Emergency Department with rigors, haemoptysis, and pleuritic chest pain. On examination, he was febrile (39°C), tachycardic (120 bpm), and had oxygen saturation of 90% on room air. He appeared lethargic, with right-sided chest crepitations. Chest radiograph revealed right lower lobe consolidation and a loculated pleural effusion. Blood tests showed leukocytosis (32.8 × 10^9/L); blood cultures were negative.

Contrast-enhanced CT of the thorax (Figure 1) revealed left internal jugular vein thrombosis (white arrow), multiple cavitary pulmonary nodules, and a multiseptated right empyema (black arrows). Pleural fluid anaerobic culture grew Fusobacterium necrophorum, confirming Lemierre's Syndrome. The patient underwent surgical drainage and decortication, followed by targeted antibiotic therapy, resulting in full clinical recovery.

Conclusion
This case underscores the need for clinical vigilance when pharyngeal infections fail to resolve or worsen. Imaging and microbiologic confirmation are critical for diagnosis. While antibiotics and drainage are standard, the role of anticoagulation remains debated.



CAS-089: From Kitchen to Catastrophe: Necrotising Fasciitis Due to Vibrio vulnificus After Crab Handling

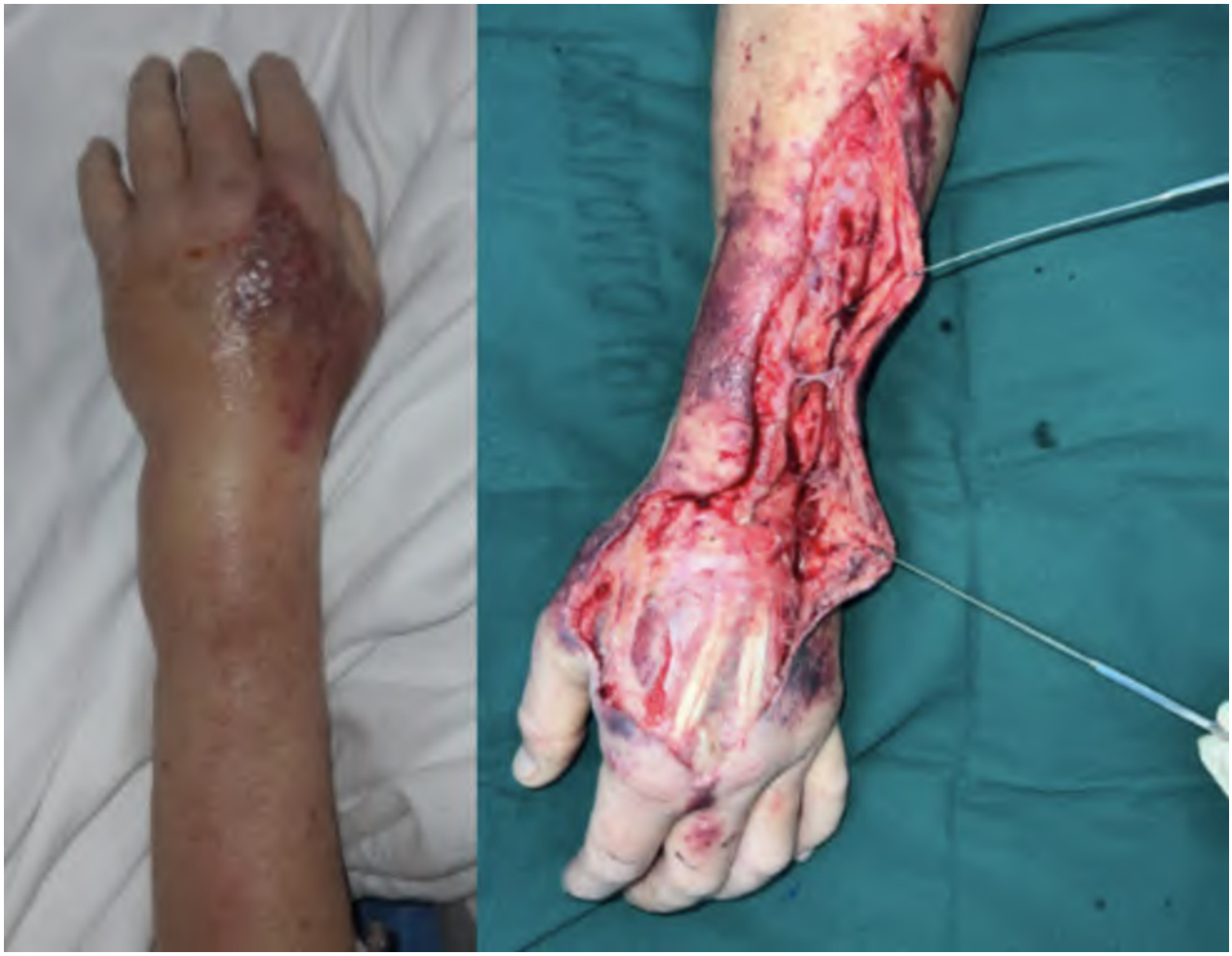
Krison Sum, Wilson Goh

MOHH

Introduction
Necrotising fasciitis is an uncommon but life-threatening soft tissue infection, with an incidence of 0.3–1.3 cases per 100,000 in developed countries. However, significantly higher rates—up to 15.5 per 100,000—are reported in Southeast Asia. One contributing factor is the cultural and occupational exposure to raw or live seafood, which increases the risk of Vibrio vulnificus infections, particularly among individuals with chronic illnesses or frequent seafood handling.

Case Presentation
A 64-year-old man with poorly controlled diabetes and a history of previous hepatitis B presented with acute right-hand pain, swelling, and erythema one day after being cut by a crab shell while cooking. On arrival, he was febrile (38.2 °C) and hypotensive (BP 80/50 mmHg). Laboratory findings included leukocytosis (21 × 10^9/L) and elevated CRP (55 mg/L); LRINEC score was 2. Empirical intravenous benzylpenicillin, clindamycin, and ceftazidime were initiated. Surgical debridement and fasciectomy were performed (Figure 1), and intraoperative cultures identified Vibrio vulnificus. Antibiotics were subsequently adjusted to IV ceftriaxone and oral doxycycline. The patient underwent further debridement and skin grafting, leading to full recovery.

Conclusion
This case highlights the need for early recognition and management of necrotising fasciitis, particularly in patients with seafood-related injuries. It underscores the importance of considering V. vulnificus in soft tissue infections associated with shellfish. Additionally, this case questions the diagnostic utility of the LRINEC score in Vibrio-associated necrotising fasciitis, where values often fall below the threshold of 6. Preventative education for high-risk groups is also warranted.



CAS-090: A Rare Case of Pyrazinamide-Induced Warm Autoimmune Haemolytic Anaemia and Polyuria in a HIV-negative Patient with Pulmonary Tuberculosis and Dual Malignancies

Wen Jie Lau

Bintulu Hospital, Sarawak, Malaysia

Introduction

Pulmonary tuberculosis (PTB) remains endemic in Malaysia, with higher prevalence among immunocompromised patients. Common adverse effects of antituberculosis therapy (ATT) typically include rash and hepatotoxicity. We present a unique case of smear-positive PTB with a rare constellation of adverse drug reactions against the backdrop of newly diagnosed dual malignancies.

Case Presentation

A 58-year-old man was diagnosed with smear- and culture-positive PTB in February 2025 and initiated on standard ATT. He developed ethambutol-induced maculopapular rashes after one month, prompting regime modification to HRZ. In May 2025, he presented with warm autoimmune haemolytic anaemia (AIHA) and significant polyuria (~6-7L/day). Polyuria resolved following pyrazinamide withdrawal, confirmed by normalised urine osmolality and retrospective analysis of fluid balance during prior sequential ATT rechallenge. Notably, AIHA also resolved without further transfusions. ATT was adjusted to HRO for 9 months. Further evaluation of violaceous skin lesions and generalized lymphadenopathy via biopsies revealed Kaposi sarcoma and classical Hodgkin lymphoma respectively. Viral screening was repeatedly negative. Prior to chemotherapy initiation, he developed invasive fungemia requiring intravenous amphotericin B. A CTPA performed due to difficulty weaning from oxygen revealed a “crazy-paving” pattern, prompting empiric treatment for Pneumocystis jirovecii pneumonia with trimethoprim-sulfamethoxazole, resulting in clinical improvement. Monthly sputum TB cultures have remained negative since April 2025.

Conclusion

Pyrazinamide-induced warm AIHA and polyuria are exceedingly rare, and their resolution upon drug withdrawal supports causality. This case highlights the importance of considering dual pathologies in PTB patients with typical features. A multidisciplinary approach was essential to navigate the diagnostic and therapeutic complexities in this immunocompromised patient.

Timeline of clinical events, diagnostics, interventions and associated outcomes

Month	Clinical events	Findings	Intervention	Outcome
February 2025	Diagnosed with smear- and culture positive PTB	CXR: Right middle zone infiltrates	Started standard ATT (EHRZ)	Initial response
March - April 2025	Rash onset	Generalized maculopapular rash	Ethambutol stopped, continued with HRZ	Rash resolved
Middle May 2025	Anaemia and polyuria (~6-7L/day)	Hb ↓, haemolytic markers raised, DAT: IgG 3+, c3D 3+; cold agglutinin test negative	Pyrazinamide withdrawn	Polyuria and AIHA resolved
June 2025	Violaceous skin lesions and generalized lymphadenopathy	Skin biopsy: Kaposi Sarcoma; right cervical LN biopsy: classical Hodgkin Lymphoma	Oncology and haematological referral	Awaiting chemotherapy
July 2025	Invasive fungemia	Left tonsil biopsy: numerous hyphae and yeast elements seen	IV Amphotericin 2 weeks followed by tablet fluconazole	Clinical improvement
July 2025	Unable to maintain saturation under room air	CTPA: worsening bilateral consolidations of the lungs and chronic changes with new onset of “crazy-paving” pattern	TMP-SMX empirically started for Pneumocystis jirovecii pneumonia	Improved oxygenation
February - July 2025	Ongoing sputum surveillance	Smear converted since March 2025, monthly sputum TB cultures have remained negative since April 2025	Planned for a 9-month course of HRO	Stable under modified ATT

Abbreviations: PTB: pulmonary tuberculosis; CXR: chest radiograph; ATT: antituberculosis therapy; EHRZ: ethambutol, isoniazid, rifampicin, pyrazinamide; Hb: haemoglobin; DAT: direct antiglobulin test; IgG: immunoglobulin G; AIHA: autoimmune haemolytic anaemia; LN: lymph node; IV: intravenous; CTPA: computed tomography pulmonary angiography; TMP-SMX: trimethoprim-sulfamethoxazole; HRO: isoniazid, rifampicin, ofloxacin

CAS-091: Severe Multi-Drug Hypersensitivity and Hepatotoxicity During Antituberculosis Therapy: A Management Challenge

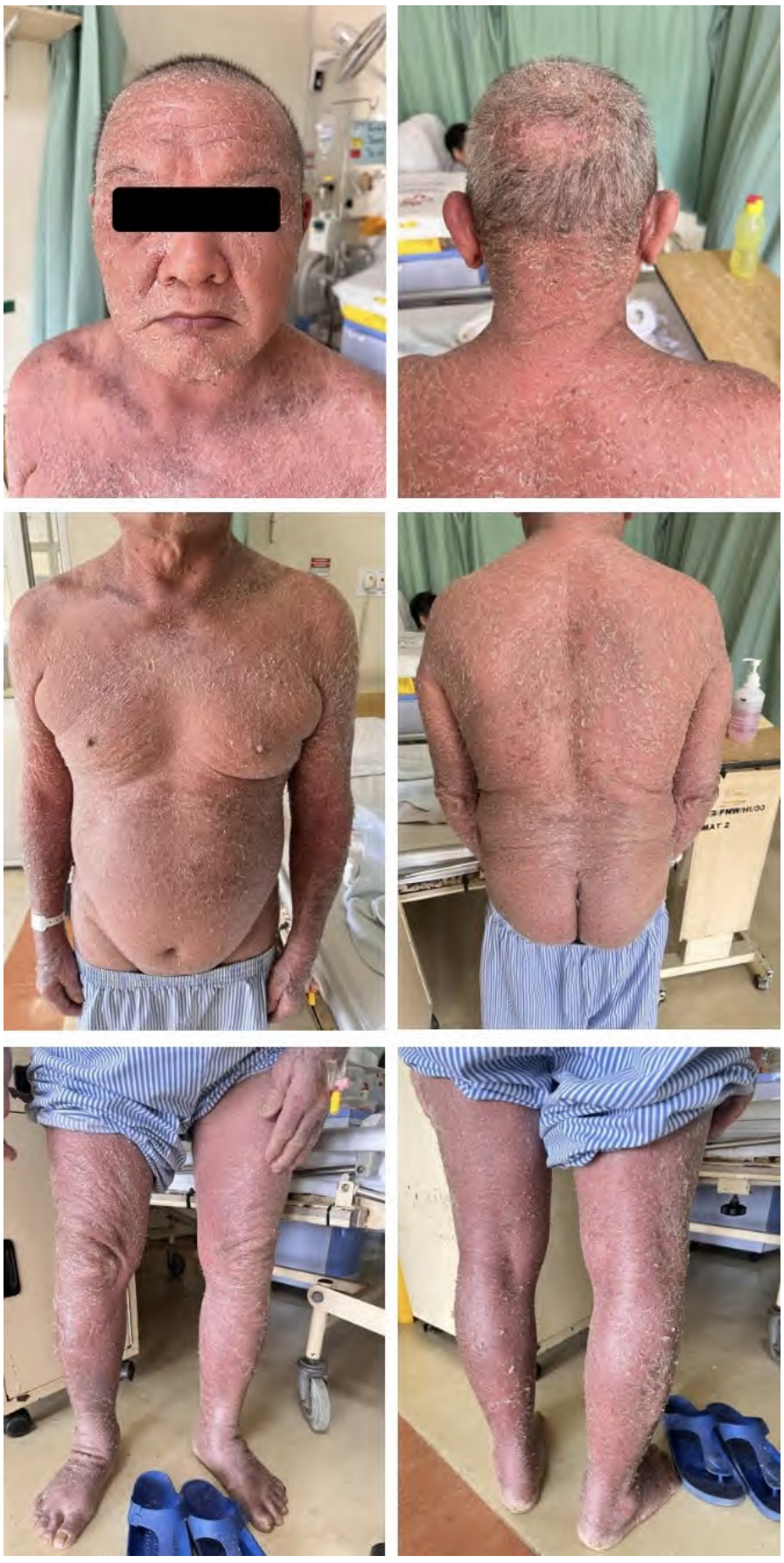
Wen Jie Lau

Bintulu Hospital, Sarawak, Malaysia

Introduction
Pulmonary tuberculosis (PTB) is commonly treated with first-line antituberculosis therapy (ATT), comprising rifampicin, isoniazid, ethambutol and pyrazinamide. While generally effective and well tolerated, ATT may rarely trigger severe cutaneous adverse drug reactions (SCARs), such as exfoliative dermatitis (ED), typically attributed to a single agent. We report a rare case of ED involving multiple first-line agents and ofloxacin, further complicated by pyrazinamide-induced liver injury, presenting a major therapeutic challenge.

Case Presentation
A 67-year-old man with underlying COPD GOLD E was diagnosed with smear-negative, culture-positive, pan-sensitive PTB in October 2024. Viral screening was non-reactive. Baseline chest radiograph showed minimal disease. He was started on fixed-dose first-line ATT. After completing the 2-month intensive phase, he developed a generalized erythematous, scaly, pruritic rash across the entire body, prompting ATT discontinuation and hospitalization in February 2025. Laboratory parameters revealed eosinophilia without liver or kidney impairment. Skin biopsy confirmed ED. Systemic corticosteroids were initiated. Individual drug rechallenge after rash resolution revealed recurrence of ED with rifampicin, isoniazid, ethambutol and ofloxacin. Additionally, pyrazinamide rechallenge resulted in drug-induced liver injury (DILI). He was transitioned to a second-line regime of clofazimine, cycloserine and linezolid by July 2025. Serial sputum TB cultures remained negative.

Conclusion
This case highlights a rare, severe hypersensitivity to nearly all first-line ATT agents, compounded by pyrazinamide-induced hepatotoxicity. Management required immediate drug withdrawal, prolonged corticosteroid use, cautious rechallenge and eventual shift to second-line therapy, raising the risk of dissemination, treatment failure and steroid-related complications. It underscores the importance of individualized, multidisciplinary care in managing extensive SCARs during TB treatment.



CAS-094: Hidden Threats: Dematiaceous Fungi as Emerging Agents of Pulmonary Infection - A Case series

Pratiksha Kamboj[1], Sowjanya Perumalla[2], Amber Prasad[2], Minakshi Singh[2], Binal Mangroliya[2]

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Introduction
Pulmonary phaeohyphomycosis represents a rare yet clinically significant manifestation of fungal lung disease, predominantly affecting immunocompromised individuals. Interestingly, isolated cases have also emerged in immunocompetent hosts, underscoring its unpredictable nature. The presentation is often subtle and non-distinct, frequently mirroring common respiratory infections such as bacterial pneumonia, making early identification and accurate diagnosis a challenge. This diagnostic ambiguity can hinder prompt therapeutic intervention, emphasizing the need for heightened clinical vigilance. We hereby present a series of 5 cases in the past one year (2024-2025).

Case Presentation
Five male patients presented to AIIMS Rishikesh with pulmonary complications linked to various underlying risk factors including bronchiectasis, pulmonary tuberculosis, lung carcinoma and diabetes. Occupational backgrounds varied, suggesting no singular occupational link. Respiratory samples were analyzed and the laboratory findings identified several dematiaceous and opportunistic fungi as causative agents. With the right diagnosis and following antifungal treatment, patients exhibited notable clinical recovery and were subsequently discharged in stable condition. Their commitment to regular follow-up allowed for continued monitoring, with progressive improvement observed both symptomatically and radiologically.

Conclusion
The emergence of clinically significant dematiaceous fungi in the foothills of Indian Himalayan region marks an important shift in the landscape of pulmonary mycoses. Early and accurate diagnosis is essential for guiding effective antifungal therapy, as delays can lead to adverse outcomes. Strengthening diagnostic capabilities and clinician preparedness will be critical in improving patient care and managing the growing burden of fungal diseases.

CAS-095: False Positive Result in Urinary TB LAM Test among HIV Patients with Disseminated Nocardiosis: A Case Report

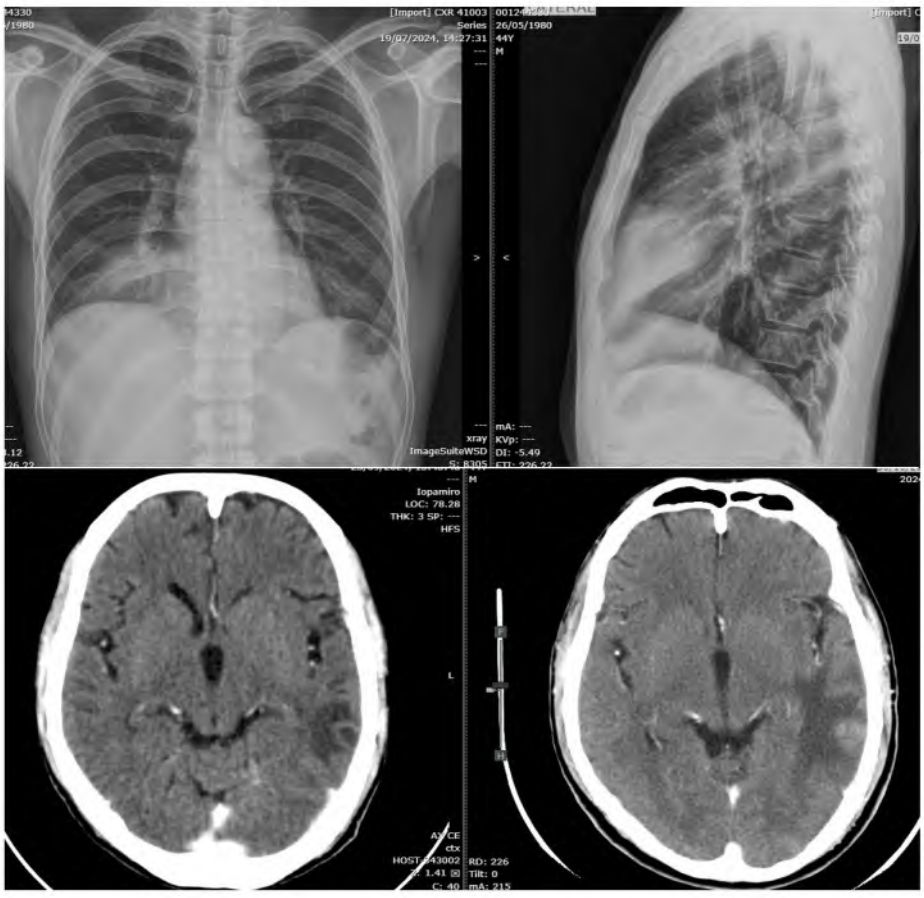
Laddarat Srikham

Sakon Nakhon Hospital, Kasetsart University

Introduction
Lipoarabinomannan (LAM) is M. tuberculosis cell wall component. A point-of-care lateral flow assay was detected LAM in urine, these testing could improve TB diagnosis in HIV patients. Higher sensitivity and specificity were in HIV-infected patients with CD4 cell counts below 100 cells/mm3.

Case Presentation
A 44-year-old Thai man from Sakon Nakhon. Six-weeks prior, He had productive cough with chest discomfort. He was diagnosed with pneumonia and treated with cefixime but clinical did not improved. Four-weeks prior, he had progressive of productive cough. On the day of admission, he had shortness of breath. Physical examination showed temperature of 38°C, RR 24-bpm, PR 100-bpm, BP 110/60 mmHg, fine crepitation at right lower-lung, no hepatosplenomegaly, skin show pruritic papular eruption and no neurological deficit. A Chest-radiograph showed consolidation at right middle lung (Figure 1). Sputum AFB, mAFB and PCR for TB were negative. Anti-HIV was positive and CD4 count 24 cells/mm3. Urine LAM was positive. A bronchoalveolar lavage (BAL) was performed, BAL-fluid for gram stain, AFB, PCR for TB were negative, but mAFB demonstrates positive filamentous branching beaded-like organism. CT-Brain was performed, showed ring enhancing hypodense lesion size 1.4x1.1 cm. at left temporal lobe (Figure 2). The BAL-fluid culture final growth Nocardia spp. The patient was given co-trimoxazole and imipenem for 4 weeks and discharged with oral co-trimoxazole. After 3-months of co-trimoxazole, his chest-radiograph was significant improvement.

Conclusion
Urine LAM can be false-positive results with several conditions like Non-tuberculous-mycobacterial infections, nocardiosis and cryptococcosis. Clinical signs and symptoms should be correlated, and caution should be exercised in interpreting TB LAM results.



CAS-097: When Microbes Work Together: The Importance of Clinical Microbiology in Diagnostic Stewardship and The Challenges of Polymicrobial Infections in Descending Necrotizing Mediastinitis

Eka Cania B, Febi Arfini, Amin Soebandrio

Faculty of Medicine, University of Indonesia

Introduction

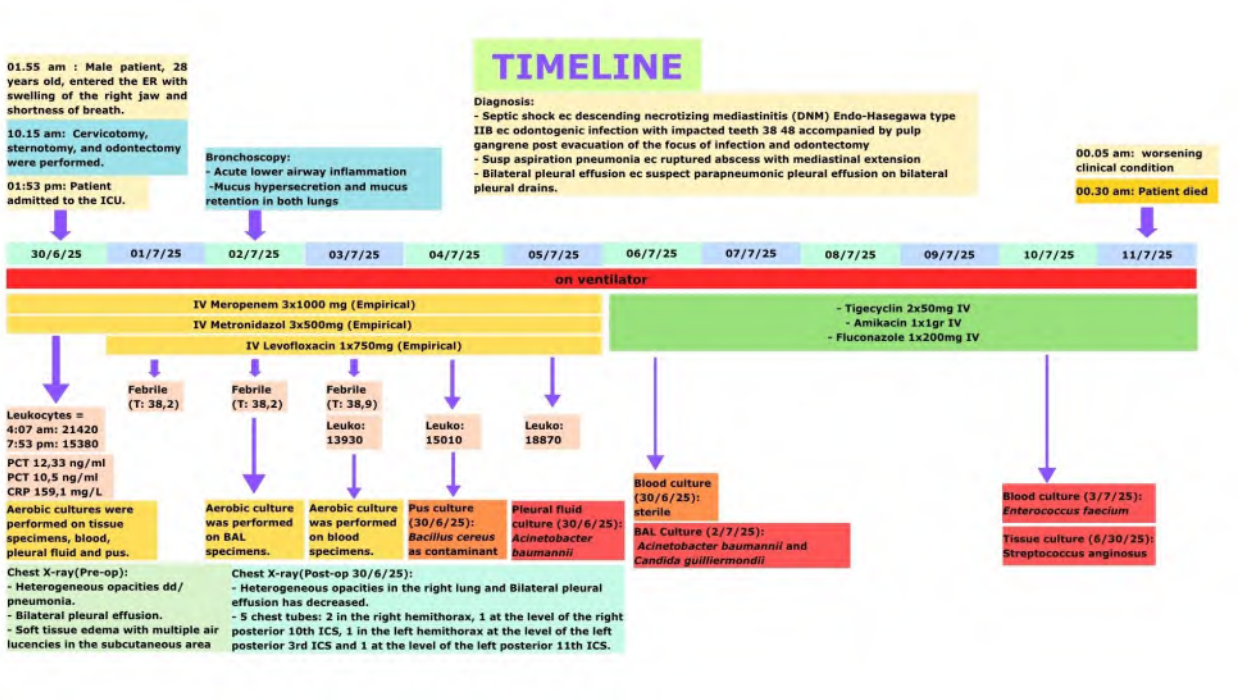
Descending Necrotizing Mediastinitis (DNM) is a rare but life-threatening infection that typically originates from oropharyngeal or cervical infections and rapidly spreads to the mediastinum through fascial planes. The condition is frequently caused by polymicrobial infections, often involving anaerobes and members of the Streptococcus anginosus group (SAG). Early recognition and appropriate intervention are crucial, but missteps in diagnostic processes can delay life-saving care. The integration of clinical microbiology into diagnostic stewardship plays a central role in ensuring accurate pathogen identification and guiding antimicrobial therapy.

Case Presentation

A 28-year-old, male who presented with fever, odynophagia, and progressive dyspnea. Neck X-ray showed soft tissue thickening with multiple air lucencies in the retropharynx, submandibular, right and left necks with suspected of mediastinal expansion. Chest X-ray showed heterogeneous opacities in both lungs, bilateral pleural effusion and Soft tissue edema with multiple air lucencies in the subcutaneous area. Empirical broad-spectrum antibiotics and surgical drainage were initiated. However, due to the lack of early microbiological result, the etiologic agents remained unknown during the initial management. The patient's condition deteriorated rapidly, and he succumbed to sepsis on day three of hospitalization. Cultures revealed a polymicrobial infection dominated by Streptococcus anginosus and Acinetobacter baumannii on culture.

Conclusion

Polymicrobial DNM underscores the urgent need for coordinated diagnostic and therapeutic strategies. Clinical microbiology must be embedded into frontline diagnostic decision-making as a core element of diagnostic stewardship. Doing so improves the precision of infectious disease management and supports the broader goals of antimicrobial stewardship.



CAS-098: Unmasking IRIS in Advanced HIV: Disseminated Histoplasmosis Following HAART in a Case of Smear-Negative Tuberculosis Complicated with Septic Shock and Iatrogenic Pneumothorax

Nurul Aqila Binti Ramlee[3], Siti Nurul Fazlin Binti Abdul Rahman[3], Azlyn Binti Mazlan[3], Amy Rose Aeriyanie Binti A. Rahman[3], Roesnita Binti Baharudin[3], Shahril Fikri Bin Zul Hasnan Najib[1], Noorlina Binti Nordin[2]

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Introduction
Advanced RVD infection is often complicated by multiple opportunistic infections, which may present with overlapping clinical features, thus creating significant diagnostic and therapeutic challenges, especially in patients who develop critical care complications, leading to further management complexity.

Case Presentation
We reported a case of 47 years old man, newly diagnosed advanced RVD and was started on HAART as outpatient. Later he presented to hospital with fever and generalized lethargy for 1 week, with history of prolonged cough. On examination, he was febrile, tachycardic with oral candidiasis. Chest x-ray on arrival revealed cavitating lesions of both upper lobes. Laboratory investigation showed seropositive syphilis infection and persistent negative of AFB smear. As his CD4 level is 0 cells/uL, we proceeded with urine TB LAM, and it was positive. Anti-tuberculous and benzathine penicillin treatment was commenced and HAART was continued.

This patient was prematurely started on HAART without further screening of his underlying opportunistic infections, which led to immune reconstitution inflammatory syndrome (IRIS). He was later diagnosed with disseminated histoplasmosis, as confirmed by fungal cultures and internal transcribed spacer (ITS) sequencing, supported by histopathological findings from skin and rectal biopsies. He was treated with liposomal amphotericin B, however complicated hospital-acquired infections and required broad-spectrum antibiotics. He was eventually discharged in a stable condition with continuation of HAART, anti-tuberculosis and histoplasmosis maintenance treatment.

Conclusion
This case highlights the potential for unmasking IRIS in advanced RVD and underscores the importance of early recognition, multidisciplinary management, and supportive care to achieve favorable outcomes.

CAS-101: Tale of the Two Tonsillectomies: Elusive Cases of Tonsillar Actinomycosis – A Case Series

Christian Jade Berino, Honey Jane Blanco-Limos

Eastern Visayas Medical Center

Introduction

Tonsillar actinomycosis is a rare but important etiologic agent in chronic and recurrent tonsillitis. It is often under-recognized due to its indolent course and lack of distinctive clinical features. There have only been five case reports that links actinomycosis as a potential etiologic agent for chronic, recurrent and hypertrophic tonsillitis. While some consider it a saprophyte, accumulating case-level evidence supports a link to chronic, recurrent, and hypertrophic tonsillitis. It is usually diagnosed post-operatively through histopathological examination. A high degree of clinical suspicion is essential for appropriate diagnosis and management.

Case Presentation

We report two cases of tonsillar actinomycosis presenting with chronic, recurrent, and hypertrophic tonsillitis. Both had a prolonged history of tonsillar enlargement and recurrent sore throat repeatedly treated with antibiotic therapy with minimal improvement. Diagnosis was confirmed post-tonsillectomy by histopathology revealing colonies of Actinomyces spp. with features of chronic suppuration and suppurative cryptitis. Following diagnosis, both patients were treated with intravenous penicillin 24 million units daily for two weeks followed by oral amoxicillin two grams daily for six weeks, resulting in favorable outcomes.

Conclusion

The two reported cases emphasize the importance of considering actinomycosis as a potential cause of chronic and recurrent tonsillitis, especially in patients unresponsive to standard treatment. Routine histopathologic examination of excised tonsils can aid in timely diagnosis which allows targeted antimicrobial therapy and prevent recurrence.

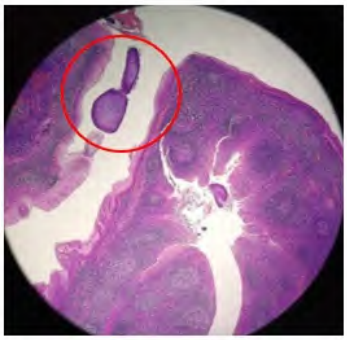

Figure 1-A (Case 1). H&E stain. 40x magnification. Histopathologic section of left palatine tonsil showing prominent lymphoid follicles with germinal centers *(purple lobules)* and a central tonsillar crypt *(white space)*. Actinomyces colony *(red circle)*

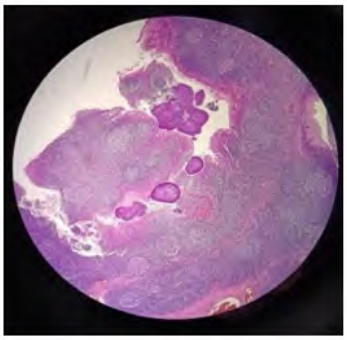

Figure 1-B (Case 1). H&E stain. 40x magnification. Histopathologic section of right palatine tonsil showing hyperplastic lymphoid follicles with prominent germinal centers and crypts filled with basophilic colonies consistent with *Actinomyces species*. The adjacent epithelium appears eroded and surrounding tissue demonstrates chronic inflammatory infiltrates.

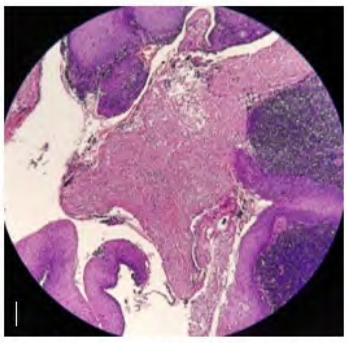

Figure 2-A (Case 2). H&E stain. 100x magnification. Microsection showing tonsillar crypt with necrotic debris and fibrinous exudate consistent with cryptitis.

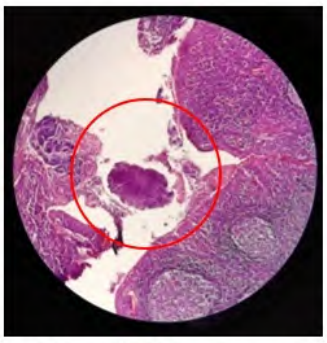

Figure 2-B (Case 2). H&E stain. 100x magnification. Microsection of left palatine tonsil showing basophilic colony *(red circle)* consistent with *Actinomyces spp.* within a crypt. The colony is surrounded by necrotic debris and degenerating neutrophils, indicating suppurative cryptitis.

CAS-102: Persistent Mycobacterium abscessus Bacteremia with Pulmonary Involvement in a Haemodialysis Patient: An Underrecognised Cause of Disseminated Catheter-related Bloodstream Infection

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[2]Medical Department, Hospital Al-Sultan Abdullah, Universiti Teknologi MARA, Selangor, Malaysia

Introduction

Mycobacterium abscessus, a rapidly growing non-tuberculous mycobacterium (NTM), is an increasingly recognised but uncommon pathogen of catheter-related bloodstream infections (CRBSIs), particularly in immunocompromised hosts and haemodialysis-dependent patients. Diagnosis is often delayed due to non-specific symptoms and empirical antibiotics lacking NTM coverage, posing diagnostic and therapeutic challenges.

Case Presentation

We present a case of a 62-year-old woman with diabetes, hypertension, ischaemic heart disease, and end-stage renal disease on haemodialysis, who presented with two days of breathlessness and reduced effort tolerance following incomplete dialysis. She was febrile but haemodynamically stable. Empirical intravenous (IV) amoxicillin-clavulanate and azithromycin were initiated for suspected pneumonia, then escalated to IV cefepime due to persistent fever and rising CRP. Serial blood cultures, taken five days apart from peripheral vein and dialysis catheter, grew Mycobacterium abscessus complex. Susceptibility testing showed sensitivity to amikacin (MIC 16 µg/mL) and clarithromycin (MIC 0.5 µg/mL), with intermediate resistance to imipenem (MIC 16 µg/mL). Whole-body CT revealed lung and pleural nodules suggestive of dissemination. The catheter was removed, and she received IV imipenem and amikacin for two months, resulting in fever resolution and CRP normalization. Treatment was transitioned to oral azithromycin and clofazimine, planned for one year due to persistent bacteremia with pulmonary involvement. She remained clinically stable at five-month follow-up.

Conclusion

This case highlights Mycobacterium abscessus as an emerging cause of persistent CRBSI in haemodialysis patients. Prompt catheter removal, susceptibility-guided antimicrobial combination therapy, and evaluation for dissemination are crucial for successful outcomes.

CAS-103: Culture-Positive, Vegetation-Negative Infective Endocarditis: A Case Report of Aggregatibacter actinomycetemcomitans Infection and Review of Diagnostic

Siti Rohani Binti Abdul Hadi, Muhammad Zaki Amali Bin Basiron

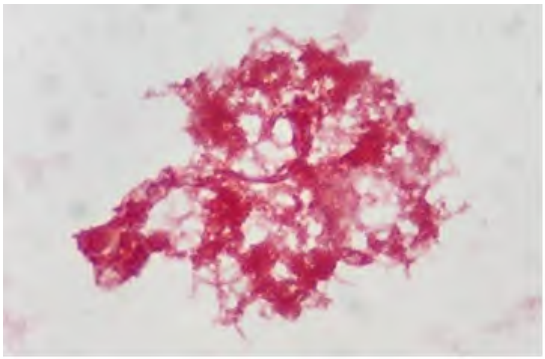
Hospital Sultanah Bahiyah

Introduction
Infective endocarditis (IE) remains a severe condition with high mortality, often caused by diverse pathogens including Aggregatibacter actinomycetemcomitans, a member of the HACEK group known for subacute IE presentations. This is a complex congenital heart disease and aortic valve replacement (AVR) patient who presented with symptoms suggestive of IE. Despite no visible vegetations on echocardiography, the case highlights the importance of advanced microbiological detection methods in accordance with the 2023 Duke-International Society for Cardiovascular Infectious Diseases (Duke-ISCVID) criteria.

Case Presentation
A 58-year-old male with a history of AVR and congenital heart defects presented with lethargy, low-grade fever, dizziness, and presyncope. Blood cultures identified Aggregatibacter actinomycetemcomitans, a fastidious HACEK organism with growth observed after prolonged incubation on enriched media and confirmed by MALDI-TOF mass spectrometry.

Molecular diagnostic methods, including PCR and next-generation sequencing (NGS), are crucial when traditional cultures are negative or inconclusive. This case underscores the need for a comprehensive diagnostic approach integrating microbiological findings with clinical and imaging data, especially when echocardiographic results are unremarkable as echocardiography showed no vegetations. The patient met one major criterion (positive blood cultures) and two minor criteria (fever and prosthetic valve), supporting a probable diagnosis of IE. Treatment involved intravenous gentamicin followed by cefotaxime.

Conclusion
The diagnosis of IE caused by Aggregatibacter actinomycetemcomitans requires a thorough integration of clinical, microbiological, and imaging data. Positive blood cultures, even without echocardiographic vegetations, can confirm IE when other Duke-ISCVID criteria are met. Advanced diagnostic techniques and a high index of suspicion are essential for effective management.



CAS-104: Lung Abscess as an Atypical Manifestation of Invasive Non-Typhoidal Salmonella in a High-Risk Host with Multiple Metabolic Comorbidities

Wan Nurliyana Wan Ramli, Ummu Afeera Zainulabid, Afiq Iddin Rosli, Suzanne Lo Shushan

Department of Internal Medicine, Sultan Ahmad Shah Medical Centre, International Islamic University Malaysia, Pahang, Malaysia.

Introduction

Invasive non-typhoidal Salmonella (iNTS) infections are uncommon in immunocompetent adults but may occur in those with underlying metabolic comorbidities. Lung abscess is a rare pulmonary manifestation of iNTS.

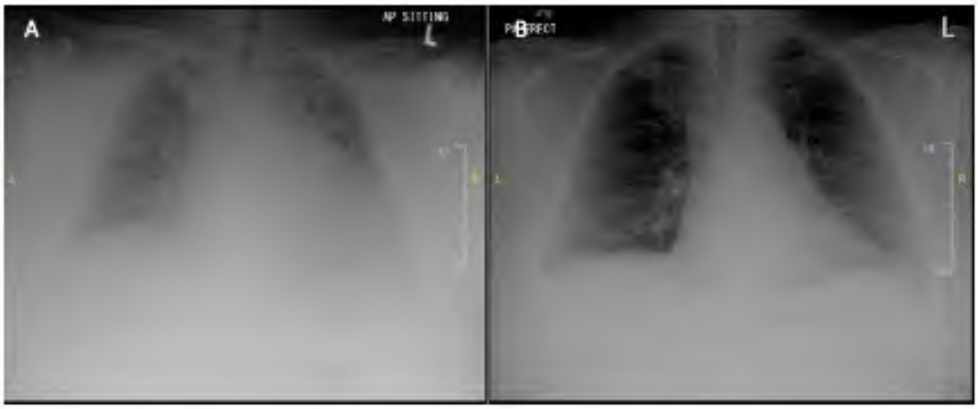
Case Presentation

A 39-year-old man with hypertension, class III obesity, and active smoking presented with acute breathlessness, two weeks of productive cough, and three days of diarrhoea. On arrival, he was severely tachypnoeic with SpO_2 65% on room air. Arterial blood gas confirmed type 2 respiratory failure. He was started on non-invasive ventilation and admitted to ICU. Due to worsening CO_2 retention, he was intubated and later developed a pneumothorax requiring chest tube insertion. Empirical intravenous ceftriaxone and azithromycin were initiated for severe pneumonia with ARDS. Blood cultures grew Salmonella group, sensitive to ceftriaxone, ciprofloxacin, ampicillin, and trimethoprim-sulfamethoxazole. CT thorax revealed a right lung abscess with mediastinal lymphadenopathy. IV ciprofloxacin was initiated but withheld due to suspected allergy; ceftriaxone was resumed. He was extubated on day six. On day eight, therapy was switched to oral trimethoprim-sulfamethoxazole, followed by successful ciprofloxacin rechallenge. Laboratory workup revealed newly diagnosed diabetes (HbA1c 6.5%). Full-body CT at week three (NTSVI score 2) excluded vascular involvement and showed regression of pulmonary lesions. He completed 51 days of antibiotics with clinical and radiological resolution.

Conclusion

This case underscores the importance of recognising metabolic and lifestyle-related vulnerabilities, such as undiagnosed diabetes, obesity, and smoking, in patients with invasive Salmonella infections presenting with atypical manifestations like lung abscess. Comprehensive risk assessment and tailored management strategies are critical to ensure timely recovery and prevent complications.

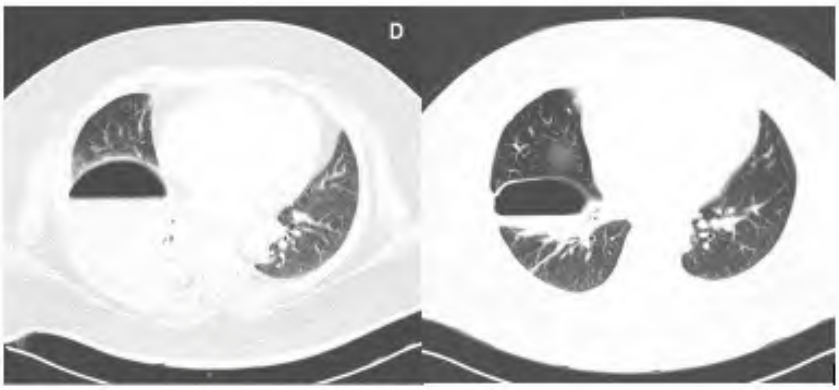
Figure 1 Serial Chest X-rays



A. Initial chest radiograph demonstrated multiple airspace opacities, a cavitary lesion in the right lower lobe, and bilateral pleural effusions.

B. Follow-up chest radiograph upon completion of antibiotics showed resolution of airspace opacities and right lower lobe cavitation, with improvement of bilateral effusions.

Figure 2 Serial CT thorax



C. CT thorax on day 12 of antibiotics revealed a right lower lobe cavity with air-fluid level, moderate right pleural effusion with adjacent collapsed consolidation and diffuse ground glass opacity (GGO) bilateral lungs.

D. CT thorax performed 2 weeks later showed smaller right lower lobe cavity with air-fluid level with improved right lower lobe collapsed consolidation. The right pleural effusion and diffuse GGO had resolved.

CAS-107: An Emerging Endemic Focus: Histoplasmosis in the Philippines

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Introduction

Histoplasmosis is present in the Philippines but is underreported due to challenges in its diagnosis. Untreated disseminated histoplasmosis is fatal; therefore, heightened clinical suspicion especially among immunocompromised patients with skin lesions and consistent systemic symptoms is crucial. This case series underscores the importance of being familiar with the peculiarities of this infection to provide life-saving treatment.

Case Presentation

We detail three cases of histoplasmosis in male patients with HIV/AIDS from a single tertiary hospital. These cases illustrate a broad spectrum of clinical presentations, ranging from disseminated infection with multi-organ involvement to chronic, non-healing cutaneous lesions. Two cases (1 and 2) presented with disseminated histoplasmosis and severe, life-threatening inflammatory conditions. Case 1 developed septic shock and multiorgan failure requiring ICU admission, while Case 2 progressed to secondary hemophagocytic lymphohistiocytosis (HLH), necessitating pulse steroids. Both were successfully treated with liposomal amphotericin B, followed by itraconazole maintenance therapy. Case 3, presented with a chronic, non-healing wound over the malleolus of the right foot, which responded to local wound care following debridement. Histoplasma was detected via skin biopsy in all three cases and in peripheral smear and bone marrow of Case 2. In Case 3, Histoplasma capsulatum was confirmed through molecular identification of the paraffin-embedded tissues.

Conclusion

These cases strongly suggest that Histoplasma capsulatum is present in the Philippines. The protean manifestations often mimic other common opportunistic infections, complicating diagnosis and delaying appropriate treatment. A more aggressive diagnostic approach is critical to ensure timely intervention and improve patient outcomes in regions where the disease is likely underreported.

TABLE 1. SUMMARY OF THE PERTINENT CHARACTERISTICS OF EACH CASE

Patient details upon diagnosis of histoplasmosis	CASE 1	CASE 2	CASE 3
Gender	Male	Male	Male
Age	35	34	34
HIV Status	Positive	Positive	Positive
CD4 count (cells/mm³)	9	73	40
On ART	No	Yes	No
Disseminated Histoplasma	Yes	Yes	No
SHDU admission	Yes	No	No
Intubation	Yes	No	No
Renal Replacement Therapy	Yes	No	No
Organ involvement	Skin, lung, bone marrow, CNS, lymph nodes	Skin, bone marrow	Skin
Site positive for Histoplasma capsulatum	Skin	Skin, blood, bone marrow	Wound tissue
Diagnostic tests performed	Histopathologic, immunohistochemical and molecular evidence of Histoplasma capsulatum	Histopathologic evidence of Histoplasma spp.	Histopathologic evidence of Histoplasma spp.
Antifungal treatment during admission	14 days of Amphotericin B followed by Itraconazole 100mg/cap 2 caps BID	14 days of Amphotericin B followed by Itraconazole 100 mg tablet 3 tablets BID	Not admitted. No antifungal treatment
Outcome	Discharged	Discharged	Discharged

CAS-108: Dengue and COVID-19 Co-Infection Complicated by Oxidative Hemolytic Crisis with Methemoglobinemia and Macrophage Activation Syndrome in a Patient with G6PD Deficiency

Priscillia Lye

NUHS

Introduction

A common presentation in the Emergency Department is a patient with hypoxia and a positive COVID-19 test. These patients are often diagnosed with COVID-19 pneumonia and commenced on intravenous remdesivir and dexamethasone. However, there are alternative life-threatening causes of hypoxia. We report a fatal case of Dengue and COVID-19 co-infection presenting with oxidative hemolytic crisis with methemoglobinemia in a patient with G6PD deficiency.

Case Presentation

A 65-year-old male with a history of ischemic heart disease, asthma, hypertension, hyperlipidemia presented with fever for 5 days. He had no cough, chest pain or shortness of breath. His COVID-19 Antigen Rapid Test was positive. His saturations on room air was 78%, and on 15L of oxygen, his saturations was 82%. On examination, vesicular breath sounds were heard, no wheeze, no crepitations, no bronchial breath sounds. The arterial blood gas showed a pH 7.44, pO2 400 mmHg, pCO2 26.5 mmHg, bicarbonate of 17.9, base excess of -6. A methemoglobin level was sent in view of the oxygen saturation gap and returned as 10.3% (reference range 0-2%). His G6PD level was deficient qualitatively. His dengue PCR also returned positive. He was commenced on intravenous ascorbic acid and exchange transfusion. He developed multiorgan failure and demised within 72 hours.

Conclusion

This patient presented with tissue hypoxia with an oxygen saturation gap, where there is absence of hypoxemia despite evidence of hypoxia. This raises suspicion for methemoglobinemia and would not be in keeping with pulmonary embolism or COVID-19 pneumonia. It is also important to identify the presence of G6PD deficiency.

CAS-109: Purpureocillium lilacinum Pneumonia in a Patient with Myositis-Associated ILD on Chronic Immunosuppression: A Rare and Elusive Diagnosis

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Department of Internal Medicine, Sultan Ahmad Shah Medical Centre, International Islamic University Malaysia, Pahang, Malaysia.

Introduction

Purpureocillium lilacinum is a rare environmental mould that occasionally causes opportunistic infections in immunocompromised hosts, including transplant recipients, patients with haematological malignancies, and those on corticosteroids. Pulmonary involvement is uncommon, with typical CT features such as nodular infiltrates or cavitating lesions. To our knowledge, this is the first reported case

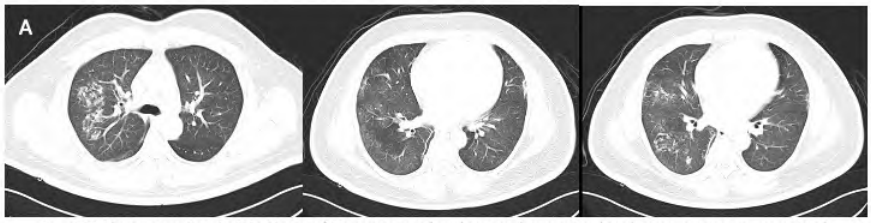
Case Presentation

A 37-year-old man with Anti-Jo-1 positive myositis-associated interstitial lung disease (ILD), on long-term mycophenolate mofetil (MMF) and high-dose prednisolone, presented with nine days of haemoptysis, dyspnoea, and reduced effort tolerance, with five days of fever and diarrhoea. He also had right-sided heart failure due to obstructive sleep apnoea. On admission, he was hypoxic with type 1 respiratory failure and bilateral coarse crackles. Pulmonary haemorrhage due to ILD flare was suspected, and intravenous hydrocortisone was commenced. Empirical ceftriaxone and azithromycin were also initiated. CT thorax revealed patchy consolidations with tree-in-bud appearance, ground-glass opacities, and mediastinal lymphadenopathy, prompting bronchoscopy which showed blood-stained secretions from the right upper lobe. Bronchoalveolar lavage culture grew Purpureocillium lilacinum. Due to unresolved haemoptysis, oral itraconazole was commenced, while MMF and prednisolone were withheld. Antifungal therapy was extended to 12 weeks due to persistent symptoms, after which CT demonstrated complete resolution. A follow-up scan three months later confirmed no recurrence.

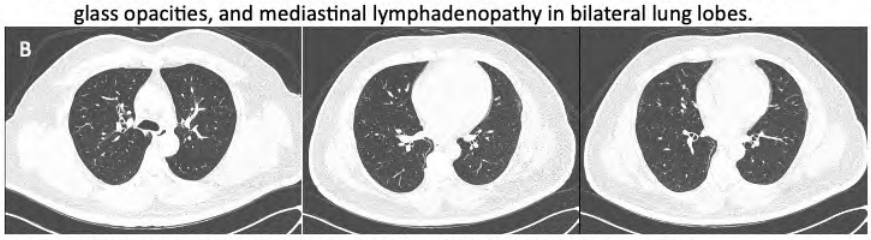
Conclusion

This case underscores the need to consider this rare opportunistic fungal pathogen in patients with autoimmune disease on high dose corticosteroids, persistent respiratory symptoms, and atypical CT findings. Early bronchoscopy, fungal diagnostics, and timely antifungal therapy are essential to improve outcomes in this vulnerable population.

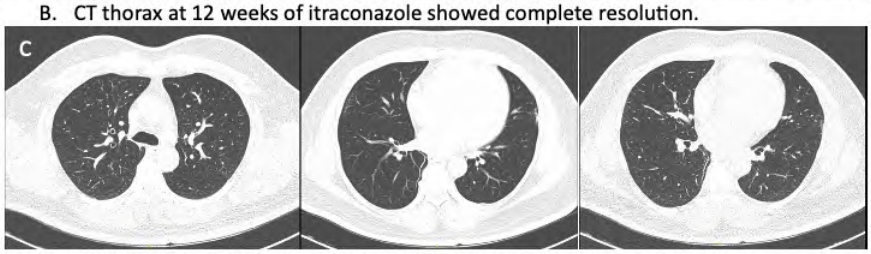
Figure 1 Serial CT Thorax



A. CT thorax prior initiation of itraconazole showed tree-in-bud appearance, ground-glass opacities, and mediastinal lymphadenopathy in bilateral lung lobes.



B. CT thorax at 12 weeks of itraconazole showed complete resolution.



C. CT thorax 3 months post cessation of itraconazole showed no recurrence.

CAS-110: Seroreversion in a 45 year old Filipino with HIV: A Case Report

Adrian Kevin Agonoy, Mark Pasayan, L. Angelique Duran

Research Institute for Tropical Medicine

Introduction
HIV antibody seroreversion occurs when antibodies decrease below detectable levels in a patient with good virologic response to antiretroviral therapy.

Case Presentation
This is a case of a 45-year-old bisexual cis-gender male diagnosed with HIV-1 in August 2009 during blood donor screening. Particle Agglutination for HIV 1/2, Vironostika HIV Ag-Ab, Genscreen HIV Ag-Ab, and Genelabs Western Blot were used in the diagnostic algorithm. (Baseline CD4+ count was 390 cells/uL. He was started on Zidovudine/ Lamivudine + Nevirapine and taken with good adherence. HIV RNA was undetectable after six onths of ART and remained undetectable in subsequent follow-up monitoring.

On December 2023, he self-conducted an HIV RDT (Abbott Bioline HIV 1/2 3.0), revealing non-reactivity. Blood was sent to SLH-SACCL on January 2024 showing nonreactivity to CLEA, reactivity to ELFA, and indeterminate immunochromatography (ICT), with one band for GP41, rendering indeterminate results. He was advised to continue ART and repeat testing after 3 months. On March 2024, CLEA and ELFA were reactive; ICT was positive, with two bands for gp160 and gp41. He was advised on his false-negative RDT, and his positive confirmatory test. He continues to take his ART with good compliance.

Conclusion
This case reflects seroreversion in a virologically suppressed PLHIV with long-term ARV. Seroreversion is usually documented using 2nd/3rd generation RDTs, with lower sensitivities than EIAs in detecting gp41, the major antibody detected in PLHIV. False-negative RDTs can be problematic when erroneously used in PLHIV started early treatment with ART due to disappearance of antibody in virologic suppression.

CAS-112: A Ruptured Mycotic Aneurysm in a Patient with Diabetes Mellitus and Cirrhosis

Yi-Ching Huang

Jen-Ai Hospital, Taichung

Introduction
A mycotic aortic aneurysm is a serious and life-threatening disease with the risk of rupture. The classic presentation is a painful, pulsatile, and enlarging mass with fever, back or abdominal pain. The diagnosis depends on imaging findings and microbiological examination of blood and/or the aneurysm wall. The treatment consists of antibiotic therapy combined with aggressive surgical debridement and vascular repair.

Presentation
A 65-year-old man with diabetes mellitus and liver cirrhosis presented to our emergency department with back soreness for 10 days and delirium. An abdominal CT scan showed a ruptured abdominal aortic aneurysm. He then received endovascular aneurysm repair. The blood and abscess cultures yielded Escherichia coli. After that, he had received percutaneous drainage for left iliopsoas muscle abscess, debridement and drainage for pyogenic spondylodiscitis of the third and fourth lumbar vertebrae, and Girdlestone procedure and antibiotic-loaded cemented mobile spacer for pyogenic arthritis of the left hip.

Conclusion
Source control and long-term antimicrobial therapy played the important roles in the management of the ruptured mycotic aneurysm and deep-seated infections.

CAS-113: Severe Nasomalar MPOX Infection in a Male with Advanced HIV Disease

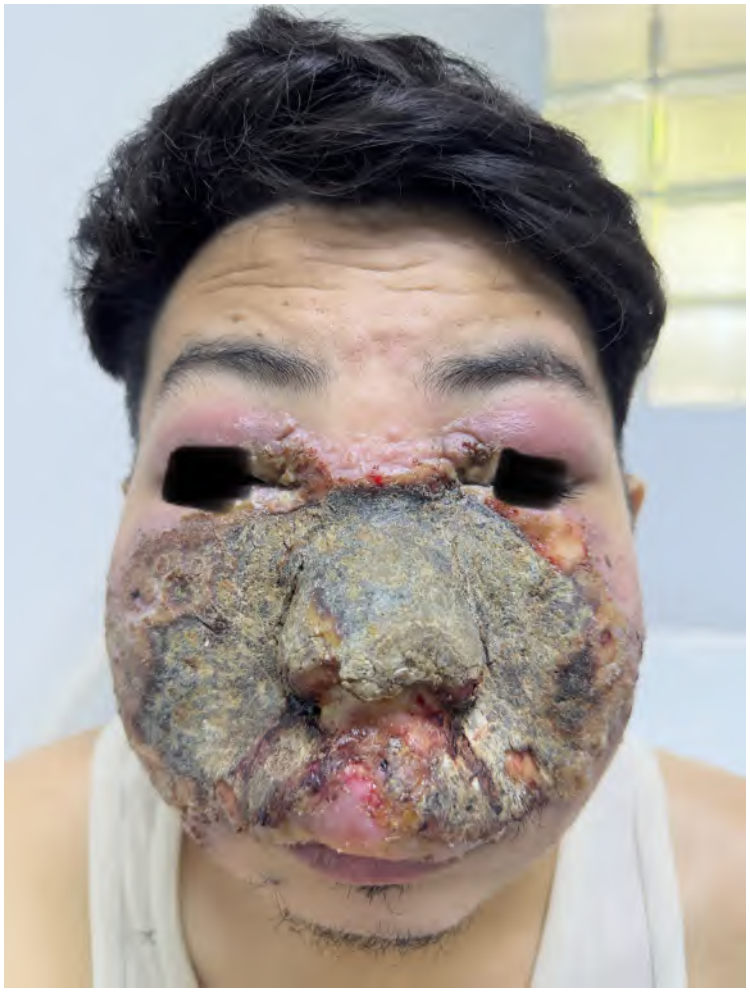
Adrian Kevin Agonoy, Kirk Ilew Quijote, Joland San Juan, Mark Pasayan

Research Institute for Tropical Medicine

Introduction
While MPOX infections typically manifest as macular to umbilicated papular lesions in the ano-genital area as observed in more recent outbreaks, there have been a number of accounts of MPOX manifesting atypically, such as in ocular, facial, and even nasal involvement, especially in severely immunocompromised individuals.

Case Presentation
This is a case of a 33 year old male with known HIV since 2018 who was not linked to care, coming initially for a two month history of an appearance of a maculopapular lesion above the philtrum which would progress to ulcerate and form several other similar lesions to coalesce into a larger ulcerated lesion to eventually form a crust involving the alae, the bridge, extending to the malar regions of the face, prompting different consultations with various dermatologists, with prescribed topical antbiotics and steroids to which there was no improvement. He eventually went to our institution for evaluation where his CD4 was at 33 cells/μL, with a tissue PCR of the crust eventually revealing a positive result for MPOX (Clade II). The patient was given Tecovirimat 600mg twice daily for 14 days without improvement and was referred to dermatology for chemical debridement of the lesion.

Conclusion
MPOX infections may manifest atypically especially in uncontrolled HIV infection. Tecovirimat may have better role in early infection, and surgical and/or chemical debridement may have a role in settings where medical management have failed to improve clinical status of the patient, requiring a multidisciplinary approach including Infectious Diseases, Dermatology and Plastic Surgery for holistic management.



CAS-115: Comparative Evaluation of Western Blot and Geenius HIV 1/2 Confirmatory Assay in an Acute HIV Infection Case

Yumi Taniguchi[1], Ai Okamoto[1], Akiko Murakami[1], Yasunori Takasuka[1], Hisamichi Tauchi[3], Koichiro Suemori[2]

[1]Department of Clinical Laboratory, Ehime University Hospital
[2]Department of Hematology, Clinical Immunology and Infectious Disease, Ehime University Graduate School of Medicine
[3]Division of Infection Control, Ehime University Hospital

Introduction
In 2020, Japan revised HIV diagnostic guidelines, introducing the Geenius HIV 1/2 Confirmatory Assay (ICA) as a replacement for conventional Western Blot (WB). Geenius has demonstrated improved sensitivity and specificity. This study compares antibody detection dynamics between WB and Geenius in acute HIV infection.

Case Presentation
A man in his 20s was diagnosed with acute HIV infection at a previous hospital in early March 20XX, based on reactive screening, HIV-1 RNA 9.8×10^6 copies/mL, WB negativity, and CD4+ count of 136/μL. ART was initiated. Due to persistent fever, diarrhea, and fatigue, he was transferred to our hospital on March 23 (day 1). CMV co-infection was diagnosed, prompting ART discontinuation and ganciclovir initiation. ART was resumed on day 106.

Methods: Samples from day 1 to day 223 were tested using WB (LAV Blot I/II) and Geenius. Band patterns and interpretation were visually compared.

Results: WB showed multiple bands from day 1 but remained indeterminate; HIV-1 positivity was confirmed on day 55 with detection of gp120 and gp41.

Geenius detected p31 on day 6 (indeterminate) and confirmed HIV-1 positivity on day 27 via p31, gp160, and gp41—28 days earlier than WB.

For HIV-2, WB showed persistent p26 from day 1, while Geenius transiently detected gp140 on day 6, which resolved by day 17.

Conclusion
Geenius enabled earlier HIV-1 detection and reduced HIV-2 cross-reactivity. Differences in antigen composition between reagents and antigen-antibody complexes in the specimen may have influenced band patterns. Additionally, altered immune responses due to CMV co-infection may have affected antibody production, warranting further investigation.

LB-CAS-001: Herpes Zoster Virus Infection Associated Neuromyelitis Optica Spectrum Disorder: Two Case Reports

Alex Tanoto Lim

NCID

Introduction

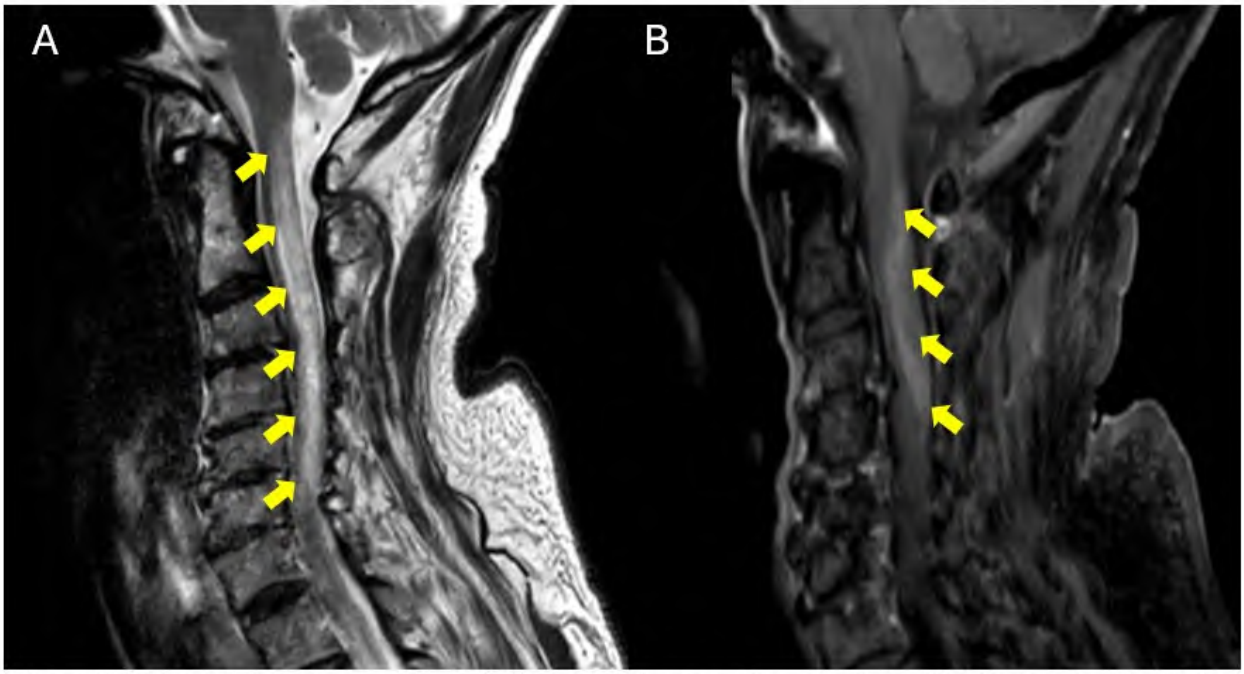
Herpes-zoster infection (shingles) is a worldwide endemic disease caused by reactivation of the varicella-zoster virus (VZV). An estimated 14.9 million cases of shingles occurred globally in 2020 in individuals aged >50 years, and the number is predicted to increase to 19.1 million cases by 2030. Herpes-zoster by itself can very rarely cause transverse myelitis. However, there is growing evidence for its role in triggering the neuroinflammatory disorder neuromyelitis optica spectrum disorder (NMOSD), a separate process from primary infective myelitis. The neurological prognosis of post-infectious NMOSD is much worse than that of VZV infectious myelitis, and the treatment required is much more intensive.

Case Presentation

We discuss two cases of older adults, a 68-year old patient breast cancer on anti-HER cyclin dependent kinase inhibitor (Abemaciclib) and a 96-year old patient with multiple comorbidities including chronic kidney disease who presented with rapid onset pseuoathetosis from spinal cord dysfunction within a week of shingles reactivation in cervical dermatomes. They were both eventually diagnosed with VZV-associated NMOSD. Both had poor neurological outcomes despite appropriate treatment for NMOSD with steroids, plasmapheresis and eventual steroid-sparing agents. We present literature review and learning points from other published reports.

Conclusion

These case reports and literature review aims to raise awareness amongst infectious disease physicians on the differential diagnoses for patients with shingles who present with neurological symptoms, and to improve the understanding about VZV-associated NMOSD.



A: Sagittal T2 MRI of the cervical spine showed a longitudinally extensive T2 hyperintense lesion extending from C2 to C7 with cord oedema (arrows)
B: Sagittal STIR (Short Tau Inversion Recovery) MRI of the cervical spine with contrast showed patchy enhancement over the cord lesion (arrows)

LB-CAS-005: Testicular Tuberculosis Revealing HIV infection: Case Report

Fatima Ihbibane[1], Jean Claude Bucumi[2], Inas Ouggane[2], Mustapha Sodqi[2], Latifa Marih[2], Ahd Ouladlahsen[2], Kamal Marhoum El Filali[2]

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Introduction
Testicular tuberculosis accounts for less than 1% of cases of extrapulmonary TBK. Rare, it often presents as a scrotal mass simulating a tumor. Its diagnosis is frequently delayed due to the absence of specific symptoms. Furthermore, its association with HIV infection is documented, but it may be the mode of revelation of HIV positivity.

Case Presentation
A 58-year-old patient with no particular medical history consulted for a painless swelling of the left testicle that had been developing for several months. Clinical examination revealed a firm mass with no local inflammatory signs. A testicular ultrasound revealed a heterogeneous lesion suggestive of a tumor. An orchiectomy was performed. The pathological analysis showed a typical caseofollicular granulomatosis of tuberculosis, without signs of malignancy. A systematic search for coinfections revealed HIV seropositivity, confirmed by viral load.

Discussion: Pseudotumoral testicular tuberculosis is a rare differential diagnosis of testicular tumors. In HIV-positive patients, immunosuppression promotes atypical and extrapulmonary forms of tuberculosis. Here, the clinical picture was misleading, initially suggesting a tumor. The concomitant discovery of HIV infection underlines the importance of systematic screening in cases of extrapulmonary tuberculosis.

Conclusion
Our case demonstrates the importance of considering tuberculosis in the differential diagnosis of testicular masses, particularly in atypical contexts or in the presence of risk factors for immunosuppression. Early and coordinated management of tuberculosis and HIV infection is essential to improve prognosis.

LB-CAS-006: Cellulolosimicrobium Cellulans Septicaemia in a Post Bone Marrow Transplant Recipient: A Case Report from a Tertiary Care Cancer Set Up from India

Sujata Lall, Vivek Bhat, Nayana Baraskar, Syeda Munawar, Shrutkirti Gupta, Navin Khattry, Ananat Gokarn, Sachin Punatar, Akanksha Chichra, Sumeet Mirgh

ACTREC TMC Navi Mumbai

Introduction
Cellulosimicrobium species, a gram-positive bacilli belonging to the order Actinomycetales rarely cause infections in humans. Most of the cases have been reported from patients suffering from a variety of chronic underlying illnesses that involved immune dysfunction. We report a case of Cellulolosimicrobium cellulans septicaemia from western India in a post bone marrow transplant recipient.

Case Presentation
A 31-year-old patient presented with back pain in August 2018 and then diagnosed to have Pre T acute lymphoblastic leukaemia with CTG QC. No history of Tuberculosis, Asthma, COVID or prior surgery was there. He Received Allogenic Bone Marrow transplant in March 2025.Post-transplant status was significant for parainfluenza virus respiratory illness presenting with cough cold, fever treated with Oseltamivir. He was admitted in august for high grade fever Hickman central lumen catheter blood culture was sent on two days. Both of them isolated a gram positive coryneform diptheroid. It was lemon yellow colored, smooth transparent circular colony on Blood agar. It was confirmed as Cellulosimicrobium cellulans by both VITek-2 Compact and MALDI-TOF spectrometry. The isolate was susceptible to Vancomycin, Linezolid, Teicoplanin and Meropenem using CLSI M45 breakpoints for Corynebacterium diptheroids. The patient reported improvement in counts and clinically with injection meropenem.

Conclusion
Awareness regarding this pathogen should be there especially in centres treating immunocompromised population as rare pathogens are increasing in prevalence due to high survival rate of immunocompromised patients, extensive application of long-term medical devices, and advances in microbiological diagnostic techniques. Such Gram positive bacilli should not be considered as contaminants while treating post-transplant population.

LB-CAS-007: Multifactorial Encephalopathy and Seizure Episodes in a Middle-Aged Male: A Diagnostic and Therapeutic Challenge in a Post-Splenectomy Patient

Llovinila Faith Eder, Jenni Shannin Alip, Ralph Aniceto

Divine Word Hospital

Introduction
Overwhelming Post-Splenectomy Infection (OPSI) is a rapidly progressive and potentially fatal condition, often caused by encapsulated organisms such as Streptococcus pneumoniae. Its diagnosis becomes particularly challenging in patients with multiple comorbidities.

Case Presentation
We present a case of a 53-year-old Filipino male with history of splenectomy, no vaccination, poorly controlled Type 2 Diabetes Mellitus, Hypertension and Chronic Kidney Disease who presented with fever, chills, and altered mental status. On admission, he was febrile, hypertensive, tachypneic and with altered sensorium. Laboratory workup showed leukocytosis, severe hyperglycemia, elevated serum creatinine, metabolic acidosis and hyperkalemia. Imaging revealed multifocal cerebral infarcts. Blood cultures grew Streptococcus pneumoniae and endotracheal aspirate culture revealed Klebsiella pneumoniae (ESBL-positive). Thyroid function tests supported thyroid storm (Burch-Wartofsky score 75). He was admitted to the intensive care unit and was given broad-spectrum antibiotics, antiepileptics, insulin infusion, renal replacement therapy and thyroid storm medications. Despite aggressive treatments, the patient's seizures persisted and ultimately succumbed on the fourth hospital day.

Conclusion
This case highlights a catastrophic progression of OPSI, complicated by overlapping syndromes—sepsis, metabolic encephalopathy, cerebral infarction, thyroid storm and acute renal failure—each contributing to diagnostic ambiguity and therapeutic complexity. Diagnostic limitations due to instability prevented MRI and lumbar puncture. The absence of a spleen likely facilitated the rapid dissemination of Streptococcus pneumoniae, contributing to septic shock and probable septic emboli. Early recognition and rapid interdisciplinary management are critical. This case reinforces the high mortality, unpredictable onset, and complex presentation of OPSI, underscoring the need for preventive vaccination and heightened clinical suspicion in asplenic patients.

LB-CAS-008: Therapeutic Challenges: A Case of Cryptococcal Pneumonia in an Immunocompetent Host

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Introduction
Cryptococcus neoformans is an opportunistic fungal pathogen. While its pulmonary manifestations are typically associated with advanced immunosuppression, diagnosis is often significantly delayed in seemingly immunocompetent individuals or those on modest immunosuppression due to its non-specific symptomatology, which closely mimics tuberculosis or malignancy.

Case Presentation
A 62-year-old gentleman known diabetes mellitus and myasthenia gravis, on low-dose prednisolone; he presented with a two-week history of fever, productive cough, and a significant 10 kg weight loss over three months. A key history of exposure to pigeon droppings was elicited. On admission, he was tachypnoeic, hypoxic, and required supplemental oxygen. Initial laboratory findings revealed leucocytosis and markedly elevated inflammatory markers. Contrast-enhanced CT thorax demonstrated extensive bilateral consolidations with cavitation and air-bronchograms. An exhaustive diagnostic workup ruled out tuberculosis and bacterial pathogens. The diagnosis of cryptococcal pneumonia was established by the isolation of Cryptococcus neoformans from bronchoalveolar lavage (BAL) culture and a positive serum cryptococcal antigen. Initial management with intravenous amphotericin B deoxycholate was complicated by the development of acute kidney injury and fluid overload, highlighting therapeutic challenge. Consequently, therapy was switched to fluconazole. The patient was well and showed marked clinical improvement, leading to discharge. Sixth months follow-up revealed clinical and radiological resolution.

Conclusion
This case underscores the diagnostic pitfalls of cryptococcal pneumonia and the imperative for a high clinical suspicion, particularly with a history of environmental exposure. It also exemplifies a core management dilemma, where first-line therapy-induced toxicity necessitated an individualized approach, balancing antifungal efficacy against potential drug toxicities in a patient with significant comorbidities.

LB-CAS-009: A Diagnostic Odyssey: Successfully Treated Cytomegalovirus-Induced Immunodeficiency with Tuberculosis Coinfection Presenting as Fever of Unknown Origin in a Young Male

John Vincent Pagaddu, John Delgado

University of Santo Tomas Hospital

Introduction
Fever of unknown origin (FUO) in tuberculosis-endemic regions presents a significant diagnostic challenge. This complexity is heightened when concurrent infections and immune dysregulation, such as that caused by cytomegalovirus (CMV), confound the clinical picture and mimic other immunodeficiency states.

Case Presentation
A previously healthy 20-year-old Filipino male presented with a three-week history of intermittent fever, malaise, and left cervical lymphadenopathy. An extensive workup for common infectious, autoimmune and malignant causes was unrevealing. However, laboratory testing revealed CMV viremia (463 copies/mL) with CD4+ T cell lymphopenia (332 cells/µL), despite a negative HIV evaluation. An excisional lymph node biopsy confirmed rifampicin-sensitive Mycobacterium tuberculosis, while bacterial culture also yielded Enterobacter cloacae. The patient received sequential antibacterials, then two weeks of valganciclovir — resulting in CMV clearance (undetectable viral load) and CD4+ T cell recovery (661 cells/µL). A follow-up examination four months later confirmed sustained CMV clearance and normal CD4+ T cell count (695 cells/µL). Anti-tuberculosis therapy, complicated by a drug-induced rash but successfully rechallenged, was completed with excellent tolerance and full clinical recovery.

Conclusion
This case illustrates the diagnostic complexity of FUO in endemic areas, highlighting how CMV-induced immunosuppression, even in immunocompetent individuals, can mimic HIV infection and predispose to opportunistic coinfection. Careful evaluation and thorough infectious workup were pivotal in achieving diagnostic clarity and therapeutic success.

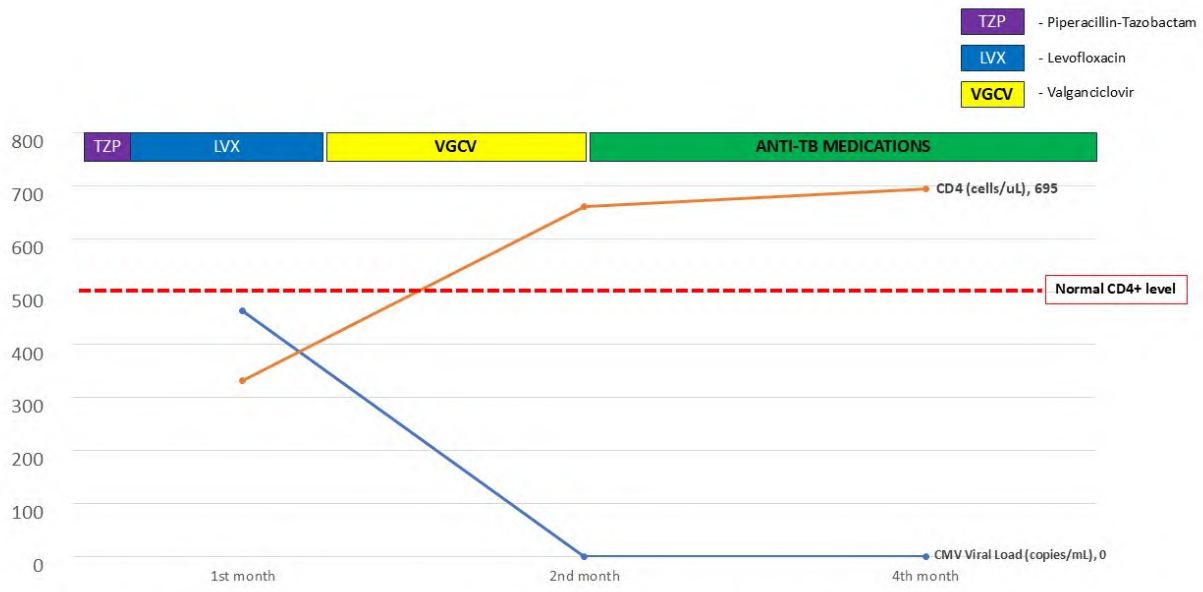

Figure 1. Timeline of antimicrobial therapy and trends of CD4+ absolute cell count and CMV Viral load

LB-CAS-010: Nontyphoidal Salmonella Bacteraemia Presenting with Respiratory Failure, Pulmonary Embolism and Mediastinal Lymphadenopathy in a Patient with Post-Tuberculosis Bronchiectasis

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Introduction
Nontyphoidal Salmonella (NTS) bacteraemia typically occurs in immunocompromised individuals and is usually preceded by gastrointestinal symptoms. Extraintestinal involvement, particularly pulmonary manifestations, is rare. We report an atypical case of NTS bacteraemia in a patient with structural lung disease, without gastrointestinal symptoms.

Case Presentation
A 65-year-old man with a history of treated pulmonary tuberculosis 20 years ago and post-tuberculosis bronchiectasis presented in mid-August 2025 with a two-day history of productive cough and dyspnoea. He was afebrile and reported no gastrointestinal complaints. He required non-invasive ventilation initially for type 2 respiratory failure. Blood cultures grew NTS; stool cultures, tuberculosis workup (GeneXpert, AFB smears) and viral screening were negative. He received 14 days of intravenous ceftriaxone and was planned for 4 weeks of oral trimethoprim-sulfamethoxazole. Despite clinical and biochemical improvement, he remained oxygen-dependent. CT pulmonary angiography revealed bilateral segmental and subsegmental pulmonary embolism with mediastinal lymphadenopathies (largest 2.9 cm). Echocardiography showed a loculated pericardial effusion (0.9 cm at the left ventricular inferior wall). Therapeutic anticoagulation was initiated. He remained hemodynamically stable with no indications for thrombolysis. He is scheduled for bronchoscopy with biopsy of the mediastinal lesions for further evaluation.

Conclusion
This case highlights a rare extraintestinal manifestation of NTS bacteraemia in a relatively immunocompetent patient with post-tuberculosis bronchiectasis. The absence of gastrointestinal symptoms, combined with pulmonary embolism, mediastinal lymphadenopathy and pericardial effusion, presents a diagnostic and management challenge. In tuberculosis-endemic regions, a multidisciplinary approach is essential, with careful coordination of prolonged antibiotic therapy, anticoagulation and further diagnostic workup to rule out malignancy or tuberculosis reactivation.

LB-CAS-011: The Great Mimicker: Osteoarticular Sporotrichosis Masquerading as Tuberculosis

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Introduction
Sporotrichosis, caused by the dimorphic fungus Sporothrix schenckii, causes a significant diagnostic challenge in immunocompromised host due to its ability to closely mimic more prevalent granulomatous diseases, particularly tuberculosis (TB). This case exemplifies a classic diagnostic conundrum in a vulnerable population.

Case Presentation
A 51-year-old lady with systemic lupus erythematosus (SLE) and class IV lupus nephritis, on immunosuppressive therapy, presented with six months right wrist pain and cutaneous nodules. MRI revealed osteomyelitis of distal radius and infective arthritis along with intraoperative findings of multiple rice bodies prompting the initiation of empilical anti-tuberculous (TB) therapy for musculoskeletal tuberculosis. However, the lack of clinical response to anti-TB treatment after several weeks prompted the consideration of alternative etiologies. Histopathological examination of tissue biopsy revealed chronic inflammation with necrotic tissue and fungal culture isolated Sporothrix schenckii. This diagnostic sequence underscores a major clinical overlap between sporotrichosis and tuberculosis can readily lead to misdiagnosis, resulting in delayed appropriate treatment and potential disease progression with irreversible tissue damage. Antifungal agent itraconazole was initiated and yielding a significant clinical improvement within two weeks and demonstrating excellent treatment response.

Conclusion
This case emphasizes the critical imperative for clinicians to maintain a high index of suspicion for fungal mimics like sporotrichosis in immunocompromised individuals presenting with treatment-refractory presumed TB. Microbiological and histopathological confirmation remains crucial to guide appropriate and timely therapy, thereby optimizing therapeutic outcomes and preventing long-term musculoskeletal sequelae.

LB-CAS-012: Rare Anaerobic Peritonitis Due to Paeniclostridium sordellii: A Case of Successful Eradication

Lorenz Lista, Armin Masbang

St. Luke's Medical Center - Quezon City

Introduction
Paeniclostridium sordellii is an anaerobic, spore-forming, gram-positive bacillus rarely implicated in human disease. Reported infections, particularly in gynecologic and injection drug use settings, have been associated with fulminant sepsis and high mortality. Peritonitis due to P. sordellii is exceedingly rare, especially in immunocompetent individuals.

Case Presentation
We describe a 47-year-old Indian male residing in the Philippines who presented with a month-long history of abdominal pain, hematemesis, and progressive abdominal distension. On admission, he had fever, chills, and hematochezia. Laboratory workup revealed anemia, elevated transaminases, and ascites with high SAAG. Imaging showed splenomegaly, heterogeneous liver parenchyma, and massive ascitic fluid collection. Initial empiric therapy with ceftriaxone failed to resolve fever. Paracentesis yielded 2400 mL of clear yellow ascitic fluid (SAAG >1.1; ANC 424, 80% lymphocytes). Antibiotics were shifted to piperacillin-tazobactam, with subsequent defervescence. On the fourth hospital day, ascitic fluid culture grew gram-positive bacilli, later confirmed as Paeniclostridium sordellii on day 9. Due to persistent ascites, an abdominal pigtail catheter was inserted, and repeat cultures demonstrated complete eradication of the organism. The patient successfully completed intravenous therapy and was discharged improved.

Conclusion
Isolation of anaerobes in spontaneous bacterial peritonitis is rare, with P. sordellii cases in literature often rapidly fatal due to potent exotoxins. We present, to our knowledge, the first documented case of P. sordellii peritonitis in an immunocompetent adult, successfully treated with piperacillin-tazobactam. This unusual case highlights the importance of vigilance and consideration of anaerobic pathogens in non-responsive peritonitis. Early recognition and appropriate antimicrobial coverage for anaerobes are essential in this case.

LB-CAS-013: A Case Report of Fusariosis in a Filipino Patient with a Solid Tumor

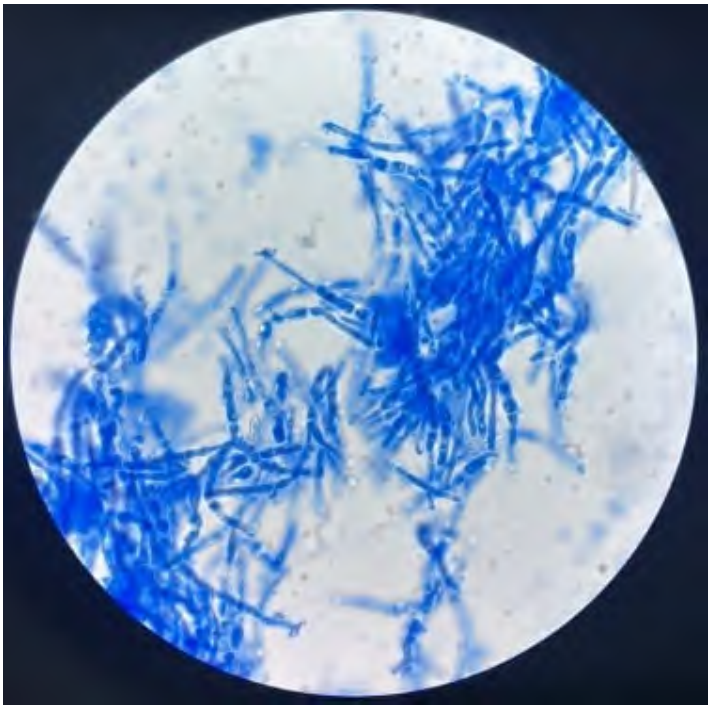
Marji Umil

St. Luke's Medical Center Quezon City

Introduction
The fungal organism, Fusarium spp. can cause infection, especially in patients with hematologic neoplasms. Only a few reports of fusariosis in patients with solid organ malignancies exist.

Case Presentation
We report a 59-year-old hypertensive Filipino female presenting with one month history of intermittent abdominal pain, jaundice, pruritus, and vomiting. An abdominal ultrasound revealed cholecystolithiasis and dilated common bile duct. Further evaluation with whole abdominal magnetic resonance imaging demonstrated a porta hepatis mass infiltrating the common hepatic and proximal common bile ducts, causing marked intrahepatic biliary dilatation. A biliary duct neoplasm was the primary consideration. The healthcare team inserted a percutaneous transhepatic internal biliary drainage catheter and performed laparoscopic gastrojejunostomy. Histopathology of the hepatoduodenal lymph node showed metastatic adenocarcinoma. Thus, a bile duct neoplasm with nodal metastasis was considered. On postoperative day two, the patient developed high-grade fever and underwent septic workup. Blood culture grew Fusarium spp., sensitive to amphotericin B and voriconazole. Voriconazole therapy was initiated, resolving her fever. She was discharged after repeat blood culture on day 3 of treatment turned negative. Voriconazole was continued with advice for close follow-up. Upon discharge she was compliant with therapy; however, by week 3, family noted poor appetite and progressive generalized weakness. Her condition deteriorated, but further evaluation was deferred per her wishes. She eventually expired by week 5 of treatment.

Conclusion
A high index of suspicion for fusariosis among those with solid neoplasms is essential because delay in diagnosis and treatment can result in catastrophic consequences.



LB-CAS-014: Tuberculous Meningitis without Pleocytosis in an Immunocompetent Patient: A Case Report

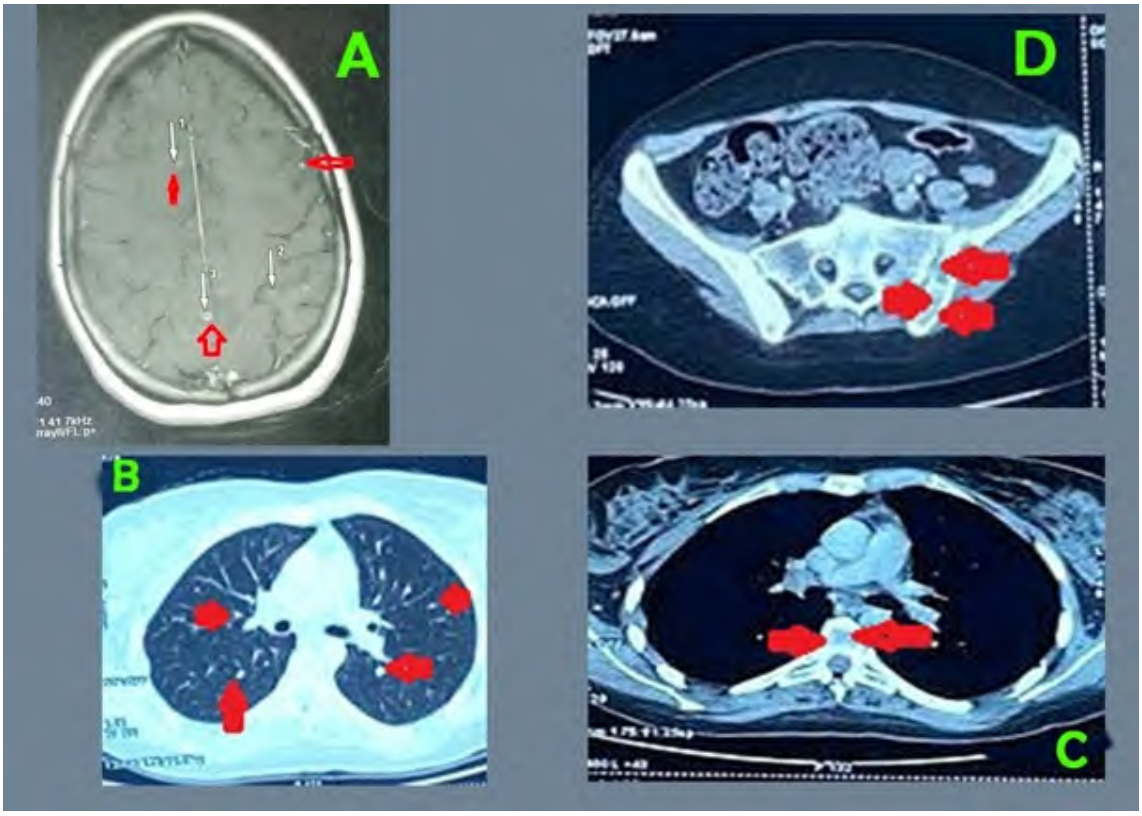
Hassan Kamena Mwana-Yile , Fatima Ihbibane, Raissa Bongungu, Latifa Marih

Ibn Rochd University Hospital, Faculty of Medicine and Pharmacy, Hassan II University, Morocco

Introduction
CSF pleocytosis is an important factor in confirming a diagnosis of meningitis. However, its absence can present a diagnostic challenge for clinicians when meningitis is suspected, especially in cases of tuberculous meningitis in immunocompetent patients. The aim is to report a case of tuberculous meningitis without CSF pleocytosis in an immunocompetent patient.

Case Presentation
Patient EI, aged 27, with no history of specific pathologies, presented with a meningeal syndrome, an infectious syndrome (fever 39 °C), and signs of basilar involvement associated with a hacking cough with whitish sputum and night sweats, evolving in a context of weight loss for 15 days. Brain MRI revealed multiple sub-centimetric intra-axial supratentorial and sub-tentorial lesions. Cytobacteriological and chemical examination of the cerebrospinal fluid showed a white blood cell count of fewer than three cells/mm3, hyperproteinorachy at 1.54 g/L, and hypoglycorachy at 0.08 g/L. BK PCR in CSF isolated Mycobacterium tuberculosis DNA without rifampicin resistance. Thoracic-abdominal-pelvic CT revealed micronodules in both lung fields, giving a millet-grain appearance, associated with mediastinal adenopathy and osteolytic lesions of the sacroiliac joint. Pulmonary localization was confirmed by sputum Genexpert. HIV-1 and 2 serology and Lupus work-up were negative, and plasma protein electrophoresis did not reveal hypergammaglobulinemia. Antibacillary chemotherapy and bolus corticosteroids were started as a matter of urgency. Cytobacteriological and chemical examination of the CSF from the follow-up lumbar puncture revealed acellular meningitis, with hyperproteinorachia at 1g/L and hypoglycorachia at 0.25 g/L.

Conclusion
The lack of CSF pleocytosis in tuberculous meningitis should not rule out this diagnosis in immunocompetent patients.



LB-CAS-015: Atypical Ocular Bartonellosis: A Case Report

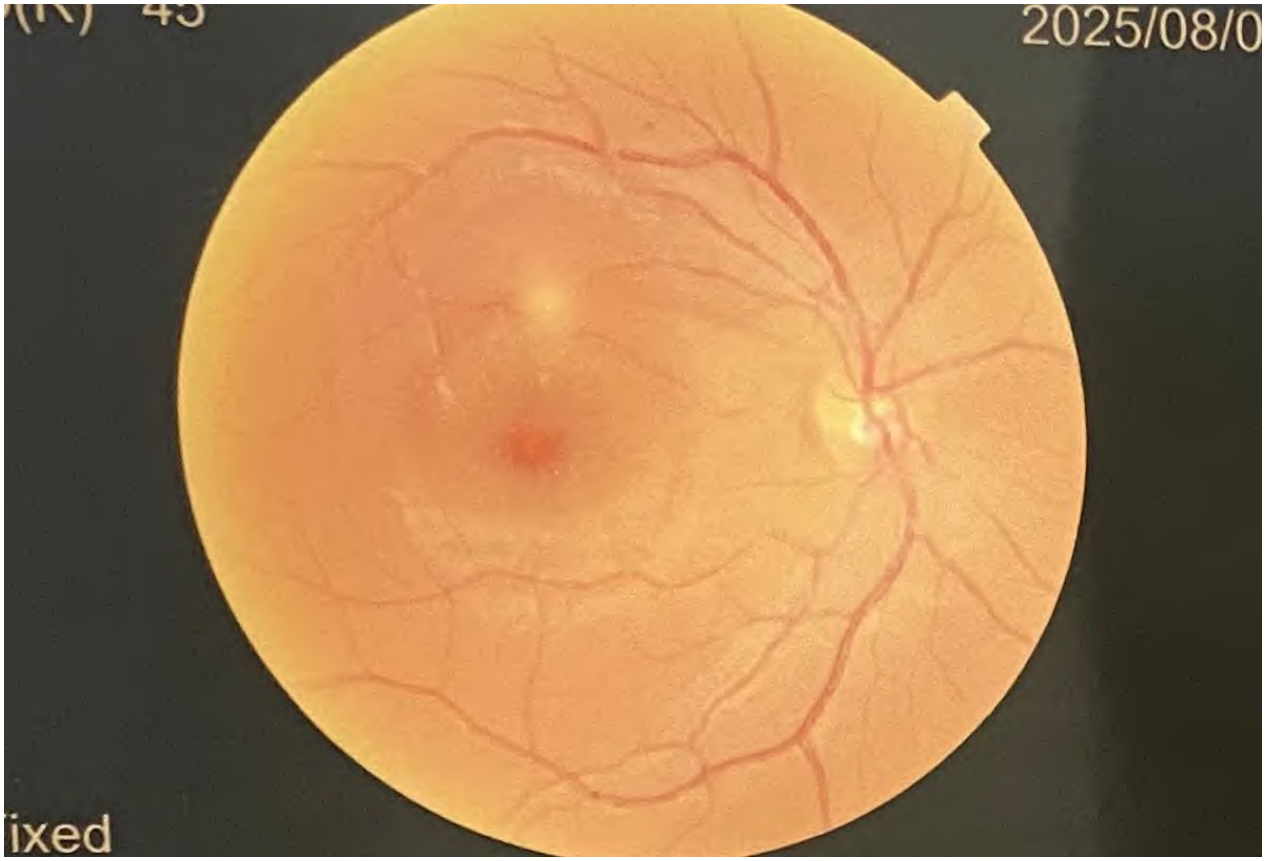
Hassan Kamena Mwana-Yile, Fatima Ihbibane, Latifa Marih

Ibn Rochd University Hospital, Faculty of Medicine and Pharmacy, Hassan II University, Morocco

Introduction
Bartonella henselae is a Gram-negative bacillus responsible for causing bartonellosis who can present in various clinical forms, ranging from isolated lymphadenopathy to systemic involvement, and occurs in both immunocompetent and immunocompromised individuals. Some rare systemic complications have been documented, including neuroretinitis. We report a case of chorioretinitis caused by B. henselae in an immunocompetent patient, which occurred without the presence of papilledema.

Case Presentation
A 27-year-old female patient with a history of multiple cat scratches presented on August 28, 2025, with a gradual decline in visual acuity in her right eye. This decline had been developing for three weeks following scratches from cats and was accompanied by a fever of 39°C. Optical coherence tomography revealed serous retinal detachment with associated epithelial detachment. Fluorescein angiography showed a hyperfluorescent perimacular focus in the superior temporal region, consistent with chorioretinitis characterized by star-shaped macular exudates, and there was no evidence of papilledema. HIV-1 and 2 serology was negative. Serum protein electrophoresis returned normal results, and the HbA1c level was 5.5%. Bartonella henselae serology was positive (IgG) in indirect immunofluorescence with a titer greater than 1/1280. The treatment plan included doxycycline (100 mg every 12 hours), rifampicin (300 mg every 12 hours), and corticosteroid therapy (1 mg/kg) for 4 weeks. Throughout the course of the illness, the patient did not develop a fever. A follow-up ophthalmological examination is scheduled at the end of treatment.

Conclusion
Ocular bartonellosis can lead to unusual eye damage, specifically chorioretinitis, even in the absence of papilledema.



LB-CAS-018: A Rash Decision: A Case of Disseminated Fusariosis in a Patient with Acute Lymphoblastic Leukemia

Ma. Kathleen Jane Villaruel, Lorenz Lista, Catherine Yu

St. Luke's Medical Center - Quezon City

Introduction
Fusarium species are ubiquitous filamentous fungi that cause invasive infections, particularly in immunocompromised hosts. Disseminated fusariosis, though rare, is associated with high morbidity and mortality. It should be suspected in patients with prolonged neutropenia and persistent fever unresponsive to broad-spectrum antimicrobials, especially when accompanied by sudden onset of characteristic skin lesions. The infection is typically acquired through inhalation, direct inoculation, or environmental exposure, including hospital water systems.

Case Presentation
We report a 64-year-old female with precursor B-cell acute lymphoblastic leukemia who developed profound neutropenia after induction chemotherapy with HyperCVAD. She presented with persistent fever and progressive cough despite empiric broad-spectrum antimicrobials, and initial blood cultures were negative. One week post-chemotherapy, erythematous maculopapular lesions appeared on her extremities, which evolved into necrotic plaques. Repeat blood cultures grew Fusarium solani complex, confirming disseminated fusariosis. Combination antifungal therapy with liposomal amphotericin B and voriconazole led to defervescence and clearance of the organism on subsequent blood cultures.

Conclusion
Disseminated fusariosis is a life-threatening fungal infection that should be considered in persistently febrile, neutropenic patients with new skin lesions. Early recognition, comprehensive diagnostic evaluation, and prompt initiation of appropriate antifungal therapy are essential. Combination therapy with lipid-based amphotericin B and voriconazole is recommended while awaiting susceptibility results, and clinical outcomes largely depend on recovery from immunosuppression, particularly neutrophil recovery.

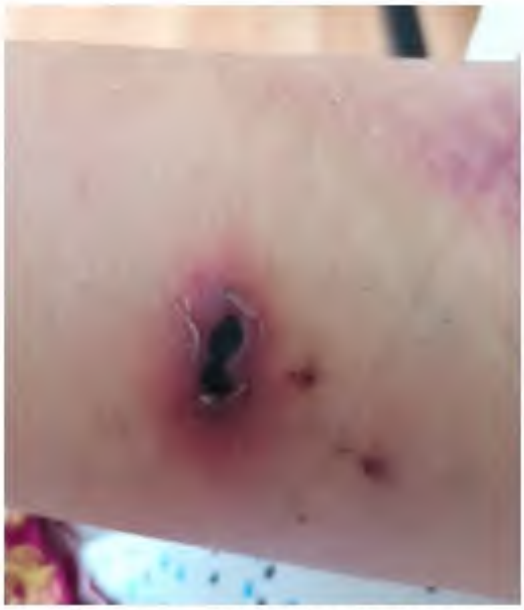


Figure A. A solitary, well-defined, irregular shaped ulcer on an erythematous base with necrotic eschar on the ventral aspect of the patient's right forearm

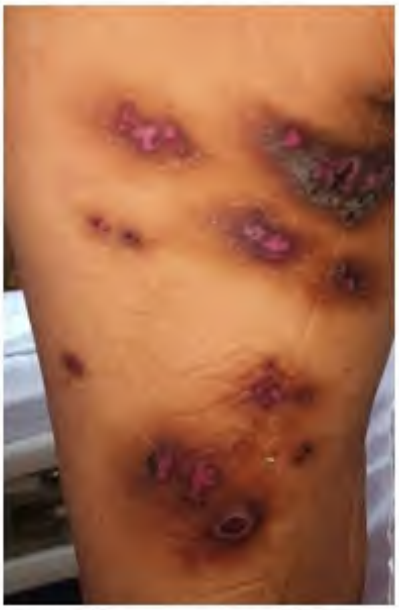


Figure B. Multiple well-demarcated ulcerative and necrotic lesions with violaceous raised borders, some with necrotic eschar and surrounding erythema over the patient's lower extremity

LB-CAS-019: From Gut to Bile: Arcobacter butzleri as an Unusual Cause of Biliary Sepsis in the Setting of Pancreatic Malignancy

Lorenz Lista, Catherine Yu

St. Luke's Medical Center - Quezon City

Introduction
Arcobacter butzleri is an emerging enteric pathogen primarily associated with gastroenteritis and foodborne illness. Extraintestinal infections are exceedingly rare, with only isolated reports of bacteremia, peritonitis, and biliary sepsis. This case demonstrates the clinical relevance of A. butzleri in an uncommon biliary tract infection, highlighting its expanding pathogenic potential, particularly in patients with malignancy and biliary instrumentation.

Case Presentation
We report a case of a 67-year-old male with obstructive jaundice due to a pancreatic head mass and choledocholithiasis who underwent endoscopic retrograde cholangiopancreatography (ERCP) with stent placement. One month later, he presented with fever, chills, hypotension, progressive jaundice, and severe anemia. Laboratory studies revealed leukocytosis (22,150/μL, 90% neutrophils), hemoglobin of 4.2 g/dL, and elevated creatinine. Imaging showed intrahepatic ductal dilatation, hepatic lesions suggestive of metastases, and gallbladder wall thickening. We initiated empiric piperacillin–tazobactam. Repeat ERCP with stent exchange yielded bile cultures that grew A. butzleri. We switched antibiotics to azithromycin, which resulted in defervescence and marked clinical improvement alongside definitive

Conclusion
This case underscores A. butzleri as an emerging opportunistic pathogen capable of causing biliary sepsis, likely facilitated by biofilm formation and translocation from the gut in patients with malignancy and biliary prostheses. We emphasize the importance of considering this organism in device-associated infections and prioritizing culture-guided therapy and timely source control to optimize outcomes.

LB-CAS-020: Beyond Colonization: Diagnostic and Therapeutic Challenges of Mycobacterium simiae and Kodamaea ohmeri Coinfection in Structural Lung Disease

Lorenz Lista, Armin Masbang

St. Luke's Medical Center - Quezon City

Introduction
Mycobacterium simiae is a slow-growing, photochromogenic nontuberculous mycobacterium (NTM) that causes pulmonary disease primarily in individuals with structural lung abnormalities or compromised immunity. Although fungal coinfections are rare, their presence can significantly worsen outcomes. Kodamaea ohmeri is an opportunistic yeast usually associated with bloodstream infections; its isolation from respiratory specimens is exceptionally uncommon, making dual infection with M. simiae particularly challenging.

Case Presentation
We present a case of a 67-year-old woman with a history of treated pulmonary tuberculosis and bronchiectasis who was admitted for worsening productive cough, dyspnea, weight loss, and hypoxemia. Chest imaging revealed multifocal bronchiectasis, nodular opacities, consolidation, and ground-glass infiltrates. Initial tests for Mycobacterium tuberculosis were negative, but sputum cultures later grew M. simiae, susceptible to clarithromycin, moxifloxacin, and trimethoprim-sulfamethoxazole, prompting targeted therapy.

During hospitalization, the patient’s condition deteriorated with persistent fever, hypotension, and neurological changes, requiring mechanical ventilation and central venous catheter insertion. Blood and sputum cultures both grew K. ohmeri, confirming the rare coexistence of fungemia and pulmonary fungal infection. Antifungal therapy with fluconazole, later escalated to voriconazole, was initiated alongside ongoing antimycobacterial treatment. With combined antimicrobial therapy, intensive supportive care, and close monitoring, the patient gradually improved, and blood cultures became sterile.

Conclusion
This case illustrates a rare and complex coinfection caused by M. simiae and K. ohmeri involving both bloodstream and respiratory tract. Shared mechanisms, including impaired mucociliary clearance, biofilm formation, and immune dysfunction, likely facilitated this dual infection. Early recognition, accurate microbial identification, and coordinated therapy are crucial to improving outcomes in such high-risk patients.

LB-CAS-021: Disseminated Clostridium Septicum Infection Presenting with Hepatic Abscess in a Patient with Metastatic Colon Adenocarcinoma

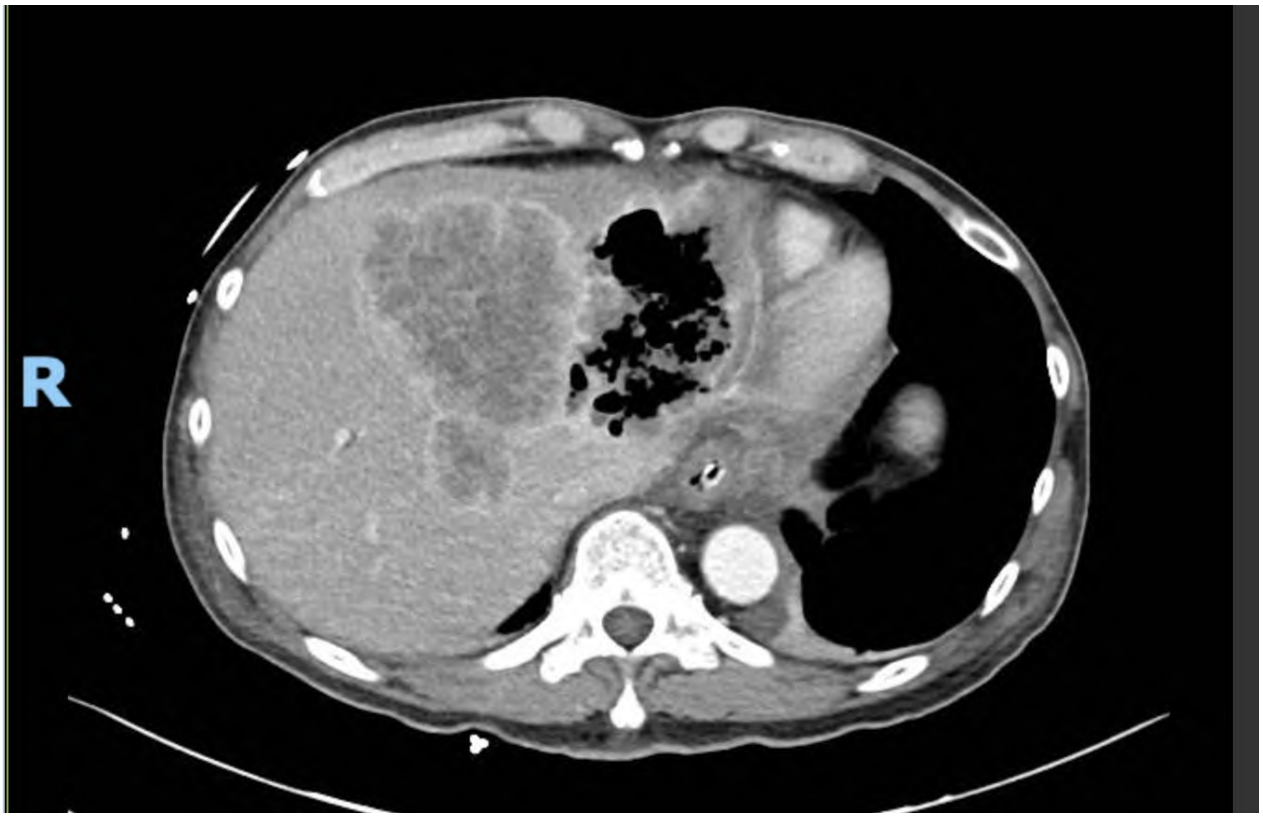
Ma. Kathleen Jane Villaruel, Jenny Mae Quinivista-Yoon

St. Luke's Medical Center - Quezon City

Introduction
The association between certain bacterial infections and malignancy has been demonstrated by several case reports in literature. Disseminated infection, particularly with Clostridium septicum, an aero-tolerant species of Clostridium and an intestinal commensal organism is rare and represents only 2-11% of clostridial infections. Clostridium septicum sepsis has been associated with underlying colorectal malignancies and often results in a high mortality rate. A concomitant C. septicum hepatic abscess in patients with liver metastases is also infrequently encountered.

Case Presentation
We report a case of a 72-year-old male with Stage IV colonic adenocarcinoma with liver and lung metastases who presented with a one-day history of fever, abdominal pain, and altered sensorium. At the emergency room, he was hypotensive, tachycardic and persistently febrile. Initial workup revealed leukocytosis, elevated transaminases, bilirubin and alkaline phosphatase. Due to history of multiple hospitalizations and antibiotic use, he was started empirically on Piperacillin-Tazobactam. CT scan of the whole abdomen was done which showed multiple air locules within the hepatic lesions, likely from abscess formation. He subsequently underwent percutaneous drainage of the hepatic abscess. Blood cultures and anaerobic abscess culture obtained were both positive for Clostridium septicum. Intravenous Metronidazole was then added to the initial antibiotic regimen.

Conclusion
Clostridium septicum infection should be suspected in patients with colorectal malignancy presenting with sepsis and hepatic abscess. Its identification warrants immediate treatment and emphasizes the importance of screening for underlying gastrointestinal malignancies in cases of unexplained Clostridium septicum bacteremia. Early recognition and the combined medical-surgical management remain critical to improving patient outcomes.



LB-CAS-022: The Double Burden Unveiled: When Dengue Meets Malaria Co-Infection in the Heart of Kapit District, Sarawak, Malaysia

Kiat Jeng Liew[1, 2], Tat Chee Calvin Chang[1, 2], Yih Hoong Lee[1, 2], Weng Yuen Wong[1, 2], Selwyn Wai Zhe Chin[1, 2], Yashine Rama Rao[1, 2], Rahjeswary Ramalinggam[1, 2],

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Introduction
Malaria and dengue are mosquito-borne infections that carry a high morbidity and mortality rates, commonly seen in endemic regions. However, co-infection with both diseases in a single patient is extremely rare and likely under-reported, as they are transmitted by distinct mosquito species. Hence, effective clinical reasoning and judgment are crucial in managing such complex cases.

Case Presentation
We report a case of a 57-year-old Iban woman who presented with a 4-days history of fever, generalized myalgia, arthralgia, and poor appetite. Her blood film for malaria parasites (BFMP) confirmed the presence of Plasmodium knowlesi trophozoites. Laboratory results revealed leukopenia and thrombocytopenia. Interestingly, she hailed from a dengue-endemic area, and her husband, who exhibited similar symptoms, was diagnosed with dengue on the same day. The constellation of clinical history, symptoms, and laboratory parameters heightened suspicion for dengue fever, prompting further diagnostic testing. She tested positive for the non-structural protein 1 (NS1) antigen on Day 4 of illness. Hence, a diagnosis of malaria-dengue co-infection was made. The patient was admitted and commenced on antimalarial therapy and dengue fluid management following national protocols. On Day 7 of illness, her dengue serology showed positive for both dengue immunoglobulin M (IgM) and dengue immunoglobulin G (IgG), consistent with the recovery phase of dengue. The patient demonstrated clinical improvement and was discharged uneventfully.

Conclusion
Malaria may mimic dengue, particularly in its early febrile phase. Physicians should be aware that co-infection with malaria and dengue is possible and that early recognition and prompt treatment are essential to achieve favourable outcome.

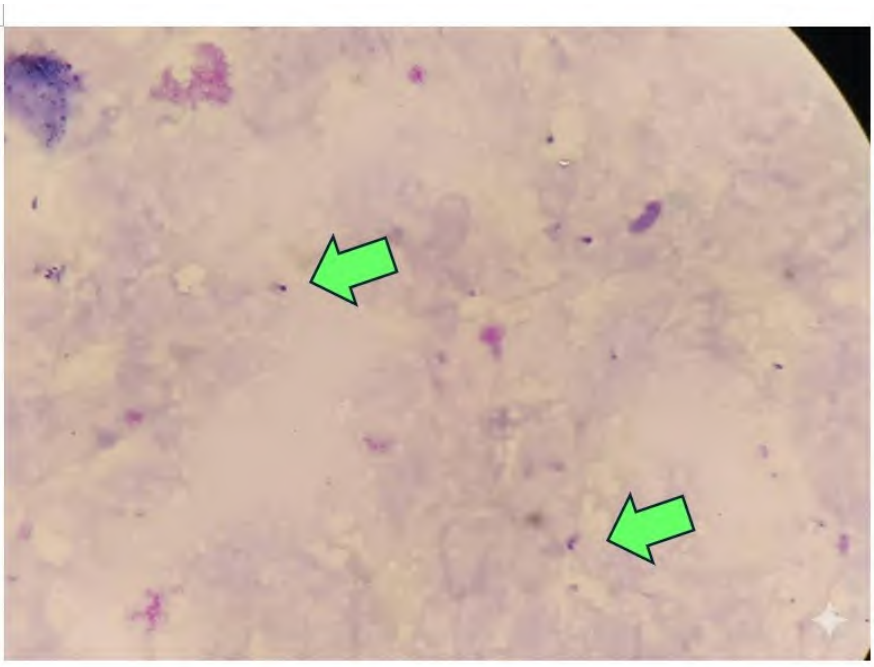
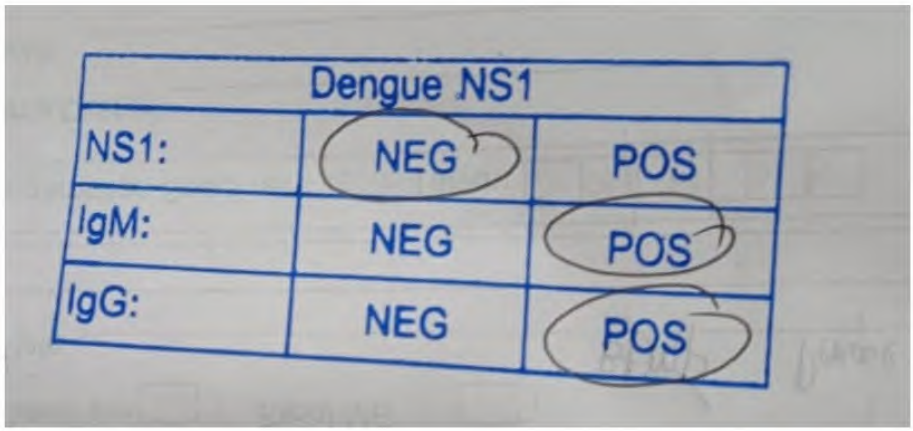


Figure A: Blood Film for malaria parasites (BFMP) 18/09/25: showing *Plasmodium knowlesi* Trophozoites (Green Arrows).



Dengue NS1		
NS1:	NEG	POS
IgM:	NEG	POS
IgG:	NEG	POS

Figure B: Repeated Dengue Rapid Test: on Day 7 of illness displayed non-structural protein 1 (NS1) negative and showed positive for both dengue immunoglobulin M (IgM) and dengue immunoglobulin G (IgG).

LB-CAS-A018: Case Report of Melioidosis and Urosepsis Due to Candida albicans

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Universitas Syiah Kuala

Introduction

This case report presents a 65-year-old male with poorly controlled diabetes mellitus who developed a rare co-infection involving Burkholderia pseudomallei and Candida albicans and is hospitalized for unstable angina and hyperglycemic hyperosmolar nonketotic syndrome (HHNS).

Case Presentation

The patient with a 10-year history of type 2 diabetes and hypertension presented to the emergency department with chest pain, nausea, and vomiting. The initial ECG was unremarkable to acute coronary syndrome nor STEMI. Lab findings revealed hyperglycemia (643 mg/dL) and metabolic acidosis. During hospitalization, the patient developed progressive pulmonary and urinary symptoms, and a brain MSCT revealed cerebellar infarction. Yeast and pseudo hyphae were detected in urine; Candida albicans was confirmed by VITEK® 2.0 Compact. The patient was subsequently admitted to the intensive care unit (ICU) due to the need for ventilatory support. Cultures from the endotracheal aspirate and central venous catheter (CVC) revealed Burkholderia pseudomallei and pseudo hyphae as observed on direct gram stain and KOH wet mount. The patient is hospitalized for 20 days. Targeted therapy with meropenem and voriconazole led to significant clinical improvement.

Conclusion

Melioidosis and candidiasis rarely occur together, especially in hospital settings. Diabetes mellitus is a known risk factor for both infections. Both organisms pose a significant risk to individuals with compromised immune systems. This report highlights the complexity of managing opportunistic infections in diabetic patients. It underscores the need for clinicians to consider opportunistic infections in ICU patients with metabolic comorbidities and to pursue early culture-based diagnosis.

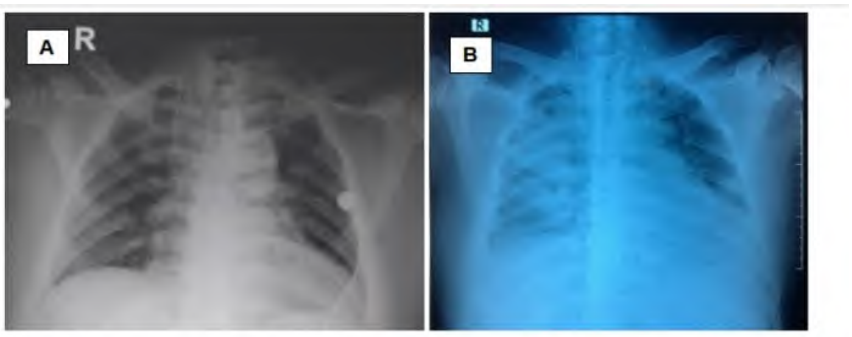

Figure 1. A. CXR on admission. Empiric antibiotics with ceftriaxone were administered
Figure 1. B. CXR 4 days hospitalization showing early pulmonary edema and worsening pneumonia

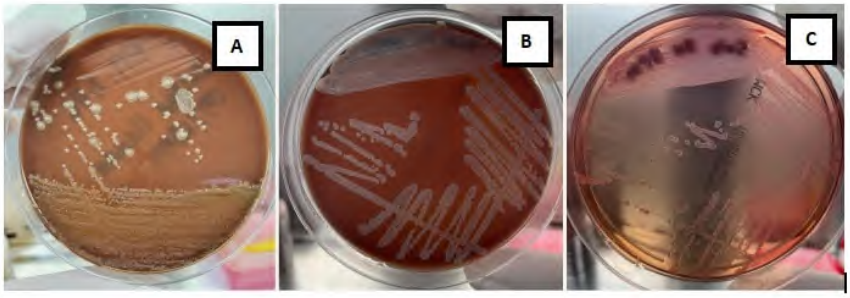

Figure 2. A. Direct ETT specimen inoculated on Chocolate Blood Agar after incubated for 72 hrs incubation with CO_2 5%
Figure 2. B. Direct ETT specimen inoculated on Sheep Blood Agar after incubated for 72 hrs incubation without CO_2 5%
Figure 2. C. Direct ETT specimen inoculated on MacConkey Agar after incubated for 72 hrs incubation without CO_2 5%

LB-RES-001: Significant Overlap in Disease Phenotype Between Genotypically Defined Hypervirulent and Classical Klebsiella Pneumoniae Among Bacteraemic Patients in Endemic Area

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Background
Hypervirulent Klebsiella pneumoniae (hvKP) has been described as an invasive syndrome of liver abscess and/or metastatic infection in Asia, and this syndrome is emerging as a global disease.

Method
This study investigated the relationship between disease phenotypes and hypervirulence markers in 273 patients with Klebsiella pneumoniae (KP) bacteraemia from three hospitals in Hong Kong from 2019 to 2023. Whole genome sequences were analysed by Kleborate and Kaptive. Epidemiological background, clinical manifestation, virulence genes, and AMR data were analysed. Genotypically defined hvKP (g-hvKP) was defined as having iucA, iroB, rmpA, rmpA2, and peg-344. KP other than g-hvKP are classified as classical KP (cKP).

Results
The mean age was 72.2 years. The M:F ratio was 1.3:1. The 14-day mortality rate was 19.8%. 216 isolates were cKP and 57 were g-hvKP. Using community-onset liver abscess and/or metastatic infection as clinical gold standard of hvKP, g-hvKP has a sensitivity of 46% and specificity of 86%. g-hvKP caused only 51% of liver abscess. g-hvKP was not significantly associated with mortality, disease severity, metastatic infection, or pneumonia. Similar results were obtained when using rmpA/rmpA2 as the definition of g-hvKP.

The commonest K types were K1 (10.6%) and K2 (13.9%). The commonest ST was ST 23 (8.8%). g-hvKP were less resistant to cephalosporins ($p = 0.02$) and fluoroquinolones ($p = 0.01$). BlaESBL was present in 42 isolates, 90% being cKP. None carried carbapenemases.

Conclusions
Significant overlap exists in disease phenotype between cKP and g-hvKP, ranging from liver abscess to other manifestations. g-hvKP was not associated with mortality or disease severity.

LB-RES-002: Respiratory Syncytial Virus Among Hospitalized Filipino Adults: A Study on Prevalence, Clinical Presentation, and Outcomes in a Tertiary Hospital

Lorenz Lista[2], Minette Claire Rosario[2], Mark Ronver Engracia[1], Lourdes Carolina Dumlao[1], Marji Umil[2], Carmenchu Marie Villavicencio[1], Zenith Alano[1]

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[2]St. Luke's Medical Center - Quezon City

Background
Respiratory syncytial virus, long known as a pediatric pathogen, is increasingly recognized as an important cause of illness in adults, especially the elderly and those with comorbidities. Its impact among hospitalized Filipino adults remains poorly described.

The objectives of this study are to determine the prevalence, clinical features, and outcomes of RSV infection in adults admitted with acute respiratory tract infections (ARTIs), and to compare these with non-RSV viral infections.

Method
We conducted a retrospective cohort study in two tertiary centers of St. Luke's Medical Center from April 2022 to December 2024. Adults admitted with ARTIs who underwent respiratory panel testing within five days were included. Patients with multiple viral co-detections or hospital-acquired infections were excluded. RSV cases were compared with non-RSV viral infections (excluding SARS-CoV-2).

Results
The overall prevalence of RSV was 5.7%, with most cases clustering in the last quarter of the year. RSV patients were older (68.0 vs. 58.9 years) and more often female. Asthma and chronic renal failure were the more common comorbidities. Cough, crackles, and radiographic pneumonia were significantly more frequent. P. aeruginosa and S. marcescens co-infections occurred more often. RSV was linked to longer hospital stay and higher mortality.

Conclusions
RSV is a substantial contributor to severe respiratory illness in hospitalized adults. It is associated with distinct clinical and epidemiologic features, and worse outcomes compared to non-RSV viral infections. These findings underscore the need for increased clinical awareness, especially among high-risk populations, and support the importance of adult RSV surveillance and prevention strategies, including vaccination.

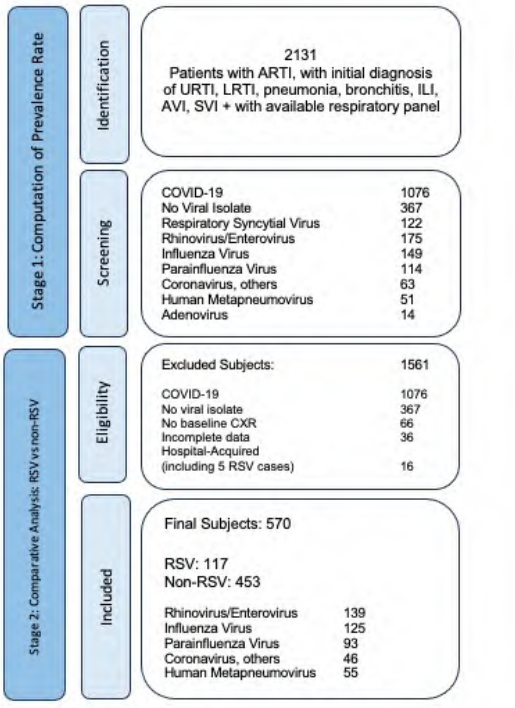

Figure 2. Flow diagram for selection of subjects.

LB-RES-003: Prevalence of Hepatitis C Infection among Immunocompromised Patients at St. Luke's Medical Center – Quezon City: A Five-Year Retrospective Cohort Study

Lorenz Lista, Minette Claire Rosario

St. Luke's Medical Center - Quezon City

Background
Introduction: Hepatitis C virus (HCV) infection remains a global health concern, with an estimated prevalence of 2.5% (177.5 million adults). Data on HCV among immunocompromised patients in the Philippines are lacking. This study examined the prevalence, characteristics, and outcomes of HCV coinfection among immunocompromised individuals at St. Luke's Medical Center, Quezon City.

Objectives: To determine the prevalence of HCV coinfection among patients with HIV, end-stage renal disease (ESRD), cancer, and organ transplants.

Method
We conducted a retrospective cohort study of adults admitted from September 2018 to September 2023. Inclusion criteria were HIV, ESRD on hemodialysis, malignancies, or solid organ/bone marrow transplantation with documented HCV testing. Demographic, clinical, testing, and treatment outcomes were analyzed using descriptive statistics.

Results
Of 2,470 patients, 35 had HCV, yielding an overall prevalence of 1.42%. Prevalence was highest among HIV (2.74%) and ESRD (1.59%) patients. While older patients were more common, prevalence was similar across age groups. Risk indicators included low CD4 counts, multiple sexual partners, and history of blood transfusion. Among HCV-positive patients, 77.1% did not undergo confirmatory HCV RNA testing, and only 17.1% received antiviral therapy.

Conclusions
HCV coinfection prevalence was low overall but higher in HIV and ESRD groups, underscoring the need for enhanced surveillance and targeted interventions. The underutilization of confirmatory testing and treatment highlights significant gaps in care, emphasizing the importance of improving diagnostic and therapeutic pathways for immunocompromised patients in the Philippines.

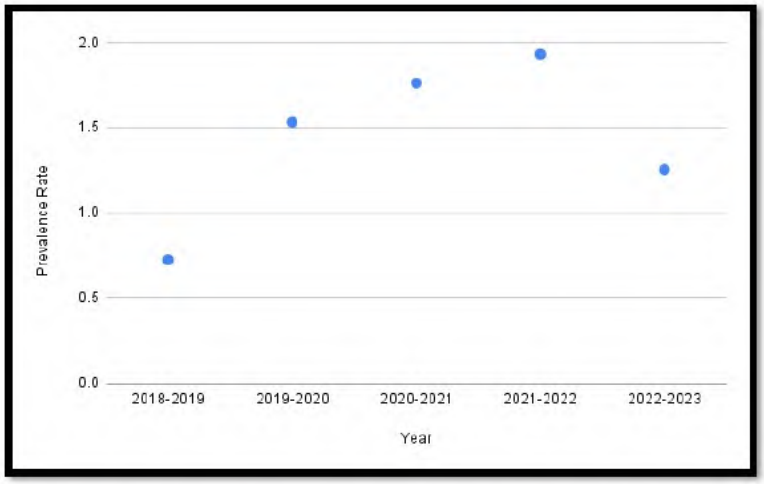

Figure 3. Prevalence rate of hepatitis C infection per year, SLMC-QC, 2018-2023

The graph illustrates the prevalence rate of hepatitis C coinfection over five years from 2018 to 2023. It shows a clear upward trend from 2018-2019 to 2021-2022. Starting at 0.72% in 2018-2019, it more than doubled by 2019-2020, reaching 1.53%. This increase continued through the following years, climbing to 1.76% in 2020-2021 and peaking at 1.93% in 2021-2022. These periods of upward trend coincided with the Covid-19 pandemic. However, the trend shifted in 2022-2023, with the prevalence rate decreasing to 1.25%.

LB-RES-004: Clinical Profiles and Patterns of Children with Leprosy from a Tertiary Hospital in the Philippines: A 10-Year Retrospective Study

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Department of Dermatology, Jose R. Reyes Memorial Medical Center, Philippines

Background
Leprosy is a chronic bacterial infection with affinity for the skin and peripheral nerves. Despite global efforts, leprosy remains prevalent in some countries. Children represent one of the most vulnerable groups due to their immature immune systems and close contact with infected family members.

Method
The study determined the incidence and clinico-demographic profile of children with leprosy confirmed by slit-skin smear and/or histopathological studies from 2014 to 2023 at the Department of Dermatology, Jose R. Reyes Memorial Medical Center. This research was a descriptive cross-sectional study. Demographic information, clinical presentation, laboratory findings, diagnosis and treatment, and follow-up outcomes were collected.

Results
Seventy-nine pediatric patients were included. Majority of the cases were from 2014-2019, predominantly adolescent aged 11–18 years (75.9%), mostly males (60.8%), presented with multibacillary disease (79.7%), had more than five skin lesions (73.4%), and ulnar nerve affectation (6.32%). Median duration of disease until consultation was 1 year. Final diagnosis was mostly lepromatous leprosy (38%). Slit-skin smears were positive (75.9%), with a mean bacteriological index (BI) of 3.13. Lepra reactions occurred (34.2%). Despite high bacillary loads, only some had documented disabilities (20.3%). Treatment was completed in more than half of patients (59.5%), while some required treatment extension (13.9%) and had relapsed (1.3%).

Conclusions
Leprosy among children remains a significant public health concern. The predominance of multibacillary forms, high BI, and delayed diagnosis in children suggest ongoing community transmission. The results highlight the significance of early detection, improved contact tracing, bacteriological monitoring, and adherence support to lessen disability and stop transmission in endemic areas.

Table 1. Disease characteristics and treatment variables in pediatric leprosy patients

Disease and Treatment Characteristics	Pediatric Leprosy Patients (*n* = 79)
Lepra Reaction (*n*, %)	
Absent	44 (55.7)
Type 1	18 (22.8)
Type 2	17 (21.5)
Lepra Reaction Symptoms* (*n*, %)	
Pain/Arthralgia/Myalgia	15 (30.6)
Swelling/Edema	10 (20.4)
Nodules	10 (20.4)
Fever	8 (16.3)
Tenderness	4 (8.1)
Papules/Plaques	2 (4.0)
Disability (*n*, %)	
Absent	69 (87.3)
Grade 1	6 (7.6)
Grade 2	4 (5.1)
Final Diagnosis (*n*, %)	
Indeterminate	10 (12.7)
Lepromatous	34 (43.0)
Borderline lepromatous	11 (13.9)
Mid-borderline	10 (12.7)
Borderline tuberculous	9 (11.4)
Tuberculous	5 (6.3)
WHO Classification (*n*, %)	
Pauci-bacillary	8 (10.1)
Multi-bacillary	71 (89.9)
Treatment Completion (*n*, %)	
Incomplete	29 (36.7)
Completed	50 (63.3)
Treatment Duration (*n*, %)	
1-6 months	29 (36.7)
7-12 months	40 (50.6)
13-24 months	9 (11.4)
>24 months	1 (1.3)
Treatment Adherence (*n*, %)	49 (62.0)
Disease Relapse (*n*, %)	1 (1.3)
Treatment Extension (*n*, %)	11 (13.9)

*
N = 49 for lepra reaction symptoms

LB-RES-005: Prevalence and Epidemiology of Onychomycosis in Filipino Patients of a Tertiary Hospital in the Philippines

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Department of Dermatology, Jose R. Reyes Memorial Medical Center, Philippines

Background
Onychomycosis is a fungal nail infection which results in discoloration, thickening, and detachment from the nail bed. Approximately 10% of the overall population and 50% of those over 70 years experience onychomycosis. Dermatophytes are responsible for 60–70% of infections.

Method
Forty-one Filipino patients with suspected onychomycosis, seen from 2024 to 2025, at the outpatient dermatology clinic of Jose R. Reyes Memorial Medical Center in the Philippines, underwent clinical evaluation, dermoscopy, Wood's lamp examination, potassium hydroxide (KOH) smear, and fungal culture. Clinical type, risk factors, comorbidities, and Onychomycosis Severity Index (OSI) were documented.

Results
Patients had a mean age of 53.1 years and most were female (61%). Common comorbidities included hypertension (36.6%) and obesity (34.1%). Risk factors included frequent wet work (75.6%) and use of open footwear (56.1%). The most common clinical type was distolateral subungual onychomycosis (58.5%). Over half of cases (51.2%) were classified as severe (mean OSI 16.3) and had KOH smear positive (68.3%). Fungal culture revealed non-dermatophyte molds with Candida (36.6%) and Aspergillus (34.1%) as the most common isolates, followed by dermatophytes such as Trichophyton (9.8%). The most common dermoscopic finding was chromonychia. An inverse relationship between disease duration and OSI was noted in distolateral subungual onychomycosis.

Conclusions
This study highlights a predominance of non-dermatophyte fungal infections among Filipino patients with onychomycosis in contrast to global studies. Neither clinical diagnosis, KOH smear, nor fungal culture alone is fully reliable for diagnosing onychomycosis. These findings underscore the evolving epidemiology of onychomycosis and the need for updated diagnostic strategies in local practice.

Table 1. Results of diagnostic tests in onychomycosis patients

Diagnostic Test Results	Onychomycosis Patients (*n* = 41)
Woods Lamp (*n*, %)	
None	39 (97.5)
Fluorescence	1 (2.5)
KOH Smear (*n*, %)	
None	13 (31.7)
Spores	11 (26.8)
Yeast Cells	1 (2.5)
3+	14 (34.1)
4+	2 (4.9)
Final Culture (*n*, %)	
None	5 (12.2)
Aspergillus	15 (36.6)
Candida	15 (36.6)
Penicillium	2 (4.9)
Trichophyton	4 (9.8)
Dermoscopy Results (*n*, %)	
Longitudinal white striae	30 (75.0)
Jagged proximal edge	28 (70.0)
Intermittent spiked pattern	31 (77.5)
Chromonychia	38 (95.0)
Distal irregular termination	33 (82.5)
Trachyonychia	29 (72.5)
Linear edge	27 (67.5)

LB-RES-006: Characterization of Antimicrobial Resistance and Hypervirulent Traits of Klebsiella Variicola Isolates Collected in South Korea

Dokyun Kim

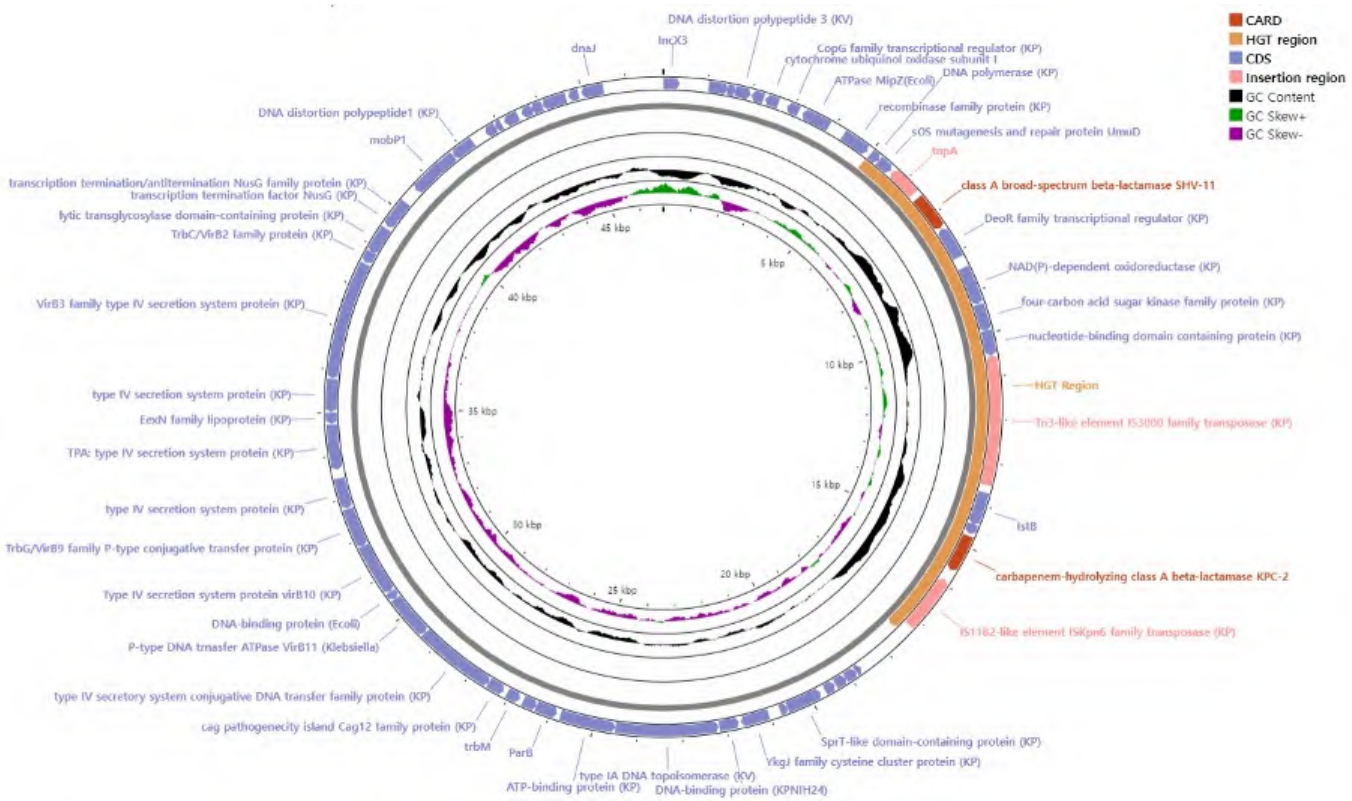
Yonsei University College of Medicine

Background
The Klebsiella pneumoniae complex includes five species including K. variicola. K. variicola had been recognized as a pathogen causing opportunistic infections to immunocompromised patients, however, the incidence has been recently increased. Recent studies revealed that the K. variicola strains with increased virulence and multidrug resistance have been reported.

Method
A total of 76 K. variicola isolates were collected from 12 local clinics in South Korea. The bacterial species were identified by Bruker Biotyper. Antimicrobial susceptibility was tested using disk diffusion according to the CLSI guideline. According to the resistance profile, putative beta-lactamase producers were selected, and common resistance determinants were investigated through PCR and sequencing methods, as described previously. Hypervirulent trait were determined by string tests, and capsular type were determined by wzi sequencing. Whole genome sequencing was performed to 18 isolates to compare the virulence factors.

Results
The antimicrobial resistance rates were below 10% for all tested antimicrobials. The resistance rate to piperacillin was 5.3%, and those to third-generation cephalosprion including cefotaxime and ceftazidime were 5.3% and 4.0%, respectively. Only one isolates were resistant to ertapenem. All four cefotaxime-resistant isolates harbored the blaCTX-M-9 gene. One carbapenem resistant isolates carried blaKPC-2 in its plasmid co-harbored with blaSHV-11. Five isolates were positive to string test, and two of them belonged to wzi201, and the remaining isolates to wzi671, wzi413, and wzi687.

Conclusions
The MDR or hypervirulent strains were still not common in South Korea. Further investigation should be performed to monitor the emergence of hypervirulent and resistant K. variicola clones in South Korea.



LB-RES-007: Biliary sepsis Caused by Burkholderia cepacia: A Rare Presentation

Lee Matthew Ponce, Gelza Mae Zabat

St. Luke's Medical Center Quezon City

Introduction
B. cepacia is a common pathogen causing nosocomial pneumonias. Literature on infections outside the respiratory tract is scarce. It is notorious for being inherently resistant to many drug classes. We present a case of biliary sepsis caused by B. cepacia in an immunocompromised host.

Presentation
A 53-year old Filipino male, recently diagnosed case of lung adenocarcinoma, presented with two month history of jaundice. Initial workups showed a leukocytosis with neutrophilic predominance. elevated transaminases and bilirubin levels. Alkaline phosphatase was also increased. A dynamic Computed Tomography scan of the liver revealed irregular hypodense nodules scattered in both hepatic lobes suggestive of metastases. Endoscopic retrograde cholangiopancreaticography (ERCP) with sphincterotomy and stent insertion was done. Post procedure, he developed fever episodes hence managed as a case of cholangitis. Piperacillin-tazobactam was started. Blood cultures obtained grew B. cepacia sensitive to Meropenem, Levofloxacin and co-trimoxazole. Antibiotics were eventually shifted to Meropenem. On the third day of antibiotics, patient still had fever episodes. The team then decided to do percutaneous transhepatic biliary drainage. Bile cultures were requested also yielded B. cepacia with the same antibiotic sensitivity. Blood cultures were repeated but still remained positive hence levofloxacin was added. The patient improved after two days, and repeat blood cultures showed clearing. Patient was then sent home with oral levofloxacin.

Conclusion
This paper describes one of the few cases of B. cepacia bacteremia secondary to a biliary tract infection. Burkholderia cepacia should be considered as a differential in immunocompromised patients who develop nosocomial biliary tract infections.

LB-RES-008: The Immunomodulatory and Antiviral Effects of Lactococcus lactis strain Plasma (LC-Plasma) in Healthy Vietnamese Medical Students During Clinical Placements – a Randomized Placebo-controlled Double-blind Parallel Group Study

Osamu Kanauchi

Kirin Holdings Co., Ltd.

Background
The global rise in viral infections, worsened by ecological changes, demands new prevention strategies beyond vaccines and antivirals, which are often compromised by viral mutations.

Method
This randomized, double-blind, placebo-controlled trial evaluated the immunomodulatory and antiviral effects of Lactococcus lactis strain Plasma (LC-Plasma) in healthy Vietnamese medical students, who represent healthcare workers (HCWs) at high risk of infection. Participants received oral LC-Plasma or placebo for four weeks. Clinical symptoms and immune responses from peripheral blood mononuclear cells (PBMCs) were assessed.

Results
The LC-Plasma group had significantly fewer cumulative days with fever and fatigue compared to placebo. Immune analysis showed increased expression of interferon-stimulated genes (ISGs), especially MxA, in the LC-Plasma group. Additionally, adding CpG ODN 2216, a mild TLR9 agonist, enhanced interferon-α (IFN-α) production in LC-Plasma participants with initially low IFN-α responses. Humoral factors from LC-Plasma-primed PBMCs inhibited dengue virus replication in vitro. These results suggest LC-Plasma activates plasmacytoid dendritic cells, boosting IFN-α production and systemic antiviral immunity through ISG upregulation. This enhanced immunity likely contributed to reduced viral symptoms and infection risk.

Conclusions
In summary, LC-Plasma supplementation may be a beneficial adjunct preventive measure to reduce HCWs from the symptoms of viral infections during outbreaks by modulating immune responses.

LB-RES-009: Comparative Genomics to Investigate the Resistome and Bacterial Heterogeneity in the Creekside Ecosystem in Navotas City: An Exploratory Research

Mariae Janselle Pamposa, Zamantha Bernadette Convento, Jhoanna Loraine Fabela, Khris Angelique Manalo, Duane Miguel Mariano, Eulce Jashen Regala, Hana Yesha Uthayasurian, Maria Ruth Pineda-Cortel, Sherill Tesalona

University of Santo Tomas

Background
Rapid urbanization and untreated sewage discharge have degraded aquatic ecosystems, particularly the Navotas River. This study aimed to assess antimicrobial resistance (AMR) patterns in bacterial communities to support rehabilitation efforts.

Method
A descriptive-correlational design was used at three creekside sites with varying human activity. Triplicate water samples (600 mL/site) were collected during the first and fourth weeks of January 2025. DNA was extracted and validated using Qubit, NanoDrop, and gel electrophoresis. Shotgun metagenomic sequencing was performed via Illumina NovaSeq (15 million reads/sample). Taxonomic classification used QIIME, KRAKEN, and BRACKEN, while ARGs were identified through Q2-RGI with the CARD database. One-way ANOVA assessed differences in bacterial and ARG abundance across sites.

Results
DNA quality met sequencing requirements, and physicochemical parameters were within normal limits. A diverse microbial community with known pathogenicity was found, including Pseudomonas, Sulfitobacter, Streptomyces, and Rhodococcus. The most abundant ARG was rpoB mutant in Bifidobacterium adolescentis (35.41%), conferring rifampicin resistance, followed by rpoB2 in Nocardia (20.94%). Other notable ARGs included sul1 (8.61%) and tlrC (4.90%), which are associated with sulfonamide and macrolide-lincosamide resistance. β-lactamases, including VIM, NDM, and OXA variants, were detected in P. aeruginosa and Klebsiella spp. Aminoglycoside-resistance genes were identified in P. aeruginosa and Serratia marcescens. No significant ARG abundance differences were found across sites ($p = 0.997$; $p = 0.777$).

Conclusions
The presence of antibiotic-resistant bacteria and ARGs, particularly rpoB mutants and β-lactamases, signals a silent AMR crisis in Navotas River. These findings highlight the urgent need for policy intervention and continuous AMR surveillance in aquatic environments.

LB-RES-012: Decoding Carbapenemase Resistance: A Comparative Analysis of MCIM and PCR

Sharifah Aisyah Sayed Hitam

Hospital Raja Perempuan Zainab II

Background
Carbapenemase-producing organisms (CPOs) represent a serious challenge in healthcare due to their multidrug resistance and high transmission potential. Prompt and accurate detection is critical for infection control. While Polymerase Chain Reaction (PCR) remains the gold standard for detecting carbapenemase genes, it is costly and less accessible in resource-limited settings. The Modified Carbapenem Inactivation Method (MCIM) offers a simpler and more affordable alternative. This study aims to evaluate the diagnostic performance of MCIM compared to PCR

Method
A total of 62 bacterial isolates were tested using both MCIM and PCR to detect carbapenemase genes. Concordance between the two methods was analyzed. Diagnostic performance was evaluated through sensitivity, specificity, diagnostic accuracy and Cohen's Kappa (κ).

Results
Among 62 evaluable isolates, 10 were excluded due to indeterminate MCIM results despite PCR positivity. Among the remaining 52 evaluable isolates, MCIM demonstrated a sensitivity of 95% (95% CI; 83.5% - 98.6%) and specificity of 33.3% (95% CI; 13.8% - 60.9%). Overall diagnostic accuracy was 80.8% (95% CI; 68.1% - 89.2%), with a Cohen's Kappa of 0.34, indicating fair agreement.

Conclusions
MCIM demonstrates high sensitivity with acceptable overall accuracy and fair agreement with PCR. While it cannot fully replace molecular methods, it may serve as a practical screening tool for CPOs in resource-limited settings. Its ease of use and reasonable performance support its integration into routine laboratory workflows for the early detection of carbapenemase producers.

LB-RES-014: Early Practice of Intravenous-to-Oral Switch of Antibiotics: An Interventional Prospective Study in a Tertiary Hospital in Kelantan, Malaysia

Hanan Hayati Mamat, Nur Maisarah Abu Bakar, Nur Aishah Che Mohd Zaid, Aisyah Nuha Mohd Sor, Muhammad Hafiz Abd Rahim

Hospital Raja Perempuan Zainab II

Background
Hospitalized patients initially on intravenous antibiotics can be safely switched to an oral equivalent within two to four days of admission once clinical stability is established. This study aimed to evaluate the outcomes of early switching of IV to oral antibiotics in medical ward HRPZ II.

Method
This was an interventional study conducted in HRPZII. In the standard of care phase, pharmacists performed the conventional practice of reviewing practice of IV-PO switches while attached printed checklists which contained IV-PO switch criteria to patients' medical notes on the day patients were eligible for the switch in the intervention phase.

Results
163 patients were recruited consisting of two groups; standard care (n=83) and intervention group (n=80). Majority were started with IV amoxycillin-clavulanic acid which was converted to oral prior to discharge (standard care: 56.6%, intervention: 61.3%). Timeliness of the switch was improved 1.98 days in the intervention phase (95% CI 1.32:2.65 days, $p<0.001$). Mean duration of IV antibiotics in the intervention phase was shorter than standard care (3.30 days (SD=1.36) vs 5.43 days (SD=2.79), $p<0.001$). Length of hospital stay in the intervention phase was shortened by 2.64 days ($p<0.001$). Median antibiotic cost savings for standard care (RM42, IQR=194.85) while for intervention phase (RM87.90, IQR=296.10), $p=0.39$).

Conclusions
Pharmacists initiated printed AMS recommendations are successful in improving the timeliness of IV-PO switch, reducing the duration of IV and length of hospitalization. However, in terms of antibiotic cost savings, there is not so much difference between both groups as tablet amoxycillin-clavulanic acid is more expensive than its intravenous form.

LB-RES-016: Water Flow Direction and Spatial Distribution of Schistosoma Cercariae in Peripheral Water Sites Around Naujan Lake, Oriental Mindoro: A Retrospective Study

Bea Alessandrine Maalihan, Gabrielle Andrea Genuino, Ma. Nelyn Joy Lascano, Rio Lorenzo Malapitan, Sophia Gabrielle Grecia

University of Santo Tomas

Background
Schistosomiasis remains a major health concern in developing countries. In the Philippines, S. japonicum primarily infects humans, with Oriental Mindoro among the most affected provinces. Water flow direction influences the distribution of Oncomelania snails and parasite spread, shaping transmission dynamics. Yet, studies on environmental determinants of snail survival are either limited or outdated. This study examined the relationship between water flow and the distribution of snails and cercariae in municipalities surrounding Naujan Lake. Recruitment has been completed, and analysis has been finalized.

Method
A retrospective study design analyzed GPS-mapped snail data from four municipalities. Samples were tested for Schistosoma infection, while government datasets on water current directions were correlated with infection rates. ArcGIS was used to map infected sites, and Chi-square tests in SPSS assessed associations between water flow and parasite prevalence, with significance at P<0.05.

Results
Findings revealed significant variation in snail abundance and infection linked to water flow. In Socorro and Victoria, snails and infected cercariae were concentrated in midstream-to-upstream and downstream zones, with strong correlations (P<0.05). Pola showed minimal presence and no significant association. Spatial mapping highlighted clusters of infected snails near river mouths and lake edges in southern and southwestern areas, particularly in Socorro and Victoria, identifying them as high-risk transmission zones.

Conclusions
Water flow direction strongly shapes snail habitats and parasite dispersal in Oriental Mindoro. The results emphasize targeted, site-specific interventions to control snail populations and interrupt transmission, supporting WHO’s elimination goals and improving resource allocation for schistosomiasis control.

Water Flow Direction and Spatial Distribution of Schistosoma Cercariae in Peripheral Water Sites Around Naujan Lake, Oriental Mindoro: A Retrospective Study

FIGURES & TABLES

Table 1. *Flow Pattern-Based Distribution of Oncomelania Snails in Endemic Municipalities of Oriental Mindoro*

Municipalities	Flow Pattern	Mean
Socorro	Downstream	19.8
	Midstream	0
	Midstream to downstream zone	0
	Midstream to upstream	119
Victoria	Downstream	64
	Midstream	0
	Midstream to downstream zone	44
	Midstream to upstream	0
Pola	Downstream	0
	Midstream	1
	Midstream to downstream zone	1
	Midstream to upstream	0

Table 2. *Flow Pattern-Based Distribution of Schistosoma cercariae in Endemic Municipalities of Oriental Mindoro*

Municip-alities	Flow Pattern	Positive	Negative
Socorro	Downstream	2.8	4
	Midstream	0	0
	Midstream to downstream zone	0	0
	Midstream to upstream	11	0
Victoria	Downstream	3	61
	Midstream	0	0
	Midstream to downstream zone	4	40
	Midstream to upstream	0	0
Pola	Downstream	0	0
	Midstream	0	0
	Midstream to downstream zone	0	0
	Midstream to upstream	0	0

Table 3. *Chi-Square Analysis of the Association Between Water Flow Patterns and the Presence of Oncomelania Snails and Schistosoma Cercariae in Oriental Mindoro*

	Chi-square test	Degree of freedom	P-value
Socorro	13.440	6	0.037
Victoria	28.000	6	0.000
Pola	1.283	2	0.526

Note: A p-value greater than 0.05 indicates no statistically significant correlation, while a p-value less than 0.05 indicates a statistically significant correlation.

Figure 2. *Spatial distribution of Oncomelania snails found in different municipalities: Socorro, Victoria, and Pola.*

Figure 3. *Spatial distribution of Schistosoma cercariae found in different municipalities: Socorro, Victoria, and Pola*

LB-RES-017: LC-Plasma Counters Heat-Stress–Induced Suppression of pDC IFN-α to Inactivated H1N1 In Vitro

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Kirin Holdings Co., Ltd.

Background
Heat stress can attenuate plasmacytoid dendritic cell (pDC) function, limiting type I interferon responses to viruses. Lactococcus lactis strain Plasma (LC-Plasma) activates pDCs, but direct evidence that it enhances responses to inactivated influenza and offsets heat-stress–induced suppression has been limited. This study tested whether LC-Plasma pre-exposure preserves pDC interferon-α (IFN-α) production under an external heat-stress condition in vitro.

Method
Human pDCs were isolated from PBMCs by magnetic beads as CD123^high/BDCA-2–positive cells at >90% purity and cultured. We set 38.5 °C as the heat-stress condition. H1N1 was inactivated by thimerosal/β-propiolactone treatment. IFN-α in supernatants was quantified by ELISA.

Results
Exposure to 38.5 °C abolished H1N1-induced IFN-α compared with 37 °C. LC-Plasma pre-exposure markedly enhanced IFN-α at 37 °C relative to non–pre-exposed controls, providing a direct demonstration consistent with prior human studies (Sugimura et al., 2015) that had suggested such enhancement ex vivo. Imaging analysis further showed that IFN-α induction by inactivated H1N1 involves phagocytosis of H1N1 virions. Under heat stress (38.5 °C), LC-Plasma pre-exposure enabled pDCs to produce sufficient, quantifiable IFN-α in response to inactivated H1N1, in clear contrast to the near-absent levels without pre-exposure.

Conclusions
In an in-vitro human pDC model, external heat stress (38.5 °C) abolished IFN-α responses to inactivated H1N1, whereas LC-Plasma pre-exposure enhanced responses at 37 °C and supported sufficient IFN-α production under heat stress. These data provide direct evidence that LC-Plasma augments pDC responses to inactivated influenza and suggest a practical approach to maintain type I interferon competence during environmental thermal stress.

LB-RES-018: Assessment of Antibacterial Property of Recombinant Endolysin Against Carbapenemase-Producing Carbapenem-Resistant Enterobacterales

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Universiti Putra Malaysia

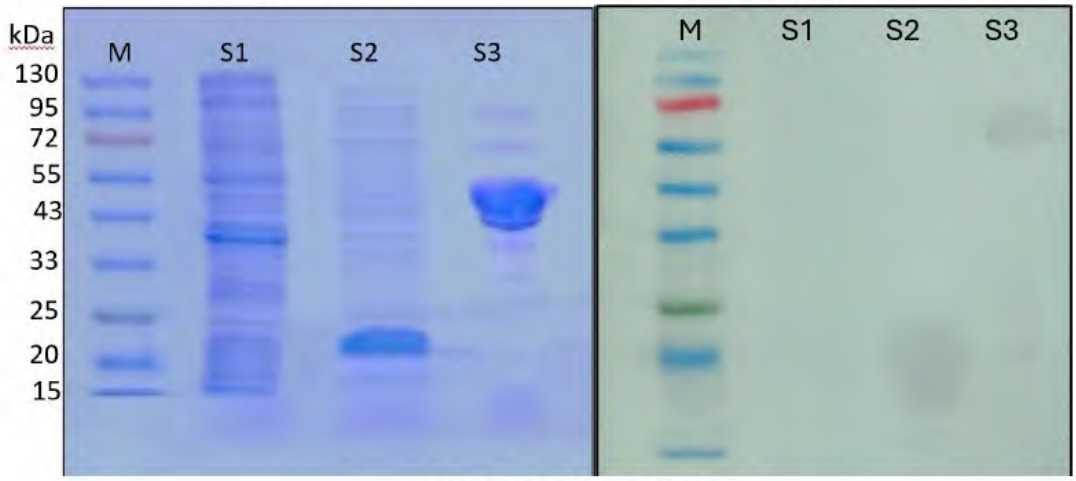
Background
Carbapenem-resistant Enterobacterales (CRE) represent a critical threat in modern healthcare. These gram-negative bacteria have developed resistance to carbapenems, a class of β-lactam antibiotics often regarded as the last line of defence against multidrug-resistant bacterial infections. The emergence of CRE highlights the dire need for novel substitutes to traditional antibiotics. In contrast, phage-derived endolysins, enzymes capable of lysing bacterial peptidoglycan layer, are being extensively investigated as potential agents to combat antimicrobial resistance. The aim of this study is to develop an alternative antimicrobial agent targeting CRE.

Method
Using an in silico approach, phage genomes were screened, and an endolysin encoded by Enterobacter phage E-2 was identified as a potential candidate. The predicted lysozyme-domain endolysin was cloned and transformed into Escherichia coli BL21 (DE3). Induction of IPTG efficiently triggered recombinant endolysin production, which was subsequently purified via immobilized metal affinity chromatography (IMAC). Protein expression was confirmed via sodium-dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) and Western blot analysis. The antimicrobial activity of the recombinant endolysin was assessed against CRE samples by measuring the optical density at 600nm (OD600) of treated and untreated bacterial cultures.

Results
The recombinant endolysin significantly inhibited the growth of carbapenemase-producing K. pneumoniae, E. coli, E. cloacae and E. kobei at a concentration of 100µg/mL, and bacterial growth was undetectable at 500µg/mL.

Conclusions
These findings suggest that the recombinant endolysin exhibit broad-spectrum lytic activity against multiple CRE species, hence may be a promising antimicrobial agent to treat CRE infections.

SDS-PAGE **Western blot**



Absorbance readings

Sample / Concentration	Absorbance at 600nm			
	Sample only	**100 µg/mL**	**250 µg/mL**	**500 µg/mL**
K. pneumoniae 1706	0.355	0.048	0.045	0.040
E. coli 25922	0.393	0.051	0.043	0.039
E. cloacae 1143	0.596	0.065	0.050	0.042
K. pneumoniae (blaNDM-1)	0.444	0.288	0.088	0.042
K. pneumoniae (blaNDM-1+KPC)	0.329	0.238	0.102	0.041
K. pneumoniae (blaKPC)	0.311	0.102	0.042	0.041
K. pneumoniae (blaNDM-1+OXA-48)	0.409	0.268	0.099	0.042
K. pneumoniae (blaOXA-48)	0.429	0.087	0.041	0.040
E. coli (blaNDM-1+KPC)	0.200	0.041	0.040	0.040
E. cloacae (blaNDM-1)	0.297	0.125	0.041	0.041
E. kobei (blaNDM-1+KPC)	0.498	0.179	0.041	0.041
MHB broth	0.042	-	-	-
Tris-HCl buffer	0.040	-	-	-

LB-RES-019: Identification of Non-Tuberculosis Mycobacteria as the cause of Pulmonary Disease Using Nanopore Sequencing with MLSTverse Analysis and Maldi-Tof

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Background
In Indonesia lung infections caused by nontuberculous mycobacteria (NTM) are increasingly common, particularly among people with lung infection and weak immune systems. These infections are often misdiagnosed as tuberculosis (TB) thus leading to treatment delays that worsen patient outcomes. Species identification of NTM can help clinicians in Indonesia's hospitals to start treatment sooner, improving care and reducing the spread of these serious infections.

Method
Specimens were collected in 2024-2025. Forty-six clinical isolates were obtained from sputum or bronchoalveolar lavage (BAL) samples of patients with suspected TB, MDR-TB, XDR-TB, or chronic lung diseases, who tested positive for acid-fast bacilli (AFB) staining but negative or indeterminate by Xpert MTB/RIF assay. The specimens were growth in liquid or solid media, DNA was extracted based on protocol study, and identification using a portable device (MinION) and a web interface application called MLSTverse to identify NTM quickly and accurately. Parallelly the identification of NTM suspected isolates were also done by Matrix-Assisted Laser Desorption/Ionization Time-of-Flight or MALDI-TOF.

Results
Sequencing achieved species-level identification in 47.8% isolates and 43.5% identified at the subspecies level. MLSTverse analysis, utilizing the mlstdb. NTM database with 184 genes, revealed Mycobacteroides abscessus as the dominant species (47.8%), with subspecies abscessus (28.3%) and massiliense (10.9%) predominant. Identification using Maldi-Tof was done only in 16 isolates and all the results are the same with sequencing method.

Conclusions
MinION with MLSTverse and Maldi-tof have significant implications for addressing Indonesia's NTM-PD burden, offering a rapid, scalable diagnostic tool that supports personalized medicine and public health surveillance in resource-limited settings.

LB-RES-020: Experimental Reverse Zoonosis of Plasmodium Falciparum in Mouse Erythrocytes Reveals Key Cellular Pathways for Anti-Malarial Drug Discovery

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Background
Malaria remains a significant and life-threatening global health challenge, primarily caused by Plasmodium parasites, with Plasmodium falciparum responsible for the most severe cases. Although P. falciparum can invade mouse red blood cells (mRBCs), it cannot complete its intraerythrocytic cycle, suggesting the presence of host-specific factors that restrict parasite maturation. Elucidating these species-specific cellular pathways is vital for novel antimalarial strategies.

Method
To investigate host species barriers, we infected mRBCs with P. falciparum and conducted microarray hybridization to assess host cellular responses. Comprehensive transcriptomic analyses, including weighted gene co-expression network analysis (WGCNA) and differentially expressed gene (DEG) analysis, were performed to identify genes and pathways with altered regulation during infection, compared to established responses in human erythrocytes.

Results
Transcriptomic profiling revealed marked transcriptional changes in mRBCs upon P. falciparum infection. WGCNA identified gene modules linked to impaired parasite development, notably at the ring stage. Key DEGs were associated with parasite membrane protein expression, nutrient metabolism, and stress response pathways. Several candidate genes emerged as possible determinants of parasite developmental arrest in mRBCs, highlighting critical host factors in cross-species restriction.

Conclusions
Our findings uncover distinct molecular responses in mRBCs that impede P. falciparum maturation, elucidating species-specific barriers at the transcriptomic level. The identification of pathways and genes tied to inhibited ring stage development provides new targets for antimalarial drug discovery, potentially informing future strategies for malaria control and eradication.

LB-RES-021: Exploring the Association Between Resolution of Pyuria and Bacteriuria on Urinalysis and a Negative Urine Culture Among Patients Treated for Complicated Urinary Tract Infections at a Tertiary Hospital in Manila

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Background
Complicated urinary tract infections (cUTIs) contribute substantially to morbidity and healthcare costs. Current guidelines recommend repeat urine culture to confirm microbiologic cure, yet this practice is costly and often impractical in resource-limited settings. This study evaluated whether the resolution of pyuria and bacteriuria on repeat urinalysis can reliably predict a negative urine culture after appropriate antibiotic therapy, offering a simpler and more sustainable approach to post-treatment monitoring.

Method
We conducted a prospective analytical study of 88 adult patients with cUTI at the Jose R. Reyes Memorial Medical Center, Manila, Philippines. All patients underwent baseline urinalysis and urine culture followed by guideline-directed antibiotic therapy. After treatment completion, repeat urinalysis and urine culture were obtained. Diagnostic accuracy measures of pyuria and bacteriuria in predicting negative culture were calculated, including sensitivity, specificity, predictive values, and receiver operating characteristic (ROC) analysis.

Results
The mean age was 45.3 years, with an equal distribution of sexes. Escherichia coli was the most common isolate (43.2%). After antibiotic therapy, 93.2% achieved negative urine cultures. Pyuria demonstrated poor discriminatory capacity (AUC <0.7). In contrast, bacteriuria was highly predictive: post-treatment bacteriuria <45/hpf yielded 98.8% sensitivity, 100% specificity, and 98.9% overall accuracy, with a negative predictive value of 85.7%. A ≥93% reduction in bacteriuria from baseline also demonstrated excellent diagnostic performance (AUC 0.984).

Conclusions
Resolution of bacteriuria on repeat urinalysis strongly predicts microbiologic cure in cUTI. This low-cost alternative to routine repeat urine culture improves sustainability and optimizes healthcare resource use, particularly in government hospitals where access and cost remain critical constraints.

Table 3. Measures of diagnostic testing accuracy for the detection of culture conversion by measures of post-treatment pyuria and bacteriuria and percentage change from baseline.

Parameter	Cutoff	Sens.	Spec.	PPV	NPV	Accuracy	DOR
Post-treatment Pyuria	**<5**	73.2%	50%	95.2%	12.0%	71.6%	2.72
	<22	90.2%	33.3%	94.9%	20.0%	86.4%	4.63
% change pyuria	>89%	98.8%	16.7%	94.2%	50.0%	93.2%	16.2
	>95%	96.3%	16.7%	94.0%	25.0%	90.9%	5.27
	>99.65%	45.1%	83.3%	97.4%	10.0%	47.7%	4.11
Post-treatment Bacteriuria	**<5**	67.1%	100%	100%	18.2%	69.3%	-
	<45	98.8%	100%	100%	85.7%	98.9%	-
	<47	98.8%	83.3%	98.8%	83.3%	97.7%	405.00
% change bacteriuria	>93%	97.6%	83.3%	98.8%	71.4%	96.6%	200.00
	>95%	96.3%	83.3%	98.8%	62.5%	95.5%	131.67
	>96.9%	92.7%	100%	100%	50.0%	93.2%	-

PPV = positive predictive value, NPV = negative predictive value, DOR = diagnostic odds ratio

LB-RES-023: Ultrasound Gel as a Vector: Investigation and Containment of a Burkholderia Cepacia Outbreak

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Background
Burkholderia cepacia (B. cepacia) is an emerging opportunistic pathogen among immunocompromised patients. It frequently contaminates saline, fluids and ultrasound Gel used in hospitals.

Method
The Infection Control team identified a sudden surge in B. cepacia cultures. A Total of 31 patients tested positive with most isolates from blood cultures (19 cases), followed by urine (9) and single cases from wound swab, tracheal aspirate and tissue culture. Most patients didn't develop active infections but two (2) BMT unit patients developed Central Line associated Blood Stream Infections (CLABSI). Both received treatment, responded well and were discharged.

To identify the source, environmental cultures were carried out from various areas. Samples were collected from water sources, hand hygiene products, antiseptic solutions, and multiple ultrasound gel containers (in-use, new, single-use sterile gel).

Results
Multiple samples from the ultrasound gel were tested positive for B. cepacian (Table 1).

Conclusions
The outbreak of B. cepacia was linked to contaminated ultrasound gel used in various areas. Timely investigation, environmental sampling and identification of the point source enabled effective containment. Widespread infections did not occur and affected patients responded well to treatment. Contaminated gels were replaced by single use sterile gel. Practices for using, storing, and handling of ultrasound gel were improved. Staff were educated on infection control measures, emphasizing proper handling and disposal of contaminated materials.

Table # 1: Summary of the collected Samples and Results			
Sr.#	**Sample Type**	**Growth**	**Department**
1.	Main Counter Tap Water	Negative	Dialysis
2.	Main Counter Soap	Negative	
3.	Hand Sanitizer Solution	Negative	
4.	Pyodine Solution	Negative	
5.	Potable tank Water	Negative	
6.	Pyodine Solution	Negative	Acute Medical Unit (AMU)
7.	Ultrasound Gel (in use)	Burkholderia cepacia	
8.	New Ultrasound Gel container	Burkholderia cepacia	
9.	Swab from AMU sink	Aeromonas hydrophilla, AcinetobacteSpp ,Burkholderia cepacia	
10.	Ultrasound Gel (in use)	Burkholderia cepacia	Intensive care unit (ICU)
11.	New Ultrasound Gel container	Burkholderia cepacia	
12.	Recently Filled Gel	Burkholderia cepacia	
13.	Gel (Bottle with Red Cap)	Burkholderia cepacia	
14.	Gel (bottle with White Cap)	Burkholderia cepacia	
15.	Single Use Sterile Gel (pouch)	Negative	
16.	New Ultrasound Gel container	Burkholderia cepacia	Bone marrow transplant (BMT)
17.	Ultrasound Gel (in use)	Burkholderia cepacia	
18.	Single Use Sterile Gel (pouch)	Negative	
19.	New Ultrasound Gel container	Burkholderia cepacia	Supply Chain Department
20.	Single Use Sterile Gel (pouch)	Negative	
21.	Single Use Sterile Gel (pouch)	Negative	
22.	Single Use Sterile Gel (Tube)	Negative	

LB-RES-028: Prevalence of Acinetobacter Baumanii Infection in a Tertiary Hospital: Antimicrobial Resistance Pattern and Outcome

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Divine Word Hospital

Background
Acinetobacter baumannii is a significant pathogen responsible for hospital-acquired infections, especially in intensive care units, and among critically ill patients. Known for its multidrug resistance, it presents significant challenges in treatment.

Method
A total of 11,576 inpatient requests for culture and sensitivity tests were reviewed from the Bacteriology Laboratory with 131 patients testing positive for A. baumannii. Demographic and clinical profiles were gathered, including age, sex, comorbidities, types of admission, during of hospital stay, and presence of invasive medical devices, along with culture and sensitivity results, and clinical outcomes of patients with the infection.

Results
The prevalence of A. baumanii infection in our center is 1.13%. Majority of these patients were over 60 years of age (53%), with females constituting 52% of the cases. Comorbidities such as cardiovascular diseases (34%), endocrine/ metabolic diseases (20%), renal diseases (16%) and pulmonary diseases (13%) were commonly observed in affected patients. 79% of the patients with the infection were admitted at the ward. The presence of invasive medical devices like Foley catheters (29.6%), nasogastric tubes (20%), and endotracheal tubes (12.6%) was associated with higher infection rates. Ceftriaxone showed a high resistance rate of 58%. 70% of the patients improved and 19% of patients were discharged but not improved, and 11% expired.

Conclusions
This study underscores the urgent need for improved infection control measures, antibiotic stewardship, and ongoing surveillance to combat the growing threat of drug-resistant A. baumannii in healthcare settings. The findings contribute valuable data for healthcare providers, pharmaceutical companies, and policymakers.

LB-RES-029: Genomic Analysis of Staphylococcus aureus from a Chinese Pig Farm Reveals SCCmec V/VII Co-Existence and Dual-Copy of blaZ-blaR1-blaI in a Highly Oxacillin- Resistant Isolate

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2Prince of Wales Hospital; S.H.Ho Research Centre for Infectious Diseases, The Chinese University of Hong Kong
3Shenzhen Institutes of Advanced Technology, CAS

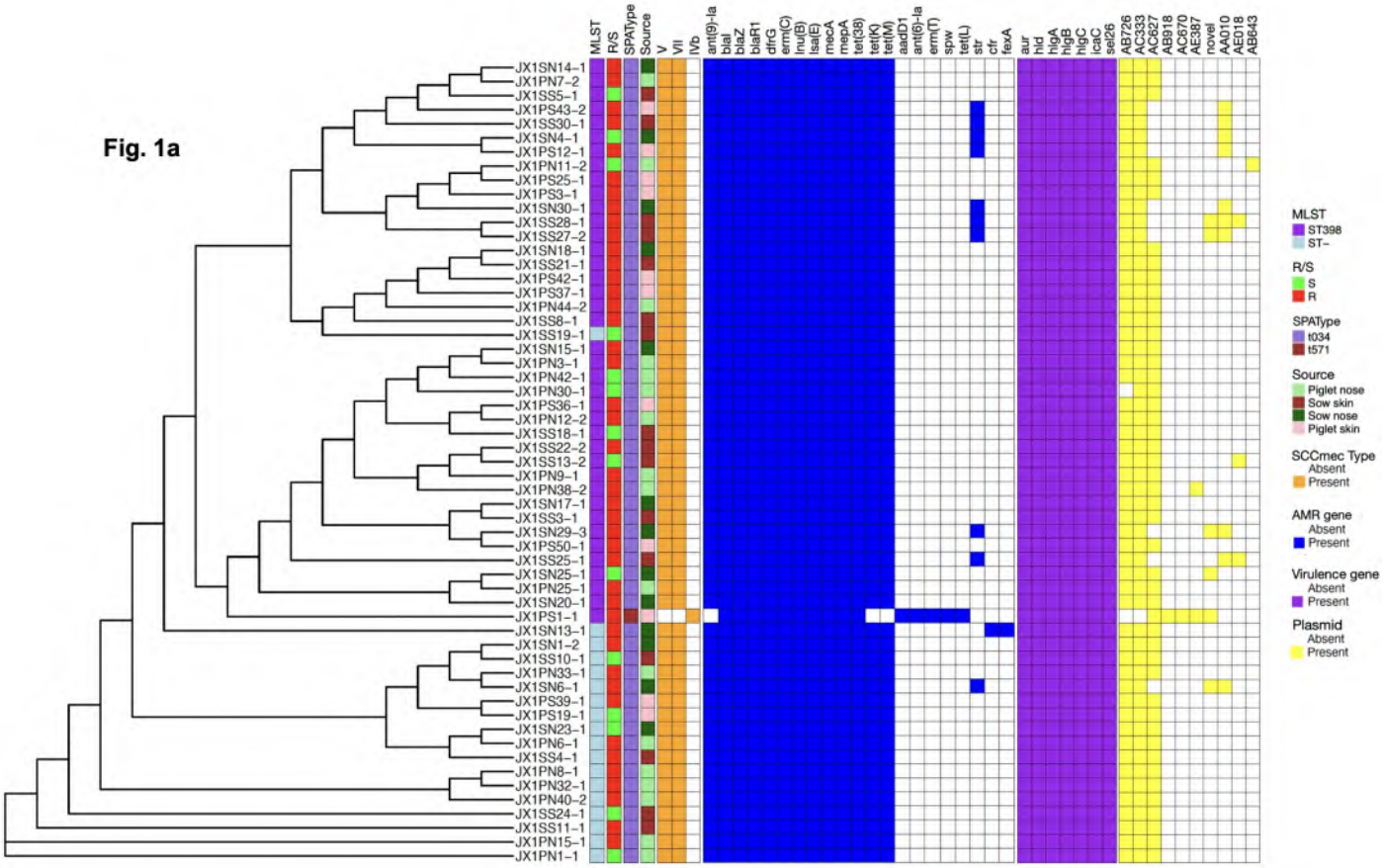
Background
From a One Health perspective, methicillin-resistant Staphylococcus aureus (MRSA) in pigs may serve as a reservoir of resistance for humans MRSA. To characterize the antimicrobial resistance phenotypes and genomic features of MRSA circulating in a Chinese pig farm.

Method
Skin and nasal swabs (n=160) from sows and piglets were collected from a pig farm in Jiangxi Province, China. Staphylococci were isolated on high-salt selective media, and single colonies were confirmed by MALDI-TOF. Methicillin resistance was assessed by cefoxitin disk diffusion and microbroth oxacillin tests. Whole-genome sequencing (WGS) via short read sequencing was performed followed by genome analysis.

Results
A total of 67 S. aureus isolates were recovered. 17 (25.4%) were cefoxitin-susceptible and 50 (74.6%) were methicillin resistant. Notably, isolate JX1PS1 exhibited no cefoxitin inhibition zone and an oxacillin MIC of 128 ug/ml, indicating high-level resistance. 57 strains passed quality control and were predominantly of ST398 or SLV398, a livestock-associated MRSA lineage. SCCmec analysis revealed all but JX1PS1, co-harbored SCCmec V and SCCmec VII elements—an uncommon configuration in pigs and, to our knowledge, the first report of widespread SCCmec V/VII co-existence in Chinese swine S. aureus (Figure 1a). JX1PS1 carried SCCmec IVb and contained duplicated bla regulatory/structural modules (blaZ-blaR1-blaI), which may have contribute to its high-level β-lactam resistance phenotype (Figure 1b).

Conclusions
MRSA ST398 in a Chinese pig farm carried both SCCmec V and VII types, with one strain carrying dual-copy of blaZ-blaR1-blaI. Continued genomic surveillance across the livestock–human interface is warranted to prevent potential zoonosis.

Fig. 1a


MLST
R/S
SPAType
Source
V
VII
IVb
ant(9)-Ia
blaI
blaZ
blaR1
dfrG
erm(C)
Inu(B)
lsa(E)
mecA
mepA
tet(38)
tet(K)
tet(M)
aadD1
ant(6)-Ia
erm(T)
spw
tet(L)
str
cfr
lexA
aur
hld
higA
higB
higC
icaC
sel26
AB726
AC333
AC627
AB918
AC670
AE387
novel
AA010
AE018
AB643
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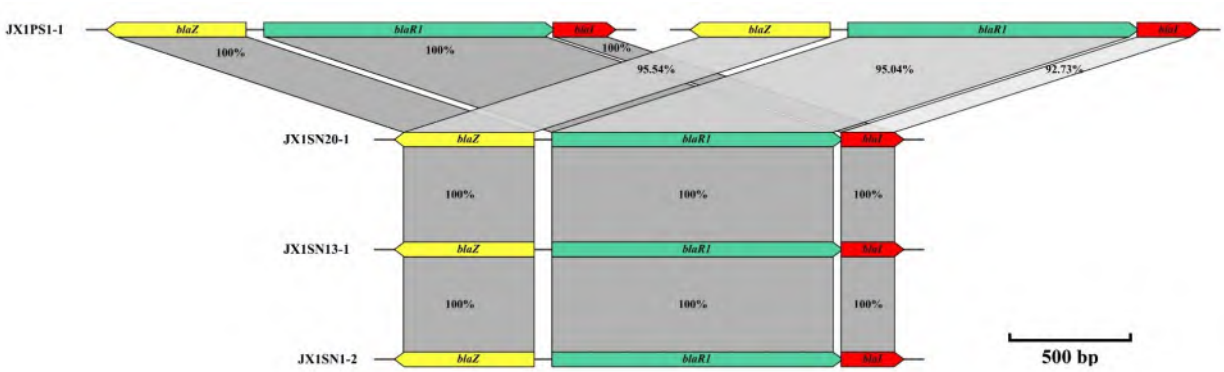
MLST
ST398
ST-
R/S
S
R
SPAType
t034
t571
Source
Piglet nose
Sow skin
Sow nose
Piglet skin
SCCmec Type
Absent
Present
AMR gene
Absent
Present
Virulence gene
Absent
Present
Plasmid
Absent
Present

Fig. 1b


JX1PS1-1
blaZ
blaR1
blaI
100%
100%
100%
95.54%
95.04%
92.73%
JX1SN20-1
JX1SN13-1
JX1SN1-2
100%
100%
100%
500 bp

LB-RES-036: Oral Pathobionts in Cancer: Mechanistic Insights into Prevotella Intermedia and Fusobacterium nucleatum in Tumor Development

I-Hsiu Huang

Oklahoma State University Center for Health Sciences

Background
Oral squamous cell carcinoma (OSCC) is the most common oral cancer, responsible for over 180,000 deaths annually. Early diagnosis yields a 90% 5-year survival rate, but late detection reduces survival to 68% due to rapid progression and diagnostic challenges. Risk factors include tobacco, alcohol, HPV infection, and possibly the oral microbiome. The oral cavity harbors over 600 microbial taxa, and dysbiosis has been linked to chronic inflammation and systemic diseases. Recent studies implicate Prevotella intermedia and Fusobacterium nucleatum in OSCC progression, but mechanisms remain unclear.

Method
Multiple strains of P. intermedia and F. nucleatum were isolated from saliva of patients with and without OSCC. Phenotypic and sequencing analyses confirmed their identity. These isolates were co-incubated with human colorectal and OSCC cell lines to measure proliferation and migration. Selected isolates underwent whole-genome sequencing to identify cancer-promoting genes. qPCR and RNA-seq were used to evaluate altered cancer-related signaling pathways.

Results
F. nucleatum isolates showed variable effects on proliferation and migration, with preliminary evidence suggesting increased oxygen tolerance may enhance progression. We demonstrated for the first time that live P. intermedia promotes proliferation, though not migration. The secreted cysteine protease InpA may activate the cancer regulator PAR2. Gene expression analyses confirmed P. intermedia upregulates oncogenic pathways, including PCNA1, IL-8, PI3K/AKT, and MAPK/ERK.

Conclusions
Our findings identify F. nucleatum and P. intermedia as contributors to OSCC progression through distinct mechanisms. Ongoing studies include RNA-seq analysis and development of a mouse model to further define cancer signaling pathways.

LB-RES-037: Leaf Extract of Murraya koenigii Disrupts the Biofilm Strengthening Amyloids of Staphylococcus aureus

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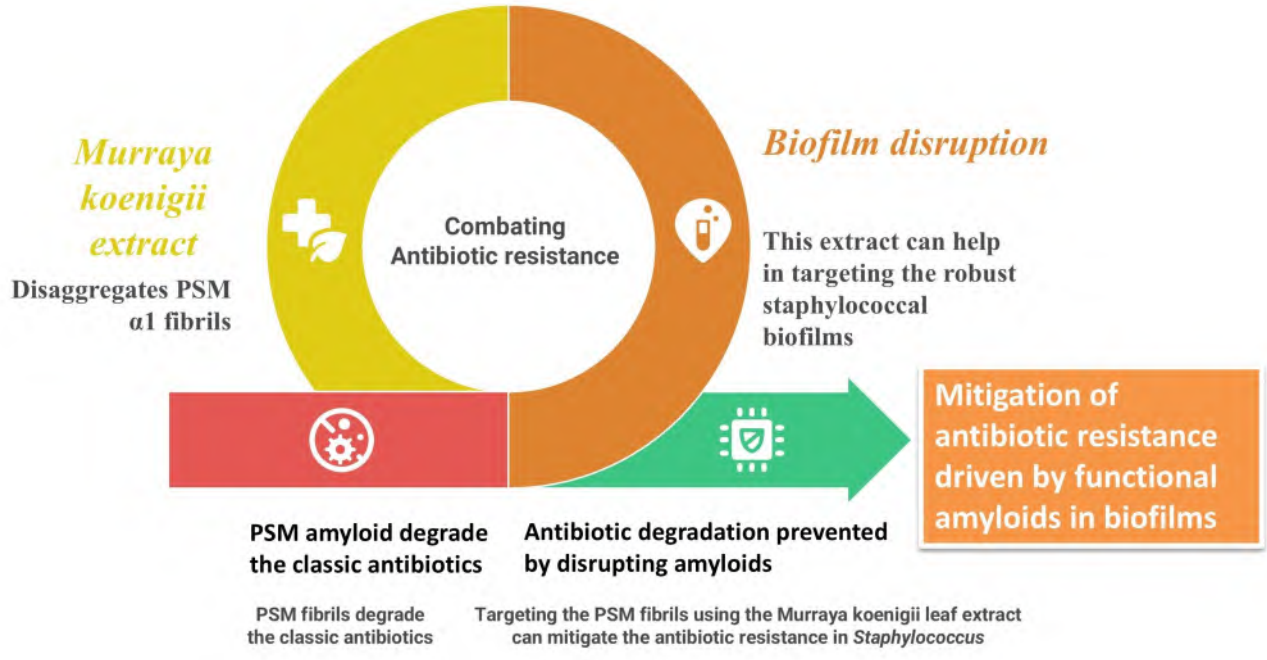
BITS Pilani KK Birla Goa Campus

Background
Antimicrobial resistance triggered by the biofilms of Staphylococcus aureus are a global concern due to the serious threat they pose to human health. Functional amyloids formed by the aggregation prone proteins and peptides of Staphylococcus aureus, provide architecture to the biofilms and promote antibiotic resistance. These aggregates reinforce staphylococcal biofilms by developing an extracellular amyloid fibrillar structure.

Method
In our present study, we put forward novel insights on the amyloid modulatory and putative anti-biofilm potential of the leaf extract of Murraya koenigii. The leaf extract of this plant disrupts the mature amyloids of staphylococcal virulent peptides, phenol soluble modulins (PSMs). We have used a combination of fluorescence spectroscopy, electron microscopy and biophysical techniques to study the effect of the methanolic leaf extract of Murraya koenigii on the PSM amyloids.

Results
A systematic analysis using biophysical assays and high-end microscopy has revealed the amyloid modulatory potential of phytochemicals present in the methanolic leaf extract of Murraya koenigii. Morphological analysis using high-end microscopy, dynamic light scattering and secondary structural studies using circular dichroism studies also revealed the disaggregation of the biofilm strengthening functional amyloids of PSM α family. Collectively, our data proposes a novel anti-biofilm activity of this leaf extract, by specifically targeting the staphylococcal functional amyloids derived from PSM α1.

Conclusions
Our study underscores that these phytochemicals in the leaf extract of Murraya koenigii can be used as a scaffold for the rational discovery of potent biofilm inhibitors targeting the biofilm strengthening amyloids which can further help in combating the antibiotic-resistant infections.



LB-RES-040: Rapid Multiplex PCR-Based Identification of Tuberculous Meningitis Among Infectious Meningitides

Qingge Li

Xiamen University

Background
Differentiating tuberculous meningitis (TBM) from other infectious meningitides remains challenging in high tuberculosis (TB) burden regions due to nonspecific presentations and limited diagnostic sensitivity.

Method
We began with the evaluation of MeltArray CNS, a rapid multiplexed PCR assay capable of detecting 85 meningitis-associated pathogens, using 85 plasmid targets, 619 clinical isolates, 18 reference strains, and 66 bronchoalveolar lavage fluid specimens. We then applied the assay to cerebrospinal fluid (CSF) samples from 158 patients with suspected meningitis. Additionally, we analyzed CSF biochemical parameters to identify potential biomarkers for TBM and viral meningitis.

Results
The MeltArray CNS assay demonstrated detection limits of 50 copies/reaction for 84 pathogen-specific targets and 5 copies/reaction for Mycobacterium tuberculosis (MTB) DNA. It exhibited 100% analytical sensitivity against 619 clinical isolates and 13 reference strains and showed no cross-reactivity with 5 non-target species. It accurately identified pathogens in all 66 bronchoalveolar lavage fluid samples. Against a composite reference standard, the assay achieved 100% sensitivity (3/3; 95% CI: 38.25–100.00) for definite TBM. When evaluated using consensus clinical criteria, sensitivity was 44.74% (17/38; 95% CI: 30.14–60.30) with 100% specificity (49/49; 95% CI: 91.32–100.00). CSF leukocyte count discriminated TBM effectively (area under the curve [AUC] 0.932; 95% CI: 0.832–1.000), while a multi-parameter model identified viral meningitis (AUC 0.964; 95% CI: 0.915–1.000). Co-infections were frequent in TBM (57.1%), highlighting diagnostic complexity.

Conclusions
The MeltArray CNS assay provides rapid, accurate, and multiplexed pathogen detection. This capability is vital for managing TBM in high-burden regions, as it identifies prevalent co-infections to guide timely, targeted therapy.

LB-RES-041: Assessing Antibiotic Resistance in Helicobacter pylori: Comparative Insights from Phenotypic and Genotypic Resistance Testing

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Background
Antibiotic resistance in Helicobacter pylori remains a major challenge in clinical management, particularly for clarithromycin and levofloxacin. While phenotypic methods such as the E-test are widely used in routine practice, genotypic assays targeting resistance-associated mutations provide rapid and precise alternatives. This study aimed to compare phenotypic and genotypic resistance testing in H. pylori isolates.

Method
Twelve clinical isolates of H. pylori were subjected to antimicrobial susceptibility testing against clarithromycin and levofloxacin using the E-test. In parallel, genotypic resistance analysis was performed by Sanger sequencing. Sequencing targeted the 23S rRNA gene, focusing on mutations A2142G and A2143G associated with clarithromycin resistance, and the gyrA gene, focusing on amino acid substitutions at codons N87K and D91N/Y linked to levofloxacin resistance. Results of phenotypic and genotypic testing were compared to assess concordance.

Results
For clarithromycin, concordance between E-test and genotypic testing was observed in 10 of 12 isolates. Two isolates exhibited phenotypic resistance without detectable 23S rRNA mutations. For levofloxacin, concordance was also 10 of 12 isolates: one isolate harbored resistance-associated gyrA mutations despite phenotypic susceptibility, while another demonstrated phenotypic resistance in the absence of genotypic alterations. Overall, 20 of 24 comparisons (83.3%) were concordant across both antibiotics.

Conclusions
This study demonstrated a high degree of concordance between phenotypic and genotypic methods for detecting clarithromycin and levofloxacin resistance in H. pylori. Incorporating genotypic assays into routine diagnostics holds the potential to enhance the precision of resistance detection, enabling more effective and individualized antimicrobial therapy for H. pylori infection.

LB-RES-042: Carbapenem-Resistant Klebsiella Pneumoniae Before and After COVID-19 Pandemic

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Background
Carbapenem-Resistant Klebsiella pneumoniae have become an emerging global threat as patients due to CRKP increase annually. Within the COVID-19 pandemic, abuse of antibiotics occurred as it has affected molecular epidemiological dissemination of carbapenem-resistant Enterobacteriaceae.

Method
We obtained 125 clinical isolates of CRKP from patients, 53 from patients before COVID-19 and 72 from after. In order to investigate the molecular epidemiological characteristics, we performed MLST. Minimum inhibitory concentrations (MIC) using 10 antibiotics and VITEK was also tested to check antibiotic resistances. Also, to check production of carbapenemase, Modified Hodge Test was first performed and later carba-NP test was performed to enhance accuracy and Polymerase chain reaction (PCR) was held to check which carbapenemase gene Klebsiella pneumoniae possessed. High Virulence was checked by phenotypic method as string test and genotypic method as PCR, checking gene rmpA, magA, aerobaction also capsule typing.

Results
Before COVID19, there were only two ST307 isolates among 53 but increased to 48 among 72. MIC and VITEK result both showed meropenem showed high resistance after COVID-19 compared to before the pandemic. MHT and carbaNP test showed mostly CRKP positive to create carbapenemase. Most carbapenemase gene were KPC2, however there was one isolate possessing NDM1 and another one possessing blaVIM26. High Virulence String test 2 isolates were hv-CRKP before pandemic and 7 isolates after pandemic.

Conclusions
This study shows, ST307 have increased dramatically after COVID and also meropenem resistance isolates have increased 59% to 93%. This could lead to a new strategy usage of antibiotics facing Carbapenem-Resistant Klebsiella pneumoniae.

LB-RES-044: Safety and Efficacy of Amoxycillin- Potassium Clavulanate Oral Suspension in Children with Upper Respiratory Tract Infections or Lower Respiratory Tract Infection: A Phase IV Study

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Background
This study aimed to assess safety and efficacy of Amoxycillin and Potassium Clavulanate Oral Suspension (600 mg + 42.9 mg / 5 ml) in Children with Upper Respiratory Tract Infection (URTI) or Lower Respiratory Tract Infection (LRTI)

Method
A total of 174 patients (aged ≥3 months to <18 years) with Upper RTI (Tonsillopharyngitis, acute bacterial sinusitis and acute otitis media) or Lower RTI (Lobar pneumonia and/or bronchopneumonia) were enrolled and received the study treatment for 5-10 days. The primary endpoint was safety assessment. The secondary endpoints (efficacy) were clinical cure, failure, improvement, relapse, and time to symptom resolution. [Clinical Trial registration: CTRI/2023/08/056267].

Results
The clinical cure rates were highest among patients with acute bacterial sinusitis (95.8%), followed by tonsillopharyngitis (83.7%), acute otitis media (76.9%) and lower respiratory tract infections-lobar pneumonia or bronchopneumonia (76.5%) with total clinical cure (82.8%) Clinical improvement was reported in tonsillopharyngitis (16.3%), acute bacterial sinusitis (4.2%), acute otitis media (23.1%), and lobar pneumonia and/or bronchopneumonia (23.5%). Patients with clinical failure or relapse were not reported in the study. Overall, 23 adverse events (AEs) reported in 21 (12.1%) patients. Most common AE was Diarrhoea (11 events). There was no discontinuation due to AEs.

Conclusions
Amoxycillin and Potassium Clavulanate Oral Suspension (600 mg + 42.9 mg / 5 ml) was safe and efficacious for treating upper or lower respiratory infections in children.

LB-RES-045: Enhanced Confirmative Diagnosis of Tuberculous Pleurisy Through Multiplex Droplet Digital PCR Detection of Mycobacterium Tuberculosis Cell-Free DNA In Pleural Effusion

Qingge Li

Xiamen University

Background
As the most prevalent form of extrapulmonary tuberculosis manifestation in adults, tuberculous pleurisy (TBP) presents significant diagnostic challenges due to its paucibacillary nature. This study aims to characterize Mycobacterium tuberculosis (MTB) cell-free DNA (cfDNA) in pleural effusion and to establish an optimal molecular assay for confirmative TBP diagnosis.

Method
Using droplet digital PCR, we quantified MTB cfDNA/gDNA concentrations and characterized MTB cfDNA fragment profiles in pleural effusion specimens. A novel multiplex ddPCR assay was developed, targeting three insertion sequence regions of IS6110 and IS 1081 with ultra-short amplicons (49-59 bp) to enhance detection efficiency. Diagnostic performance was prospectively validated in 356 consecutive adults with radiological confirmed pleural effusion, using composite microbiological/histopathological criteria as the diagnostic gold standard.

Results
MTB cfDNA demonstrated significantly higher detection rates than gDNA in definite TBP cases (median 32.4 vs 4.8 copies/mL, P=0.009), with predominant fragment lengths of 60-80 bp. The multiplex assay achieved exceptional sensitivity, detecting 0.2 genome equivalents/reaction (95% CI 0.1-0.4). In microbiologically-confirmed TBP patients (n=104), assay sensitivity reached 94.2% (95% CI 88.1-97.3%), significantly outperforming Xpert MTB/RIF (52.0%, P<0.0001) and liquid culture (35.3%, P<0.0001). Specificity remained 97.0% (95% CI 93.8-98.6%) in non-TB effusions (n=252).

Conclusions
Our findings establish MTB cfDNA as the predominant nucleic acid form in tuberculous pleural effusion. The optimized multiplex ddPCR platform, through synergistic use of multi-copy targets and size-adapted amplification, provides unprecedented diagnostic sensitivity while maintaining high specificity. This paradigm-shifting approach addresses critical limitations in current TBP diagnostics and shows immediate clinical translation potential.

LB-RES-046: Diagnostic Performance of an Automated Image Analyzer for Single Pattern Recognition in Antinuclear Antibody (ANA) Test

Muhammad Asyraf Bin Mohamad Kamil

Ministry of Health

Background
Indirect immunofluorescence (IIF) is the gold standard technique for antinuclear antibody (ANA) testing and plays a crucial role in guiding clinicians for management of patients suspected of systemic autoimmune rheumatic diseases (SARD). To address high sample volumes, automation of ANA IIF test using automated image analyzers has been introduced. However, several studies have reported mixed findings regarding the accuracy of these analyzers in pattern recognition.

Method
Our study evaluated 129 positive ANA IIF samples with a single pattern, using the EUROPattern Suite (EUROIMMUN, Lübeck, Germany). These samples were sent to Immunology Laboratory of Hospital Canselor Tuanku Muhriz between May and July 2025 for routine ANA test and comparison were made with manual IIF readings as the gold standard.

Results
The essential agreement (i.e., exact pattern match) ranged from 0% to 100%, with an overall agreement of 50.4%. Centromere pattern had the highest agreement (based on a small sample size), while more common patterns such as homogeneous and speckled showed moderate agreement (61.1% and 65.8%, respectively). Notably, 46.5% of samples were discordant with manual readings due to the machine interpreting them as mixed patterns. However, if mixed patterns (where the true pattern is included) are considered acceptable, the overall agreement increased to 90.7%. Interpretation of the DFS70 pattern remained particularly challenging, with only 33.3% agreement.

Conclusions
Our findings suggest that the automated system tends to overinterpret patterns, emphasizing the need for caution in reporting. Nevertheless, its ability to include the true pattern within a mixed result may assist laboratory personnel in improving diagnostic accuracy.

Manual IIF readings	Automated Image Analyser readings												Essential agreement (%)	Agreement with mixed pattern (true pattern included) (%)
	Homogenous	Speckled	Nucleolar	Nuclear dots	Centromere	DFS70	Centromere	Nuclear envelope	Mitotic spindle	Cytoplasmic	Mixed pattern (with true pattern included)	Mixed pattern (with true pattern excluded)		
Homogenous (n=18)	**11**	2	-	-	-	-	-	-	-	-	5	-	61.1	88.9
Speckled (n=73)	1	**48**	-	-	-	-	-	-	-	-	23	1	65.8	97.2
Nucleolar (n=11)	-	-	**1**	-	-	-	-	-	-	-	9	1	9.1	90.9
Nuclear dots (n=1)	-	1	-	-	-	-	-	-	-	-	-	-	0	0
Centromere (n=2)	-	-	-	-	**2**	-	-	-	-	-	-	-	100	100
DFS70 (n=9)	-	-	-	-	-	**1**	-	-	-	-	2	6	11.1	33.3
Cytoplasmic (n=15)	-	-	-	-	-	-	-	-	-	**2**	13	-	13.3	100
Nuclear envelope (n=0)	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Mitotic spindle (n=0)	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Total (n=129)	12	51	1	-	2	1	-	-	-	2	52	8	50.4	90.7

RES-002: Risk Factors Assessment for Dry Socket: A Focus on Antimicrobial Associations

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Background
Antimicrobial resistance (AMR) has become a global problem, and many fields are working on AMR countermeasures; however, there remains much room for improvement in the appropriate use of antimicrobial agents in dental practice. Dry socket (DS) is a relatively common complication of third molar surgery, and the use of antimicrobial agents to prevent DS is widespread but also controversial. The purpose of this study was to clarify the DS rate after third molar surgery and to identify factors associated with the efficacy of antimicrobial agents and the increased risk of DS.

Method
A retrospective study was conducted using patient medical records from patients who underwent third molar surgery at the study hospital over a span of 10 years (2014-2023). Patient backgrounds and factors related to DS were extracted from their medical records. A multivariate analysis using binomial logistic regression was performed for each factor, with DS as the dependent variable.

Results
A total of 3,271 cases in 1,714 patients (1,113 females and 601 males; age 14-90 years) were included in this study. A total of 222 (6.8%) patients had DS, and the variable that significantly influenced the occurrence of DS was BMI (odds ratio: 1.05; 95% CI: 1.01-1.09; $p<0.05$). The type and duration of antimicrobial agents used did not significantly affect the occurrence of postoperative infections.

Conclusions
Antimicrobial agents did not significantly reduce the risk of DS after third molar surgery.

RES-005: Clinical Profile and Outcomes among Patients with Elizabethkingia meningoseptica Infections: A Single Center Tertiary Hospital Study

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[2]St. Luke's Medical Center - Quezon City

Background
Elizabethkingia meningoseptica is a gram-negative aerobic bacillus recently identified as an emerging hospital-acquired pathogen. It has typically been isolated in water supplies and medical devices. Notably, E. meningoseptica has intrinsic resistance to many antibiotics commonly used in hospital settings, including β-lactams, aminoglycosides, and carbapenem. Infections by this pathogen have been reported in many parts of the world with a high mortality rate especially among immunocompromised patients. However, until now, there have been no published reports from other Southeast Asian and resource-limited countries.

Method
This is a descriptive retrospective study of the demographic profile and clinical outcome of patients with Elizabethkingia meningoseptica infections at the St. Luke's Medical Center Quezon City from January 2018 and June 2023.

Results
Over five years, Elizabethkingia meningoseptica was isolated from 15 patients (53.3% male, mean age 69.7 years). Common risk factors included recent hospitalization, prolonged ICU admission, mechanical ventilation (all 80%), and acute renal failure (67.7%). All had significant comorbidities, most commonly hypertension and diabetes (66.7%). Infections were primarily nosocomial, with isolates from endotracheal aspirates (46.7%) and blood (33.3%). Resistance to fluoroquinolones was high (86.7%), and 80% of the isolates were multi-drug resistant. Most patients received combination antimicrobial therapy. Mortality was high at 46.7%.

Conclusions
E. meningoseptica infections, though rare, pose serious risks in critically ill older adults. High resistance rates and diagnostic challenges demand timely diagnosis, susceptibility testing, and combination therapy. In low-resource settings like the Philippines, these hurdles may compromise care, underscoring the need for clinician awareness and strict infection control.

Table 1. Antimicrobial susceptibility test results of *Elizabethkingia meningoseptica*.

Antimicrobial	Sensitive (%)	Intermediate (%)	Resistant (%)
Amikacin	0	0	8/8 (100)
Aztreonam	0	0	8/8 (100)
Cefepime	1/15 (6.7)	0	14/15 (93.3)
Ceftriaxone	0	0	15/15 (100)
Ceftazidime	1/15 (6.7)	0	14/15 (93.3)
Ceftolozane-Tazobactam	1/15 (6.7)	0	14/15 (93.5)
Ciprofloxacin	2/15 (13.3)	0	13/15 (86.7)
Colistin	0	0	2/2 (100)
Gentamicin	0	1/6 (16.7)	5 / 6 (83.3)
Imipenem	0	0	8/8 (100)
Levofloxacin	3/15 (20)	1/15 (6.7)	11/15 (73.3)
Meropenem	1/15 (12.5)	0	7 / 8 (87.5)
Piperacillin-tazobactam	2/15 (13.3)	0	13/15 (86.7)
Co-trimoxazole	7/15 (46.7)	0	8/15 (53.3)
Vancomycin	2/2 (100)	0	0

RES-006: The Impact of Non-Indicated CSF Testing on the True Incidence of Viral Encephalitis – A Single-Centre Retrospective Study

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Background timely and accurate diagnosis is required for viral encephalitis, which can lead to devastating consequences. However, inappropriate CSF sampling may underestimate the true incidence of viral encephalitis. Our study aims to evaluate the pattern of ordering CSF viral testing and estimate the true incidence of Herpes simplex (HSV) and Varicella Zoster virus (VZV) infection in adult patients with clinical features of encephalitis.

Method
A retrospective study was conducted on CSF specimens from adult patients received at National Hospital-Galle between December 16, 2023, and December 15, 2024. Request forms were screened and grouped into specimens from clinical encephalitis and non-encephalitic patients based on the British Neurologists and British Infection Association (BIA) National Guidelines. The HSV and VZV infection incidences were compared between two groups to assess the appropriateness of viral testing and its diagnostic yield.

Results
Out of 224 CSF specimens, 89 met the criteria of clinical encephalitis, while 135 were grouped as non-encephalitic cases. The incidence of HSV and VZV in the encephalitis group was 6.74%, whereas in the non-encephalitis group, it was 0%. Statistical analysis showed a higher diagnostic yield of viral infections in the clinical encephalitis group (p-value = 0.0026). Of the six positive samples, one was positive for HSV-1, and the remaining five were positive for VZV.

Conclusions
This study highlights that CSF viral testing is indicated and yields higher diagnostic value in encephalitic cases. Furthermore, non-indicated testing may underestimate the true incidence of viral encephalitis. Therefore, optimizing CSF testing by improving diagnostic stewardship through establishing criteria is essential.

RES-012: Factors Affecting Timeliness in Vaccination of Under-five Children in India: A Cross-sectional Study using Health Survey during COVID-19

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Background
Immunization is an essential intervention that protects millions of children against Vaccine Preventable Diseases (VPDs) across the World. Despite improvement in coverage and technology to deliver vaccines to the beneficiaries, timeliness of vaccine administration remains a significant challenge impact health of many children in India and COVID-19 pandemic had further worsen the situation This study examines the factors associated with untimeliness of childhood vaccinations in India.

Method
A cross-sectional study using Kids Recode (KR) dataset of National Family Health Survey (NFHS) 5 was done that includes 232920 children under 5 years of age. Timeliness was considered as four days earlier and up to twenty-eight days after standard date in comparison with National Immunization Schedule (NIS). Using STATA MP v18, Regression analysis was used after to assess impact of factors related to Child, Mother, Household, Community and COVID-19 on timeliness by deriving adjusted Prevalence Ratios.

Results
Timeliness at birth was highest (94.6%), however, it declined for subsequent doses at 6 weeks (74.2%), and 14 weeks (67.5%). Untimeliness at 14 weeks was mainly due to Polio 3 (60.2%) and Rotavirus 3 (58.0%) vaccines. Factors associated with untimeliness include low birth weight, fewer antenatal visits, non-institutional delivery, no maternal education, rural residency and belonging to lower socio-economic strata. Children residing in Central and Northeast zones had the highest prevalence of untimeliness in receiving vaccines. Despite COVID-19 disruptions, the timeliness of vaccination was comparable pre-and-post COVID-19.

Conclusions
This study shows that the untimeliness of vaccination is influenced by factors related to Child, Mother, Household and Community.

RES-019: Performance Evaluation of Two Newly Developed Korean Mycobacteria RT-PCR Kits for the Identification of Culture Isolates

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Hanyang University College of Medicine

Background
Korea has one of the highest tuberculosis incidence rates among OECD countries, and nontuberculous mycobacteria (NTM) infections are also rising. RT-PCR kits for mycobacteria detection have been widely used in Korea to identify Mycobacterium tuberculosis (MTB) and NTM from both clinical specimens and acid-fast bacilli (AFB) culture isolates. Recently, two new RT-PCR kits have been developed, necessitating performance evaluation.

Method
We assessed AFB culture isolates identified as MTB or NTM using the Anyplex MTB/NTM Real-time Detection kit (Seegene). For NTM species identification, 47 isolates were selected based on MolecuTech REBA Myco-ID (YD Diagnostics) results. The performance of two new RT-PCR kits, NextGene MTB/NTM Detection Kit (EoneBiotech) and NeoPlex TB/NTM Detection Kit (Genematrix), was evaluated.

Results
For MTB isolates (n = 30), all three RT-PCR kits yielded concordant results, with EoneBiotech and Genematrix showing similar Ct values, while Seegene exhibited slightly higher Ct values. For NTM isolates (n = 47), all kits provided consistent results. However, for M. fortuitum complex, Genematrix produced higher Ct values than EoneBiotech, with a mean Ct difference of 4.04.

Conclusions
The newly developed RT-PCR kits demonstrated comparable performance to existing methods. Their additional advantages suggest potential for widespread clinical adoption.

RES-021: Bacterial Dynamics Inside Host Cells During Model Urinary Tract Infections

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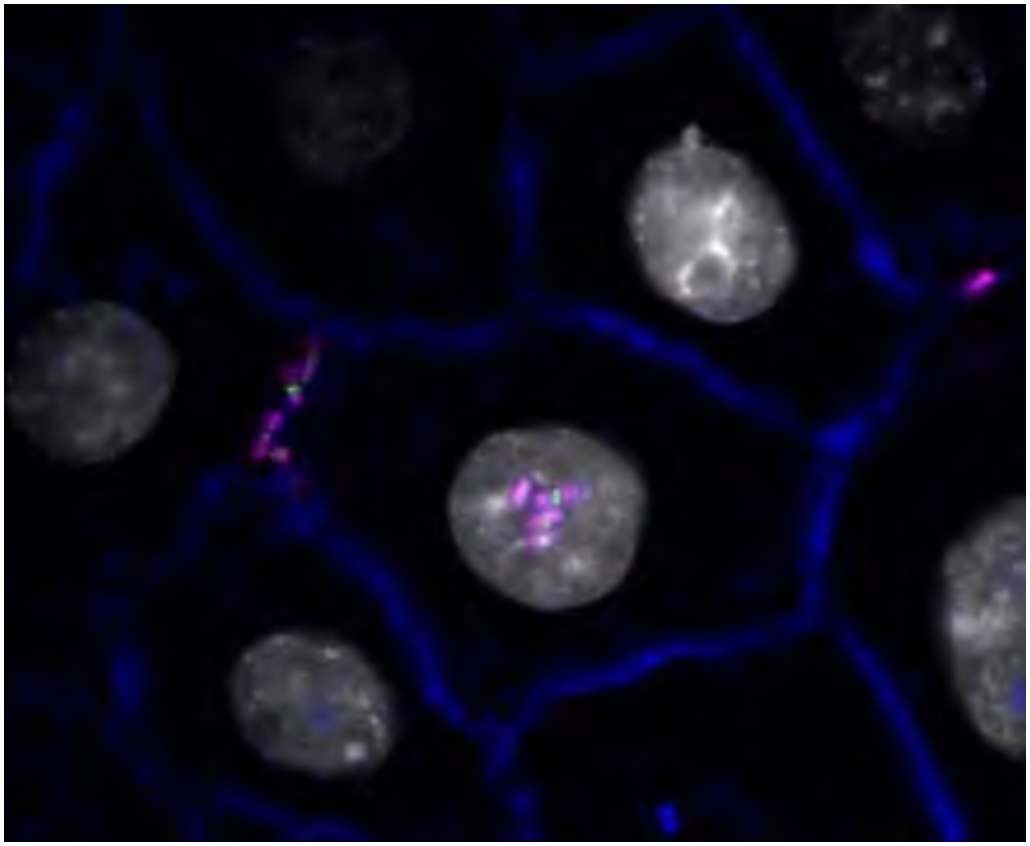
University of Technology Sydney

Background
Urinary tract infections are one of the most commonly diagnosed infections world-wide today, where Uropathogenic Escherichia coli (UPEC) is the main causative agent. With the rising threat of antimicrobial resistance, there is a need to find alternative approaches combating bacterial infections. However, one major bottleneck in this endeavour is that we still do not know enough fundamental microbial molecular biology to approach this issue in an effective manner.

Method
Here we have examined UPEC growth, proliferation and protein dynamics (e.g., division machinery and chromosomes) inside human urothelial bladder cells at a single cell level using a combination of live cell and single-molecule microscopy.

Results
Using a microfluidics based in-vitro infection model, we visualise molecular responses at single bacterial cell levels to common clinically used antibiotics, e.g. the Trimethoprim/sulfamethoxazole combination treatment for UTI, while the bacteria are intracellular. We also show what happens in the host cytoplasm when it is overrun by bacteria and how UPEC transition from rods to filaments inside live bladder cells prior to escaping for the hosts.

Conclusions
By mapping single cell bacterial growth dynamics at high-resolution, we can begin to understand intracellular interactions and how bacteria are spatially localized inside hosts during infection. A better understanding of bacterial proliferation inside host cells can lead to the discovery of new pathways for novel therapeutics.



RES-022: HLA-Recognized SARS-CoV-2 Peptides Trigger Antiviral Defenses in A549-hACE2-TMPRSS2 Cells

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Universiti Malaya

Background
Host genetic variability, particularly within the human leukocyte antigen (HLA) system, significantly influences immune responses to SARS-CoV-2. Identifying viral peptides that are effectively presented by HLA molecules can inform peptide-based interventions. This study aimed to profile the expression of antiviral genes in A549-hACE2-TMPRSS2 cells treated with SARS-CoV-2-derived peptides previously predicted to bind common HLA alleles.

Method
A549-hACE2-TMPRSS2 cells were cultured and treated with selected SARS-CoV-2 peptides (predicted high-affinity binders to HLA-A and HLA-B alleles prevalent in Malaysian populations). Cells were harvested at defined timepoints post-treatment, and total RNA was extracted. Antiviral gene expression was analyzed using a custom-designed qPCR array targeting key innate immune genes (PKR, OAS-3, MX-2, and ISG-15). Expression levels were compared with untreated and mock-treated controls.

Results
Treatment with specific SARS-CoV-2 peptides significantly upregulated the expression of multiple antiviral genes. Notably, ISG-15 and MX-2 exhibited >5-fold increases compared to controls, suggesting activation of the type I interferon pathway. Distinct expression profiles were observed depending on the peptide-HLA binding prediction, highlighting differential host cell responses. No cytotoxicity was observed at the tested concentrations.

Conclusions
SARS-CoV-2-derived peptides predicted to bind specific HLA alleles can induce robust antiviral gene expression in lung epithelial cells expressing ACE2 and TMPRSS2. These findings support the potential of HLA-targeted peptide immunogens to enhance innate antiviral defenses and contribute to future peptide-based vaccine or therapeutic development.

Table 1. MHC Class I processing prediction

Allele	#	Start	End	Peptide Length	Peptide	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
HLA-A*02:01	1	1	9	9	VLSEARQHL	1.51	0.42	-2.38	1.93	-0.45	241.2
HLA-A*02:01	1	1	9	9	VMVELVAEL	1.38	0.48	-0.96	1.86	0.89	9.2
HLA-B*15:03	1	1	14	14	TRFQTLLALHRSYL	1.33	0.52	-2.70	1.86	-0.84	501.1
HLA-B*18:01	1	1	8	8	DEFVVVTV	1.24	0.11	-2.72	1.35	-1.37	527.1
HLA-B*58:01	1	1	9	9	RSFIEDLLF	1.23	1.21	-0.72	2.44	1.72	5.3

Table 2. MHC Class I & II binding affinity prediction

Allele	#	Start	End	Peptide Length	Peptide	Distance	Score	Percentile Rank
HLA-A*02:01	1	1	9	9	VLSEARQHL	0	0.570751	0.21
HLA-A*02:01	1	1	9	9	VMVELVAEL	0	0.848575	0.06
HLA-B*15:03	1	1	14	14	TRFQTLLALHRSYL	0	0.000461	21
HLA-B*18:01	1	1	8	8	DEFVVVTV	0	0.881991	0.03
HLA-B*58:01	1	1	9	9	RSFIEDLLF	0	0.933645	0.04
HLA-DRB1*11:04	1	1	15	15	SASAFFGMSRIGMEV		0.2648	8.1

RES-023: Application of Starch-Based Alpha-Amylase Depletion to Enhance Salivary Proteomic Analysis in Periodontitis.

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Background
Saliva is a clinically informative biological fluid that provides a non-invasive medium for diagnostics. However, the dominance of high-abundance proteins, particularly alpha-amylase, hampers the detection of low-abundance proteins, including those linked to disease. This limitation complicates the identification of microbial agents such as Trichomonas tenax, a protozoan implicated in periodontitis. This study aimed to enhance salivary proteomic analysis by depleting alpha-amylase and comparing protein profiles between periodontitis patients and healthy controls, with and without T. tenax.

Method
Saliva samples from 30 individuals (15 periodontitis patients and 15 healthy controls) were carefully screened and analyzed. Following that, alpha-amylase was depleted using a starch-based depletion method. The protein concentration of the elution was estimated using the BCA assay, and SDS-PAGE was performed to assess the success of the process. A distinct band in non-depleted samples, predicted to be consistent with alpha-amylase, was excised, and the protein identity will then be confirmed by LC–MS/MS.

Results
Protein concentration was significantly higher in non-depleted saliva than in depleted saliva across all samples ($p < 0.001$), confirming the effectiveness of alpha-amylase depletion. In both conditions, protein concentrations were notably higher in periodontitis patients compared to healthy controls. SDS-PAGE of non-depleted saliva showed a distinct 59-62 kDA band which disappeared after depletion. LC–MS/MS analysis revealed the similarity of the peptides to human salivary alpha-amylase.

Conclusions
The starch-based depletion protocol effectively depletes salivary alpha-amylase, improving the resolution of low-abundance proteins. This approach enhanced salivary proteomic profiling and may facilitate the identification of biomarkers associated with Trichomonas tenax-related periodontitis.

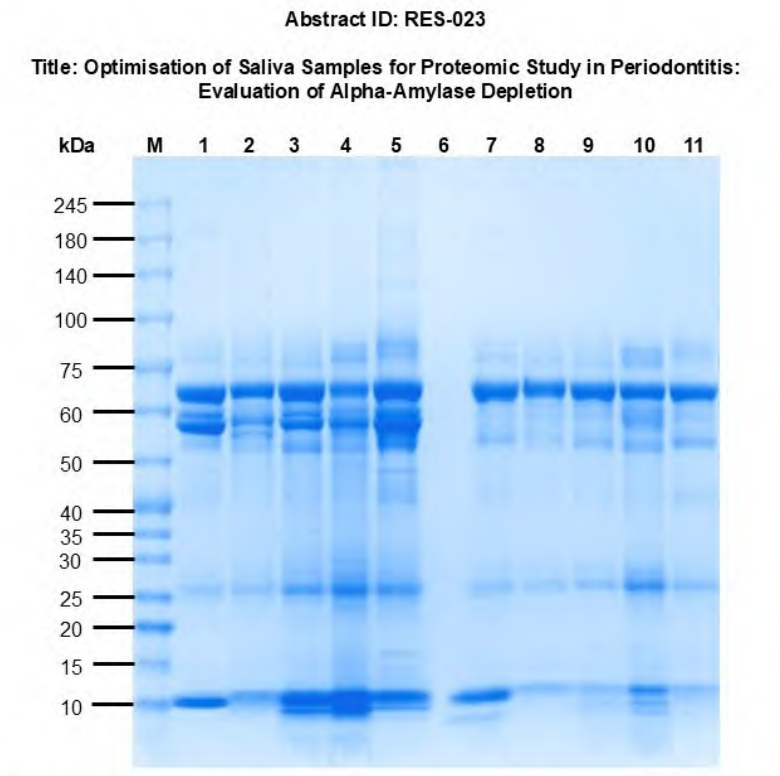

Figure 1. SDS-PAGE gel image showing protein profiles of undepleted saliva samples (Lanes L1–L5) and depleted saliva samples (Lanes L7–L11).

RES-024: Cysticercosis/T. solium Taeniasis, a Potential Public Health Concern in Non-Endemic Country, Kuwait: A New Diagnostic Method to Screen T. solium Taeniasis Carriers Among the Expatriate Population

Jamshaid Iqbal

College of Medicine, Kuwait University, Kuwait

Background
Kuwait is non-endemic for Taenia solium infection due to strict restriction pork consumption however, several cases of cysticercosis and neurocysticercosis were detected among Kuwaiti nationals with no history of travel to endemic countries. Infected domestic helpers/food handlers from endemic countries who may not have been detected of infection by microscopy at the time of their arrival into Kuwait were suspected as the possible source of infection. This study determined the seroprevalence of T. solium among domestic helpers/food handlers by using a sensitive taeniasis-specific anti-rES33 antibody assay.

Method
Subjects and Methods: Newly arriving five hundred domestic helpers and five hundred food handlers from endemic countries were enrolled during 2015-2017. T. solium-specific rES33 antigen was expressed and purified from human embryonic kidney (HEK) 293-6E cells using the pTT5 mammalian expression vector. Stool samples were processed for microscopy, and blood samples were screened to detect anti-T. solium taeniasis-specific IgG antibodies by ELISA.

Results
All stool samples were negative for Taenia parasite eggs by microscopy. However, 42 individuals (4.2%) tested positive for T. solium taeniasis-specific IgG antibodies. Though statistically not significant, the IgG seropositivity was higher among individuals with lower education levels, low-income background, and higher frequency of hand washing.

Conclusions
Conclusions: This is the first report from Kuwait and the Middle East on the detection of anti-T. solium taeniasis-specific serum IgG antibodies among the high-risk expatriate population. The results emphasize the importance of efficient and sensitive screening of T. solium carriers and thus the prevention of infection transmission and development of cysticercosis in the local population.

RES-028: Bactericidal Effects of High-Speed Water Nanodroplet Technology Against Spore-Forming Pathogens

Yurina Tamura[1], Kei Kaimori[1], Masato Kawamura[1], Takehiko Sato[2], Tomoki Nakajima[2], Siwei Liu[2], Takumi Sato[1], Shigeru Fujimura[1]

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[2]Tohoku University

Background
Spore-forming bacteria, including Clostridioides difficile and Bacillus anthracis, are public health threats. In 2017, we developed a high-speed nanodroplet generation technology using water only as a new sterilization method. This technology produces droplets less than 100 nm in diameter at a velocity of ~30 m/s from a distance of 10 cm, without wetting the contact surface. This study evaluated its bactericidal effect of nano-droplets on the spores of Clostridium and Bacillus species.

Method
Bacillus subtilis ATCC6633 spores were prepared in difco sporulation medium at 37°C for 3 days with shaking. The spores of Clostridium butyricum were obtained after anaerobic incubation on Brucella HK agar at 37°C for 5 days and suspended in milli-Q water. Sporulation was confirmed by Schaeffer-Fulton stain. After exposure to nanodroplets for 2–20 minutes at 37.5 MPa, morphological changes were observed by scanning electron microscopy, and viable counts were measured.

Results
After 2 minutes of exposure to high-speed nanodroplets, projections appeared on B. subtilis spores, which dented over time and flattened by 20 minutes. In C. butyricum, projections were observed at 2 minutes, with holes forming at 10 minutes. Initial viable counts were 1×10^5 CFU/mL. After 20 minutes, B. subtilis decreased to 3.53×10^2 CFU/mL, while C. butyricum remained at 7.87×10^4 CFU/mL.

Conclusions
B. subtilis spores were flattened and killed by the impact pressure of 37.5 MPa, while damage to C. butyricum was limited. These results suggest C. butyricum spores possess a more robust structure than those of B. subtilis.

RES-030: Comparison of Treatment Outcomes Between Isavuconazole and Voriconazole for Suspected Invasive Aspergillosis: A Single-Center Retrospective Cohort Study

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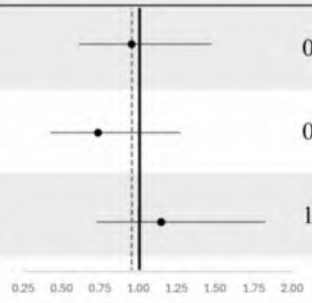
Background
Invasive aspergillosis (IA) is a life-threatening infection and has been increasingly identified. According to published guidelines, voriconazole (VORI) is the first-line agent and isavuconazole (ISAV) plays an alternative role. However, supporting evidence is primarily derived from studies of heterogeneous populations with various fungal infections. This study aimed to evaluate treatment outcomes among patients with suspected IA who initiated ISAV or VORI.

Method
This retrospective cohort study enrolled hospitalized non-HIV adults with suspected IA who initiated ISAV or VORI at a tertiary medical center in Taipei, Taiwan between January 2019 and February 2024. Patients who received ISAV or VORI for ≤ 2 days, exposed to amphotericin B or anti-mold triazoles in previous 6 months, were excluded. The primary outcome, 42-day in-hospital mortality, was analyzed by using Cox proportional hazards model. Sensitivity analyses were performed to validate major findings using a stricter definition of IA and inverse probability of treatment weighting. Drug safety, such as liver dysfunction, was also assessed.

Results
Of the 407 patients included, 74 received ISAV and 333 received VORI. The crude 42-day in-hospital mortality were similar (33.8% vs 34.5%, HR: 1.03; 95% CI: 0.67–1.59). After adjustment for confounders including age, ICU admission, and immunosuppressive status, no significant difference was observed (Table). Notably, ALT elevation >5× ULN occurred more frequently in the ISAV group (10.5% vs. 4.9%; p = 0.082), though not statistically significant.

Conclusions
ISAV demonstrated similar 42-day in-hospital mortality to VORI, which supports its role as a first-line therapy for suspected IA. Liver dysfunction during IA treatment warrants continued monitoring.

	no. of events/total no. (%)			Adjusted HR (95% CI)	*p* value
	Total patients	ISAV group	VORI group		
Main analysis† (All patients)	140/407 (34.4)	25/74 (33.8)	115/333 (34.5)	0.95 (0.61-1.47)	0.815
Patients met specific mycological evidence‡	90/252 (35.7)	16/53 (30.2)	74/199 (37.2)	0.73 (0.42-1.27)	0.267
IPTW§	128/407 (31.4)	56/197 (28.4)	72/210 (34.3)	1.14 (0.72-1.82)	0.579



† Main analysis: Included patients with clinical suspicion of IA and supporting mycological evidence who received ISAV or VORI as initial treatment.
‡ Specific mycological evidence: GM antigen ≥1.0 or positive non-sputum PCR/culture.
§ After IPTW (Inverse Probability of Treatment Weighting), variables with ASD > 0.2 (index year, solid organ transplant history, hematological malignancy, and ESRD) were adjusted in the multivariable Cox regression.

RES-031: Parechovirus Develops Normocellular Meningitis; Retrospective Analyses from 33 Cases of Meningitis/Encephalitis Confirmed by Multiplex PCR

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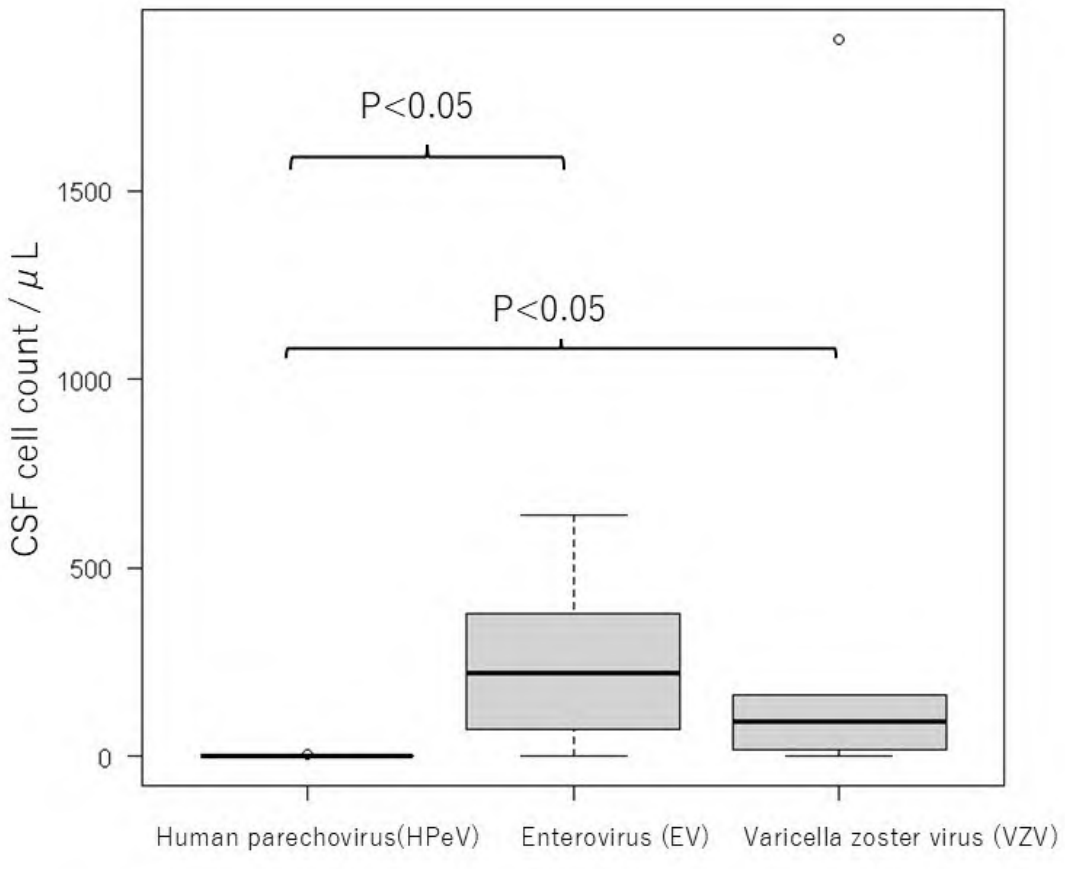
Tokyo Medical University Hachioji Medical Center

Background
A multiplex PCR can detect causable pathogen within an hour regardless of cerebrospinal fluid (CSF) cell count.

Method
To show the correlation between CSF cell count (CCC) and pathogen derived from CSF samples among patients with meningitis/encephalitis. Tokyo Medical University Hachioji Medical Center is a 610-beded tertiary care hospital. A retrospective analysis was conducted on CSF samples obtained from patients with meningitis/encephalitis, using the Film Array Meningitis/Encephalitis Panel (FA-M/E: BioMérieux Japan) from April 2023 to March 2024. Information on the patient's age, gender, underlying disease, pathogen from CSF, CSF cell counts (CCC), CSF protein, and clinical outcome were collected.

Results
33 cases were included; median age was 28.9 years(range:0-90). 57.6% were under 10 years old. The types of pathogens were Virus 78.8%, Bacteria 12.1%, and Fungus 9.1%. The three most common pathogens were Enterovirus (EV) 23.5%, Human parechovirus(HPeV) 20.6%, Varicella zoster virus (VZV) 17.6%. Median CSF cell counts were 232.2(1-2160)/μL. The CCC in HPeV 2.2(1-3)/μL were significantly lower than EV 248.2(0-38) /μL, and VZV 378.5(1-1904) /μL by the Mann-Whitney U test ($p<0.05$).

Conclusions
Low-normal range (LNR) CCC meningitis are known as cryptococcus meningitis in PLWH. Our results revealed that HPeV cause LNR CCC meningitis among infants ≤ 3month old*. The Multiplex PCR including FA-M/E can make rapid definitive diagnosis of LNR CCC meningitis/encephalitis. Even if the CCC is normal range, meningitis/encephalitis cannot be ruled out. Further investigation is needed.
* Journal of NeuroVirology (2022) 28:46–51



RES-033: Analysis of Blood Myxovirus Resistance Protein A for Diagnosis of Upper Respiratory Viral Infections

S. Kim

Gyeongsang National University College of Medicine

Background
Myxovirus resistance protein A (MxA) is induced by interferon after viral infections and inhibits viral replication. Elevated level of MxA indicates the viral infections. We analyzed MxA blood level for the respiratory viral infected patients.

Method
We evaluated the clinical performance of AFIAS MxA (Boditech Med, Inc., Korea) using blood collected from patients (N=66) with upper respiratory tract infections during Jan-Feb, 2024. Healthy people (N=48) without respiratory symptoms were recruited as a control group. The Allplex™ Respiratory Panel 1, 2, 3 and Allplex™ SARS-CoV-2 Assay multiplex real-time RT-PCR kit (Seegene, Korea) was used to confirm viral infections for the nasopharyngeal swab specimens.

Results
The AFIAS MxA showed excellent sensitivity (98%-100%) and specificity (92%-94%) for the EDTA blood regardless of virus type (SARS-CoV-2, n=19; Influenza A, n=11, Influenza B, n=39; Human Rhinovirus, n=4) based on the manufacture's cutoff, 30 ng/mL. Area under the ROC (receiver operating characteristics) curve ranged 98.7%-99.6% and optimal cut-off was from 35.04 ng/mL (AFIAS-10) to 58.69 ng/mL (AFIAS-3). Heparinized blood or capillary blood showed the similar sensitivity and specificity.

Conclusions
AFIAS MxA was useful to screen respiratory viral infections. MxA test could be adopted as one of effective strategy to save antibiotics to reduce antibiotic resistance problem. As MxA of the capillary blood showed a compatible result with either EDTA- or heparinized blood, it could be considered as a point-of-care test in the outpatient clinic.

RES-040: Prescribing Practices and Stewardship Gaps in a Surgical Department at the National Hospital of Sri Lanka: A Prospective Study to Combat Antimicrobial Resistance

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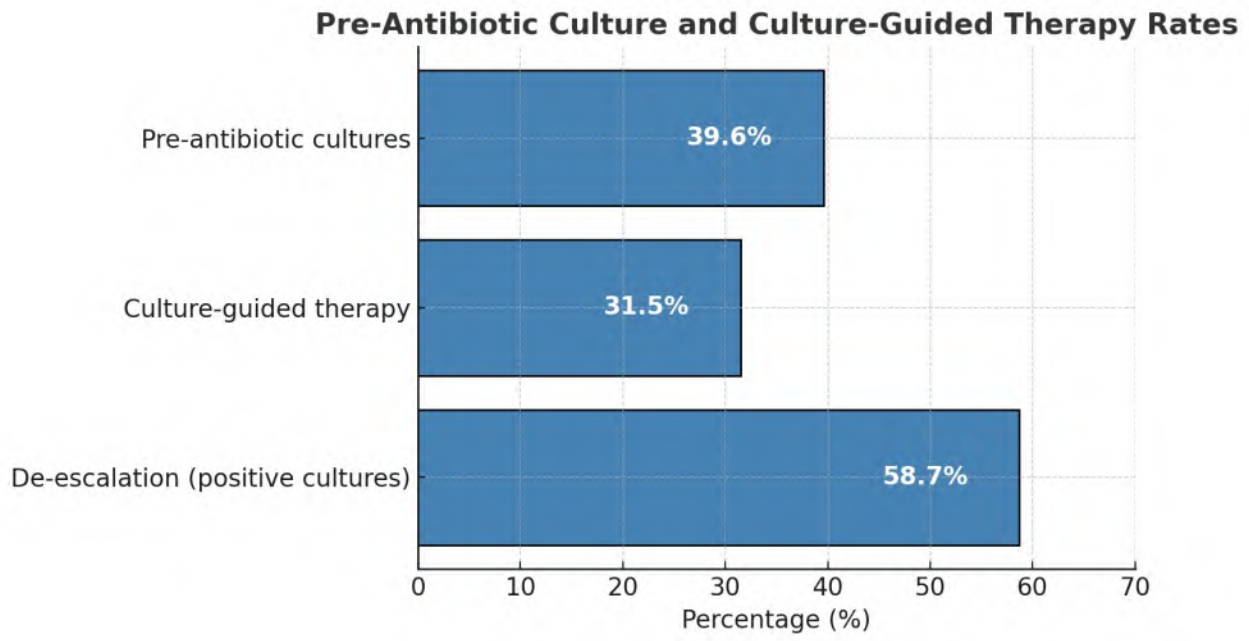
Background
Antimicrobial resistance (AMR) is a growing global threat, exacerbated by inappropriate antibiotic use. This study assessed the knowledge, attitudes, and prescribing behaviours of healthcare professionals in a surgical ward to identify gaps and inform targeted antimicrobial stewardship (AMS) interventions.

Method
A prospective study of 500 postoperative patients was conducted from January to March 2025. Data was collected on antibiotic choice, dosing, documentation, and review practices using a structured questionnaire.

Results
Pre-antibiotic cultures were taken in only 39.6% of patients. Appropriate dose, route, and duration were observed in 83.2% of cases. Culture-guided therapy occurred in 31.5%, with de-escalation implemented in 58.7% of positive-culture cases. Reviews were often conducted at 48–72 hours (51.0%), with timely review linked to significantly higher de-escalation rates (70.3%) versus delayed reviews (>72h; 40.7%).

Use of the newly introduced national antimicrobial chart (H 1338) was only in 29.5% of patients. Strong positive correlations (r >0.6) were found between documentation practices and culture-guided prescribing. WHO AWaRe classification showed 58.4% of prescriptions were from the Access group, narrowly missing the ≥60% target.

Conclusions
Suboptimal review timing, documentation, and multidisciplinary engagement limit effective AMS. Strengthening stewardship through mandatory pre-treatment cultures, structured 48-hour reviews, consistent chart use, and team-based oversight is vital to reduce AMR and optimize antibiotic use.



RES-041: Aerosolised Methicillin-resistant Staphylococcus aureus (MRSA) particles and their Role in Hospital Surface Contamination and Transmission Dynamics: An Interim Analysis

Stephanie Sutjipto

Society of Infectious Diseases Singapore

Background
Understanding the transmission modes of methicillin-resistant Staphylococcus aureus (MRSA) in hospitals is crucial for effective prevention. While direct contact is likely the primary transmission route, the role of aerosolized MRSA in environmental contamination and patient-to-patient transmission is unknown.

Method
At Woodlands Health Campus, MRSA and non-MRSA cubicles are co-located within the same ward, separated by half-wall partitions with natural airflow (Figure 1). This study encompasses three main components: active air sampling via SASS-3100 air sampler, passive air sampling via settle plates, and surface sampling (Figure 2). 505 environmental samples were collected from 30 MRSA-colonized patients over five sampling sessions (21 October- 18 November 2024), with an additional passive air sampling from non-MRSA patients.

Results
MRSA was cultured from active and passive air samples from various areas surrounding patients and from air samples from the opposite non-MRSA cubicle (Table 1). Sampling of high-touch surfaces revealed heavy MRSA growth on patient chairs and bed railings; moderate growth on railings and cardiac tables; and light growth on bedside lockers and light switches. No MRSA contamination was found in common areas on the sampling day. Findings are summarized in Table 1.

Conclusions
MRSA was frequently cultured from air samples collected within MRSA cubicles (4/9, 44% positive) and potentially dispersed in the air to the opposite non-MRSA cubicles (2/7, 29% positive). Whole genome sequencing to explore correlations of MRSA from patients and environments is ongoing. Further longitudinal study with larger sample size is needed to understand the role of aerosolized MRSA in healthcare-associated transmission.

Figure 1. (i) Ward setup with MRSA and non-MRSA cubicles located within the same wards, separated by half-wall partitions with natural airflow; (ii) Percentages of positive MRSA cultures captured by active air samplings in the cubicles (*dotted boxes*).

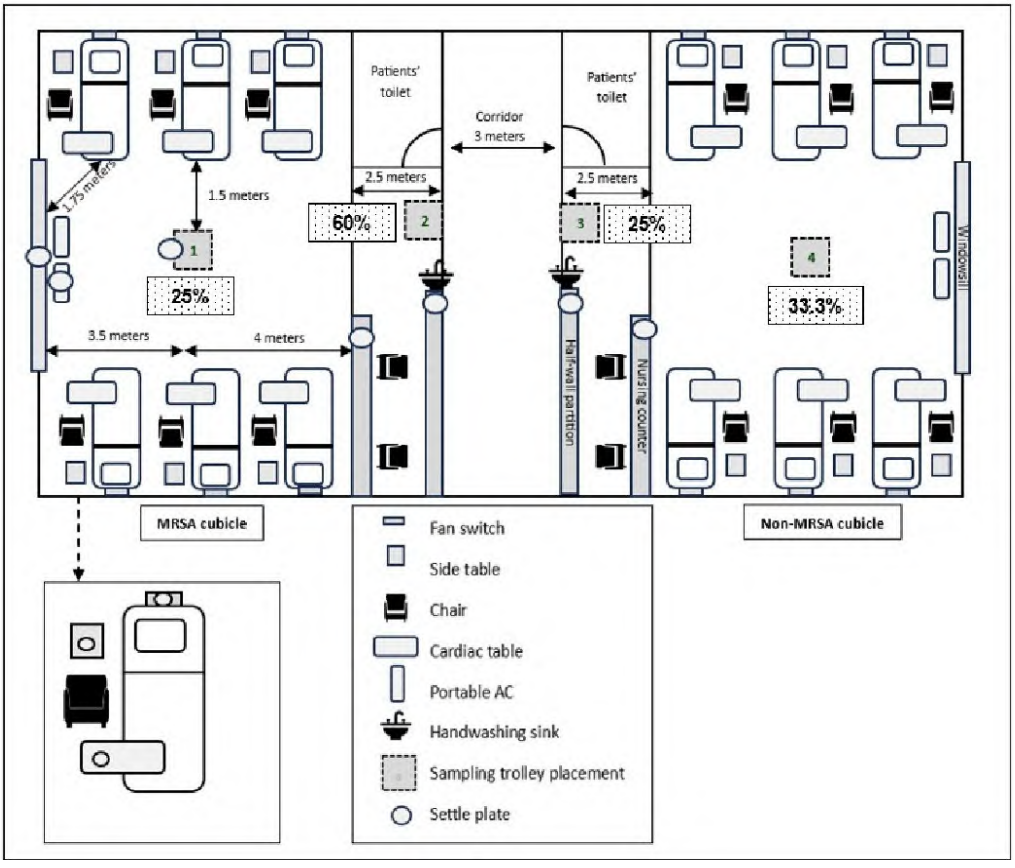


Figure 2. **Study design with three main investigational components: air sampling (active and passive samplings), surface sampling, and whole genome sequencing (WGS) technology**

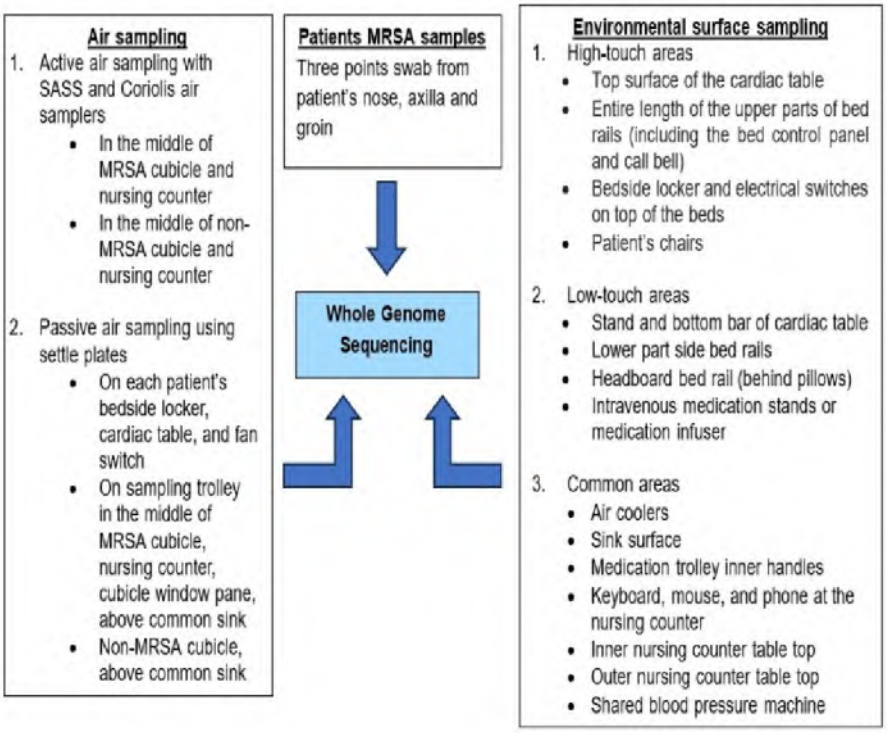


Table 1. Results of (i) Active air sampling using the SASS 3100 air sampler; (ii) Passive air sampling with settle plates; (iii) Environmental surface swabbing

(i) Active air sampling using the SASS 3100 air sampler				
Sample trolley placement	**Growth on Brilliance™ agar**	**MRSA growth (samples)**	**Number of air sample collections (samples)**	**Positivity rate (%)**
MRSA cubicle, middle of the room	Heavy	1	4	25%
MRSA cubicle, nursing counter	Heavy	3	5	60%
Non-MRSA cubicle, nursing counter	Heavy	1	4	25%
Non-MRSA cubicle, middle of the room	Heavy	1	3	33.3%
Total	-	**6**	**16**	**37.5%**
(ii) Passive air sampling with settle plates				
Placement of settler plates	**Location of settle plates**	**Number of settle plates collected (plates)**	**Number of settle plates with MRSA growth (plates)**	**Positivity rate (%)**
Patients' surroundings	MRSA patients' bedside locker	30	6	20%
	MRSA patients' cardiac table	30	7	23.3%
	MRSA patients' fan switch	30	5	16.7%
	Non-MRSA patients' bedside locker, cardiac table, fan switch (*1 round of sampling*)	18	0	0%
Common areas	MRSA cubicle, middle of the room	6	3	50%
	MRSA cubicle, windowsill	6	2	33.3%
	MRSA cubicle, nursing counter	6	0	0%
	MRSA cubicle, above the sink	5	2	40%
	Non-MRSA cubicle, nursing counter	1	0	0%
	Non-MRSA cubicle, above sink	5	0	0%
Total	-	**137**	**25**	**18.2%**

(iii) Environmental surface swabbing				
Site for environmental surface sampling		**Heavy growth of MRSA (isolates)**	**Moderate growth of MRSA (isolates)**	**Light growth of MRSA (isolates)**
MRSA cubicle, high-touch areas around patients	Cardiac table (top), including handle	1	4	4
	LEFT side length of upper part of bed rail, including bed control panel and call bell	1	5	1
	RIGHT side length of upper part of bed rail, including bed control panel and call bell	2	1	1
	Patient's Chair	5	6	1
	Bed side lockers and light switches on top of bed	2	1	3
MRSA cubicle, low-touch areas around patients	Stand and bottom bar of cardiac table	7	5	2
	Lower part side of bed rails	3	1	1
	Headboard bed rails	4	5	2
	Drip stand/ medication infuser (if applicable)	0	0	1
MRSA cubicle common/shared areas	Air cooler	0	0	1
	Sink surfaces	0	0	0
	Medication trolley inner handle	0	0	0
	Keyboard, mouse, and phone on the nursing counter	0	0	0
	Nursing counter table facing the patients' cubicle	0	0	0
	Nursing counter table facing the main corridor	0	0	0
	Shared blood pressure machine	0	0	0

RES-042: Evaluating the Clinical Utility of TORCH Screening in Neonates with Isolated IUGR: A Single Centre Retrospective Analysis

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National Hospital Galle

Background
Perinatal TORCH infections (Toxoplasma gondii, rubella, cytomegalovirus [CMV], herpes simplex virus [HSV]) cause significant foetal and neonatal morbidity and mortality. TORCH screens are often ordered to investigate isolated IUGR, but there is limited evidence to support screening for these infections in the absence of other clinical manifestations. However, the clinical utility of routine TORCH screening in neonates with isolated IUGR, in the absence of other clinical signs, remains controversial. The study aims to assess the diagnostic yield and clinical relevance of TORCH screening in neonates presenting with isolated IUGR.

Method
A retrospective study was conducted on postnatal TORCH testing between January 2024 and December 2024 at the National Hospital, Galle. Records were reviewed to identify indications for testing and serology results.

Results
Requests of 155 neonates were reviewed. TORCH serology was performed for the following indications: isolated IUGR in 81 patients (52.3%) and neonates presented with other symptoms in addition to IUGR (47.7%). Screens ordered for isolated IUGR were positive in 0%, while the 3 (4.05%) neonates of the second cohort had positive torch screening results. (95% CI 0.84 to 11.39%). Among them, two were positive for HSV and one for CMV.

Conclusions
Routine TORCH screening in neonates with isolated IUGR yields low diagnostic and clinical utility. Selective screening based on additional clinical findings or maternal history may be more cost-effective and clinically appropriate.

RES-043: Serotype Distribution, Multilocus Sequencing Type, and Antimicrobial Susceptibility of Invasive Streptococcus Pneumoniae Isolates from Adults in Hokkaido, Japan

Mitsuyo Kawaguchiya[3], Meiji Soe Aung[3], Noriko Urushibara[3], Nobuhide Ohashi[3], Nobuyuki Kobayashi[1], Kenji Kudo[2], Masahiko Ito[2], Nobumichi Kobayashi[3]

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[2]Sapporo Clinical Laboratory Inc.
[3]Sapporo Medical University School of Medicine

Background
In Japan, the 23-valent pneumococcal polysaccharide vaccine (PPSV23) for adults aged >65 years was incorporated into the national immunization program in 2014. The present study aimed to investigate the molecular characteristics and antimicrobial resistance of Streptococcus pneumoniae isolates from adults with invasive pneumococcal disease (IPD) in Hokkaido, the northern main island of Japan.

Method
From September 2017 to December 2023, a total of 45 pneumococcal isolates from patients with IPD (41 inpatients; 4 outpatients) were collected throughout Hokkaido, Japan. All isolates were serotyped by sequential multiplex PCR and direct sequencing. Multilocus sequence typing scheme for pneumococcus was performed to identify the sequence types (STs). Minimum inhibitory concentrations to 11 antimicrobials were measured by broth microdilution test using a Dry Plate.

Results
Among a total of 45 isolates, serotype 3-ST180 (24.4%) was the most prevalent, followed by 23A-ST338/ST5242 (13.3%), 23F-ST242/ST1437/ST3543 (8.9%), and 6D-ST282, 15A-ST63, 35B-ST558, and 34-ST1439/ST7388 (6.7% each), collectively accounted for 73.4% of all isolates. Overall, the proportion of the PPSV23 serotypes was 44.5%. The rate of non-susceptibility to penicillin was 24.4%, and most of them (n=10/11, 90.9%) were also non-susceptible to erythromycin and tetracycline. Among the non-PPSV23 serotypes, 23A, 6D, 15A, 35B, and 6E showed multiple drug resistance (3 or more classes), along with non-susceptibility to penicillin.

Conclusions
The present study revealed the high prevalence of non-PPSV23 serotypes among isolates from IPD in adults, associated with high rates of non-susceptibility to antimicrobial agents. These findings indicated the need for continuous surveillance of S. pneumoniae in Japan.

RES-044: Why Do Some People Not Get COVID-19? A Mixed Methods Study Among Household Members With and Without COVID-19 in Singapore

Smeetha Nair[1, 2], Moses Lim Yaorong[2], Paul Anantharajah Tambyah[1], Natasha Howard[2, 3]

[1]National University Hospital
[2]National University of Singapore
[3]London School of Hygiene and Tropical Medicine

Background
The COVID-19 pandemic has spread globally in successive waves, infecting much of the world's population. However, a small subset of individuals appears to have never contracted the virus. While genome-wide association studies have not identified genetic markers of protection, few studies have examined behavioral differences between those who have and have not been infected.

Method
We conducted a mixed-methods study using semi-structured dyadic interviews and an online survey to explore behavioral factors influencing COVID-19 infection risk. Participants were recruited via purposive and snowball sampling and through an online group.

Results
Interview data from 40 individuals (20 dyads) were analyzed thematically, while survey responses from 256 participants were analyzed descriptively using independent sample t-tests and Fisher's exact tests. Survey findings indicated that individuals who avoided crowds (OR = 0.46, 95% CI [0.24, 0.87]) and consistently wore masks since 2020 (OR = 0.18, 95% CI [0.08, 0.44]) had lower odds of self-reported infection. In contrast, those who used traditional medicine had higher odds of infection (OR = 2.01, 95% CI [1.04, 3.88]), though interviewees often cited it as a means of immune strengthening. While mask use and social distancing were seen as protective in the survey, these did not emerge as major themes in the interviews. Vaccination did not appear to be a major factor in either analysis.

Conclusions
These findings underscore the need for more in-depth multi-modal research to identify appropriate and sensitive risk communications taking into account local cultures and beliefs. Effective health communication will be critical in preparing for the next pandemic.

RES-045: Cefiderocol Resistance in a KPC-Producing Hypervirulent Klebsiella pneumoniae Strain Mediated by envZ Mutation and Downregulation of Iron Transport Genes

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[1]China-Japan Friendship Hospital
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Background
Cefiderocol is a last-resort antibiotic for carbapenem-resistant hypervirulent Klebsiella pneumoniae (CR-hvKP). While resistance often involves metallo-β-lactamases, mechanisms in KPC-producing strains are unclear.

Method
A clinical cefiderocol-susceptible KPC-2-producing CR-hvKP strain (K27356) evolved under sub-lethal cefiderocol pressure to generate resistant mutants (K27356M1-M3). Resistance mechanisms were investigated using whole-genome sequencing, transcriptomics, genetic manipulation, antimicrobial susceptibility testing, siderophore quantification (CAS/Arnow assays), single-cell ICP-MS for iron content, growth kinetics, and macrophage phagocytosis/survival assays.

Results
All resistant mutants exhibited high-level cefiderocol resistance (MIC >128 mg/L) and harbored a gain-of-function mutation in the sensor kinase gene envZ (V145G). The envZ mutation/deletion alone in K27356M1 conferred an 8-fold MIC decrease, but additional unidentified factors contributed to high-level resistance. Further transcriptomics revealed significant downregulation of genes involved in catecholate siderophore biosynthesis (entABCEF), iron transport (cirA, fepA, fhuA, fecA, cjrC), TonB energy transduction (exbB, exbD), and sulfate assimilation (cysAT). Functional validation confirmed reduced siderophore production (particularly catechol type) and impaired intracellular iron accumulation in mutants under normal and iron-limited conditions. K2756M1 exhibited significant fitness costs, including impaired growth, reduced resistance to oxidative stress, and diminished survival within macrophages.

Conclusions
A novel cefiderocol resistance mechanism in KPC-producing CR-hvKP involves an envZ (V145G) mutation, disrupting the EnvZ/OmpR two-component system and downregulating iron/siderophore transport genes. This impairs cefiderocol uptake and iron homeostasis, leading to high-level resistance. However, substantial fitness costs may limit transmission. These findings highlight the role of regulatory mutations in cefiderocol resistance and inform strategies to combat resistant CR-hvKP.

RES-046: Pseudomonas Aeruginosa with Difficult-to-Treat Resistance Cases: A Single-Center Review

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NHO Kyoto Medical Center

Background
Pseudomonas aeruginosa (PA), which is of particular importance among resistant bacteria, has recently been defined as Difficult-to-treat resistance Pseudomonas Aeruginosa (DTR-PA) and has been alerted. We attempted to adopt Tazobactam/Ceftolozane (TAZ/CTLZ) for DTR-PA; however, the actual frequency of DTR-PA and its antimicrobial susceptibility were unknown. Therefore, we investigated the frequency of DTR-PA detection, its background, and prognosis in our hospital.

Method
DTR-PA identified in culture at our institution from October 2016 to December 2024 were analyzed retrospectively.

Results
During the period, 427 cases of PA were detected; 9 (2.2%) were DTR-PA. We detected DTR-PA from sputum, pleural fluid and urine. Five (55.6%) out of 9 cases were assumed to be the causative organism. PA had been previously detected in 5 (55.6%) cases, and antibiotics had been used within the past one month in all cases. Major comorbidities consisted of chronic kidney disease, bronchiectasis, diabetes mellitus, and cerebrovascular disease. All of the 6 cases that were available for testing remained susceptible to TAZ/CTLZ. Aminoglycosides and polymyxins were administered to 4 cases (44.4%) and 0 case, respectively. Both 30-day and in-hospital mortality rates were 3 (33.3%) cases. Of the 4 cases administered aminoglycosides, one case died (25%). The median duration of treatment was 8 days. Adverse events occurred in 3 (33.3%) cases, but only mild ones.

Conclusions
In our hospital, the frequency of DTR-PA was relatively low, but the mortality rate of DTR-PA was high and the prognosis was poor.

RES-047: Knowledge, Attitudes, and Practices on the Control and Prevention of Soil-transmitted Helminthiases Among Residents of San Antonio, Quezon, Philippines

Johanna Camille Liwanagan, Mary Jane Flores

De La Salle University

Background
Soil-transmitted helminths (STH) is one of the neglected tropical diseases that affect more than 48 million children in the Philippines despite the implementation of control and prevention strategies such as mass drug administration, access to clean water, sanitation, hygiene, and education. This study described the knowledge, attitudes, and practices to control and prevent STH infections of the residents in San Antonio, Quezon.

Method
Single-type focus group discussions were conducted once among selected residents in eighteen (18) barangays of 20 barangays in San Antonio, Quezon.

Results
Residents demonstrated inadequate knowledge about STH's biology, signs and symptoms of infection, transmission, and epidemiology. In addition, several misconceptions about STH were mentioned by the participants such as being infected with STH has importance in one's life, a person can be infected with STH by consuming raw rice grains and sugar, and that Amoeba is an STH. Regarding attitudes, only the residents from 4 (Buliran, Bulihan, Poblacion, and San Jose) of the 18 barangays claimed that they followed the deworming protocol. To prevent STH infections, the residents practice washing of hands, wearing slippers or shoes, and refraining from open defecation.

Conclusions
In general, the residents of San Antonio, Quezon have good hygiene and sanitary practices but lacked knowledge about STH and exhibited negative attitude towards deworming. The health education strategy should be strengthened to ensure that the residents are aware of the different ways they can prevent STH infections among the members of the community.

RES-048: Establishment of Antimicrobial stewardship (AMS) Program at a Tertiary Cancer Center: A 2-years' Experience at University Medical City/ Sultan Qaboos Comprehensive Cancer and Research Center (SQCCCRC)

Eyad Al-Madhoun, Bassem Awada, Amna Al Hashar, Athar Al-Khirbash, Ramesh Bora

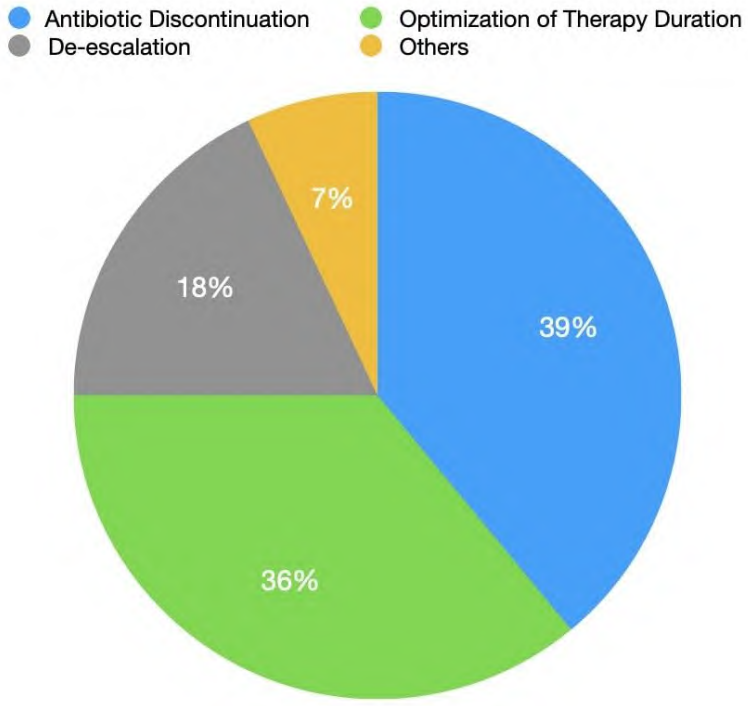
Sultan Qaboos Comprehensive Cancer Care and Research Center

Background
Antimicrobial stewardship programs (ASP) are essential in oncology settings to optimize antimicrobial use, reduce resistance, and improve patient outcomes. At Sultan Qaboos Comprehensive Cancer Care and Research Center (SQCCCRC), a fully electronic, real-time ASP model was implemented from the center's inception to guide daily antimicrobial decision-making process.

Method
A validated electronic ASP platform was developed to document interventions and generate automated reports. Daily stewardship reviews focused on broad-spectrum antibiotics and carbapenems sparing strategy in medical wards and intensive care unit. A retrospective descriptive analysis was conducted from January 2023 to December 2024 to evaluate key performance indicators (KPIs), including the ASP interventions, Days of Therapy (DOT) per 1,000 patient-days, prevalence of multi-drug-resistant organisms (MDROs) from clinical isolates, and most common bloodstream infections pathogens.

Results
Over the two-year period, 2,519 antimicrobial stewardship interventions were recorded, with a compliance rate of 93%. The most frequent interventions included antibiotic discontinuation (39%), optimization of therapy duration (36%), and de-escalation (18%). The median DOT per 1,000 patient-days was 61.5 (IQR: 20) for carbapenems, 133 (IQR: 42.75) for Piperacillin-Tazobactam, and 34 (IQR: 16.5) for vancomycin. The prevalence of carbapenems-resistant Enterobacterales (CRE) ranged from 1.8 to 4.8 per 1,000 patient-days; methicillin-resistant Staphylococcus aureus (MRSA) ranged from 2.2 to 4.1; and multi drug-resistant Acinetobacter ranged from 0 to 1.6 per 1,000 patient-days.

Conclusions
The ASP at SQCCCRC demonstrated sustained implementation with high compliance and impactful, targeted interventions. The program contributed to reduced use of broad-spectrum antibiotics and close monitoring of resistance trends, highlighting the value of real-time, integrated stewardship.



RES-051: Impact of Population Ageing on Pathogen Distribution and Clinical Outcomes in Bloodstream Infections: A 17-Year Retrospective Cohort Study in South Korea

Min Hyuk Choi

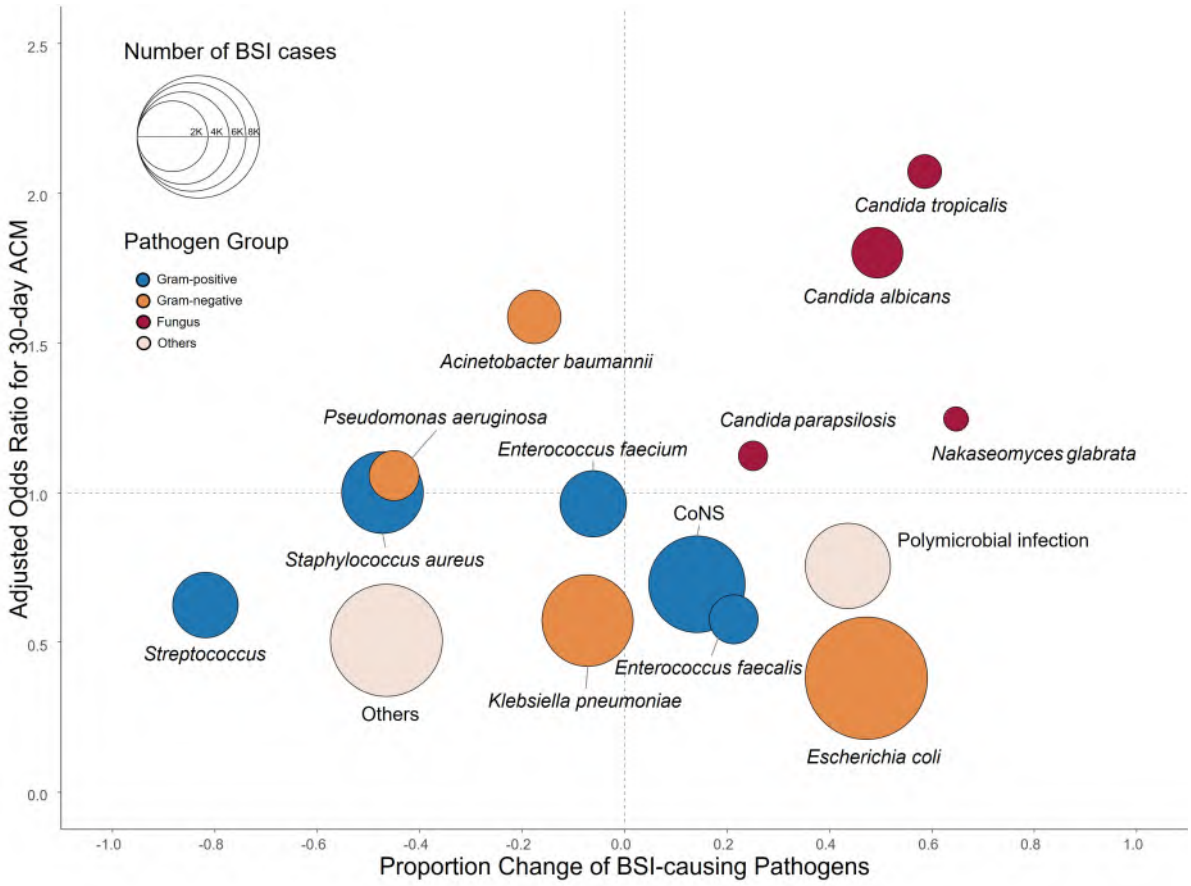
Yonsei University College of Medicine

Background
As global population aging progresses, its impact on the epidemiology and prognosis of bloodstream infections (BSIs) remains insufficiently explored. We assessed how ageing affects pathogen distribution and 30-day mortality among patients with BSI.

Method
This retrospective study analyzed 37,100 BSI cases from two tertiary hospitals in South Korea (2006–2023). Statistical models and machine learning (ML) approaches were used to examine age-related temporal trends, predictors of 30-day mortality, and shifts in pathogen proportions. Structural equation modeling and SHapley Additive exPlanations (SHAP) interpretation were used to identify direct and indirect age effects.

Results
The mean age of patients was 64.6 years (SD 15.0), with 55.7% aged ≥65. Advanced age was independently associated with a high 30-day mortality via a shift in pathogen distribution. The figure summarizes pathogen-specific characteristics in terms of the number of cases, adjusted mortality risk, and age-related changes in distribution. ML models predicted an increasing proportion of BSIs caused by Escherichia coli, Enterococcus faecalis, coagulase-negative staphylococci, and fungi with ageing and a decreasing proportion of those caused by Staphylococcus aureus, streptococci, Pseudomonas aeruginosa and Acinetobacter spp. Fungemia contributed to the highest adjusted mortality rate. The advantage of E. coli-BSI being associated with low 30-day mortality was diminished in strains not susceptible to third-generation cephalosporins.

Conclusions
Population aging is associated with distinct shifts in BSI pathogen distribution and outcomes. Our findings highlight the need for age-tailored antimicrobial stewardship and infection control strategies to address the rising burden of BSIs in older adults.



RES-052: Strengthening Carbapenems Usage Monitoring Through Antimicrobial Stewardship Program as an Effective Measure in Reducing Carbapenem-Resistant Enterobacterales (CRE) Cases – A Single Centre Experience from Miri Hospital, Sarawak, Malaysian Borneo.

Tonnii Sia, Salasiah Jaidil, Lee-Hwa Chu, Nurul Aimi Abdul Rahman, Nancy Uhai, Siew-Moi Chang, Marylisa Abai, Siew-Chen Ten, Ling-Weng Wong, Mohd Taha Ariff Isa Ali

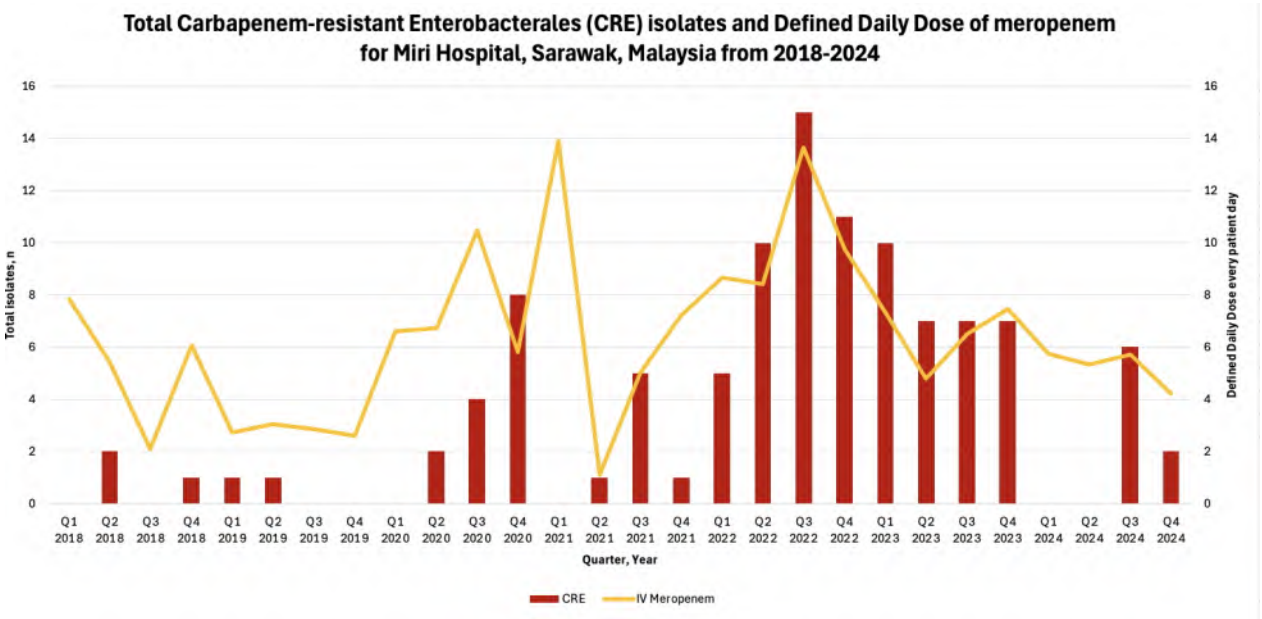
Miri Hospital

Background
Carbapenem-resistant Enterobacterales (CRE) is an alarming hospital-acquired infection in Malaysia as it carries high mortality and limited treatment options. CRE are driven by broad-spectrum antibiotic use, especially carbapenems. Miri Hospital is the sole government-funded tertiary centre in Northern Sarawak. Since 2020, CRE cases have risen significantly, from 2–3 cases annually in 2018–2019 to 30–40 cases annually, between 2020-2023.

Method
This is a retrospective analysis of CRE surveillance and antimicrobial consumption data from 2018-2024. Antimicrobial consumption is measured using the Defined Daily Dose (DDD). Since June 2023, Antimicrobial Stewardship Programme (ASP) was strengthened to ensure carbapenem use was compliance with national antimicrobial guideline (NAG).

Results
106 CRE cases were recorded during study period. 48.1% (n=51) was isolated from blood, 22.6% from respiratory tract secretions, 14.1% from urine and 15.1% was from other samples. 75.5% (n=80) were classified as infection and others as coloniser. A sharp increase in CRE cases was observed from 2020-2023 (Figure 1). COVID-19 pandemic caused low admission in 2021. The median meropenem DDD increased from 2.95 prior to 2020 to 9.20 in 2022. The rise in CRE cases paralleled an increase in meropenem usage. Following intensified ASP efforts (timely 72 hours reviews of treatment indications, evaluation of microbiological culture results, and strict adherence to NAG), the median meropenem DDD declined to 5.52 in 2024 and so as the number for CRE cases.

Conclusions
Strengthening ASP is effective in reducing hospital-acquired CRE. Continuous prescriber education and regular feedback on antimicrobial use are essential.



RES-054: Uncovering Dengue Virus Host Factors: Paving the Way for Innovative Antiviral

Shin-Hong Shiao

National Taiwan University

Background
Incidence of dengue virus (DENV) and Zika virus (ZIKV), two mosquito-borne flaviviruses, is increasing in large parts of the world. Vaccination and medication for these diseases are unsatisfactory. Here, we developed a novel antiviral approach, using a virus-inducible gene expression system, to block virus replication and transmission.

Method
Constructs containing the smallest replication units of dengue virus serotype 2 (DENV2) with negative-stranded DENV2 artificial genomes and genes of interest were established in an Aedes aegypti cell line, resulting in expression of target genes after DENV2 infection. Green fluorescent protein (GFP) assays confirmed the system was virus-inducible.

Results
When we used one of two apoptosis-related genes, A. aegypti michelob_x (AaMx) and inhibitor of apoptosis (IAP)-antagonist michelob_x-like protein (AaIMP) instead of GFP, the production of viral RNA and proteins were inhibited for all five viruses tested (DENV1–4 and ZIKV), and effector caspase activity was induced. The system thus inhibited the production of infectious virus particles in vitro, and in mosquitoes it did so after DENV2 infection.

Conclusions
This is a novel broad-spectrum antiviral approach using a flavivirus-inducible gene-expression system, which could lead to new avenues for mosquito-borne disease control.

RES-056: Bacteremia Caused by Carbapenem-Resistant E. coli In Children from a Tertiary Care Hospital

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Background
Antimicrobial resistance (AMR) has emerged as a significant global public health challenge, especially in developing countries like India, where infectious diseases are prevalent, and antibiotic use often lacks proper regulation. This research aimed to explore the epidemiological connection among patients infected with carbapenem-resistant Escherichia coli.

Method
A total of 80 isolates were collected from children suffering from diarrhea. Conventional phenotypic methods were performed, and antibiotic susceptibility testing was conducted using CLSI guidelines. Bacteremias caused by E. coli were registered in 28 children. Various bacteriological and molecular biological methods (PCR-RT and MLST) were used to identify isolates.

Results
All 28 children with bacteremia were in isolated wards. Out of these, carbapenem resistance in E. coli was detected in 12 children. In two carbapenem-sensitive E. coli isolates, the NDM-1 gene was detected. No antibiotic resistance genes were found in the hospital environment or other samples. Comparative genomic analyses of 8 E. coli isolates revealed differences in common loci, possibly due to variations in plasmid sequences.

Conclusions
This study established group colonization in E. coli strains due to translocation of intestinal flora. Genomic surveillance of priority pathogens will help identify high-risk AMR clones regionally and globally, and groups at risk of infection. This will enable correlation of virulence factors with patient outcomes, aiding in early outbreak detection.

RES-057: One Health Genomic Surveillance of AMR in Western India: A First-of-Its-Kind Ecosystem-Wide Study Linking Human, Animal, and Environmental Resistomes to Policy

Pravinkumar Dudhagara, Rajesh Patel

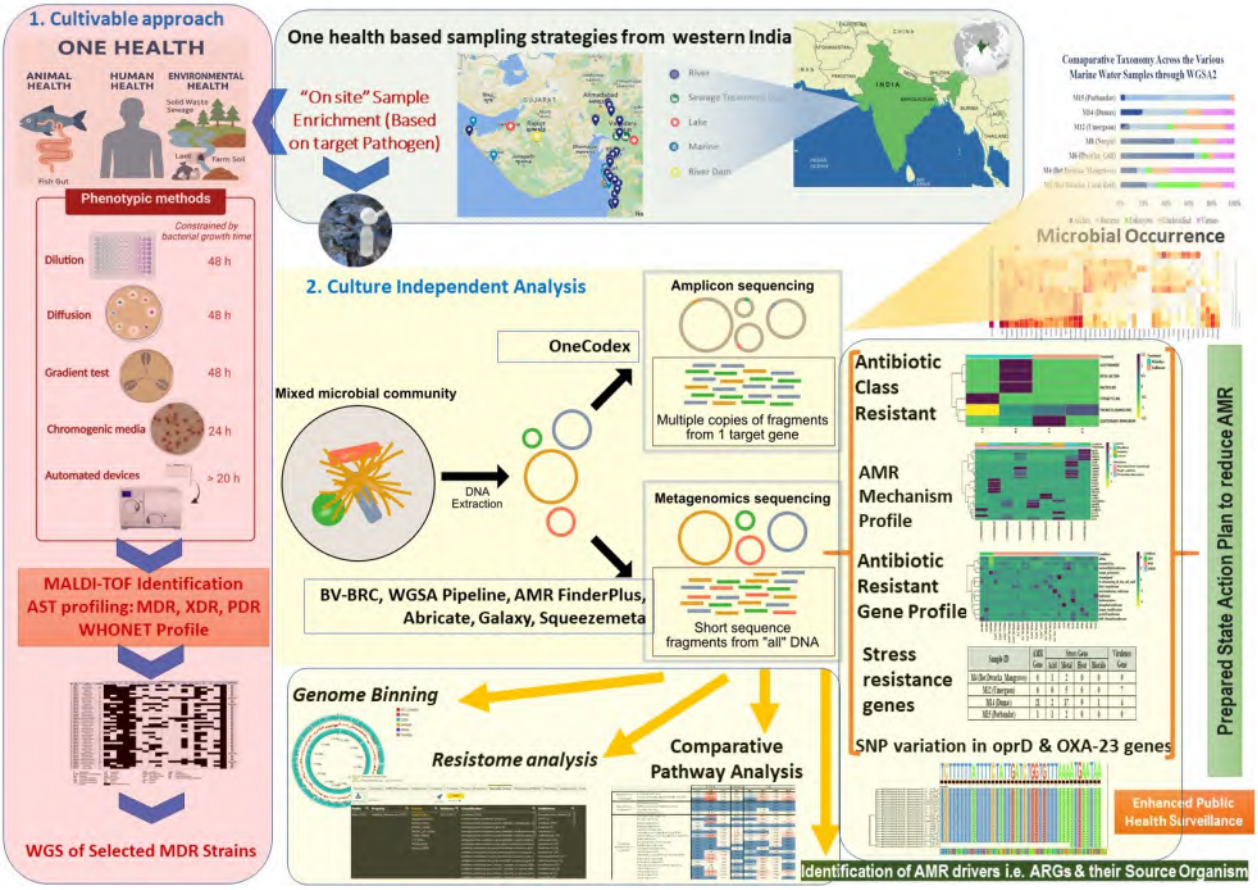
Veer Narmad South Gujarat University

Background
AMR is a serious global threat, increasingly driven by the complex interactions between human, animal, and environmental ecosystems. To address this, first-of-its-kind One Health-based AMR Surveillance strategy implemented across Western India, focusing on microbial samples from three sectors: animal (fish gut), human (urban sewage), and environment (rivers, lakes, farm soil, and solid waste).

Method
The first phase utilized a culture-dependent approach, employing MALDI-TOF identification and antibiotic susceptibility testing (AST) to detect and profile MDR, XDR, and PDR organisms. Select MDR isolates underwent WGS to identify key resistance determinants. The second phase involved a metagenomic analysis using advanced pipelines i.e. BV-BRC, WGSA, AMR FinderPlus and SqueezeMeta.

Results
This revealed high microbial diversity and widespread antibiotic resistance genes (ARGs) across all sampled ecosystems. ARGs conferring resistance to β-lactams, vancomycin, and tetracycline were prevalent, and stress resistance genes (e.g., for heavy metals) were detected, indicating co-selection pressures. SNP variations, particularly in oprD and OXA-23, were identified, demonstrating genetic adaptation in resistance genes. Genome binning and resistome profiling provided insights into the microbial hosts of ARGs and enabled the mapping of resistance mechanisms to specific ecological niches. The analysis confirmed gamma-Proteobacteria and other taxa as key ARGs source organisms, underlining the evolutionary and ecological complexity of AMR. Based on these findings, a State Action Plan was developed to mitigate AMR risks, emphasizing enhanced public health surveillance, environmental monitoring, and cross-sectoral policy integration.

Conclusions
This study reinforces the importance of integrated genomic surveillance and provides a foundational framework for AMR containment through the One Health lens.



RES-058: Promising Strategies for the Prevention and Treatment of Viral Diseases Due to Lactococcus lactis strain Plasma

Masato Kawamura, Yurina Tamura, Shigeru Fujimura

Tohoku Medical and Pharmaceutical University

Background
Biogenic and probiotics in healthy foods and supplements have been reported to regulate the intestines and activate the immune system. This study investigated interferon-α (IFN-α) production and the phagocytic ability of plasmacytoid dendritic cells (pDCs) in response to each biogenic or probiotic bacteria.

Method
Nine probiotic strains were isolated from the supplements and yoghurt products; Lactococcus lactis strain Plasma, Lactobacillus acidophilus L-92, Gluconacetobacter hansenii GK-1, Lactiplantibacillus plantarum L-137, Lacticaseibacillus paracasei MCC1849, Lactobacillus delbrueckii subsp. Bulgaricus OLL1073R-1, Bifidobacterium longum subsp. longum BB536, Lactbacillus gasseri SBT2055, and Lactocaseibacillus rhamnosus CRL1505. Each of these bacteria were inoculated mouse-pDCs and determined production of IFN-α. Briefly, the pDCs were differentiated and developed using the Flt3 ligand from mouse bone marrow cells and the IFN-α concentration was measured using ELISA kits. Additionally, the phagocytic activity of the pDCs was evaluated. First, the pDCs were isolated using a negative selection method. Second, the probiotic strains were stained with FITC and different probiotic strains were inoculated with the pDCs. These were cultured 24 h at 37℃ under 5% CO2. The pDCs stained with Alexa Fluor 546 were observed using by fluorescence microscopy and laser scanning confocal fluorescence microscopy.

Results
L. lactis Plasma were phagocytosed by pDCs, resulting in the production of IFN-α at a concentration of 74 pg/mL.

Conclusions
L. lactis strain Plasma, a novel therapeutic agent, may be effective for treatment and prevention of viral infection.

RES-061: Pilot Study of Epidemiology of Coliform Bacteria in Different Area of Public Bathroom of Outpatient Department, Siriraj Hospital

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Background
Hospital public restrooms are high-risk areas for bacterial spread due to heavy use. Studies show that the toilet seat is often the most contaminated surface especially by coliform bacteria. Regular cleaning may not fully eliminate bacteria, highlighting the need for better infection control strategies.

Method
We conducted a pilot study to investigate the epidemiology of coliform bacteria in public restrooms at Siriraj Hospital, Bangkok, Thailand. We randomly collected samples from six locations within each of six restrooms in the outpatient clinic of the Internal Medicine Department. We used a cotton swab soaked in normal saline to collect samples from an area of approximately 10 cm^2, which were then transferred to normal saline transport media. A 100-microliter loop was subsequently used to spread the samples onto MacConkey agar. After a 24-hour incubation period, colonies were counted and reported as colony-forming units (CFU).

Results
Table 1 presents colony counts (median [min-max]) by location and bacterial type (fermentative vs. non-fermentative). The highest fermentative counts were on the sink faucet (0[0-58]), toilet seat cover (0[1-16]), and flush handle (0[0-16]). For non-fermentative bacteria, the top sites were the sink faucet (201[0-1000]), toilet seat cover (2[0-19]), and bidet hose (1[0-98]. The predominant gram-negative bacteria species were identified as E. coli, K.pneumoniae, and P.aeruginosa.

Conclusions
In conclusion, the sink faucet was the most contaminated area, harboring not only coliform bacteria but also nosocomial pathogens. This area requires special attention, and cleaning staff should be particularly vigilant, as it may pose potential health risks within the healthcare facility.

	Count of Fermentative bacteria (colony forming unit)						
	Male room-1	Male room-2	Female room-1	Female room-2	Accessible room-1	Accessible room-2	Median [min-max]
1. Inner door lock	0	0	0	0	0	0	0
2. Toilet seat cover	1	0	16	0	0	0	0 [0-16]
3. Flush handle	0	16	0	0	0	0	0 [0-16]
4. Bidet hose	0	0	0	0	0	0	0
5. Sink faucet	3	0	0	58	0	0	0 [0-58]
6. Handrail	-	-	-	-	0	0	0
	Count of Non-fermentative bacteria (colony forming unit)						
	Male room-1	Male room-2	Female room-1	Female room-2	Accessible room-1	Accessible room-2	Median [min-max]
1. Inner door lock	2	1	0	0	0	0	0 [0-2]
2. Toilet seat cover	19	0	2	0	2	8	2 [0-19]
3. Flush handle	0	32	0	0	0	0	0 [0-32]
4. Bidet hose	1	0	0	0	1	98	0.5 [0-98]
5. Sink faucet	667	402	0	1000+	0	0	201 [0-1000]
6. Handrail	-	-	-	-	0	0	0

RES-062: Gut Microbiota Signatures Predict Antihistamine Efficacy in Burn-Related Pruritus

Yoon Soo Cho, Yeongyun Jung

Hangang Sacred Heart Hospital

Background
Post-burn pruritus (PBP) is a frequent and distressing complication of burn injury. Antihistamines are commonly prescribed, yet their efficacy varies among patients. Recent evidence suggests that gut microbiota can modulate immune responses and influence drug effectiveness. However, their role in mediating antihistamine response in PBP remains poorly understood.

Method
Fifty-six male burn patients were categorized into three groups: no pruritus (NP), histamine-responsive (HR), and histamine-nonresponsive (HNR). Fecal samples were collected at baseline and 8 weeks after antihistamine administration. Microbiota composition was analyzed via 16S rRNA gene sequencing. Functional predictions were generated using PICRUSt2.

Results
Alpha and beta diversity did not differ significantly between groups. However, genus-level analysis identified group-specific patterns: Sutterella was enriched in the HR group, while Faecalimonas, Ligilactobacillus, and Catenibacillus were more abundant in HNR patients. Post-treatment, the HR group showed increased microbial richness and upregulated proteolytic and antioxidant pathways. In contrast, the HNR group demonstrated enrichment of amino acid and fatty acid metabolism with reduced redox-related functions.

Conclusions
Distinct gut microbiota signatures and functional traits are associated with antihistamine efficacy in burn-related pruritus. These findings highlight the potential of gut microbial profiling as a predictive tool for personalized management of post-burn pruritus.

Acknowledgments: This research was supported by Basic Science Research Program through the National Research Foundation of Korea (NRF) funded by the Ministry of Education (NRF-2020R1I1A3074150).

RES-063: Emergence of Multidrug-Resistant and Extended-Spectrum β-lactamase-producing Shigella flexneri 2a Clinical Isolates in Japan

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[2]Nagoya University Graduate School of Medicine
[3]National Institute of Infectious Diseases, Japan Institute for Health Security

Background
The emergence of fluoroquinolone- and third-generation cephalosporin (3GC)-resistant Shigella spp., including extended-spectrum β-lactamase (ESBL)-producing strains, is an increasing public health concern, with incidence rates continuing to rise. In this study, we report for the first time in Japan the genomic characterization of multidrug-resistant (MDR) and ESBL-producing Shigella flexneri 2a strains, focusing on their antimicrobial resistance and virulence profiles.

Method
Two Shigella isolates were obtained in Japan in 2023 from family members who had traveled to Southeast Asia. Bacterial identification was performed using biochemical testing, ipaH gene detection, and serotyping. Antimicrobial susceptibility testing was conducted to determine the minimum inhibitory concentrations of ceftriaxone, ciprofloxacin, and azithromycin. Whole-genome sequencing was carried out to characterize antimicrobial resistance genes, plasmid profiles, and virulence factor genes.

Results
Both isolates were identified as S. flexneri 2a and were found to harbor the ESBL gene blaCTX-M-15 and the fluoroquinolone resistance gene qnrS1, integrated into the chromosomal prophage region. Although these isolates were obtained from members of the same family, single nucleotide variant analysis revealed that they were genetically distinct. Additionally, one isolate carried an IncB/O/K/Z-type plasmid harboring macrolide resistance genes such as mphA and ermB, and exhibited resistance to azithromycin.

Conclusions
We identified two distinct MDR Shigella flexneri isolates, raising concerns about the MDR Shigella strains originating from Southeast Asia. In Japan, no genomic analyses of MDR Shigella have previously been reported. This study provides valuable insights into the genetic characteristics of MDR Shigella isolates. The emergence of MDR Shigella strains poses a significant challenge to effective antimicrobial therapy.

RES-064: Efficacy of Ceiling-Mounted Mosquito Nets for Malaria Vector Control in a Peruvian Amazon Riverine Community: A Stepped-Wedge Cluster Randomized Trial

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[2]Universidad de Ingeniería y Tecnología
[3]Universidad Nacional de la Amazonía Peruana, Loreto, Peru
[4]World Vision Korea, Seoul, Korea
[5]World Vision Peru, Loreto, Peru

Background
Malaria remains a critical public health threat in tropical regions, including the Peruvian Amazon. Structural modifications to reduce human–mosquito contact have gained interest as sustainable vector control strategies. This study evaluated the impact of ceiling-mounted mosquito nets on indoor and outdoor densities of Anopheles mosquitoes, the primary malaria vectors.

Method
We conducted a stepped-wedge cluster-randomized trial from March to December 2024 in Llanchama, San Juan Bautista district, Loreto, Peru. Sixty-nine households were assigned to three clusters, receiving the intervention—installation of ceiling-mounted nets and sealing of open structural gaps—at staggered three-month intervals. Entomological surveillance included human landing catches to quantify Anopheles density, bites per person per night (BPN), and bites per person per hour (BPH), both indoors and outdoors.

Results
In per-protocol analysis, intervention households showed a 55% reduction in indoor Anopheles counts (95% CI: 33%–74%; p = 0.004), a 60% decline in indoor BPN (95% CI: 27%–78%; p = 0.003), and a 61% decrease in indoor BPH (95% CI: 15%–83%; p = 0.018) relative to non-intervention households. No significant differences were observed for outdoor entomological indices.

Conclusions
Ceiling-mounted mosquito nets significantly reduced indoor exposure to Anopheles mosquitoes, supporting their potential as a scalable structural intervention to complement malaria control efforts in endemic riverine settings.

Table 1: Estimated Effects of CMMNs on Mosquito Density and Biting Rates

Model Parameters	Indoor mosquitoes count	Outdoor mosquitoes count	Overall mosquitoes count	Indoor BPN	Outdoor BPN	Overall BPN	Indoor BPH	Outdoor BPH	Overall BPH
	IRR (95% CI)	IRR (95% CI)	IRR (95% CI)	IRR (95% CI)	IRR (95% CI)	IRR (95% CI)	IRR (95% CI)	IRR (95% CI)	IRR (95% CI)
CMMN	**0.45**** **(0.26 – 0.77)**	0.94^{ns} (0.75 – 1.17)	0.78^{ns} (0.59 – 1.03)	**0.40**** **(0.22 – 0.73)**	0.93^{ns} (0.73 – 1.19)	0.75^{ns} (0.55 – 1.02)	**0.39*** **(0.17 – 0.85)**	0.92^{ns} (0.57 – 1.49)	0.71^{ns} (0.47 – 1.08)
Time									
Baseline	Reference	Reference	Reference	Reference	Reference	Reference	Reference	Reference	Reference
3rd month	0.20*** (0.14 – 0.30)	0.20*** (0.16 – 0.25)	0.20*** (0.16 – 0.24)	0.21*** (0.14 – 0.30)	0.20*** (0.16 – 0.25)	0.20*** (0.16 – 0.25)	0.10*** (0.07 – 0.16)	0.20*** (0.14 – 0.28)	0.20*** (0.15 – 0.27)
6th month	0.09*** (0.05 – 0.16)	0.10*** (0.08 – 0.13)	0.10*** (0.07 – 0.13)	0.10*** (0.06 – 0.18)	0.10*** (0.08 – 0.13)	0.10*** (0.07 – 0.13)	0.05*** (0.02 – 0.11)	0.10*** (0.06 – 0.18)	0.10*** (0.07 – 0.16)
9th month	0.45*** (0.26 – 0.77)	0.19*** (0.14 – 0.26)	0.17*** (0.12 – 0.24)	0.12*** (0.05 – 0.26)	0.19*** (0.14 – 0.27)	0.17*** (0.11 – 0.26)	0.06*** (0.02 – 0.20)	0.21*** (0.11 – 0.39)	0.20*** (0.11 – 0.35)
Household type									
Type B	Reference	Reference	Reference	Reference	Reference	Reference	Reference	Reference	Reference
Type C	1.07^{ns} (0.66 – 1.73)	0.88^{ns} (0.67 – 1.15)	0.92^{ns} (0.71 – 1.19)	1.04^{ns} (0.67 – 1.61)	0.86^{ns} (0.65 – 1.13)	0.91^{ns} (0.70 – 1.18)	0.84^{ns} (0.56 – 1.27)	0.73^{ns} (0.53 – 1.02)	0.79^{ns} (0.59 – 1.07)
Type D	0.45** (0.26 – 0.77)	0.76^{ns} (0.67 – 1.03)	0.69* (0.52 – 0.92)	0.46** (0.29 – 0.73)	0.73* (0.53 – 0.99)	0.68** (0.51 – 0.91)	0.51** (0.31 – 0.85)	0.56** (0.37 – 0.83)	0.56** (0.39 – 0.80)
Constant	122.0*** (94.4 – 157.5)	122.0*** (94.4 – 157.5)	197.5*** (153.6 – 254.0)	39.6*** (26.0 – 60.5)	62.6*** (48.1 – 80.3)	100.0*** (78.0 – 128.1)	7.3*** (5.0 – 10.6)	6.2*** (4.5 – 8.2)	9.5*** (7.2 – 12.5)
Ln(alpha)	-0.14*** (-0.36 – 0.08)	-1.26*** (-1.45 – -1.07)	-1.36*** (-1.55 – -1.17)	-0.43** (-0.68 – -0.17)	-1.32*** (-1.53 – -1.11)	-1.41*** (-1.62 – -1.20)	-1.34*** (-1.82 – -0.86)	-2.30*** (-3.10 – -1.51)	-2.04*** (-2.56 – -1.52)
Cluster Variance	0.02*** (<0.01 – 0.52)	<0.01^{NA} (NA)	<0.01^{NA} (<0.01 – 0.21)	<0.01^{NA} (NA)	<0.01 (NA)^{NA}	<0.01^{NA} (<0.01 – 1.27)	<0.01^{NA} (NA)	<0.01^{NA} (NA)	<0.01^{NA} (NA)

*, p value <0.05; **, p value <0.01; ***, p value <0.001; ns, non-significant; IRR, incidence rate ratio; BPN, bites per person per night; BPN, bites per person per person; Ln, Napierian logarithm; CMMN, ceiling-mounted mosquito nets.

RES-065: Evaluation of the Effect of Tetracycline and Fluoroquinolone Combination Therapy for Japanese Spotted Fever: A Comprehensive Analysis of Case Reports and Case Series

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Background
Since its first report in 1984, the incidence of Japanese spotted fever (JSF) has increased annually, with a corresponding rise in mortality. However, there has not yet been a standard treatment for JSF. The primary medication for treating rickettsial infections is tetracycline (TC). Meanwhile, there have been reported cases in clinical practice where the combined therapy of TC and fluoroquinolone (FQ) (TC+FQ) is successful.

Method
From 1984 to 2022, we searched PubMed and Ichushi Web for cases definitively diagnosed with JSF. The study extracted data on temperature and patient characteristics. We standardized the data by adjusting for patient characteristics. This research analyzed the maximum body temperatures recorded daily from the first visit (Day 1) to Day 10, or up to 1 day after a change in treatment among the TC and TC+FQ groups.

Results
We collected temperature data from 102 patients, 84 in the TC group and 18 in the TC+FQ group. There were no significant differences in complications between the two groups. The analysis of the temperature difference between the two groups on days 3 and 4 revealed that the TC+FQ group had significantly lower temperatures compared to the TC group (P = 0.042 and 0.027, respectively). Thus, the TC+FQ group had 1.5 days shorter at 37.5°C or below than the TC group.

Conclusions
The results of our study indicated that TC+FQ had a greater antipyretic effect compared to TC alone. Therefore, when defervescence serves as a measure of medical effectiveness, TC+FQ can shorten the duration of treatment.

RES-071: Therapeutic Challenges of Streptococcus pneumoniae meningitis: A Retrospective Study in Casablanca, Morocco

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Background
Pneumococcal meningitis, caused by Streptococcus pneumoniae, is a medical emergency that accounts for 70% of bacterial meningitis cases. The management of pneumococcal meningitis is further complicated by the emergence of strains with reduced sensitivity to penicillin, which necessitates the use of third-generation cephalosporins and/or vancomycin for empirical treatment. Few African studies have explored the management challenges of pneumococcal meningitis in adults, especially in Morocco. The aim is to evaluate the treatment approaches and mortality rates associated with pneumococcal meningitis in Casablanca.

Method
A retrospective descriptive study was conducted involving adults admitted to the infectious diseases department of Ibn Rochd University Hospital in Casablanca for Streptococcus pneumoniae meningitis from January 2021 to January 2024.

Results
The diagnosis of pneumococcal meningitis was confirmed through Gram staining and culture of cerebrospinal fluid (CSF) in the majority of cases. All patients tested negative for HIV-1 and HIV-2 serology. They exhibited elevated alpha-2 globulin levels on serum protein electrophoresis and underwent a contrast-enhanced cerebral CT scan. Brain MRI was performed on patients with traumatic brain injury. Ceftriaxone was the most commonly used antibiotic for empirical treatment, administered to all 16 patients (100%), followed by vancomycin (25%). Additionally, corticosteroid therapy was given to all patients. Pneumococcal vaccination was administered to recovered patients with an osteomeningeal breach. The overall mortality rate was 25%.

Conclusions
The management of pneumococcal meningitis in Casablanca and Africa faces considerable difficulties, even when international treatment guidelines are followed.

RES-072: Epidemiological Trends in Extrapulmonary Nontuberculous Mycobacterial Infections at a Tertiary Care Institution in Japan: A 10-Year Retrospective Analysis

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Background
The global incidence of nontuberculous mycobacterial (NTM) infections is demonstrating an increasing trend. Among these pathogens, respiratory infections caused by Mycobacterium avium-intracellulare complex (MAC) and Mycobacterium (M.) kansasii represent the predominant clinical entities in Japan. In the context of non-respiratory NTM manifestations, we present a case series documenting extrapulmonary NTM infections identified at a tertiary hospital in Japan.

Method
A retrospective analysis was conducted over a 10-year period, January 1, 2014, through December 31, 2023. Extrapulmonary specimens, excluding sputum and gastric aspirates, underwent bacteriological evaluation. A total of 33 cases harboring nontuberculous mycobacterial species, excluding M. tuberculosis and MAC, were identified and analyzed.

Results
Among the 33 cases, the distribution of NTM species was as follows:
Rapidly-growing mycobacteria (26 cases): M. chelonae (10), M. abscessus (5), M. fortuitum (6), M. wolinskyi (2), and M. mageritense (2).
Intermediate-growing mycobacteria (6): M. gordonae (5) and M. marinum (1).
Slowly-growing mycobacteria (1): M. szulgai (1).

Among these cases, eleven were consulted with infectious disease (ID) specialists, all of whom achieved successful therapeutic outcomes. Immunosuppressive therapy was identified as the primary predisposing factor in three cases. The predominant clinical presentations comprised cutaneous ulcerations or subcutaneous masses (n=13), followed by infections associated with continuous ambulatory peritoneal dialysis (CAPD) catheter exit sites (n=12).

Conclusions
Despite considerable regional variation, cutaneous and soft tissue infections, followed by CAPD catheter exit-site infections, constituted the predominant forms of extrapulmonary nontuberculous mycobacterial infections observed at a tertiary care university hospital in Japan. Clinical outcomes may have been enhanced through ID specialist consultation.

RES-074: Statistical Properties Regarding Partial Regression Coefficients for the Cox Proportional Hazard Model

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Background

Partial regression coefficients (β) indicate the number of changes in response variables per an increase in covariates by a unit quantity, which is 1, for regression analysis. For the Cox proportional hazard model, partial regression coefficients are calculated to analyze the hazard ratio (HR). HR is calculated using cumulative survival rates [S(t)] as shown in figure. For example, we consider the two covariates of age and adult duration (age – 20), with time-to-event data (death caused by COVID-19 during hospitalization). Based on the Cox proportional hazard model, we examined statistical properties using simulation data including these covariates.

Method

We created simulation data of the two covariates with the time-to-event data (Figure). We analyzed “an association between age and death” (Case 1) and “an association between adult duration and death” (Case 2) (n = 50).

Results

The HR and partial regression coefficients in Case 1 and Case 2 were identical (HR (95% confidence interval): 1.06 (1.03–1.10), β: 0.06). When the S(t) were arranged in descending order of the covariates in each and were assigned a number, the S(t) with the same assigned number between the Cases 1 and 2 were identical. In addition, S0(t)^exp(β×20) (S0(t): baseline S(t)) in Case 1 and S0(t) in Case 2 were identical between the same assigned numbers (Figure).

Conclusions

Partial regression coefficients are calculated by apprehending the differences between the given covariates arranged in ascending order as the number of changes.

$$\frac{-\mathrm{Log_e}(S(t)_{z=x+1})}{-\mathrm{Log_e}(S(t)_{z=x})} = \mathrm{HR} \qquad z = \text{covariates}$$

$$\exp(\beta) = \mathrm{HR}$$

$$S(t) = S_0(t)^{\exp(\beta \times z)}$$

Number	Age	Length of stay	Death (1) or discharge (0)	$S_0(t)$	$S(t)_{z=20}$	S(t)
1	90	11	1	0.9977	0.9922	0.5718
2	89	11	1	0.9977	0.9922	0.5910
3	88	12	1	0.9953	0.9842	0.3646
4	87	12	1	0.9953	0.9842	0.3870
5	86	13	1	0.9929	0.9761	0.2578
6	85	13	1	0.9929	0.9761	0.2793
7	84	14	1	0.9906	0.9684	0.2033
8	83	14	1	0.9906	0.9684	0.2234
9	82	15	1	0.9889	0.9629	0.1907
10	81	15	0	0.9889	0.9629	0.2103
11	80	11	1	0.9977	0.9922	0.7380
12	79	11	1	0.9977	0.9922	0.7514
13	78	12	1	0.9953	0.9842	0.5779
14	77	12	1	0.9953	0.9842	0.5970
15	76	13	1	0.9929	0.9761	0.4787
16	75	13	1	0.9929	0.9761	0.5000
17	74	14	1	0.9906	0.9684	0.4208
18	73	14	0	0.9906	0.9684	0.4429
19	72	15	0	0.9889	0.9629	0.4064
20	71	15	0	0.9889	0.9629	0.4286
21	70	11	1	0.9977	0.9922	0.8478
22	69	11	1	0.9977	0.9922	0.8562
23	68	12	1	0.9953	0.9842	0.7423
24	67	12	1	0.9953	0.9842	0.7555
25	66	13	1	0.9929	0.9761	0.6701
26	65	13	0	0.9929	0.9761	0.6861
27	64	14	0	0.9906	0.9684	0.6247
28	63	14	0	0.9906	0.9684	0.6424
29	62	15	0	0.9889	0.9629	0.6130
30	61	15	0	0.9889	0.9629	0.6310
31	60	11	1	0.9977	0.9922	0.9142
32	59	11	1	0.9977	0.9922	0.9191
33	58	12	1	0.9953	0.9842	0.8505
34	57	12	0	0.9953	0.9842	0.8587
35	56	13	0	0.9929	0.9761	0.8045
36	55	13	0	0.9929	0.9761	0.8149
37	54	14	0	0.9906	0.9684	0.7744
38	53	14	0	0.9906	0.9684	0.7862
39	52	15	0	0.9889	0.9629	0.7665
40	51	15	0	0.9889	0.9629	0.7787
41	50	11	1	0.9977	0.9922	0.9524
42	49	11	0	0.9977	0.9922	0.9552
43	48	12	0	0.9953	0.9842	0.9158
44	47	12	0	0.9953	0.9842	0.9206
45	46	13	0	0.9929	0.9761	0.8885
46	45	13	0	0.9929	0.9761	0.8947
47	44	14	0	0.9906	0.9684	0.8703
48	43	14	0	0.9906	0.9684	0.8775
49	42	15	0	0.9889	0.9629	0.8655
50	41	15	0	0.9889	0.9629	0.8729

Case 1

Figure

Number	Adult duration	Length of stay	Death (1) or discharge (0)	$S_0(t)$	S(t)
1	70	11	1	0.9922	0.5718
2	69	11	1	0.9922	0.5910
3	68	12	1	0.9842	0.3646
4	67	12	1	0.9842	0.3870
5	66	13	1	0.9761	0.2578
6	65	13	1	0.9761	0.2793
7	64	14	1	0.9684	0.2033
8	63	14	1	0.9684	0.2234
9	62	15	1	0.9629	0.1907
10	61	15	0	0.9629	0.2103
11	60	11	1	0.9922	0.7380
12	59	11	1	0.9922	0.7514
13	58	12	1	0.9842	0.5779
14	57	12	1	0.9842	0.5970
15	56	13	1	0.9761	0.4787
16	55	13	1	0.9761	0.5000
17	54	14	1	0.9684	0.4208
18	53	14	0	0.9684	0.4429
19	52	15	0	0.9629	0.4064
20	51	15	0	0.9629	0.4286
21	50	11	1	0.9922	0.8478
22	49	11	1	0.9922	0.8562
23	48	12	1	0.9842	0.7423
24	47	12	1	0.9842	0.7555
25	46	13	1	0.9761	0.6701
26	45	13	0	0.9761	0.6861
27	44	14	0	0.9684	0.6247
28	43	14	0	0.9684	0.6424
29	42	15	0	0.9629	0.6130
30	41	15	0	0.9629	0.6310
31	40	11	1	0.9922	0.9142
32	39	11	1	0.9922	0.9191
33	38	12	1	0.9842	0.8505
34	37	12	0	0.9842	0.8587
35	36	13	0	0.9761	0.8045
36	35	13	0	0.9761	0.8149
37	34	14	0	0.9684	0.7744
38	33	14	0	0.9684	0.7862
39	32	15	0	0.9629	0.7665
40	31	15	0	0.9629	0.7787
41	30	11	1	0.9922	0.9524
42	29	11	0	0.9922	0.9552
43	28	12	0	0.9842	0.9158
44	27	12	0	0.9842	0.9206
45	26	13	0	0.9761	0.8885
46	25	13	0	0.9761	0.8947
47	24	14	0	0.9684	0.8703
48	23	14	0	0.9684	0.8775
49	22	15	0	0.9629	0.8655
50	21	15	0	0.9629	0.8729

Case 2

RES-075: Statistical Properties of a Least Squares Method for Regression Analysis

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Background

A least squares method is used to calculate partial regression coefficients. The least squares method shows that partial regression coefficients depend on differences between covariates and a mean covariate and between response variables and a mean response variable (Figure). Thus, we examined the statistical properties using simulation data.

Method

We created simulation data for two cases. Case 1: a covariate: “duration from an admission date (a date of onset) to ‘an enforcement date of PCR for COVID-19 detection’ (PCR date)” (Admission → PCR), a response variable: threshold cycle values (CT values) of the PCR. Case 2: a covariate: “duration from a ward transfer permission date (defined as ten days after admission) to PCR date” (Transfer permission → PCR), a response variable: CT values of the PCR (Figure). The response variables were common between Cases 1 and 2. We calculated partial regression coefficients for the two cases using a least squares method (n = 10).

Results

The covariates in Case 1 were all “10 + the covariates in Case 2”. The mean of covariates in Case 1 was “10 + the mean of covariates in Case 2”. The differences between the covariates and the mean covariate, as well as the partial regression coefficients, were identical in Cases 1 and 2. The constant term (α) in Cases 1 and 2 were different (Figure).

Conclusions

Partial regression coefficients are calculated by apprehending the differences between the given covariates arranged in ascending order as the number of changes.

$$\text{Regression line: } \hat{y} = \hat{\alpha} + \hat{\beta}\, x$$

$$\hat{\alpha} = \bar{y} - \hat{\beta}\bar{x} \qquad \hat{\beta} = \frac{S_{xy}}{S_x^2} \qquad S_x^2 = \sum (x - \bar{x})^2,\ S_{xy} = \sum (x - \bar{x})(y - \bar{y})$$

Case 1	Admission → PCR (x_1)	$\bar{x}_1$	$(x_1 - \bar{x}_1)^2$	CT value of PCR (y)	$\bar{y}$	$(x_1 - \bar{x}_1)(y - \bar{y})$	$(x_2 - \bar{x}_2)(y - \bar{y})$
	11		20.25	31		20.25	20.25
	12		12.25	33		8.75	8.75
	13		6.25	34		3.75	3.75
	14		2.25	32		5.25	5.25
	15	15.5	0.25	35	35.5	0.25	0.25
	16		0.25	36		0.25	0.25
	17		2.25	37		2.25	2.25
	18		6.25	39		8.75	8.75
	19		12.25	38		8.75	8.75
	20		20.25	40		20.25	20.25
Total			Sx_1^2: 82.5			Sx_1y: 78.5	Sx_2y: 78.5
Case 2 Transfer permission → PCR (x_2)		$\bar{x}_2$	$(x_2 - \bar{x}_2)^2$	$\hat{\beta}_1$: Sx_1y/Sx_1^2	$\hat{\alpha}_1$	$\hat{\beta}_2$: Sx_2y/Sx_2^2	$\hat{\alpha}_2$
	1		20.25	0.95	20.75	0.95	30.27
	2		12.25				
	3		6.25				
	4		2.25				
	5	5.5	0.25				
	6		0.25				
	7		2.25				
	8		6.25				
	9		12.25				
	10		20.25				
Total			Sx_2^2: 82.5				

Figure

RES-076: Statistical Properties of the Risk Ratio

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Background
To examine statistical properties of the risk ratio, we supposed a comparison of effect between vaccines and placebos using risk ratio, following the conditions:
1. The number of symptomatic COVID–19 (SY) is lower in “patients injected vaccine” (vP) than in “patients injected placebo” (pP).
2. The number of asymptomatic COVID–19 (ASY) is equal between vP and pP.
3. Presence of SY or ASY is replaced with SY presence. In this case, the risk ratio becomes lower theoretically.

Method
We conducted a meta-analysis using data from a previous meta-analysis including 67 studies that provided the number of true positives, false positives, false negatives, true negatives, sensitivity, and specificity of the cytomegalovirus (CMV) antigenemia assay, using PCR as the reference standard. We proposed and calculated a metric named “Metric 1” as follows: “The number of ‘patients with positive diagnostic tests’ (PP)” (nPP) and “the number of ‘patients with negative diagnostic tests’ (NP)” (nNP) were adjusted such that total nPP and total nNP became both 100. Metric 1 = |Adjusted nPP [AnPP] with PCR–proven [AnTPP] – adjusted nNP [AnNP] with PCR–proven [AnFNP]| ÷ (AnTPP + AnFNP) (Figure). Metric 1 and the reciprocal of risk ratio were calculated for all studies, assuming that PP was replaced with pP and NP was replaced with vP.

Results
Sixty-five studies were included in this meta-analysis. Metric 1 negatively correlated with the reciprocal of risk ratio (r=–0.98, p<0.001).

Conclusions
The statistical property of the risk ratio revealed in this study may be better to be considered when interpreting risk ratio.

	PCR–proven	Not PCR–proven	
Antigenemia (+)	239	4	243
Antigenemia (–)	77	55	132
	316	59	375

↓

$239 \div 243 \times 100 \fallingdotseq 98$	$4 \div 243 \times 100 \fallingdotseq 2$	$243 \div 243 \times 100 = 100$
$77 \div 132 \times 100 \fallingdotseq 58$	$55 \div 132 \times 100 \fallingdotseq 42$	$132 \div 132 \times 100 = 100$

↓

Adjusted	PCR–proven	Not PCR–proven	
Antigenemia (+)	98	2	100
Antigenemia (–)	58	42	100

$$\text{Metric 1} = |98 - 58| \div (98+58) \fallingdotseq 0.26$$

Figure

RES-077: Co-occurrence of Intracellular Pseudomonas aeruginosa DNA in Acanthamoeba Isolates from Keratitis Patients Diagnosed at Parasitology and Medical Entomology Department, Faculty of Medicine, Universiti Kebangsaan Malaysia

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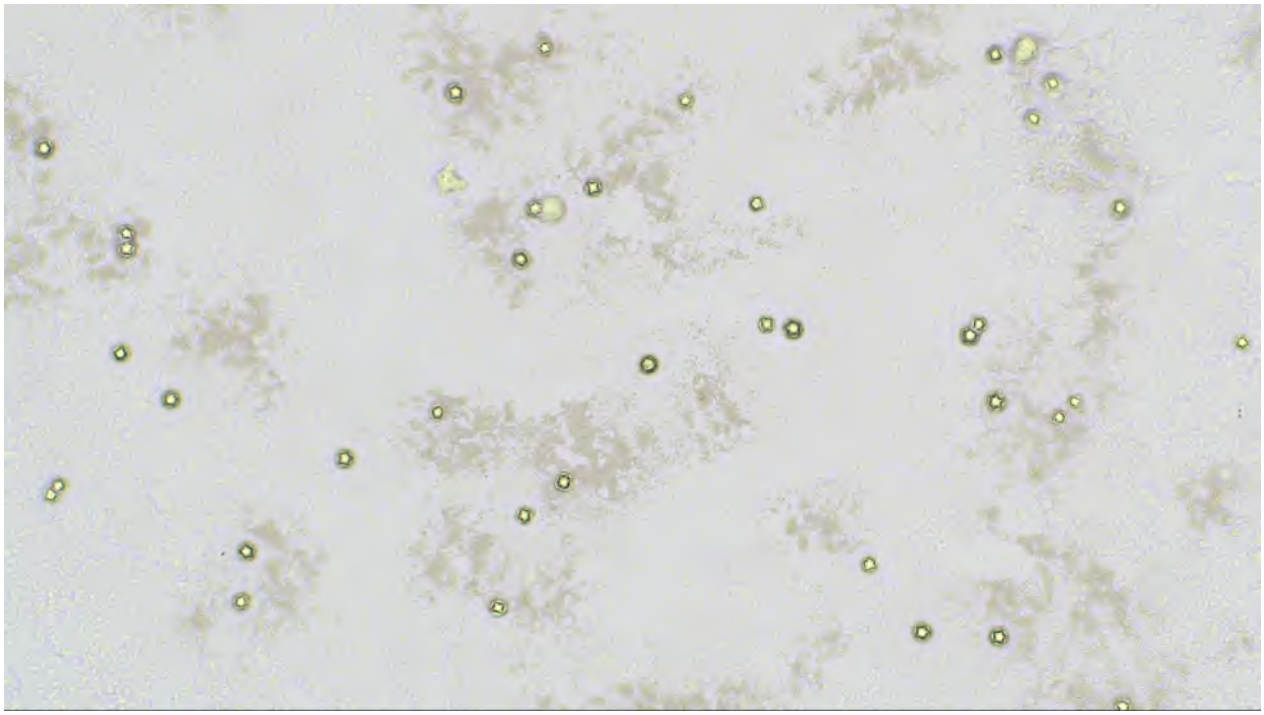
Background
Acanthamoeba keratitis (AK) is a severe, sight-threatening corneal infection caused by free-living amoebae, often misdiagnosed and quite difficult to treat. Concurrently, Pseudomonas aeruginosa is a leading cause of bacterial keratitis, notorious for its rapid progression, potent virulence factors, and increasing antimicrobial resistance. Emerging evidence suggests a complex interaction between Acanthamoeba, which can act as hosts and protect bacteria from environmental stresses, potentially enhancing their pathogenicity. This study aimed to investigate the molecular co-occurrence of P. aeruginosa within Acanthamoeba isolated from corneal scrapings of patients diagnosed with keratitis.

Method
Twenty-three Acanthamoeba isolates obtained from corneal scrapings of keratitis patients were screened for the presence of Pseudomonas spp. DNA by conventional polymerase chain reaction (PCR) targeting the 23S-5S intergenic spacer (IGS) region. Species identification was achieved by comparing the gene sequences with those in the GenBank database using the BLAST algorithm.

Results
Out of 23 Acanthamoeba isolates screened, 15 (65.2%) were positive for Pseudomonas spp. DNA. Subsequent sequence analysis confirmed that all 15 positive samples harbored Pseudomonas DNA with the highest sequence similarity to Pseudomonas aeruginosa at 91% to 99%.

Conclusions
The detection of Pseudomonas aeruginosa DNA within Acanthamoeba isolates from keratitis patients highlights a crucial correlation between these two pathogens in ocular infections. This finding is particularly important because both organisms independently cause severe keratitis, and their co-existence may have profound implications for disease progression and treatment outcomes.



RES-080: Developing a Risk Prediction Score for Hospital-associated Carbapenemase-producing Enterobacterales Acquisition in a Singaporean Tertiary Hospital

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Background
Carbapenemase-producing Enterobacterales (CPE) acquisition poses a significant challenge globally. Universal screening remains impractical due to logistic and financial barriers. Therefore, this study aimed to develop a clinically applicable predictive risk score for hospital-attributable CPE (HA-CPE) to inform targeted infection prevention (IP) measures.

Method
Retrospective matched case-control study was performed in Singapore General Hospital from February 2023 to August 2024, including 1074 cases (HA-CPE positive ≥3days post-admission) and 2148 controls, matched for age, sex and admission date. Independent predictors were identified using multivariable conditional logistic regression, reported as adjusted odds ratios (aOR) with 95% confidence intervals (CI). Model predictive performance was assessed, and internal validation was performed by bootstrapping. The risk score was derived using Sullivan method and evaluated through area-under receiver-operator curve (AUROC) and confusion matrix.

Results
Prolonged hospitalization (15–22 days, aOR: 16.2, 95% CI: 11.56–22.71) was the strongest predictor of HA-CPE acquisition. Other significant independent risk factors were dependent mobility (aOR: 2.59, 95%CI: 2.01-3.33), transfer to high-risk areas(aOR: 4.09, 95%CI: 3.17-5.27), beta-lactam administration (aOR: 3.42, 95% CI: 2.55-4.58), dementia (aOR: 1.89, 95%CI: 1.04-3.43), gastrointestinal diseases (aOR: 2.15, 95%CI: 1.64-2.82), malignant cancer (aOR: 1.61 95%CI: 1.23-2.10), liver disease (aOR: 4.45, 95%CI: 1.37-14.47), peripheral vascular disease (aOR: 2.45, 95%CI: 1.50-4.01) and renal disease (aOR: 1.46, 95%CI: 1.11-1.91) (Table 1). The model and score demonstrated good discrimination at AUROC of 0.93 and 0.87, respectively. Total score ranged from 0 to 24. At cut-off of 8.5 points, the sensitivity was 0.83 and specificity was 0.76.

Conclusions
The risk score demonstrated a good predictive performance and could be used for early identification of at-risk patients and timely implementation of IP measures.

Table 1: Independent risk factors for HA-CPE and corresponding risk points

Variables	aOR[a]	95% CI[a]	Risk Points[#]
Duration of hospitalisation[b]			
1-7 days	(Ref)	(Ref)	–
8-14 days	2.59	2.05–3.40	3
15-22 days	16.31	12.8–21.78	7
23-30 days	13.87	9.76–19.96	7
>30 days	7.95	5.89–11.26	5
Transfer to high-risk areas in preceding 30 days[c]	4.15	3.38–5.15	4
Mobility status[d]			
Dependent	2.60	2.11–3.22	3
Underlying comorbidities[e]			
Dementia	1.91	1.14–3.27	2
Gastrointestinal diseases	2.16	1.75–2.64	2
Malignant cancer	1.61	1.35–1.99	1
Moderate/severe liver disease	4.57	1.92–15.41	4
Peripheral vascular disease	2.50	1.67–3.85	2
Renal disease	1.46	1.15–1.80	1
Antibiotic treatment in preceding 90days[f]			
Beta-lactams	3.47	2.77–4.37	3

Abbreviations: aOR, adjusted odds ratio. CI, confidence interval. Ref, reference level.

[a]Step-wise backward multivariable conditional logistic regression.

*p-value <0.05 was considered statistically significant.

[#]Risk scores were developed using the Sullivan method. In this method the base level(i.e. reference level) of the categorical variable is assigned zero points(absence of the risk factor). The constant of the scoring is identified as the smallest regression coefficient in the model, and it corresponds to one-point in the risk scoring system. For each risk factor, the corresponding regression coefficient is divided by the constant to obtain the risk point value. A patient's total risk score was calculated by adding the corresponding points for all the risk factors for that patient.

[b]Duration of hospitalisation was defined as the period from admission to CPE positive date for cases and from admission date of discharge, death or study end (whichever was earlier) for controls. It is presented in categorical form.

[c]High-risk areas included intensive care units, intermediate care areas and high-dependency units. Data on transfer to high-risk areas was collected for a period of 30days before HA-CPE positive for the cases and for a period of 30days before admission date up to discharge or death or study end date, whichever was earlier, for the controls.

[d]Mobility data was collected as of admission. Dependent mobility was defined as "wheel-chair bound, "bed-bound" or "requiring assistance" status.

[e]Underlying comorbidities were identified and categorised based on the International Classification of Diseases-Tenth Revision (ICD-10) codes, as documented in the electronic medical records.

[f]Data on previous antibiotic exposure was collected for a period of 90days before HA-CPE positive date for the cases and a period of 90days before admission date up to discharge or death or study end date, whichever was earlier, for the controls. Beta-lactams included carbapenem, penicillin, cephalosporin, monobactam and beta-lactam inhibitor.

RES-081: Cox Proportional Hazard Model with a Binary Covariate to Evaluate a Chronic Event Incidence Risk for Chronic Diseases－Pilot Meta-Analysis

Soichi Takeishi

Inuyama Chuo General Hospital

Background
Censoring and non-“proportional hazards” (PH) may affect reliability of the data analyzed using Cox proportional hazard model (Cox) with a binary covariate (intervention and control).

Method
We included articles that could be searched for free using PubMed for pilot meta-analysis. The following conditions were satisfied:
1. parallel clinical trial,
2. evaluating a chronic event incidence risk,
3. using Cox, and
4. describing No. at Risk over a follow-up period.

We evaluated several important outcomes in each article. We divided outcomes into two groups using a cutoff line of “hazard ratio (HR) = 1”. We proposed metrics named eCuI, TDR, TDR/eCuI, eHR, |eHR – HR|, 95%CI range, β, and eSE, whose calculation methods were shown in Figure 1. Theoretically, an increased TDR/eCuI reflects increased censoring. Theoretically, an increase in |eHR – HR| quantitatively reflects enhanced non-PH.

Results

We included 147 outcomes from 51 studies. Figure 1 shows the correlations between metrics related to Cox in HR<1 group (n=121) and in HR>1 group (n=26). In HR<1 group, TDR/eCuI for intervention, TDR/eCuI for control, |eHR – HR|, eSE and 95%CI range had significant correlations with each other. In HR>1 group, TDR/eCuI for intervention, TDR/eCuI for control, |eHR – HR|, |β|, eSE and 95%CI range had significant correlations with each other.

Conclusions
Increased censoring may lower reliability of data analyzed using Cox with a binary covariate through enhanced non-PH. Especially in HR>1, an increase in |β| which was disfavor for research hypotheses was associated with enhanced non-PH through increased censoring.

HR<1 (n=121)	eCuI, I	eCuI, C	TDR/eCuI, I	TDR/eCuI, C	|eHR - HR|	|β|	eSE	95%CI range
eCuI, I		r=0.9	r=-0.4	r=-0.22	r=-0.04	r=-0.07	r=-0.29	r=-0.31
eCuI, C	p<0.001		r=-0.4	r=-0.24	r=-0.06	r=0.28	r=-0.1	r=-0.31
TDR/eCuI, I	p<0.001	p<0.001		r=0.71	r=0.44	r=0.15	r=0.49	r=0.52
TDR/eCuI, C	p=0.01	p=0.009	p<0.001		r=0.91	r=0.10	r=0.34	r=0.33
|eHR - HR|	p=0.64	p=0.53	p<0.001	p<0.001		r=0.16	r=0.28	r=0.18
|β|	p=0.47	p=0.002	p=0.09	p=0.27	p=0.08		r=0.65	r=0.06
eSE	p=0.001	p=0.29	p<0.001	p<0.001	p=0.002	p<0.001		r=0.74
95%CI range	p<0.001	p<0.001	p<0.001	p<0.001	p=0.04	p=0.51	p<0.001	
HR>1 (n=26)	eCuI, I	eCuI, C	TDR/eCuI, I	TDR/eCuI, C	|eHR - HR|	|β|	eSE	95%CI range
eCuI, I		0.99	-0.68	-0.59	-0.46	-0.33	-0.52	-0.49
eCuI, C	p<0.001		-0.70	-0.63	-0.46	-0.39	-0.51	-0.51
TDR/eCuI, I	p<0.001	p<0.001		0.95	0.66	0.40	0.59	0.56
TDR/eCuI, C	0.002	p<0.001	p<0.001		0.66	0.52	0.51	0.54
|eHR - HR|	0.02	0.02	p<0.001	p<0.001		0.79	0.68	0.78
|β|	0.10	0.047	0.04	0.007	p<0.001		0.51	0.74
eSE	0.007	0.007	0.001	0.007	p<0.001	0.008		0.95
95%CI range	0.01	0.008	0.003	0.004	p<0.001	p<0.001	p<0.001	

eCuI: cumulative incidence estimated to the first decimal place using Kaplan-Meier curves, total dropout rate (TDR): (‘No. at Risk. at follow-up start time [0 year]’ (‘n’) – No. at Risk. at a final follow-up year) ÷ n × 100, TDR/eCuI: TDR ÷ eCuI, eHR: $-\log_e$(‘1 – eCuI’ for intervention) ÷ $-\log_e$(‘1 – eCuI’ for control), |eHR – HR|: absolute values of ‘eHR – HR’, 95%CI range: ‘upper limit of 95% confidence interval [CI] of HR’ (U95%CI) – ‘lower limit of 95%CI of HR’ (L95%CI), |partial regression coefficients| (|β|): absolute values of $\log_e$HR, estimated standard error of β (eSE): (($\log_e$U95%CI – $\log_e$HR) ÷ 1.96 + ($\log_e$HR – $\log_e$L95%CI) ÷ 1.96) ÷ 2

Figure 1

RES-085: From Drips to Decisions: A Cost-Effectiveness Analysis of Intravenous-to-Oral Switch (IVOS) Antibiotics in a Large Acute Hospital in UK

Alice Liu, Owen Harris, Maria Girgis, Rachel Pye

Gloucestershire Hospitals NHS Foundation Trust

Background
IVOS is an important antimicrobial stewardship intervention. Research evidence confirms several IVOS benefits such as reducing hospital-acquired infections and promoting hospital discharge. In 2024, UK Government published a 5-year National Action Plan to combat antimicrobial resistance; IVOS is one of its strategies.

Method
A prospective, interventional study was conducted to identify the patients who received intravenous antibiotics (IVAB) over 24hours, met the criteria for prompt IVOS against the modified UKHSA antimicrobial decision aid tools and analyse the barriers. Patients on IVAB for prophylaxis, antifungal, antiviral treatment and in intensive or high-dependency units are excluded in the study.

Results
Thirty-six of 110 patients met the criteria for prompt IVOS. Gastro-intestinal surgery was the highest user of IVAB equivalent to 14.5% of all prescriptions (n=159). Acute Medicine was benefited most from the early intervention with 60% of patients changing to oral antibiotics by AMS team. The average IVAB length was 5.7 days; total expenditure was £5,348.83 which piperacillin-tazobactam costs 21% of the budget. The commonest reason for being unsuitable for IVOS was “one or more infection marker criteria not met”. 25 patients were “qualified” sooner than the audit day and 39 hospital-bed days could be saved.

Conclusions
The results illustrated the following recommendations for improvement:
1) Conducting a targeted AMS ward round regularly to review broad-spectrum antibiotics (eg. piperacillin-tazobactam)
2) Collaborative working relationship with surgical team to advocate IVOS
3) Promoting AMS to doctors, nurses and AHPs through local and global educational talks or seminars.
4) Using artificial intelligence for IVOS screening during clinical assessment

FROM DRIPS TO DECISIONS: AN ANALYSIS OF IVOS IN AN ACUTE NHS DISTRICT HOSPITAL, AND THE BARRIERS PREVENTING IT.

IV to oral switch
Think ACED

Alice Liu, Maria Girgis, Owen Harris, Rachel Pye
Gloucestershire Hospitals NHS Foundation Trust

NHS Gloucestershire Hospitals NHS Foundation Trust

Background

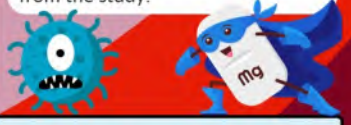
The Intravenous-to-Oral-Switch (IVOS) represents a multidisciplinary strategy that facilitates the transition of patients from intravenous to oral antibiotics when clinically appropriate (see fig 1). IVOS plays a critical role in antimicrobial stewardship, accelerates patient discharge, and mitigates both operational and financial pressures on healthcare trusts. The latest NHS Planning guidance, brings an intensified financial demand on the NHS, underscoring the importance of capitalizing on cost-saving opportunities presented by effective IVOS implementation.

Objectives

- Analyse the IV antibiotic prescribing against drug cost and highlight the cost saving opportunities if IVOS took place
- Identify the barriers preventing this in practice and make recommendations for improvement

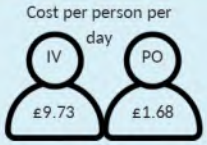
Methods

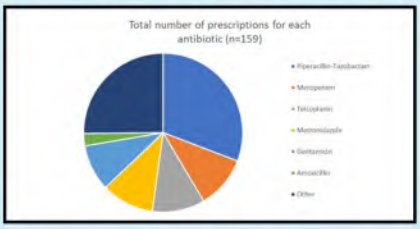
The study extracted a list of patients on intravenous antibiotics for over 24-hours from Business Intelligence (BI) and analysed it against the electronic patient record (EPR) using a modified UKHSA Antimicrobial intravenous-to-oral (IVOS) decision aid tool [1]. Patients receiving prophylactic, antifungal, antiviral treatments, and those in intensive or high-dependency units were excluded from the study.

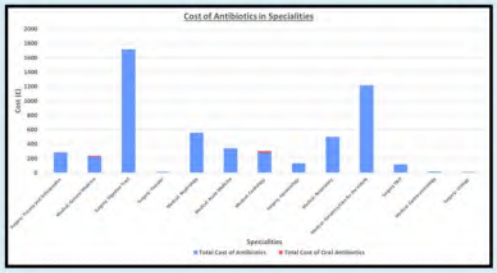


Results

- **Thirty-six out of 110 patients (33%) met the criteria1 for IVOS**
- The average length of intravenous antibiotic course was 5.7 days in total (range 2-21 days)
- **Twenty-five patients** (23%) were found to be able to switch to oral antibiotic(s) sooner than the audit day which meant that a total of **39 hospital-bed days could have been saved**, if medically fit for discharge
- Surgery in digestive tract used the highest volume of intravenous antibiotics which contributed to **14.5% of all IV antibiotic prescriptions** (n=159), **53% of these patients were suitable for IVOS.**
- The most common reason for being unsuitable for IVOS was "one or more infection marker criteria not met".
- The total expenditure of intravenous antibiotics was **£5,348.83 in which £1,124.55 (21%) was spent on piperacillin-tazobactam**; the most commonly used antibiotic in the study.
- The highest rate of IVOS was seen in acute medicine with a total of 60% of IVOS being actioned.







Conclusion

The results highlight key opportunities to maximise IVOS efficiency, by directing resources toward high IV antibiotic prescribing specialities such as GI Surgery and regular review of broad-spectrum antibiotics such as piperacillin-tazobactam. IVOS should be advocated through educational and training to doctors and nurses, regular antimicrobial stewardship ward round and advocacy of IVOS through hospital staff communications. The use of artificial Intelligence should be maximised to help "detect" the patients on IVOS whom met the criteria for oral switch and alert the clinical team for prompt review which could help reducing the unnecessary use of IV antibiotic and promote hospital discharge.

References

- [1] UKHSA Antimicrobial Intravenous IV-to-Oral Switch (IVOS) Decision Aid. V6 IVOS tool (publishing.service.gov.uk)

Acknowledgements

Thank You for the support in data collection from the Microbiology Departments and Trainee Pharmacists across Gloucestershire Royal Hosptial and Cheltenham General Hospital

RES-086: A Rapid and Accurate mNGS Method for Detecting RNA Pathogens in BALF Samples

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Micronbrane Medical Co., Ltd

Background
In the post-COVID-19 era, the demand for RNA virus detection has significantly increased, drawing renewed attention to metagenomic next-generation sequencing (mNGS) technologies. However, most commercially available kits still rely on conventional methods—such as the Trizol-based RNA extraction—which are labor-intensive, hazardous, and difficult to standardize into a streamlined protocol. Moreover, the use of toxic chemicals like Trizol and chloroform poses logistical challenges due to regulatory and shipping restrictions worldwide, making these traditional approaches unsuitable for developing practical mNGS-compatible RNA pathogen detection kits.

Method
Inactivated SARS-CoV-2 and RSV-A viruses were spiked into simulated BALF samples. The RNA virus detection workflow integrates the Devin™ host depletion filter with a standard magnetic bead-based RNA purification step to effectively reduce host-derived RNA contamination through a simple 2-minute filtration process. A high-efficiency reverse transcription module and an ultralow biomass-compatible NGS library preparation method were used to construct libraries. Sequencing was performed using 150 bp single-end reads, generating 1 Gb of data on the NovaSeq 6000 platform.

Results
In this study, we implemented a high-efficiency reverse transcription module with a conversion rate of 137%, significantly outperforming typical commercial kits, which achieve around 70%. By leveraging RNA secondary structure, our method also efficiently depletes ribosomal RNA, thereby enhancing pathogen detection sensitivity with a limit of detection as low as 100 copies.

Conclusions
In hospital diagnostic workflows, a rapid and convenient method for RNA virus detection is essential. This study presents a fast and efficient detection approach that utilizes mNGS technology for comprehensive RNA virus identification, offering hospitals a novel diagnostic solution.

RES-088: Considering the Risks of Abstention by Permanent Members of United Nations Security Council – A Review of 100 Recent Security Council Resolutions

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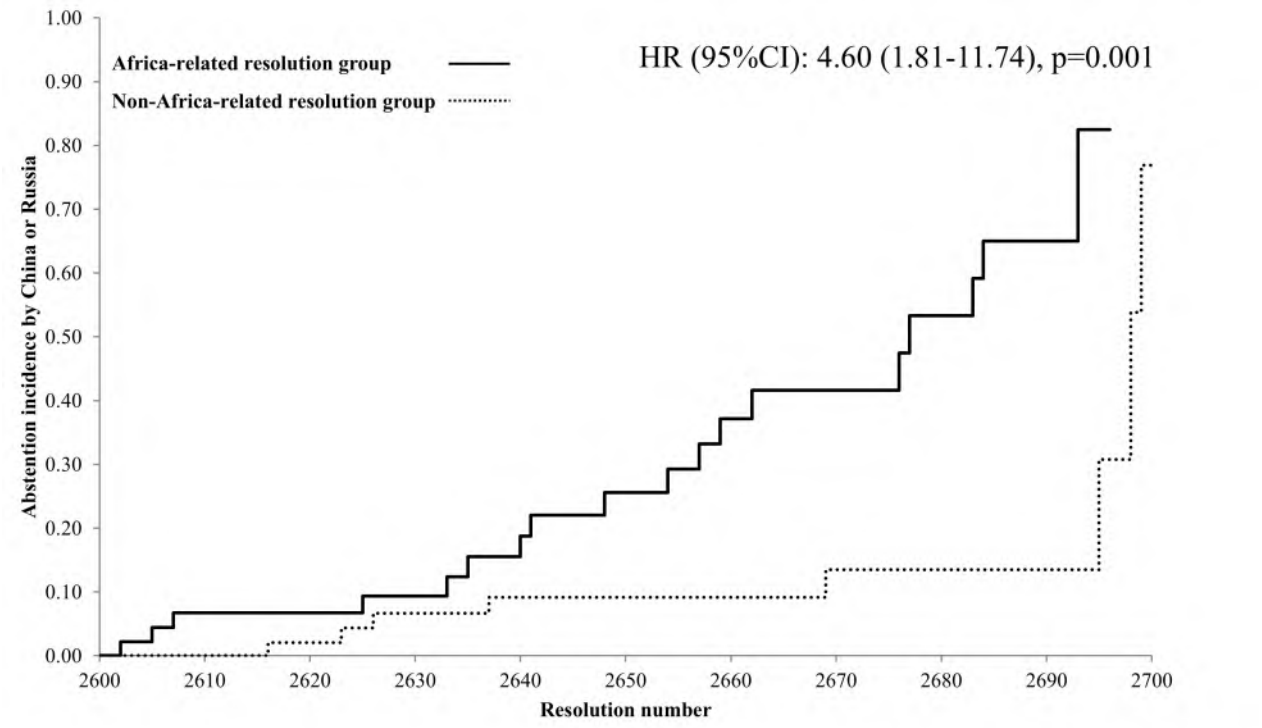
Background
Permanent members of United Nations Security Council are economic powerhouses and may often have military and economic stakes in the parties to a dispute.

Method
This study reviewed voting patterns of countries on 100 Security Council resolutions (resolution number: 2601-2700) adopted between October 29, 2021 and October 19, 2023. The risk of abstention by China or Russia in the Africa-related resolution group (n=45) compared to the non-Africa-related resolution group (n=55) was analyzed using the Cox proportional hazards model. In the 14 resolutions with abstentions by non-permanent members, the presence or absence of abstentions by African non-permanent members between the Africa-related and the non-Africa-related resolution groups was compared using Fisher's exact test.

Results
There were 30 resolutions with abstentions across the 100 resolutions, of which 27 were abstained from by permanent members; 26 of these were abstained from by China or Russia. The risk of abstention by China or Russia in the Africa-related resolution group was significantly higher than in the non-Africa-related resolution group (HR: 4.60; 95% confidence interval (CI): 1.81-11.74, p=0.001). Among the 14 resolutions with abstentions by non-permanent members, all Africa-related resolutions involved abstentions by African non-permanent members, whereas none of the non-Africa-related resolutions did (p<0.001).

Conclusions
Between October 29, 2021 and October 19, 2023, China or Russia more likely to abstained from voting on Africa-related United Nations Security Council resolutions. The present study results may reflect underlying military and economic interests shared by China, Russia, and African countries.



	Africa-related resolution group	Non-Africa-related resolution group	Total
Presence of abstentions by African non-permanent members	9	0	9
Absence of abstentions by African non-permanent members	0	5	5
Total	9	5	14

Figure

RES-090: Multi-systemic risks and disease burdens of post-acute sequelae of dengue at 2 years

Jue Tao Lim

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Background
While post-acute sequelae following dengue infection are increasingly well-characterized, existing evidence is largely restricted to the first year post-infection and lacks quantification of overall burden on healthcare systems. This study aimed to estimate the 2-year post-acute risks and rates of new-incident multi-systemic complications following dengue infection and quantify excess healthcare burdens attributable to dengue in terms of disability-adjusted life years (DALYs), hospitalizations, and mortality.

Method
National surveillance (1 Jan 2013–30 June 2022) and healthcare claims (1 Jan 2012–30 June 2024) databases in Singapore were utilized to build a retrospective population-based adult cohort with laboratory-confirmed dengue transmission. Population-level morbidity and disability burden of new-incident complications across multiple organ systems, all-cause hospitalizations and deaths post-dengue infection were systematically and comprehensively identified by contrasting versus population-based controls.

Results
A total of 68,145 dengue-infected individuals and 2,886,119 population-based controls were included. Over two years, an estimated 1,670 excess DALYs (95% CI: 849.6–2,492.0), or 2.52 DALYs per 100 cases, were attributable to post-acute dengue complications. Neuropsychiatric, endocrine, renal, and gastrointestinal sequelae contributed the largest shares to burdens. Dengue infection was associated with increased risks of death (HR: 1.259 [1.138–1.393]) and hospitalization (HR: 1.118 [1.102–1.134]). While most sequelae risks declined in the second year, elevated risks for hospitalization and gastrointestinal complications persisted.

Conclusions
Increased post-acute burdens of multi-organ complications, all-cause hospitalizations, death, and disability were observed in dengue survivors. These findings support the inclusion of post-acute morbidity and disability in dengue burden estimates used for priority setting and economic evaluation.

RES-091: What Lurks Beneath the Sink: Looking into CRE in Hand Hygiene Stations

Lera Almendral

Silliman University

Background
Carbapenem-resistant Enterobacteriaceae (CRE) are considered a major global health threat by the WHO due to their impact on immunocompromised patients. This study investigated the presence of CRE in handwashing stations at a tertiary hospital in Dumaguete City, Negros Oriental, Philippines.

Method
Swab samples from handwashing stations were diluted and cultured on CHROMagar KPC. Colonies were counted, isolated, and purified on MacConkey agar. Selected isolates underwent antimicrobial susceptibility testing to imipenem and meropenem using the Kirby-Bauer disk diffusion method to detect carbapenem-resistant Enterobacteriaceae (CRE).

Results
Forty swab samples from handwashing stations in a tertiary hospital were analyzed for CRE. CRE load significantly varied across wards, with the obstetrics ward highest. Pseudomonas spp. (38%) was most prevalent, followed by Acinetobacter, Klebsiella, Enterobacter, and Citrobacter spp. All five genera were found in each ward. Significant differences in inhibition zones were observed for Enterobacter and Klebsiella spp. when tested against imipenem and meropenem, indicating variable antimicrobial susceptibility among isolates.

Conclusions
This study confirmed the presence of carbapenem-resistant Enterobacteriaceae (CRE) in handwashing stations of a tertiary hospital in Dumaguete City. Using CHROMagar™ KPC and Kirby-Bauer testing, isolates showed resistance to imipenem and meropenem. Identified CRE included Pseudomonas spp., Acinetobacter spp., Klebsiella spp., Enterobacter spp., and Citrobacter spp., with Pseudomonas and Acinetobacter being most common, especially in ICU areas. Most sinks harbored multiple CRE species. These findings suggest that hospital sinks may serve as reservoirs for drug-resistant bacteria, posing a serious risk of nosocomial infections, particularly in vulnerable patients. Infection control measures must address this hidden environmental threat.

RES-092: Toxin-associated Gene Prevalence in Food-Derived Bacillus cereus in Japan

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[1]Graduate School of International University of Health and Welfare
[2]International University of Health and Welfare

Background
Bacillus cereus is widely distributed in the environment and foods and can cause food poisoning. Food poisoning is categorized into diarrhea and emetic types, and while most cases are mild, some are severe or even fatal. Foods that can cause food poisoning include rice dishes, noodles, and dairy products. In this study, we examined the contamination of rice balls with B. cereus and the presence of toxin-related genes.

Method
Fifty-six samples of rice balls collected from various regions of Japan were analyzed. The samples were homogenized by adding 225 mL of saline solution to 25 g of sample, and the homogenate was applied to a standard medium and cultured. Additionally, enrichment culture was performed on HIB medium. B. subtilis-like colonies were isolated, biochemical properties were confirmed, and strains that were positive for lecithinase and identified as B. cereus group by mass spectrometry were determined to be B. cereus. For each strain, toxin-related genes (hbl, nhe, cytK, entFM, ces) were detected by PCR.

Results
B. cereus was isolated from 10 of the 56 samples (17.8%). The toxin gene profiles of the 10 detected strains were as follows: hblC 4, hblD 5, hblA 4, nheB, nheA, and nheC 10 each, cytK 5, entFM 10, and ces 1.

Conclusions
Possession of toxin-related genes was generally consistent with previous studies. The suggestion of genes such as hbl, nhe, and ces is noted, but the specific ability to produce toxins remains uncertain. Therefore, toxin quantification by mass spectrometry and cytotoxicity testing will be necessary in the future.

sample	Toxin								
	HBL			*NHE*					Cereulide
	hblD	*hblA*	*hblC*	*nheB*	*nheA*	*nheC*	*cytK*	*entFM*	*ces*
Grilled Corn	+	+	+	+	+	+	+	+	−
Chicken Rice	+	+	+	+	+	+	+	+	−
Fried Rice	+	+	+	+	+	+	+	+	−
Egg Fried Rice	−	−	−	+	+	+	−	+	−
Perilla and Dried Young Sardines	+	−	−	+	+	+	−	+	+
Spicy Cod Roe with Mayonnaise	−	−	−	+	+	+	+	+	−
Tuna Mayonnaise	−	−	−	+	+	+	−	+	−
Salted	−	−	−	+	+	+	−	+	−
Chicken and Burdock Root	−	−	−	+	+	+	−	+	−
Egg Yakisoba Rice Ball	+	+	+	+	+	+	+	+	−

＋:a PCR product of the expected size was obserbed , − :no PCR product was observed

RES-096: Oteseconazole Versus Fluconazole for the Treatment of Severe Vulvovaginal Candidiasis: A Post Hoc Analysis by Candida Species

Hongjie Ruan[4,7], Fengxia Xue[6], Wei Wang[3], Shangrong Fan[2], Manhua Cui[5], Xiaowan Luo[1]

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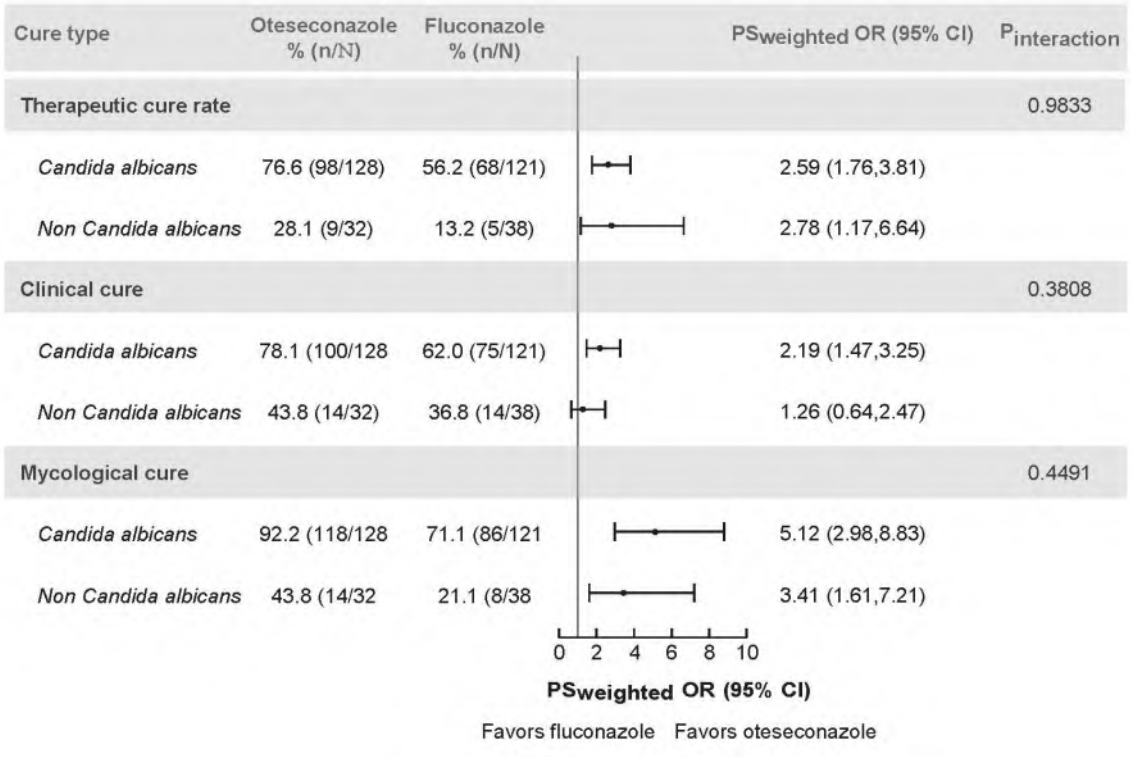
[2]Peking University Shenzhen Hospital
[3]Peking University Third Hospital
[4]Nanjing Women and Children's Healthcare Hospital
[5]The Second Hospital of Jilin University
[6]Tianjin Medical University General Hospital
[7]Women's Hospital of Nanjing Medical University

Background
Oteseconazole, a novel selective fungal CYP51 inhibitor, has demonstrated to be superior to fluconazole for the treatment of severe vulvovaginal candidiasis (SVVC). To explore the efficacy and safety of oteseconazole in SVVC caused by different Candida species.

Method
This post hoc analysis was based on a randomized, double-blinded, phase 3 trial (NCT04956419). Female participants with vulvovaginal signs and symptoms score of ≥7 and positive Candida species were randomly assigned (1:1) to receive oteseconazole (600 mg on D1 and 450 mg on D2) or fluconazole (150 mg on D1 and D4). The trial was conducted between April 2021 and October 2021 at 26 sites in China. Main study outcomes were therapeutic cure (the achievement of both clinical and mycological cure), clinical cure (absence of both VVC signs and symptoms), and mycological cure (culture-negative of vaginal swabs for Candida species) at day 28.

Results
Overall, 319 participants had a confirmed Candida-positive culture (249 positive for Candida albicans and 70 for non-Candida albicans). In the Candida albicans subgroup, oteseconazole was associated with greater odds of achieving therapeutic cure, clinical cure, and mycological cure at day 28. In the non-Candida albicans subgroup, only the odds of achieving therapeutic cure and mycological cure were greater with oteseconazole (Figure 1). No interaction was observed by Candida species (all pinteraction >0.05). Adverse events were generally consistent with oteseconazole versus fluconazole regardless of Candida species.

Conclusions
Oteseconazole shows potential benefit over fluconazole in treating SVVC caused by C. albicans and non-Candida albicans species, with tolerable toxicity.



RES-098: Designing a Novel Multi-epitope Subunit Vaccine Against Trichuris trichiura by Immunoinformatics-Guided Approach

John Kenneth Pagdanganan[2], Jose Jurel Nuevo[2], Mandy Torres[2], Kclyn Tono[2], Cyriz Tan[2], Jinyoshi Sato[2], Russel Dale Santos[2], Tricia Mae Rivera[1], Cedrick Rabanillo[2], Abegail Quimma[2], Loreynne Pangawilan[2], Wysden Muñez[2], Heart Mingoy[2], Clark Vincent Maningas[2], Marnelle Lustre[2], John Aaron Lopez[2], Kimberly Llanes[2], Erica Mae Leaño[2], Jeslea Francisco[2], Ma. Rakiel Loren Ergina[2], Clarence Cañaveral[2], Alfredo Zeus Matthew Mape[2]

[1]Our Lady of Fatima University
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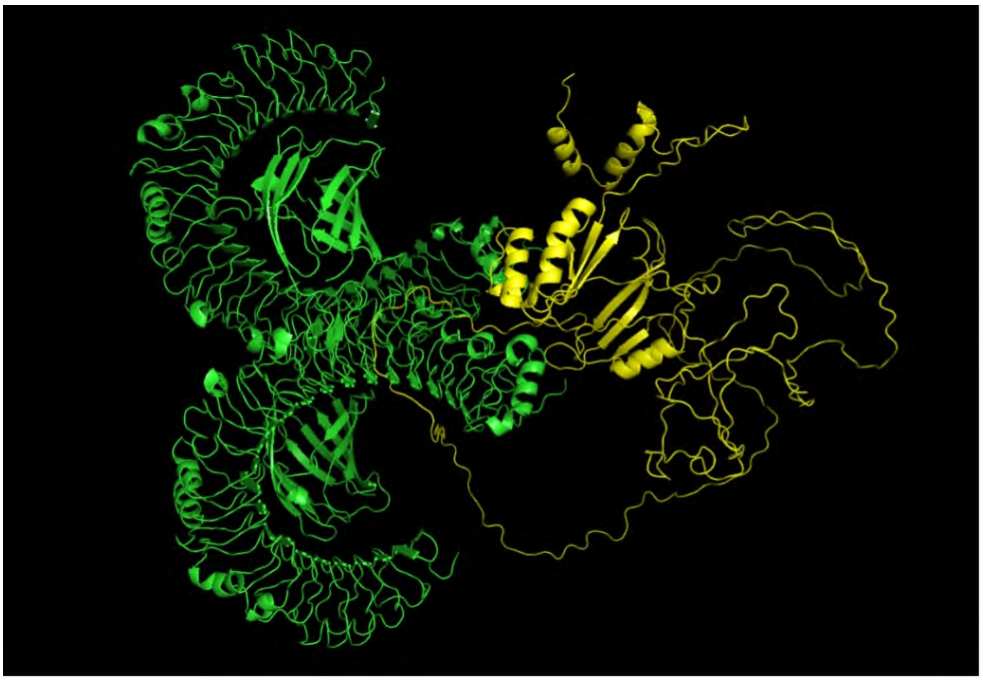
Background
Epidemiological data from the Centers for Disease Control and Prevention showed high morbidity and mortality rates among children caused by parasitic infection associated with Trichuris trichiura. This has posed a significant challenge in the field of public health in preventing diseases, promoting health, and prolonging life. This research study aims to design a multi-epitope subunit vaccine against Trichuris trichiura targeting specific epitopes present in extracted parasite egg proteins through an immunoinformatics approach.

Method
Computational-based predictive immunoinformatic tools were utilized to evaluate identified epitopes based on allergenicity, toxicity, immunogenicity, and antigenicity. The epitopes were used to arranged in an immunogenic manner, conjugated with the N-terminal region of adjuvant, and connected by linkers to determine the affinity and stability of the vaccine-receptor interaction. C-ImmSim predicted the in vitro stimulation of humoral and cellular immune responses.

Results
Sixty-three (63) Trichuris trichiura proteins that showed sequences homologous to human proteins were identified with known molecular functions. Thirteen (13) epitopes were predicted to induce antibody production (LBL), three (3) epitopes induced CTL Immune response, and four (4) HTL epitopes were predicted to induce HTL responses. The vaccine construct dynamic and molecular simulations revealed that it can be recognized and trigger immune responses with a favorable high binding affinity with the TLR4 receptor.

Conclusions
This study developed a promising in silico vaccine using computational servers, suggesting that the vaccine construct is non-allergenic, non-toxic, immunogenic, antigenic, protein-stable, water-soluble, hydrophilic, and thermostable confers its potential as a strong candidate for Trichuris trichiura vaccine development.



RES-100: Molecular Characterization of Enterobacterales Carried IncX3 Plasmid Harboring blaNDM in Tokyo

Tsukasa Ariyoshi, Yumi Uchitani, Rumi Okuno, Isao Yoshida, Hiroaki Kubota, Kohji Mori, Kenji Sadamasu, Takashi Chiba

Tokyo Metropolitan Institute of Public Health

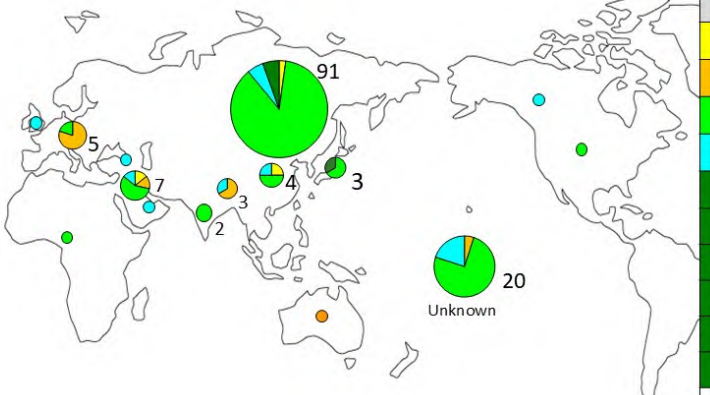
Background
Metallo-beta-lactamase (NDM)-producing Enterobacterales were mostly detected in imported cases in Japan until around 2017. However, in recent years, the number of NDM-producing Enterobacterales from patients with no overseas travel history increased especially Enterobacterales carried IncX3 plasmid harboring blaNDM became the majority in Tokyo.

Method
Among 731 carbapenem-resistant Enterobacterales strains collected through national surveillance between 2015 and 2024, 17 strains carried IncX3 plasmid harboring blaNDM (Escherichia coli [n=11], Klebsiella pneumoniae [n=4], Citrobacter sp. [n=2]), as identified by whole-genome sequencing, were further analyzed for molecular characteristics. These plasmids were introduced into E. coli DH5α by electroporation, and the resulting transformants were tested for antimicrobial susceptibility.

Results
The breakdown of the sequence type (ST) of 11 strains of E. coli were 2 each of ST167 and 617, and 1 each of ST38, 156, 410, 648, 764, 1011, and 3076, respectively. There was no specific ST bias for other species. The IncX3 plasmid sequences of these strains observed similarity with other strains, with approximately 46 kbp of plasmid sizes, although some insertions and deletions were present. Antimicrobial susceptibility testing of transformants revealed the plasmid containing a ~6,000 bp gene cassette insertion upstream of blaNDM conferred higher resistance to meropenem compared to the other plasmids.

Conclusions
In this study, we discovered that highly similar IncX3 plasmids harboring blaNDM may be widely spread in Tokyo, regardless of the species of Enterobacterales. Some of these plasmids conferred high levels of carbapenem resistance to their host strains and should be focused on from a clinical point of view.

Detection of *Enterobacterales* have IncX3 plasmid harboring bla_{NDM} around the world



bla_{NDM} variants	Number of data
NDM-1	4
NDM-4	9
NDM-5	107
NDM-7	16
NDM-16b	1
NDM-17	1
NDM-19	1
NDM-20	1
NDM-21	1
NDM-33	1
Total	142

Ariyoshi, T., *et al,* : Microbiol Spectr. 2022 Jul-Au; 10(4): e01449-22

RES-101: Reducing the Positive Rate of Legionella in Hospital Water Supply Systems in a Certain Region of Southern Taiwan

Yuen Ju Chen, Yu-Ting Tsai, Huan-Yi Wu

Pingtung Veterans General Hospital/Infection Control Office

Background
Legionella is a bacterium ubiquitously present in natural aquatic environments, soil, and man-made water systems. It preferentially colonizes warm, low-flow, or stagnant water environments, including cooling towers, hot water systems, and humidifiers, and can persist even in chlorine-treated municipal water supplies. Among high-risk populations in hospital settings, infection can lead to severe pneumonia and potentially fatal outcomes.

Method
Since opening in November 2023, our hospital conducts biannual Legionella testing at 23 sampling points across ICUs, neonatal units, and other facilities. Standards require zero tolerance in high-risk areas and <30% positivity in non-high-risk areas.

Results
Since November 2024 testing revealed 34.8% average positivity with 8 high-risk site cases (serotypes 1, 2, 5). Investigation identified insufficient cooling tower disinfection, hot water temperatures of 40-45°C, and water in unused wards is not flowing.

Implemented improvements included: cooling tower disinfection with 0.5 ppm chlorine maintenance, use ozone to disinfect when hot water systems test positive, thermostat installation maintaining >50°C temperatures, daily 2-3 minute flushing of unused wards water sources, and faucet filter installation at positive sites. After 2 months of continuous monitoring, May 2025 testing achieved 0% positivity with no healthcare-associated infections.

Conclusions
For energy conservation, the hospital maintains water at 45°C, optimal for Legionella growth. Recommendations include: daily 2-3 minute flushing of unused ward water sources, maintaining hot water >50°C, continuous HAI surveillance, using boiled water for medical care instead of tap water, avoiding direct tap water use. Upon detecting Legionella, immediate systematic response measures are essential for patient and staff safety.

RES-102: Effect of Iron on the Growth, Motility, and Biofilm Formation of Burkholderia pseudomallei isolated from Humans and Animals

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[2]Medical Technology Program, Faculty of Science, Nakhon Phanom University, Thailand

Background
Burkholderia pseudomallei is the causative agent of melioidosis, commonly found in tropical countries including Southeast Asia and northern Australia. Environmental factors, such as iron availability may influence the bacterium's survival and adaptive responses.

Method
In this study, we investigated the adaptive changes in five isolates of B. pseudomallei that were obtained from human clinical and animal samples in Thailand, and the reference strain K96243. The growth rate of B. pseudomallei strains cultured in Luria–Bertani broth containing different concentrations of iron (100-500 mM FeSO4) at 37°C were analyzed over a period of 72 hours. The bacteria were then examined the motility using the swarm plate method and assessed biofilm formation efficiency after culture under iron conditions.

Results
In response to exposure to iron, B. pseudomallei isolates showed increased growth, motility, and biofilm formation capacity. Growth curve analysis revealed that B. pseudomallei isolates exhibited the similar growth rate at 37 °C for 18 to 24 hours under conditions of 0, 100, 300 and 500 mM FeSO4. Bacterial motility was positively affected under conditions with iron. Most of B. pseudomallei isolates increased motility when grown in the presence of 100 mM FeSO4. Biofilm formation capacity of each B. pseudomallei isolate increased when grown in the presence of 0, 100, 300 and 500 mM FeSO4, respectively.

Conclusions
These findings indicate that iron contributes to the survival of B. pseudomallei and its ability to adapt in the environment. This may also play a role in the transmission and infection of melioidosis.

RES-103: Surveillance of the Antimicrobial-Resistant Bacteria in Nagasaki, Japan, 2014 to 2023

Yasuhide Kawamoto, Daisuke Sasaki, Kosuke Kosai, Norihiko Akamatsu, Katsunori Yanagihara

Department of Laboratory Medicine, Nagasaki University Hospital, Nagasaki

Background
Monitoring antimicrobial resistance (AMR) bacteria is essential for effective regional antimicrobial stewardship. This study analyzed the prevalence and trends of AMR bacteria in hospitals in Nagasaki, Japan.

Method
We collected and analyzed data on AMR bacteria from 17 hospitals in Nagasaki, Japan, between 2014 and 2023. The study focused on the following AMR bacteria: methicillin-resistant S. aureus (MRSA), vancomycin-resistant Enterococci (VRE), extended-spectrum β-lactamase (ESBL) producing bacteria, multidrug-resistant P. aeruginosa (MDRP), carbapenem-resistant Enterobacteriaceae (CRE), and carbapenemase-producing Enterobacteriaceae (CPE).

Results
The isolation rate of MRSA decreased from 50.8% in 2014 to 40.6% in 2021, after which it stabilized. VRE was isolated in only two cases, one in 2021 and one in 2023. The prevalence of ESBL-producing E. coli increased from 23.7% in 2014 to 30.5% in 2019, then stabilized. The isolation rates of ESBL-producing K. pneumoniae (avg. 5.4%) and P. mirabilis (avg. 3.5%) showed minimal fluctuations. The isolation rate of ESBL-producing K. oxytoca (avg. 6.3%) increased slightly. The isolation rates of MDRP (avg. 0.42%) and CRE (avg. 0.08%) remained stable. Among isolates identified as CRE and carbapenemase-producing Enterobacteriaceae (CPE), Enterobacter spp. was the most prevalent, accounting for 59.6% and 64.1%, respectively.

Conclusions
We identified the trends in the isolation of antimicrobial-resistant bacteria in Nagasaki, Japan over the past decade (2014–2023). Ongoing surveillance of regional drug-resistant bacteria remains imperative.

RES-105: Multiple cases of CVA16 associated with B1c clade were found for the first time Heilongjiang Province

Qian Yang

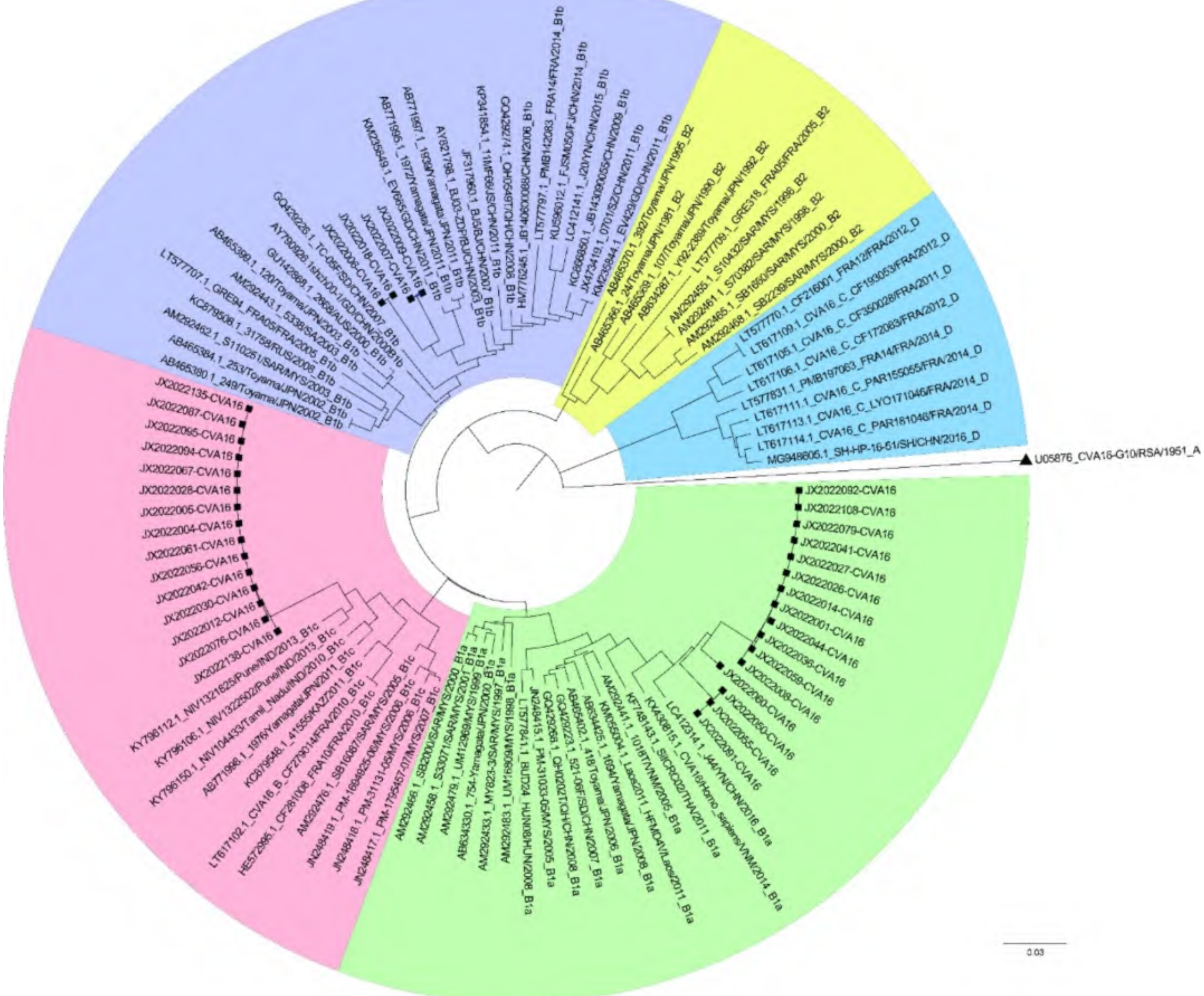
National Institute for Viral Disease Control and Prevention, Chinese Center for Disease Control and Prevention

Background
Hand, foot, and mouth disease (HFMD) is a global infectious disease mainly caused by various enteroviruses. Enterovirus A71 (EV-A71), Coxsackievirus A16 (CVA16) and Coxsackie virus A6 (CVA6) are the main pathogens of HFMD. CVA16 belongs to the genus Enterovirus and family Picornaviridae. B1a and B1b are the prevalent subtypes, while B1c is rarer.

Method
In this study, 15 cases of CVA16(B1c) clusters were found in Jixi City by detecting HFMD samples from Heilongjiang Province, China in 2022, and whole genome sequencing was further conducted. The phylogenetic origin and recombination were analyzed by combining the sequence information in GenBank.

Results
The results showed that the homology between CVA16 (B1C) in this study was high, and the nucleotide similarity in the VP1 region was 99.6-100%. The average base substitution rate of CVA16 (B1C) worldwide is 4.24×10-3 (3.47×10-3, 5.11×10-3) substitution/site/year, and the earliest common ancestor can be traced back to 2001. The earliest strain CVA16 (B1C) isolated in China can be traced back to 2011. The transmission path analysis suggested that the Chinese strain may have originated from India. Recombination analysis showed that CVA16 (B1C) had the possibility of recombination with EV-A71, CVA6 and CVA4.

Conclusions
This study detected a cluster of CVA16 (B1c) cases in Heilongjiang Province for the first time, which enriched the gene sequence library of CVA16 (B1c) in China. as well as provided an epidemiological reference for further study of CVA16 (B1c) antigen-antibody and pathogenicity.


U05876_CVA16-G10/RSA/1951_A
JX2022092-CVA16
JX2022108-CVA16
JX2022079-CVA16
JX2022041-CVA16
JX2022027-CVA16
JX2022026-CVA16
JX2022014-CVA16
JX2022001-CVA16
JX2022135-CVA16
JX2022087-CVA16
JX2022095-CVA16
JX2022094-CVA16
JX2022067-CVA16
JX2022028-CVA16
JX2022005-CVA16
JX2022004-CVA16
JX2022061-CVA16
JX2022056-CVA16
JX2022042-CVA16
JX2022030-CVA16
JX2022012-CVA16
JX2022076-CVA16
MG948605.1_SH-HP-16-51/SH/CHN/2016_D
LT617114.1_CVA16_C_PAR181048/FRA/2014_D
LT617113.1_CVA16_C_LYO171046/FRA/2014_D
0.03

RES-109: Evaluation of Confirmatory Testing for HTLV-1 in Pregnant Women in Nagasaki: Comparison of CLIA, LIA, and PCR Results

Kaori Ishihara[3], Fujiko Mitsumoto-kaseida[1,2], Maiko Yoshida[1], Daisuke Sasaki[1,2], Kosuke Kosai[2,3], Hiroo Hasegawa[1,2], Katsunori Yanagihara[1, 2]

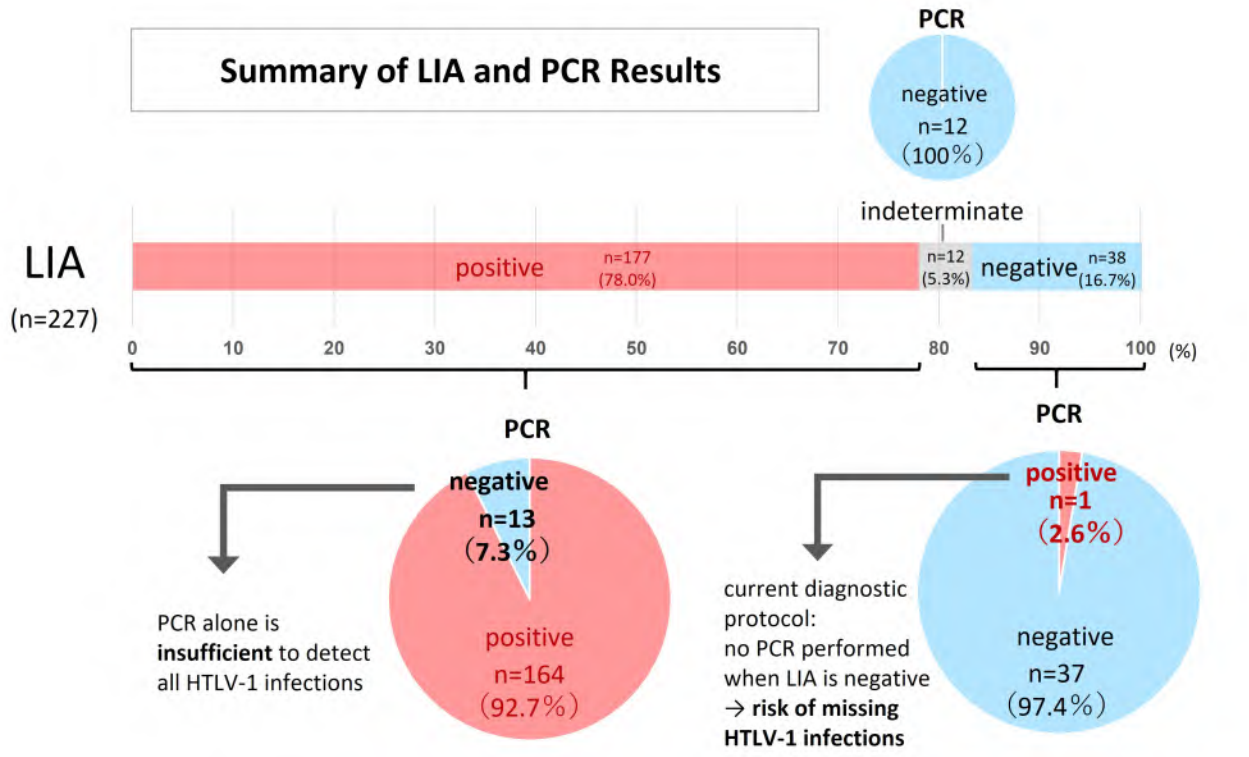
[1]Department of Laboratory Medicine, Nagasaki University Hospital
[2]Department of Laboratory Medicine, Nagasaki University Graduate School of Biomedical Sciences
[3]Nagasaki University Hospital

Background
Human T-cell leukemia virus type 1 (HTLV-1), a retrovirus causes adult T-cell leukemia (ATL), is primarily transmitted by breastfeeding. Nagasaki Prefecture, a high-prevalence region in Japan, has established HTLV-1 screening program for pregnant women since the 1980s. HTLV-1 infection is diagnosed both positive screening antibody test and positive confirming test by line immunoassay (LIA) or polymerase chain reaction (PCR).In Nagasaki prefecture, all confirmatory test (both LIA and PCR) is centralized at Nagasaki University Hospital. This study involved a comparison between screening antibody test outcomes and confirmatory test results.

Method
We retrospectively analyzed 227 pregnant women with positive screening results also tested confirmatory test (both LIA and PCR) from 2019 to March 2025. HTLV-1 antibody was measured by a chemiluminescent immunoassay (CLIA) as the initial screening test.

Results
Of the 227 cases, 177 (78.0%) were LIA-positive, and 12 (5.3%) were indeterminate, all of which were PCR-negative. One LIA-negative case was PCR-positive. Thus, 178cases (78.4%) were confirmed HTLV-1 positive. Mean CLIA cut-off values(s/co) were significantly higher in LIA-positive cases than LIA-negative (95.4 ±40.0 vs. 1.6 ± 2.5; $p < 0.05$). PCR-positive samples had significantly higher CLIA values than PCR-negative ones (98.0 ± 38.8 vs. 1.4 ± 13.4; $p < 0.05$). However, CLIA values did not correlate with proviral load.

Conclusions
High CLIA values are predictive of confirmatory test positivity. However, as one LIA-negative case was PCR-positive, LIA alone may miss HTLV-1 carriers. Combining LIA and PCR is essential for accurate diagnosis and prevention of mother-to-child transmission.



RES-110: Efficacy and Safety of Oteseconazole Versus Fluconazole for Severe Vulvovaginal Candidiasis: A Post-Hoc Analysis Based on Reproductive Tract Infection History

Zhengai Xiong[2], Bei Zhang[5], Zhiying Su[4], Qi Chen[3], Xiaoling Zhang[1]

[1]Jiangxi Maternal and Child Health Hospital
[2]The Second Affiliated Hospital of Chongqing Medical University
[3]The Second Affiliated Hospital of Nanchang University
[4]Xiamen Maternal and Child Health Hospital
[5]Xuzhou Central Hospital

Background
Vulvovaginal candidiasis (VVC), primarily caused by Candida albicans, is a common infection among women. Oteseconazole, a selective fungal CYP51 inhibitor, demonstrated superior efficacy over fluconazole in a multicenter, double-blinded, phase 3 trial in China.

Method
Women aged 18–75 years with a VVC score ≥7 and confirmed Candida infection were randomized to receive oteseconazole (600 mg Day 1, 450 mg Day 2) or fluconazole (150 mg Days 1 and 4). A post-hoc analysis using propensity score weighting (Psweighted) compared efficacy in patients with or without a history of reproductive tract infections.

Results
Among patients with prior reproductive tract infections (RTIs), 47 received oteseconazole and 60 fluconazole; in those without RTIs, 113 and 99 received oteseconazole and fluconazole, respectively. Oteseconazole consistently outperformed fluconazole in therapeutic cure (combined clinical and mycological cure), clinical cure, and mycological cure at Days 14 and 28, with fewer patients requiring rescue therapy, regardless of RTI history (Table 1). Treatment-related adverse events (TRAEs) occurred in 23.4% vs. 15.0% (with RTI) and 21.2% vs. 22.8% (without RTI) for oteseconazole and fluconazole, respectively.

Conclusions
Oteseconazole demonstrated superior efficacy and a comparable safety profile versus fluconazole for severe VVC, irrespective of reproductive tract infection history.

Table 1. Efficacy of oteseconazole versus fluconazole for severe vulvovaginal candidiasis: subgroup analysis by reproductive tract infection history

Timepoint	Endpoint	History of Reproductive Tract Infections				No History of Reproductive Tract Infections				Interaction P-value
		Oteseconazole (N=47)	Fluconazole (N=60)	Psweighted Risk Difference (95% CI)	Psweighted Odds Ratio (95% CI)	Oteseconazole (N=113)	Fluconazole (N=99)	Psweighted Risk Difference (95% CI)	Psweighted Odds Ratio (95% CI)	
Day 14	Therapeutic cure†	24 (51.06%)	19 (31.67%)	0.19 (0.06, 0.32)	2.26 (1.29, 3.95)	60 (53.10%)	42 (42.42%)	0.11 (0.01, 0.20)	1.54 (1.05, 2.27)	0.4345
Day 14	Clinical cure	24 (51.06%)	25 (41.67%)	0.09 (–0.04, 0.23)	1.46 (0.85, 2.50)	67 (59.29%)	55 (55.56%)	0.04 (–0.05, 0.13)	1.18 (0.80, 1.73)	0.6382
Day 14	Mycological cure	37 (78.72%)	40 (66.67%)	0.12 (0.00, 0.24)	1.87 (1.01, 3.44)	94 (83.19%)	66 (66.67%)	0.15 (0.07, 0.23)	2.28 (1.45, 3.61)	0.6023
Day 28	Therapeutic cure†	29 (61.70%)	27 (45.00%)	0.18 (0.04, 0.31)	2.03 (1.18, 3.51)	78 (69.03%)	46 (46.46%)	0.23 (0.14, 0.32)	2.59 (1.74, 3.85)	0.5877
Day 28	Clinical cure	31 (65.96%)	32 (53.33%)	0.11 (–0.02, 0.24)	1.56 (0.90, 2.69)	83 (73.45%)	57 (57.58%)	0.17 (0.08, 0.26)	2.10 (1.40, 3.16)	0.7118
Day 28	Mycological cure	36 (76.60%)	37 (61.67%)	0.18 (0.05, 0.30)	2.29 (1.27, 4.13)	96 (84.96%)	57 (57.58%)	0.27 (0.19, 0.35)	4.18 (2.62, 6.67)	0.1913
Overall	Use of rescue therapy	4 (8.51%)	9 (15.00%)	–0.08 (–0.17, 0.00)	0.43 (0.18, 1.05)	2 (1.77%)	14 (14.14%)	–0.12 (–0.17, –0.07)	0.11 (0.04, 0.34)	0.1152

†Therapeutic cure defined as combined clinical and mycological cure. Interaction P-values assess whether treatment effects differed significantly by reproductive tract infection history.

RES-113: Development of Cobas® UC-TIB-CPO Assay for Detection of KPC, OXA-48, NDM, and VIM/IMP

Brian Lee[1], Xun Zhuang[1], Marco Kaiser[2], Hai Nguyen[1], Qiu Yang[1], Patrick Lin[1], Indira Somanathan[1], Aishwarya Sathish[1], Brett Hanson[1], Kyle Cady[1], Ellen Ordinario[1]

[1]Roche Diagnostics Solutions
[2]TIB Molbiol

Background
Carbapenemase-producing organisms (CPO) are a significant cause of healthcare-associated infections and an urgent threat to public health. These critical pathogens have limited treatment options and are associated with high mortality, making resistance detection essential for infection prevention, antimicrobial stewardship, and epidemiological surveillance.

Method
The UC-TIB-CPO assay was designed for qualitative detection of the five major carbapenemases, KPC, OXA-48 like, NDM, and VIM/IMP (undifferentiated), on the Cobas® Utility Channel of the automated, high-throughput Cobas® 5800/6800/8800 Systems. Analytical performance was compared with the Cepheid Xpert Carba-R assay using contrived specimens spiked in rectal swab matrix with reference organisms carrying target genes or synthetic templates. Analytical exclusivity was conducted with 51 bacterial strains carrying closely related but off-target resistance markers, spiked at 1E7 colony-forming units (CFU)/mL. Additionally, in-silico inclusivity and specificity analyses were performed.

Results
With contrived swab samples, the assay demonstrated an analytical sensitivity of ~62.5 CFU/swab (KPC-2), 3.9 CFU/swab (OXA-232), 125 CFU/swab (VIM-2), 31.25 CFU/swab (NDM-1), and 3.9/7.81 CFU/swab (IMP-1/IMP-4), outperforming the Carba-R assay. Combined in silico and wet-lab studies demonstrated 100% inclusivity for all variants of the 5 major carbapenemases available in the National Center for Biotechnology Information GenBank as of March 2025. No cross-reactivity was observed either in wet-lab testing with 51 exclusivity strains or in silico.

Conclusions
Using contrived rectal swab samples, the UC-TIB-CPO assay demonstrated better analytical sensitivity than the Cepheid Carba-R assay with excellent inclusivity and exclusivity for the detection of the 5 most problematic carbapenemase-encoding genes carried by Gram-negative pathogens.

RES-120: Timeliness of Ceftazidime Initiation in Suspected Melioidosis Cases in Bintulu Hospital

Tonnii Sia[2], Cindy Lau[1], Ahnaf Rushdi Rosli[1], Mong-How Ooi[3]

[1]Bintulu Hospital
[2]Miri Hospital
[3]Sarawak General Hospital

Background
Bintulu, Malaysian Borneo is endemic for melioidosis (1). Timely antimicrobial(s) administration in sepsis saves lives (2). The need for empirical ceftazidime therapy is a day-to-day antibiotic stewardship conundrum faced by clinicians when they manage community-acquired sepsis at melioidosis-endemic areas. This study aimed to analyze ceftazidime use to advise future prescription practices at Bintulu Hospital.

Method
The study analyzed the ceftazidime prescription in melioidosis at Bintulu Hospital in 2024 as an antimicrobial stewardship activity. Cases were reviewed and classified into “Culture-confirmed”, “Probable”, “Possible” and “Not melioidosis” (3).

Results
Eighty-four cases were included. Seventy (83.3%) were male. The median age was 43.5 years (IQR 32.0–54.8). Ceftazidime was initiated in 35 (41.7%), 7 (8.3%), 11 (13.1%), and 31 (36.9%) cases ≤24 hours, 25–48 hours, 49–72 hours, and >72 hours of hospitalization, respectively. Ceftazidime was initiated ≤24 hours in 46% (16/35), 25–48 hours in 57% (4/7), 49–72 hours in 64% (7/11), and >72 hours of hospitalization in 48% (15/31) cases who had final diagnosis of culture-confirmed, probable, or possible melioidosis. Among the 37 culture-confirmed and probable cases, less than 50% received ceftazidime ≤48 hours of hospitalization. Of the 10 cases that had ceftazidime >72 hours post-admission, a median delay of 6 days (IQR 5–10) was observed. Case fatality rate of melioidosis was 11% (4/37, 2 culture-confirmed, 2 probable). Deaths occurred at a median of 45 (IQR 22–102) days post-admission.

Conclusions
Further improvement in clinical and laboratory recognition of melioidosis is required in streamlining ceftazidime use in melioidosis management at Bintulu Hospital.

Melioidosis diagnosis	Time to initiate ceftazidime				Mortality n=7
	< 24 hours (n=35)	24-48 hours (n=7)	49-72hours (n=11)	>72 hours (n=31)	
Culture-confirmed * (n=18)	6 17.1%	4 57.1%	3 27.3%	5 16.1%	2 11.1%
Probable # (n=13)	7 20.0%	0	1 9.1%	5 16.1%	2 15.4%
Possible ** (n=11)	3 8.6%	0	3 27.3%	5 16.1%	0
Not melioidosis (n=42)	19 54.3%	3 42.9%	4 36.4%	16 51.6%	3 7.1%

Footnote:
Definition of cases based on Cheng et.al (3).
* Culture-confirmed = One or more clinical samples culture-positive for *B. pseudomallei*.
# Probable melioidosis = Evidence of one or more abscesses that would be consistent with a diagnosis of melioidosis but culture not performed or negative for *B. pseudomallei*, or culture negative for *B. pseudomallei* on first presentation but represented to hospital within 1 month with culture-proven melioidosis.
** Possible melioidosis = Clinically suspected melioidosis improved after treatment with an effective antimicrobial regimen for melioidosis (ceftazidime/carbapenem drug/amoxicillin-clavulanate) or clinically suspected melioidosis but the patient died before improvement was observed.

RES-122: Real-world Clinical Outcomes of 48-hour Extended Antibiotic Infusion Using Elastomeric Pumps (RECEIVE-48): A Retrospective Observational Cohort Study from a Single Center Outpatient Parenteral Antibiotic Therapy (OPAT)

Jia Min Deborah Chong[2], Stephanie Sutjipto[3], Lihua Zhong[1], Barnaby Edward Young[3], Monica Chan[3]

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[2]Tan Tock Seng Hospital
[3]Tan Tock Seng Hospital, National Centre for Infectious Diseases

Background
Outpatient parenteral antimicrobial therapy (OPAT) enables treatment of infections needing prolonged intravenous antibiotics. While 24-hour elastomeric infusors have established stability data, evidence for 48-hour infusors is limited. At Tan Tock Seng Hospital (TTSH), ceftriaxone and cefazolin are administered via both 24-hour and 48-hour infusors as using 48-hour infusors reduces hospital visits, line manipulation, and costs.

Method
A retrospective cohort study compared clinical outcomes and adverse events in patients receiving ceftriaxone or cefazolin via 24-hour (Baxter LV10) or 48-hour (Baxter LV5) infusors. Outcomes included cure rates at treatment completion and at 3 months post-treatment. Adverse events included treatment-related side effects and readmissions from infection or antibiotics.

Results
Of 122 patients (68% male, median age 63), the most common infections were head and neck infections (21.3%) and osteomyelitis (20.5%) -Table 1. For ceftriaxone (48-hour: n=41; 24-hour: n=27), there were no significant differences in clinical outcomes or adverse events (P>.05). Radiological improvement was comparable (P> .05) – Table 2. For cefazolin (48-hour: n=8; 24-hour: n=46), there were no significant differences in clinical outcome at the end of treatment or adverse effects (P >.05); but 3-month cure rates were lower in the 48-hour group (P < .05) –Table 3. Notably, only patients with renal impairment (creatinine clearance < 35) received 48-hour cefazolin infusors due to lower doses required.

Conclusions
Ceftriaxone delivery via 48-hour infusors appears safe and effective. However, further data is needed to assess outcomes of cefazolin administration via 48-hour infusors, as current results are limited by small sample size and differences in patient population.

Table 1: Demographics

Characteristic		**TOTAL**	LV5CR	LV10CR	LV5CFZ	LV10CFZ
Total patients studied		122	41	27	8	46
Age - year	Median	63	63	55	86	63
	Interquartile range [IQR]	39 [28-67]	18 [56-74]	19 [48-67]	11 [77-88]	21 [52-73]
Gender - no. (%)	Female	39 (32.0)	12 (9.8)	7 (5.7)	2 (1.6)	18 (14.8)
	Male	83 (68.0)	29 (23.8)	20 (16.4)	6 (4.9)	28 (23.0)
Infection type - no. (%)	Urinary tract	6 (4.9)	4 (3.3)	0 (0.0)	0 (0.0)	2 (1.6)
	Intra-abdominal/ hepatobiliary	23 (18.9)	9 (7.4)	5 (4.1)	0 (0.0)	9 (7.4)
	Skin/soft tissue	4 (3.3)	0 (0.0)	0 (0.0)	0 (0.0)	4 (3.3)
	Osteomyelitis (including spine, long bones etc.)	25 (20.5)	9 (7.4)	0 (0.0)	5 (4.1)	11 (9.0)
	Head and neck (including meningitis, encephalitis, cerebral abscess, skull base osteomyelitis, complex sinusitis, malignant otitis externa etc.)	26 (21.3)	9 (7.4)	13 (10.6)	1 (0.8)	3 (2.5)
	Infective endocarditis	10 (8.2)	6 (4.9)	1 (0.8)	0 (0.0)	3 (2.5)
	Joint infection	13 (10.6)	2 (1.6)	1 (0.8)	1 (0.8)	9 (7.4)
	Bacteraemia (including Methicillin sensitive Staphylococcus aureus, *Salmonella* etc)	10 (8.2)	2 (1.6)	3 (2.5)	1 (0.8)	4 (3.3)
	Lung infection	2 (1.6)	0 (0.0)	1 (0.8)	0 (0.0)	1 (0.8)
	Others	3 (2.5)	0 (0.0)	3 (2.5)	0 (0.0)	0 (0.0)

Key: LV5CR = 48-hour infusor for Ceftriaxone, LV10CR =24-hour infusor for Ceftriaxone, LV5CFZ = 48-hour infusor for Cefazolin, LV10CFZ = 24-hour infusor for Cefazolin.

Table 2: Comparing outcomes for receiving Ceftriaxone in 24-hour infusor versus 48-hour infusor

		LV5CR (total no. =41)	LV10CR (total no. =27)	Fisher's exact test
Infection type – no. (%)	Urinary tract	4 (9.8)	0 (0.0)	Nil
	Intra-abdominal/ hepatobiliary	9 (22.0)	5 (18.5)	
	Skin/soft tissue	0 (0.0)	0 (0.0)	
	Osteomyelitis	9 (22.0)	0 (0.0)	
	Head and neck	9 (22.0)	13 (48.1)	
	Infective endocarditis	6 (14.6)	1 (3.7)	
	Joint infection	2 (4.9)	1 (3.7)	
	Bacteraemia	2 (4.9)	3 (11.1)	
	Lung infection	0 (0.0)	1 (3.7)	
	Others	0 (0.0)	3 (11.1)	
Outcome at the end of treatment – no. (%) *	Cure	37 (94.9)	24 (96.0)	$P = 1.00$
	Treatment failure	1 (2.6)	1 (4.0)	
	Demise	1 (2.6)[#]	0 (0)	
Outcome at 3 months – no. (%) *	Cure	34 (87.2)	23 (92.0)	$P = .484$
	Treatment failure	2 (5.1)	2 (8.0)	
	Demise	3 (7.7)[##]	0 (0.0)	
Radiological outcome at the end of antibiotic use– no. (%) *	Improved	22 (73.3)	20 (87.0)	$P = .541$
	Stable	4 (13.3)	1 (4.3)	
	Worse	0 (0.0)	0 (0.0)	
	Not repeated	4 (13.3)	2 (8.7)	
Readmission related to the target infection during treatment period – no. (%) *	No	38 (97.4)	24 (96.0)	$P = 1.00$
	Yes	1 (2.6)	1 (4.0)	
Readmission for antibiotic effects during treatment period – no. (%) **	No	38 (97.4)	25 (96.2)	$P = 1.00$
	Yes	1 (2.6)[###]	1 (3.8)[####]	
Treatment related adverse effects during treatment period – no. (%) ***	No	38 (97.4)	25 (92.6)	$P = .563$
	Yes	1 (2.6)[###]	2 (7.4)[####]	

Key: LV5CR = 48-hour infusor for Ceftriaxone, LV10CR =24-hour infusor for Ceftriaxone.

* Did not include data of LV5CR14 - passed on of unknown cause (admitted to non-NHG institutions); LV5CR30 - restricted access; LV10CR13 and 14- defaulted appointments.

** Does not include data of LV5CR14 -passed on of unknown cause (admitted to non-NHG institutions); LV5CR30 - restricted access; LV10CR14- defaulted appointment.

*** Does not include data of LV5CR14- passed on of unknown cause (admitted to non-NHG institutions); LV5CR30 - restricted file.

[#] The LV5CR patient who demised prior to the end of treatment had metastatic cancer and was subsequently admitted for a different infection then passed on.

[##] For the LV5CR patients who passed on within 3 months after the end of treatment, one had an aortic aneurysm with an aortoenteric fistula and was palliated, and the other had glioblastoma progression.

[###] The LV5CR patient who had treatment related adverse effects had diarrhea attributed to antibiotics and was admitted.

[####] For the LV10CR patients who had treatment related adverse effects, one had cytopenia attributed to antibiotics, and the other had anaphylaxis attributed to antibiotics and was admitted.

Table 3: Comparing outcomes for receiving Cefazolin in 24-hour infusor versus 48-hour infusor

		LV5CF (total no. = 8)	LV10CF (total no. =46)	Fisher's exact test
Infection type – no. (%)	Urinary tract	0 (0.0)	2 (4.3)	Nil
	Intra-abdominal/ hepatobiliary	0 (0.0)	9 (19.6)	
	Skin/soft tissue	0 (0.0)	4 (8.7)	
	Osteomyelitis	5 (62.5)	11 (23.9)	
	Head and neck	1 (12.5)	3 (6.5)	
	Infective endocarditis	0 (0.0)	3 (6.5)	
	Joint infection	1 (12.5)	9 (19.6)	
	Bacteraemia	1 (12.5)	4 (8.7)	
	Lung infection	0 (0.0)	1 (2.2)	
	Others	0 (0.0)	0 (0.0)	
Outcome at the end of treatment – no. (%) *	Cure	6 (75.0)	44 (97.8)	$P = .056$
	Treatment failure	1 (12.5)	1 (2.2)	
	Demise	1 (12.5) #	0 (0)	
Outcome at 3 months – no. (%) *	Cure	5 (62.5)	42 (93.3)	$P = .038$
	Treatment failure	2 (25.0)	1 (2.2)	
	Demise	1 (12.5) #	2 (4.4) ##	
Readmission related to the target infection during treatment period – no. (%)	No	6 (75.0)	45 (97.8)	$P = .054$
	Yes	2 (25.0)	1 (2.2)	
Readmission for antibiotic effects during treatment period – no. (%)	No	7 (87.5)	46 (100.0)	$P = .148$
	Yes	1 (12.5) ###	0 (0.0)	
Treatment related adverse effects during treatment period – no. (%)	No	6 (75.0)	45 (97.8)	$P = .054$
	Yes	2 (25.0) ###	1 (2.2) ####	

Key: LV5CF = 48h infusor for Cefazolin, LV10CF =24h infusor for Cefazolin.

* Did not include data of LV10CF as defaulted appointments.

LV5CF patient passed on from unknown cause (admitted to non-NHG institutions).

LV10CF patients both passed on from unknown causes (admitted to non-NHG institutions).

For the LV5CF patients who had treatment related adverse effects, one had rise in creatinine attributed to acute interstitial nephritis related to antibiotics and was admitted, the other had rash attributed to antibiotics.

The LV10CF patient who had treatment related adverse effect had leukopenia attributed to antibiotics.

RES-126: A Novel Carbapenem Resistance Screening Method (Carba Plate) Shows High Specificity and Sensitivity Against Carbapenem Resistant Enterobacterials: One Health Sample to Solution Strategy

Jayalaxmi Wangkheimayum[1], Amitabha Bhattacharjee[2]

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Background
Carbapenem resistant organisms (CROs) pose an enormous threat to human health and World Health Organization (WHO) has enlisted CRO as one among the major pathogens with critical priority. Detection of carbapenem resistance is not yet accessible in terms of daily or routine use by the hospitals of Low- and middle-income countries because the present methods are inadequate in terms of time and facility required. A novel screening method (CarbaPlate) is designed here to evaluate its efficacy in Enterobacteriales.

Method
189 isolates from clinical-environmental origin of Escherichia coli (n=125), Klebsiella pneumoniae (n=64) were selected for the study. Isolates streaked onto an inhouse developed test medium containing a chromogenic substrate of β-galactosidase and carbapenem antibiotic was incubated at 37°C for 16 hrs. (IP pending). Carba NP test and Kirby Bauer disc diffusion was used to calculate specificity and sensitivity of the newly designed media.

Results
All the carbapenem non susceptible isolates were positive and the coloration accurately predicting resistance mechanism by the test and was 100% sensitive and specific comparing with disc diffusion method. Also, the blue color and colorless colonies could differentiate between lactose and non-lactose fermenters.

Conclusions
The present screen agar-based screening method simultaneously differentiates between lactose and non-lactose/ non fermenting bacteria and also carbapenemase or non carbapenemase mediated resistance. The method is simple, deployable in routine diagnostic laboratories of resource limited countries. The screening method can holistically detect carbapenem resistance in all settings in a sample to solution approach thereby reducing diagnostic intervention by 16 hours.

RES-127: Establishment of a MALDI-TOF MS Database for Taiwanese Helicobacter pylori Isolates and Its Application to Disease Classification and Antimicrobial Resistance Analysis

Yun-Shan Lu

National Taiwan University Hospital

Background
Helicobacter pylori is closely associated with various gastrointestinal diseases, including chronic gastritis, peptic ulcers, gastric cancer, and MALT lymphoma. Although MALDI-TOF mass spectrometry (MS) has become a mainstream method for rapid bacterial identification, its performance for H. pylori remains suboptimal due to limited reference spectra in existing databases.

Method
This study collected 697 clinical H. pylori isolates from Taiwan. Spectral data from 2001 to 20000 m/z were processed, with the highest intensity in each 30 m/z bin used as input features. Each isolate was labeled with its corresponding clinical diagnosis: chronic gastritis, gastric ulcer, duodenal ulcer, gastric cancer, or MALToma. A local H. pylori spectral database was constructed. Antimicrobial susceptibility testing was performed, and machine learning models (CatBoost and LightGBM) were developed for disease classification.

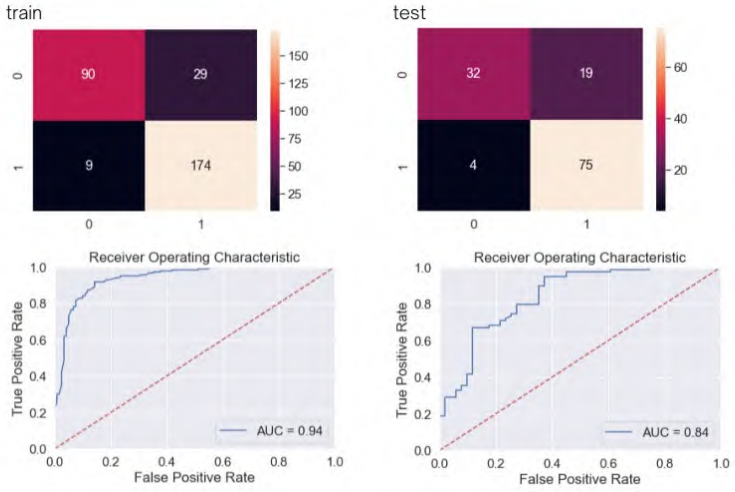
Results
The newly constructed local MALDI-TOF MS database significantly improved H. pylori identification accuracy compared to the commercial Bruker database. In disease classification tasks, CatBoost outperformed LightGBM. The 5-class model achieved an AUC of 0.85 in the test set. Two binary classification models further improved discrimination between benign (gastritis/ulcers) and malignant (gastric cancer/MALToma) conditions, with AUCs of 0.81 and 0.84, respectively. However, performance declined when applied to validation data with a different distribution, highlighting the importance of dataset consistency.

Conclusions
Integrating MALDI-TOF MS with machine learning enables accurate classification of H. pylori-associated diseases and enhances bacterial identification. Establishing a local spectral database provides a foundation for future clinical applications, including resistance prediction and personalized treatment strategies.

bin_size = 30 - CatBoost

CatBoost	AUC	accuracy	sensitivity	specificity	precision	F1
train	0.9402	0.8742	0.9508	0.7563	0.8571	0.9016
test	0.8438	0.8231	0.9494	0.6275	0.7979	0.8671

Gastritis (1)/ Ulcers(0)



RES-128: Effectiveness of Diagnosis and Antimicrobial Susceptibility Testing in the Treatment of Patients with CRE Infections: A Retrospective Analysis from Lerdsin Hospital

Parichat Boonrod, Thitirat Tangkosakul

Lerdsin Hospital

Background
Carbapenem-resistant Enterobacteriaceae (CRE) are a major clinical threat due to limited treatment options and high mortality. Rapid diagnosis and reliable antimicrobial susceptibility testing (AST) are key to guiding effective therapy.

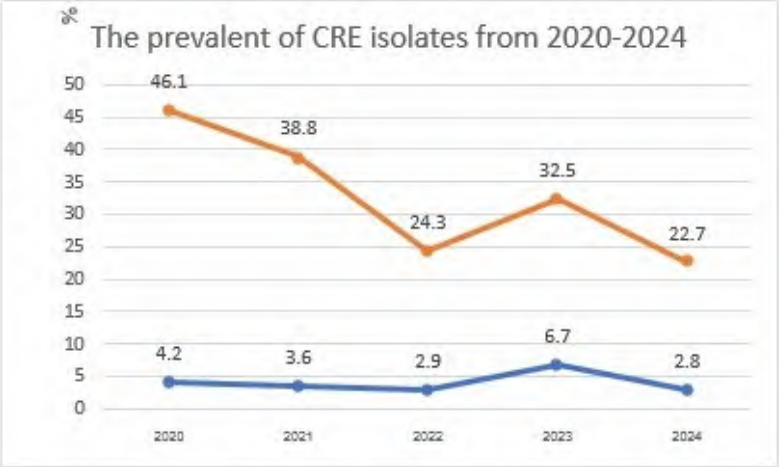
Method
A retrospective study by using laboratory data and multivariate analysis of 14-day mortality risk factors.

Results
The predominant CRE pathogens were Klebsiella pneumoniae (CRE-KP) and Escherichia coli (CRE-EC). In CRE-KP contain OXA-48 (29.0%) and NDM (9.7%), while in CRE-EC contain NDM dominated (41.2%) and OXA-48 (5.9%).

In 2024, susceptibility rates of CRE-KP were: tigecycline 47.6%, colistin 79.1%, and ceftazidime-avibactam (Cef/Avi) 49.1%. CRE-EC: 100% to tigecycline and colistin, and 86% to Cef/Avi. Colistin showed the highest in vitro activity.

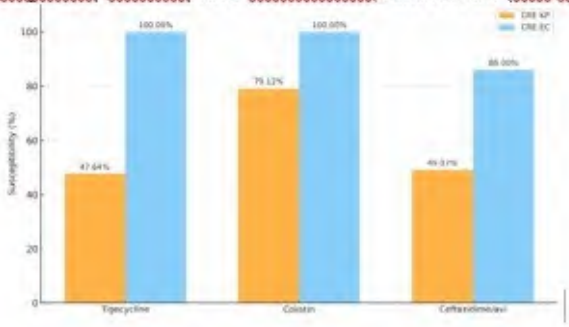
Among 61 patients with CR-GNB bacteremia, those receiving colistin-based therapy had a lower 14-day mortality rate (OR = 2.11; 95% CI; p = 0.057). Early of appropriate empirical antibiotics within 4 hours or adjustment within 48 hours was significantly improved survival rate.

Conclusions
Timely laboratory diagnosis and AST are crucial for managing CRE infections. Local antibiograms to guide empirical threatment, while early appropriate antimicrobial adjustment or novel agents can improve outcomes. Continued surveillance and stewardship are key to CRE threats improvement.



The most common CRE pathogens were Klebsiella pneumoniae (CRE-KP) and Escherichia coli (CRE-EC).

Antimicrobial susceptibility of CRE-KP and CRE-EC isolates in 2024 to Tigecycline, Colistin, and Ceftazidime/Avibactam (Cef/Avi)



- CRE-KP show susceptibility rate:
  - Tigecycline: 47.64%
  - Colistin: 79.12%
  - Cef/Avi: 49.07%
- CRE-EC show susceptibility rate:
  - Tigecycline
  - Colistin: 100%
  - Cef/Avi: 86%

Although Cef/Avi is generally effective against bacteria contain the OXA-48 resistance gene, not NDM, antimicrobial susceptibility testing of CRE-KP revealed a low prevalence of the NDM gene; however, susceptibility to Cef/Avi was observed in less than half of the isolates. While colistin demonstrated high in vitro activity but it is nephrotoxic, and its clinical use remains limited and requires caution.

RES-129: Explainable Machine Learning for Predicting CLABSI in Severe Burn Patients: A 10–Year Time-Series Analysis

Kibum Jeon

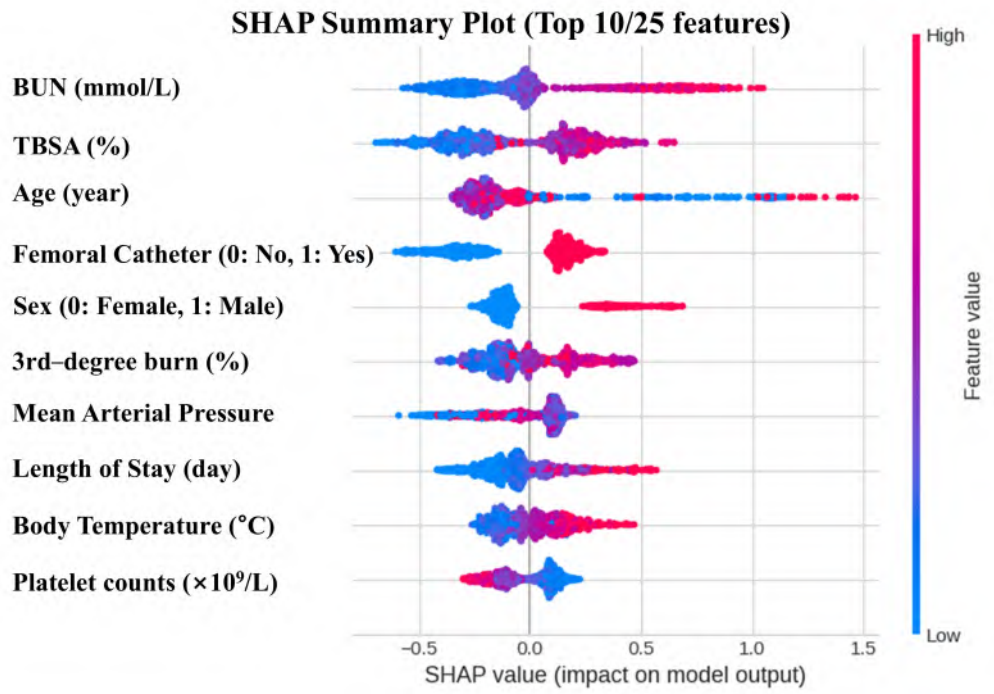
Hallym University

Background
Patients with severe burns are at a high risk for central line–associated bloodstream infections (CLABSI). This study aimed to identify risk factors for CLABSI in severe burn patients using time–series data, analyzed via a machine learning (ML) model with explainable AI (XAI).

Method
This study included patients admitted to the ICU of a Korean burn center from January 2015 to December 2024, undergoing routine central venous catheter (CVC) changes. CVC line–days with microbiologically confirmed CLABSI were defined as “case–days” and others as “control–days.” A total of 73 features, including daily laboratory test, vital signs, demographics, and burn index, were collected. Recursive feature elimination selected key features, and SHAP values ensured ML model interpretability.

Results
Over 10 years, 6,378 line–days from 860 CVCs in 286 patients were were analyzed. The CLABSI rate was 15.99 per 1,000 line–days. The most common pathogens were A.baumanii (35.3%), K.pneumoniae (25.5%), and Candida spp. (17.6%). A model using 25 features showed the best performance, with an AUROC of 0.835 (95% CI: 0.798–0.868). Key risk factors included elevated BUN, longer ICU stay, higher body temperature, greater percentage of total body surface area burned and third–degree burns. Femoral catheterization and male sex were also significant, while age and mean arterial pressure showed non-linear relationships with CLABSI risk.

Conclusions
ML model demonstrated excellent performance, and XAI revealed complex relationships between CLABSI risk and features. Daily laboratory tests and vital signs were critical, showing that integrating time-series data with baseline characteristics enhances predictive accuracy.



RES-130: Evaluating the Diagnostic Value of Absolute Eosinopenia in Culture-Positive Enteric Fever: A Case-Control Study

Kunalsen Jagatdeo, Gyanamitra Panigrahy, Sidharth S. Pattnaik

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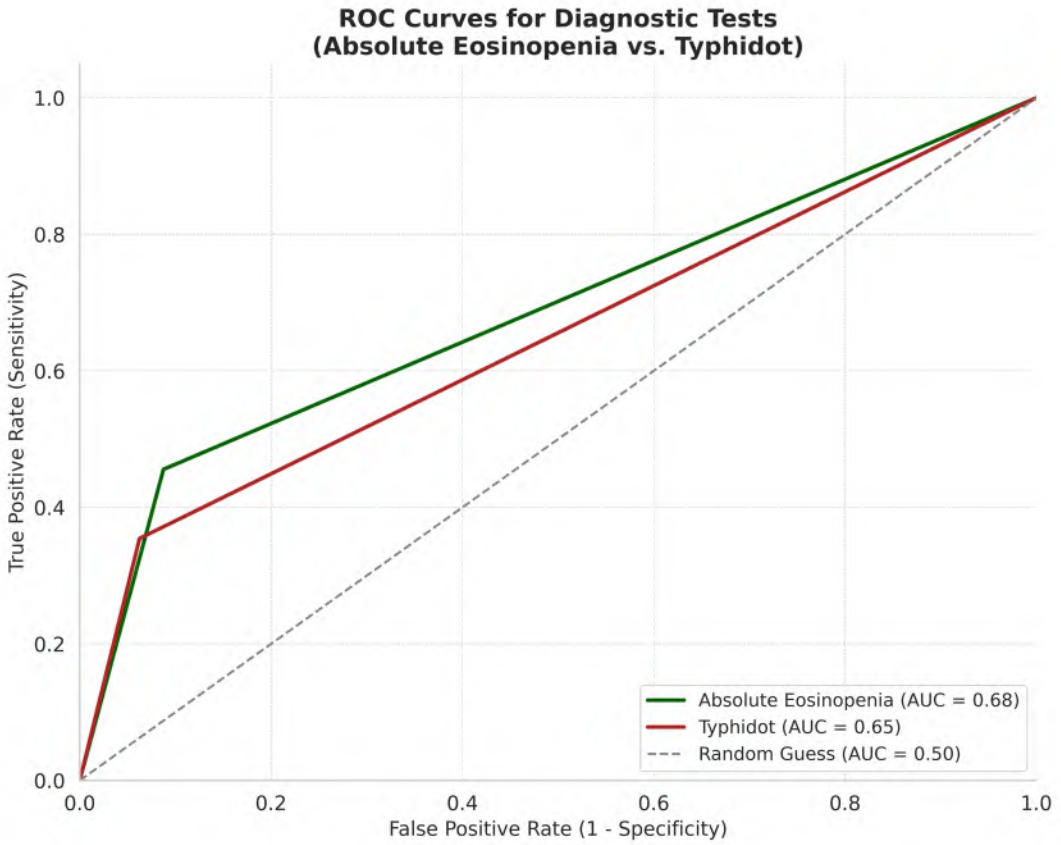
Background
Enteric fever poses a diagnostic challenge in endemic regions due to delayed results of blood cultures and the poor specificity of serological tests. Absolute eosinopenia (AEC = 0 cells/mm³), a simple low-cost haematological marker, may offer early diagnostic utility. So this study was done to evaluate the diagnostic performance of absolute eosinopenia in detecting culture-confirmed enteric fever and compare it with common serological tests.

Method
This case-control study was conducted at a tertiary care teaching hospital in Eastern India between August 2023 and June 2024. Culture-positive patients with Salmonella Typhi or Paratyphi were enrolled as cases, while febrile patients with confirmed non-enteric diagnoses were controls. Data was extracted from electronic health records. A total of 159 patients (79 cases and 80 controls) were included. Sample size was calculated using prior eosinopenia proportions (59% vs. 13%), with α = 0.05 and 80% power. Absolute eosinophil counts were obtained using an automated haematology analyser and diagnostic accuracy was compared to serological testing.

Results
Absolute eosinopenia was observed in 46.8% of enteric fever cases and 8.75% of controls. It showed a sensitivity of 45.6% (95% CI: 34.3-57.3) and a specificity of 91.3% (95% CI: 82.7-96.4), with a positive predictive value of 84.6% and a negative predictive value of 61.6%. The area under the ROC curve for AEC was 0.68 (95% CI: 0.60-0.76), demonstrating moderate diagnostic accuracy.

Conclusions
Absolute eosinopenia demonstrates high specificity and moderate overall diagnostic accuracy for enteric fever. It may serve as a rapid, adjunctive marker to support clinical suspicion in endemic, resource-limited settings.



RES-133: Strategies for Integrating Whole-Genome Sequencing into Antimicrobial Resistance Surveillance

Younggwon On, Eun-Jeong Yoon, Songmee Bae

National Institute of Health, Korea Disease Control and Prevention Agency

Background
Antimicrobial resistance remains a growing concern in global public health, requiring improved strategies for surveillance and response. While conventional methodologies including culture-based susceptibility testing and gene-targeted molecular diagnostics remain central, their limitations in resolution, speed, and scalability pose challenges to effective resistance monitoring.

Method
Whole-genome sequencing (WGS) was reviewed as a complementary approach, enabling high-resolution characterization of resistance determinants, virulence factors, and mobile genetic elements. A WGS-based surveillance framework was proposed based on five analytical domains: pathogen identification, molecular epidemiology, resistance gene detection, virulence profiling, and mobile genetic element analysis. For each domain, key bioinformatics tools were identified and organized into structured workflows applicable to both web-based and locally installed environments.

Results
The proposed framework incorporates widely used tools (e.g., Kraken2, PubMLST, AMRFinderPlus, VirulenceFinder, PlasmidFinder) and highlights their functional advantages and limitations. Web-based tools offer accessibility for resource limited settings, while locally installed pipelines provide flexibility for advanced analyses. The framework emphasizes tool interoperability, update frequency, and suitability for genomic surveillance.

Conclusions
The proposed framework supports practical integration of WGS into antimicrobial resistance surveillance by offering flexible, tool-based workflows tailored to diverse infrastructure levels. Broader application of these tools supported by advances in user interfaces and automation will enhance global capacity for genomic surveillance and antimicrobial resistance control.

RES-134: Construction of a Database for AI-Based Development of Antibiotic Resistance

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National Institute of Health, Korea Disease Control and Prevention Agency

Background
Antimicrobial resistance (AMR) is driven by four major mechanisms, among which drug inactivation plays a key role. Inhibiting this process enables the development of antimicrobial resistance inhibitors targeting drug-inactivating enzymes. Recently, user-friendly Artificial Intelligence (AI)-based simulation platforms for protein-compound docking have facilitated virtual screening of candidate compounds with affinity to target proteins. However, data remain scattered, highlighting the need for a systematic and reliable database.

Method
We collected and curated three categories of data: (i) protein structures and drug-enzyme docking data from the Protein Data Bank (PDB), focusing on carbapenemases and aminoglycoside-modifying enzymes; (ii) chemical information on antimicrobial drugs and resistance inhibitors from PubChem; and (iii) bioactivity data of antimicrobial drugs and resistance inhibitors from ChEMBL. After data curation, a relational database was constructed using MySQL, and entity relationships were visualized using an ER diagram.

Results
For each antimicrobial drug-inactivating enzyme, three tables were generated: drugs, drug-inactivating enzymes, and enzyme inhibitors with associated bioactivity data. The tables were linked using key identifiers: PDB ID and PubChem CID for drugs and drug-inactivating enzymes, and PDB ID and ChEMBL ID for drug-inactivating enzymes and resistance inhibitors. Each table contained 7–19 entries for drugs, 8–25 for drug-inactivating enzymes, and 12–648 for resistance inhibitors.

Conclusions
We established a structured, curated database to support research and development of inhibitors targeting antibiotic-inactivating enzymes, addressing urgent AMR threats. The database is currently being applied in AI-based analyses to identify promising candidate compounds for inhibiting antibiotic resistance.

RES-136: Severe Fever with Thrombocytopenia Syndrome Virus in Bats and Ticks Collected from Bat Habitats

Hye-Ryung Byun[3], Su-Jin Chae4, Seong-Ryeong Ji[3], Jae-Hyoung Jeong[3], Chul-Un Chung[2], Bumseok Kim[1], Hye-Sung Jeong[4], Joon-Seok Chae[3]

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Background
The tick-borne zoonotic infectious disease, severe fever with thrombocytopenia syndrome (SFTS), caused by the SFTS virus (SFTSV), Bandavirus dabieense, was identified in bats and ticks collected from bat habitats in the Republic of Korea.

Method
To investigate the relationship between bats and SFTSV, 1,200 ticks were collected from 12 sites in 6 provinces within 1 km of bat habitats using flagging, and 147 bat sera were collected via cardiac puncture after ether anesthesia between November 2021 and September 2022. Total RNA was extracted from the ticks and bat sera, and nested reverse transcription polymerase chain reaction (RT-PCR) was performed to amplify the S segment of SFTSV. Bat sera were analyzed for IgG antibodies against SFTSV by enzyme-linked immunosorbent assay (ELISA).

Results
Within 1 km of bat habitats, 881 H. longicornis, 209 H. flava, 96 Haemaphysalis spp., and 14 Ixodes (I.) nipponensis were identified. SFTSV was detected in 12.3% (147/1,200) of the ticks. Although no SFTSV RNA was detected in bat sera by nested PCR, 3.4% (5/147) were seropositive by ELISA.

Conclusions
While molecular evidence of SFTSV infection was not observed in bats, a few serological positives suggest possible past exposure. The detection of SFTSV in ticks collected from bat habitats suggests potential ecological interactions involving bats, ticks, and other wildlife species. These findings highlight the importance of considering both wildlife reservoirs and the indirect role of bats in the geographical spread of SFTSV.

RES-137: Metagenomic Profiles of Blood-Fed Ticks in Asian Countries Using Next-Generation Sequencing

Hye-Ryung Byun[5], Mi-Sun Rieu[5], Seong-Ryeong Ji[5], Hyun-Young Nam[5], Chang-Yong Choi[5], Seulgi Seo[5], Bui Khanh Linh[10], Hien Le Thanh[4], Morakot Kaewthamasorn[1], Ana Sahara[7], Remil L. Galay[8], Shang-Lin Wang[3], Tuvshinjargal Erdenechimeg[11], Nyambayar Batbayar[11], Shin Matsui[6], Noritomo Kawaji[2], Muhammad Avais[9], Joon-Seok Chae[5]

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[10]Vietnam National University
[11]Wildlife Science and Conservation Center of Mongolia

Background
The increasing incidence of tick-borne diseases is driven by climate change and advancements in technologies for detecting tick-borne pathogens. Asia, as a hotspot for zoonotic infectious diseases, requires region-wide surveillance efforts to monitor and prevent the spread of these pathogens.

Method
Between 2022 and 2023, 261 blood-fed ticks were collected from wild and domestic animals, birds, and reptiles across nine Asian countries: South Korea, Thailand, Japan, Indonesia, Pakistan, the Philippines, Vietnam, Taiwan, and Mongolia. Ticks from five genera (Amblyomma, Haemaphysalis, Hyalomma, Rhipicephalus, and Ixodes) were included. Pathogen detection was conducted using next-generation sequencing (NGS), targeting DNA/RNA viruses, bacteria (16S rRNA), and protozoa (18S rRNA).

Results
NGS generated 18~30 million clean reads for DNA viruses, 22~32 million for RNA viruses, 134~286 thousand for 16S rRNA, and 147~352 thousand for 18S rRNA. Analysis identified 28 RNA viruses, 13 DNA viruses, 16 bacterial species, and 4 protozoan species. Detected pathogens included zoonotic-related families such as Phenuiviridae, Rickettsiaceae, and Borreliaceae, indicating potential risks for animal-to-human transmission.

Conclusions
This study, involving nine Asian countries, highlights the diversity and distribution of tick-borne pathogens in blood-fed ticks. Strengthening collaborative research across Asia is essential, and our findings underscore the need for expanded regional partnerships to enhance tick-borne disease surveillance. The use of metagenomic NGS enabled the simultaneous detection of a broad range of pathogens, including those with zoonotic and emerging potential.

RES-138: Klebicins as Novel Therapeutics for the Treatment of Infections Caused by Drug-Resistant Klebsiella pneumoniae

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GangaGen Biotechnologies Private Limited

Background
Klebsiella pneumoniae is an urgent clinical concern due to resistance to all antibiotics. To address this challenge, novel target-specific protein antibacterials called Klebicins have been developed, demonstrating potential in treating lung infections caused by this pathogen. These precision-engineered antibacterials offer an effective alternative to conventional antibiotics.

Method
Klebicins were identified through genome analyses, cloned and expressed in E. coli vector, and purified as soluble recombinant proteins. Their antimicrobial activity was assessed in vitro via broth microdilution to determine MICs against a global panel of 444 clinical Klebsiella pneumoniae, including MDR strains. In vivo efficacy was evaluated against seven distinct K. pneumoniae strains in a 24-hour neutropenic mouse lung infection model, where Klebicins were administered intravenously, and reduction in colony-forming unit in the lung was measured.

Results
Three Klebicins namely GAN 002, GAN 010, and GAN 011 exhibited potent antibacterial activity against Klebsiella pneumoniae. Individually, they covered 60%, 65%, and 83% of clinical isolates, respectively. When combined as a cocktail, coverage rose to 95%, with MIC of 12 µg/mL. Importantly, Klebicins demonstrated bactericidal activity against MDR strains without any cross-resistance to existing antibiotic classes. Intravenous administration of Klebicin cocktail was well tolerated and showed significant efficacy in vivo, reducing bacterial load in the lung by ≥1 log in infected mice for all the tested K. pneumoniae strains.

Conclusions
Klebicin cocktail exhibits robust antibacterial activity and efficacy in the mouse lung infection model. These findings support its therapeutic potential as a viable alternative for treating Klebsiella pneumoniae lung infections and countering antimicrobial resistance.

RES-139: Epidemiological & Demographic Trends of Haemophilus Influenzae in Southern Peninsular Malaysia: Data Insights from Tertiary Hospital Network

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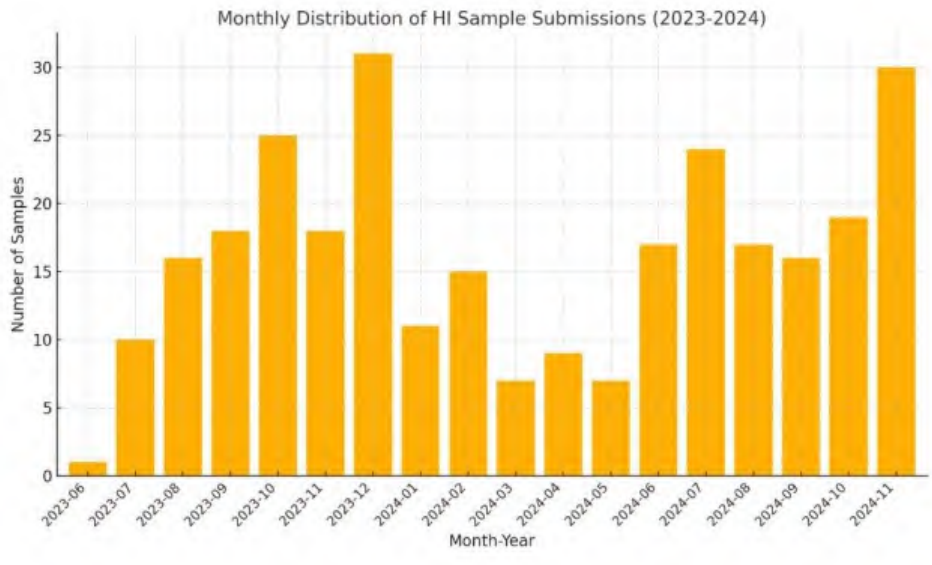
Background
Haemophilus influenzae (HI) is a leading cause of respiratory and invasive infections, with epidemiology shifting following the introduction of the Hib vaccine. The introduction of the Haemophilus influenzae B (Hib) vaccine in Malaysia in year 2002 led to a dramatic decline in Hib-associated diseases. Understanding local trends, especially the rise of non-typeable Haemophilus influenzae (NTHi), is essential for effective public health interventions in Malaysia.

Method
A cross-sectional study was conducted from June 2023 to December 2024 at a tertiary hospital in Johor Bahru and nearby district facilities. All clinical HI isolates were collected and identified using standard laboratory methods and Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrometry (MALDI-TOF-MS). Confirmatory serotyping was performed in the local reference center. Demographics, sample types, and seasonal trends were analyzed using descriptive statistics.

Results
Out of 291 clinical isolates, 96.5% were identified as NTHi. Sputum was the most frequent specimen (56.4%). Infection peaks during monsoon seasons. Infants (<1 year) and the elderly (≥65 years) were the most affected age groups. The majority of cases were Malaysian nationals; however, foreign nationals, though representing 2.1% of cases, had disproportionately higher mortality. Most samples originated from general wards (48.5%) and clinics (37.1%), with fewer from critical care units.

Conclusions
NTHi has emerged as predominant cause of HI infections in Malaysia's southern region following Hib vaccination. Seasonal variation and demographic disparities (elevated risks among infants, elderly, and foreign nationals), highlight the need for targeted public health strategies. Strengthening rural healthcare access and considering vaccine development against NTHi are crucial for reducing disease burden.



RES-142: The Implementation of Antimicrobial Consumption Surveillance and Stewardship in Human Healthcare in Post-Soviet States: A Systematic Review

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Background
Antimicrobial consumption (AMC) surveillance and antimicrobial stewardship (AMS) effectively combat increasing antimicrobial resistance (AMR) rates worldwide. Fifteen post-Soviet countries implemented AMC surveillance and AMS elements with varying success. This systematic review assesses AMC surveillance and AMS implementation across these post-Soviet countries.

Method
We compiled evidence through searches in PubMed, Google Scholar, Embase, CyberLeninka, and Scopus following the Preferred Reporting Items for Systematic reviews and Meta-Analyses (PRISMA) checklist. Eligibility criteria included AMC surveillance and AMS-related papers in human health from specified regions within defined timeframes. Three reviewers evaluated selected papers using the Joanna Briggs Institute (JBI) and Authority, Accuracy, Coverage, Objectivity, Date, Significance (AACODS) appraisal checklists.

Results
We analyzed three peer-reviewed publications and 31 documents. Eleven countries have national action plans for combating AMR with AMC surveillance and AMS implementation as strategic objectives. All 15 countries submitted AMC data to international networks and reported approved laws regulating antibiotic sales. High-income countries demonstrate comprehensive systems for most AMC surveillance and AMS elements, while lower-middle-income countries operate at lower levels (see Figure 1). Unexpectedly, some high-income countries show similar antimicrobial use optimization levels to low-middle income countries. This suggests that political prioritization, healthcare system structures, and historical antibiotic use approaches may equally determine implementation success.

Conclusions
The review demonstrates that income level alone does not guarantee implementation success, and sustained political commitment and long-term strategic planning are critical success factors. Public health authorities must prioritize enforcement mechanisms, digital health technologies for enhancing surveillance, and capacity building through coordinated investment to address regional gaps.

RES-143: Trends in Detection of Candida auris in Urine Cultures in Korea from 2021 to 2024 Using Referral Laboratory Data

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Background
The global detection frequency of Candida auris is increasing. C. auris is a key target for infection control due to its high fatality rate in immunocompromised patients. When cultured from urine, it can lead to invasive infections and spread in healthcare settings. However, there is a lack of epidemiological data on C. auris in Korea. This study examined the detection patterns of C. auris using urine culture data from a reference laboratory.

Method
Urine culture data from 492,417 urine samples from 361,353 patients (32.0% male, 68.0% female) were collected from a total of 2,667 medical institutions across all regions of Korea, submitted to the Seegene Medical Foundation from 2021 to 2024. Urine samples were quantitatively cultured on blood agar and MacConkey agar at 35°C for 24 hours, and colonies exceeding 10^4 CFU/mL were identified using MALDI-TOF MS.

Results
The number of institutions detecting C. auris rose from 1 in 2021 to 1 in 2022, 3 in 2023, and 9 in 2024. Newly identified patients increased annually: 2, 4, 7, and 11, totaling 24 by the study's end. Median age was 79 years (IQR 67–84.5), with more males (16, 66.7%) than females (8, 33.3%) ($p<0.001$, chi-square test). One institution accounted for 15 patients, 62.5% of total cases. Urine samples with C. auris grew from 2 in 2021 to 56 in 2023, then decreased to 21 in 2024.

Conclusions
The increase in C. auris cases from urine cultures in Korea is concerning. Systematic investigations of transmission patterns within individual institutions are necessary.

RES-144: The Isolation Rates of oxacillin-susceptible mecA-positive Staphylococcus aureus at Nagasaki University Hospital in Japan

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Background
Oxacillin-susceptible mecA-positive Staphylococcus aureus (OS-MRSA) has been reported in many countries, but few reports indicate isolation rates. Therefore, we investigated the isolation rates of OS-MRSA at our hospital.

Method
We included 1056 S. aureus strains isolated at Nagasaki University Hospital from 2023 to 2024. The strains with oxacillin ≥4 μg/mL or cefoxitin ≥8 μg/mL were defined as MRSA. The distribution of MIC for oxacillin and cefoxitin was analyzed. PCR was performed to detect the presence of mecA and mecC genes, particularly in MSSA strans with oxacillin MICs ranging from 0.5 to 2 μg/mL.

Results
The distribution of MICs for oxacillin was ≤0.25 μg/mL, 0.5, 1, 2 and ≥4 for 41.1% (434/1056), 25.5% (269/1056), 0.7% (7/1056), 0.2% (2/1056), 32.6% (344/1056). MRSA was 33.1%（350/1056）, and MSSA was 66.9%（706/1056）.

The mecA gene was detected in 1.5% (4/272) of MSSA strains with oxacillin MICs ranging from 0.5 to 2 μg/mL. Of these, three strains indicated oxacillin 0.5 μg/mL and cefoxitin 4 μg/mL, while one strain indicated oxacillin 0.5 μg/mL and cefoxitin ≤ 2 μg/mL. The mecC gene was not detected.

Conclusions
The results of this study showed that frequency of OS-MRSA. The prevalence of mecA gene was investigated only in MSSA strains with oxacillin MICs ranging from 0.5 to 2 μg/mL. The surveillance is needed for all MSSA strains.

RES-145: COVID-19 and Intestinal Parasitic Infections: A Retrospective Analysis from Northern India

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Background
The COVID-19 pandemic has led to a diminished focus on parasitic infections, resulting in a limited understanding of their dynamics and highlighting the need for further investigation to assess the full extent of the impact.

Method
A cross-sectional study at AIIMS Rishikesh was conducted from January 2019 to December 2022. Stool samples were examined for adult worms and wet mounts. The study divided the timeline into pre-COVID, early COVID-19 (ivermectin included), and late COVID (ivermectin withdrawn) pandemic compartments. The overall positivity rate was compared using Chi-square test and Bonferonni adjustment.

Results
A total of 5389 patients with clinically suspected intestinal parasitic infections were included in the study. Most affected age group was 21-40yrs. Positivity rate was higher in Pre-Pandemic (2.78%) vs. Pandemic (1.48%) era. Giardia 46 (45.1%) and Hookworm 20 (19.61%) were the predominant intestinal parasite infections.

During COVID-19, a maximum positivity rate (1.67%) was after the removal of ivermectin from the treatment regime by ICMR as compared to when included in the treatment regime (1.13%).

During the post-ivermectin period, there was an immediate fall in the positivity rate (0.14%) from September to December which was followed by an increase in the positivity rate (2.24%).

Conclusions
Our study showed an effect of ivermectin on giardia, but as it's not the standard treatment, further research is needed to determine if the results were due to the drug itself or to improved sanitation and lifestyle changes during the pandemic.

RES-146: Prevalence Of Methicillin Resistant Staphylococcus aureus (MRSA) Among Asymptomatic Animal Farmers in Agogo and Ejisu-Juaben

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Background
Staphylococcus aureus is a major human pathogen that causes sepsis, skin, and soft tissue infections, and has developed resistance to methicillin and other commonly used antibiotics. Farm activities such as animal handling and stall cleaning increase the risk of exposure to contaminated surfaces. While S. aureus carriage is well-documented, nasal carriage among animal farmers in Ghana requires further investigation. This study aimed to determine the prevalence of S. aureus and its resistance patterns among animal farmers in rural and semi-urban settings.

Method
A cross-sectional study was conducted from December 2022 to June 2023 involving 196 animal farmers from Ejisu-Juaben (semi-urban) and Asante-Akim North (peri-rural) districts in Ghana. Questionnaires were used to capture demographic and occupational data.Nasal swabs were collected and cultured for the identification of S. aureus and Methicillin Resistant Staphylococcus aureus (MRSA) using standard microbiological and biochemical techniques. Antibiotic susceptibility was performed using the Kirby-Bauer disk diffusion method. Polymerase Chain Reaction (PCR) was used to detect the mecA (methicillin-resistance) and Panton Valentine Leukocidin (PVL) (virulence) genes.

Results
The prevalence of S. aureus was 16.8% (33/196), with MRSA being 8.6% (17/196). Semi-urban farmers had a higher MRSA prevalence (14.5%) than rural farmers (5.5%). Cotrimoxazole was the most effective antibiotic while tetracycline was the least. Multi-drug resistance was observed in 27.2% of isolates. The PVL gene was found in 6.1% of S. aureus isolates.

Conclusions
The study reveals notable S. aureus and MRSA carriage among animal farmers, especially in semi-urban areas, emphasizing the need for antimicrobial stewardship to reduce zoonotic and resistance threats.

RES-147: Environmental Contamination from Healthcare Sinks: A Study on Splash Zone

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Hospital Raja Perempuan Zainab II

Background
Sinks have emerged as important reservoirs for multidrug-resistant organisms in hospitals. In 2015 and 2022, major outbreaks of Pseudomonas aeruginosa were detected in critical care units in Kelantan. Investigations traced the pathogen related to sinks located near to patient beds and baby incubators.

Method
A cross-sectional survey was conducted across critical care wards in three major hospitals in Kelantan. The study involved sink mapping, identification of items located within two meters of sinks, and measurement of water splash zones using tracing paper.

Results
Domestic sinks were more commonly found than clinical sinks in critical care areas. Splash zones extending beyond one meter were predominantly associated with domestic sinks, especially those with high-velocity water flow. Clinical sinks with low-velocity taps were associated with significantly smaller splash areas. Items within the splash radius often included medical equipment and patient-care materials.

Conclusions
Sink design and water flow velocity are critical factors influencing splash zone size and risk of contamination. Clinical sinks and low-velocity water taps reduce environmental contamination risks in critical areas. Ideally, items should be placed more than two meters away from sinks. Infection control teams should be actively involved in ward layout and infrastructure planning. Moving forward, water-free models may offer a safer alternative.

RES-149: Multiplex PCR Pneumonia Panel in Critically Ill Patients with Respiratory Failure: A Real-World Experience

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Background
Whilst pneumonia is a leading cause of respiratory failure and intensive care unit (ICU) admission, non-infectious mimics, e.g. autoimmune, malignancy, interstitial lung diseases and cryptogenic organizing pneumonia, are common. Multiplex PCR panels are introduced intended for the diagnosis of pneumonia.

Method
Consecutive patients presenting to 2 district general hospital ICU with respiratory failure received BioFire FilmArray Pneumonia panel (FAPN) (bioMérieux, Marcy-l'Étoile, France) from 1 Oct 2024, in a before-and-after intervention spanning 1 Jan 2024 to 30 Jun 2025. To evaluate real-world performance of FAPN, a consensus panel reviewing clinical, laboratory and radiological information, determined the cause of respiratory failure in post-intervention patients clinically suspected with pneumonia, defined with PF ratio <300mmHg with ≥1 quadrant involvement on CXR. Utility of FAPN in detecting non-infectious mimics was calculated by sensitivity and specificity.

Results
One hundred and sixteen patients were included (pre-intervention 60, post-intervention 56). Among post-intervention patients with suspected pneumonia (n=45), sensitivity and specificity of "negative FAPN and sputum culture" to diagnose mimics were 75% (95%CI: 50-100%) and 91% (95%CI: 81-100%) respectively. In multivariable logistic regression, FAPN was associated with reduced probability of antibiotic escalation (OR 0.70, p<0.01). The PPV of bacterial targets in FAPN was 0-100%, median 35%. For bacteria detected in 10^4CFU/mL, 10^5CFU/mL, 10^6CFU/mL and 10^7CFU/mL by FAPN, 8%, 7%, 48%, and 57% were identified in culture correspondingly.

Conclusions
For patients suspected with pneumonia, "negative FAPN and sputum culture" result should prompt investigation of such non-infectious mimics. FAPN was associated with reduced antibiotics escalation but has low PPV in identifying bacterial targets.

RES-151: Antifungal Activity of Isavuconazole against Candida Species and Filamentous Fungi in a Tertiary Hospital in Hong Kong

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[2]The Chinese University of Hong Kong

Background
Invasive fungal infections are one of the growing global health concerns. Isavuconazole is considered an agent of choice for the treatment of invasive aspergillosis along with voriconazole, but with the advantages of better tolerability and pharmacokinetic profiles than the latter. Antifungal susceptibility data for isavuconazole are sparse in Hong Kong and are urgently needed to guide appropriate antifungal therapy.

Method
A total of 57 archived fungal isolates from clinical samples, including 31 Candida species and 26 filamentous fungi, were included. The Thermo Scientific Sensititre ITAMYUCC Plate was used to determine the minimum inhibitory concentration (MIC) of isavuconazole, along with eight other commonly used antifungal agents. Results were read after 24 and 48 hours for a colorimetric change, with 72-hour results also being read for filamentous fungi.

Results
Isavuconazole exhibited a good in vitro activity against all Candida species isolate, with low MIC of ≤0.008μg/mL to 2μg/mL, and at least 8-fold lower in comparison to fluconazole. Isavuconazole displayed effective in vitro activity against all molds tested, including Aspergillus flavus, Aspergillus niger, Aspergillus fumigatus, and Aspergillus terreus (mode MIC: 0.12μg/mL - 2μg/mL), Scedosporium species, and Purpureocillium lilacinum. A discrepancy was noted between 24- and 48-hour readings in Candida species, with the 48-hour reading showing at least a 2-fold increase in mode MIC for almost all azoles.

Conclusions
Isavuconazole demonstrated good in vitro activity against all Candida, Aspergillus species, Scedosporium species, and Purpureocillium lilacinum indicating it is a possible substitution for traditional azoles administration in Hong Kong.

Table 1 - In vitro susceptibility of fungal organisms using Sensititre YeastOne ITAMYUCC Plate

Antifungals	Fungi		Candida species			Aspergillus species				Non-Aspergillus species
			Candida albicans	*Candida glabrata*	*Other candida species*[#]	*Aspergillus flavus*	*Aspergillus niger*	*Aspergillus fumigatus*	*Aspergillus terreus*	*Scedosporium species*
Amphotericin B	Nº isolates		7	15	9	5	3	1	1	6
	MIC range	24h	0.5-1	0.5-1	0.25-1	1 to 4	≤0.12-2	1	-	-
		48h	0.5-2	1 to 2	1 to 4	4->8	2	2	4	0.5-8
		72h	-	-	-	4->8	2 to 4	2	4	4->8
	ECV (CLSI)	µg/mL	2	2	1 to 2	4	2	0.5	4	-
	ECOFFs WT (EUCAST)	mg/L	-	-	-	≤4	(≤0.5) Tentative	≤1	≤8	-
Anidulafungin	MIC range	24h	≤0.015-0.12	≤0.015-0.12	0.03-1	>8	≤0.015->8	≤0.015	-	-
		48h	≤0.015-0.12	0.03-0.12	0.06-2	>8	>8	>8	≤0.015	1->8
		72h	-	-	-	>8	>8	>8	0.03	>8
	ECV (CLSI)	µg/mL	0.12	0.25	0.12-4	-	-	-	-	-
	ECOFFs WT (EUCAST)	mg/L	-	-	-	ND	ND	ND	ND	-
Caspofungin	MIC range	24h	0.03-0.12	0.06-0.12	0.12-1	>8	≤0.008->8	0.03	-	-
		48h	0.06-0.12	0.06-0.5	0.12-2	>8	>8	>8	≤0.008	0.25->8
		72h	-	-	-	>8	>8	>8	0.06	>8
	ECV (CLSI)	µg/mL	-	-	1	0.5	0.25	0.5	0.12	-
	ECOFFs WT (EUCAST)	mg/L	-	-	-	-	-	-	-	-
Fluconazole	MIC range	24h	0.25-1	2 to 16	0.5-32	128->256	>256	>256	-	-
		48h	0.5-1	8-256	1-128	>256	>256	>256	>256	≤0.12-32
		72h	-	-	-	>256	>256	>256	>256	32-64
	ECV (CLSI)	µg/mL	0.5	8	1 to 2	-	-	-	-	-
	ECOFFs WT (EUCAST)	mg/L		-	-	ND	ND	ND	ND	-
Isavuconazole	MIC range	24h	≤0.008	≤0.008-0.25	≤0.008-0.25	0.25-1	1	0.5	-	-
		48h	≤0.008-0.06	0.25-4	≤0.008-8	0.5-1	1 to 2	0.5	0.25	≤0.008-0.5
		72h	-	-	-	0.5-2	2	0.5	0.5	0.5-8
	ECV (CLSI)	µg/mL	-	-	-	1	4	1	1	-
	ECOFFs WT (EUCAST)	mg/L	-	-	-	≤2	≤4	≤2	≤1	-
Itraconazole	MIC range	24h	≤0.015-0.06	0.12-0.5	0.03-0.25	0.12-0.25	0.5	0.25	-	-
		48h	≤0.015-0.12	0.5->16	0.06->16	0.25	0.5	0.25	0.12	≤0.15-0.5
		72h	-	-	-	0.25-0.5	0.5	0.25	0.12	0.25-1
	ECV (CLSI)	µg/mL	-	4	0.5-1	1	4	1	2	-
	ECOFFs WT (EUCAST)	mg/L	-	-	-	≤1	≤2	≤1	≤0.5	-
Micafungin	MIC range	24h	≤0.008-0.015	≤0.008-0.015	0.03-1	>8	≤0.008->8	≤0.008	-	-
		48h	≤0.008-0.015	0.015	0.03-2	>8	>8	>8	≤0.008	0.12->8
		72h	-	-	-	>8	>8	>8	0.12	>8
	ECV (CLSI)	µg/mL	0.03	0.03	0.06-2	-	-	-	-	-
	ECOFFs WT (EUCAST)	mg/L	-	-	-	ND	ND	ND	ND	-
Posaconazole	MIC range	24h	0.015-0.03	0.12-1	0.015-0.25	0.06-0.25	0.12	0.06	-	-
		48h	0.015-0.06	0.5->8	0.03->8	0.12-0.25	0.12-0.25	0.06	0.06	≤0.008-0.25
		72h	-	-	-	0.25-0.5	0.12-0.25	0.06	0.06	0.25-1
	ECV (CLSI)	µg/mL	0.06	1	0.12-0.5	0.5	2	-	1	-
	ECOFFs WT (EUCAST)	mg/L	-	-	-	≤0.5	≤0.5	≤0.25	≤0.25	-
Voriconazole	MIC range	24h	≤0.008-0.015	0.03-0.5	≤0.008-0.25	0.25-1	0.5-1	0.25	-	-
		48h	≤0.008-0.015	0.25-4	0.015-8	0.5-1	0.5-1	0.25	0.25	≤0.008-0.25
		72h	-	-	-	0.5-2	1	0.5	0.5	0.25-0.5
	ECV (CLSI)	µg/mL	0.03	0.25	0.06-0.25	2	2	1	2	-
	ECOFFs WT (EUCAST)	mg/L	-	-	-	≤2	≤2	≤1	≤2	-

[#]Other candida species: included *Candida parapsilosis, Candida tropicalis, and Candida krusei*

RES-154: Antiviral Effects of Lactococcus lactic Strain Plasma (LC-Plasma) Against Upper Respiratory Tract Infectious Viruses

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Background
Respiratory viruses such as influenza and SARS-CoV-2 enter the body via the upper respiratory tract, sometimes causing severe illness. Despite advances in antiviral drugs and vaccines, effective prevention remains challenging. Probiotics like Lactococcus lactis strain Plasma (LC-Plasma) have been reported to boost antiviral immunity, possibly through activating plasmacytoid dendritic cells (pDCs), although the mechanisms are not fully understood.

Method
In this study, we directly exposed peripheral blood mononuclear cells (PBMCs) collected from healthy subjects without intervention to LC-Plasma, and coexisting influenza A (H1N1) virus, and/or SARS-CoV-2, and conducted immunological analyses to investigate the infection defense mechanisms of LC-Plasma.

Results
Conditioned media from LC-Plasma-stimulated PBMCs (LCP-Sup) inhibited viral replication of both H1N1 and SARS-CoV-2 in a dose-dependent manner. LCP-Sup significantly reduced SARS-CoV-2 viral load in Huh-7 cells. Higher concentrations of LCP-Sup were required to inhibit H1N1 in A549 cells compared to SARS-CoV-2 in Huh-7 cells. LC-Plasma stimulation increased expression of interferon-stimulated genes (ISGs), notably Mx-A. Additionally, LC-Plasma and CpG-DNA induced production of interferon-α (IFN-α) along with various cytokines, chemokines, and growth factors, with LC-Plasma eliciting stronger effects.

Conclusions
These findings confirm that LC-Plasma's antiviral activity involves IFN-α induction and broadly immune cell regulation, contributing to host defense against respiratory viruses.

RES-156: The Immunomodulatory and Antiviral Effects of Lactococcus lactis strain Plasma (LC-Plasma) in Healthy Vietnamese Medical Students During Clinical Placements – a Randomized Placebo-controlled Double-blind Parallel group Study

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[3]Universiti Malaya

Background
The global rise in viral infections, worsened by ecological changes, demands new prevention strategies beyond vaccines and antivirals, which are often compromised by viral mutations. This randomized, double-blind, placebo-controlled trial evaluated the immunomodulatory and antiviral effects of Lactococcus lactis strain Plasma (LC-Plasma) in healthy Vietnamese medical students, who represent healthcare workers (HCWs) at high risk of infection.

Method
Participants received oral LC-Plasma or placebo for four weeks. Clinical symptoms and immune responses from peripheral blood mononuclear cells (PBMCs) were assessed.

Results
The LC-Plasma group had significantly fewer cumulative days with fever and fatigue compared to placebo. Immune analysis showed increased expression of interferon-stimulated genes (ISGs), especially MxA, in the LC-Plasma group. Additionally, adding CpG ODN 2216, a mild TLR9 agonist, enhanced interferon-α (IFN-α) production in LC-Plasma participants with initially low IFN-α responses. Humoral factors from LC-Plasma-primed PBMCs inhibited dengue virus replication in vitro. These results suggest LC-Plasma activates plasmacytoid dendritic cells, boosting IFN-α production and systemic antiviral immunity through ISG upregulation. This enhanced immunity likely contributed to reduced viral symptoms and infection risk.

Conclusions
In summary, LC-Plasma supplementation may be a beneficial adjunct preventive measure to reduce HCWs from the symptoms of viral infections during outbreaks by modulating immune responses.

RES-157: An In-Depth Investigation of Borderline Results in QuantiFERON-TB Gold-Plus Testing

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Konkuk University School of Medicine

Background
The QuantiFERON-TB Gold Plus (QFT-Plus; Qiagen, Hilden, Germany) assay is widely used for latent TB infection (LTBI) screening; however, borderline results often show variability during follow-up. We investigated the longitudinal variability of borderline TB1 and TB2 results throughout the follow-up period.

Method
A total of 770 tests with borderline results (0.2–0.7 IU/mL) in either the TB1 or TB2 tube were retrospectively collected over a five-year period. Agreement and correlation between the initial TB1 and TB2 results were analyzed. Trends, including reversion and conversion, were assessed separately for TB1 and TB2 tubes, as well as for the overall combined results.

Results
Agreement and correlation between initial borderline TB1 and TB2 results were weak and moderate (Cohen's κ = 0.441 [95% CI, 0.401–0.480]; Spearman rank correlation coefficient = 0.640 [95% CI, 0.596–0.680], P <0.001). Variability, including reversion and conversion, was highest in TB2 during the first follow-up (33.8%, 47/139) and decreased with subsequent tests. Result variability was observed in 30.2% (13/43) of individuals with ≥2 follow-up tests, excluding those who received LTBI treatment. Initial borderline results in both TB1 and TB2 tended to show higher rates of reversion and conversion.

Conclusions
Careful interpretation is required for patients with borderline results in both TB1 and TB2. Follow-up testing is recommended, as variability decreases over time.

RES-158: Expansion of Diverse 16S Methyltransferase Mediated Aminoglycoside Resistance in Escherichia Coli From Clinical-Environmental Interface

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Background
Aminoglycosides are important antibiotics that are used as combination therapy. Wastewater and drainage systems, particularly those receiving effluents from hospitals, serve as critical convergence zones for resistant bacteria and resistance genes. Clinical-environmental interfaces support the survival and horizontal gene transfer among diverse microbial communities. Current investigation aimed to characterize acquired 16S methyl transferase genes within isolates from Clinical-Environmental interface.

Method
Total of 121 drainage samples were collected from places near PHCs and tertiary referral hospital of Silchar, Assam. MICs of isolates against aminoglycoside antibiotics and susceptibility pattern towards cephalosporins and carbapenems were determined by disc diffusion method. PCR assay was performed targeting various 16S methyltransferase genes. Horizontal transferability was determined by electroporation method and plasmid incompatibility typing was done for the transformants.

Results
A total of 79 (65.28%) were found to be resistant to atleast one of the aminoglycosides antibiotics viz; gentamicin, tobramycin, amikacin, netilmicin and kanamycin. Among 79 isolates it was observed that 45 (56.96%) were positive for 16S methyltransferase genes, viz; rmtA (n=14), rmtB (n=6), rmtC (n=9), rmtD (n=6), armA (n=4), rmtF (n=3), npmA (n=2), and rmtH (n=1). Majority of the isolates showed susceptibility towards imipenem. All the resistance genes were conjugatively transferable, and incompatibility typing showed multiple 16S methyltransferase genes originated from diverse IncFIA,

Conclusions
The current study was able to highlight the presence of diverse acquired 16S methyl transferases within this locality. The study is a starting point for investigation of transmission dynamics of resistance determinants from clinical to environmental setting and vice-versa.

RES-160: Early Sepsis Screening in Patients with Suspected Sepsis in Emergency Settings: a Sequential Strategy of Monocyte Distribution Width and Presepsin

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Background
Monocyte distribution width (MDW), an US FDA-cleared early sepsis indicator, is intended for use with adults patients presenting to the emergency departments (ED). We evaluated the clinical utility of a sequential measurement of MDW and presepsin (a soluble CD14-subtype) for the early sepsis screening in the ED.

Method
In a total of 281 patients with suspected sepsis, 128 patients (45.6%) were diagnosed as having sepsis based on the Sepsis-3 criteria. Using EDTA-K3 whole blood samples, MDW was measured in the Beckman Coulter DxH 900 analyzer, and presepsin level was measured in the Sysmex HISCL system, with a respective cut-off of 21.5 and 500 pg/mL. MDW, presepsin, and sequential strategies (MDW followed by presepsin) were compared using area under the curves (AUC) of receiver operating characteristic (ROC) curve analyses, diagnostic tests, and Chi-squared tests.

Results
MDW, presepsin, and the sequential strategy were comparable for diagnosing sepsis (AUCs: 0.52 vs. 0.65 vs. 0.52). The sequential strategy increased sensitivity to 98.4%, compared with MDW and presepsin (sensitivities of 90.6% and 89.8%, respectively). The sequential strategy significantly reduced false negative results compared with MDW and presepsin (two [1.6%] for the sequential strategy vs. 12 [9.4%] for MDW vs. 13 [10.2%] for presepsin, P <0.001).

Conclusions
Compared with individual measurement of MDW and presepsin, the sequential strategy of MDW followed by presepsin would improve early sepsis screening in ED patients with significantly reducing false negatives. This strategic approach promises more timely and accurate sepsis screening, potentially improving patient outcomes.

RES-162: In vitro Activity of Zosurabalpin and Comparator Agents Tested Against Acinetobacter baumannii-calcoaceticus Complex (ABC) Isolates from China

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Background
Zosurabalpin (ZAB, RG6006) is a first-in-class, novel tethered macrocyclic peptide that prevents intracellular transport of lipopolysaccharide by inhibition of the LptB2FGC complex. This agent is under clinical development for the treatment of difficult-to-treat ABC infections such as carbapenem-resistant ABC (CRABC). This study evaluated the activity of ZAB against 100 ABC bacterial isolates collected from hospitals in China.

Method
Isolates were collected from documented infections during 2024. Susceptibility testing was performed by the CLSI reference broth microdilution method. ZAB was tested in cation-adjusted Mueller Hinton broth (CAMHB) and CAMHB supplemented with 10% or 20% of heat-inactivated horse serum (HoS). ZAB CAMHB MIC endpoints were determined at substantial reduction (SR) and complete inhibition of growth (100%). CLSI, FDA, and EUCAST breakpoint criteria were applied for comparator agents.

Results
Against 100 ABC isolates, ZAB had potent activity when tested in HoS and CAMHB when reading SR (MIC50/90 values of 0.25/0.5 mg/L). When tested in CAMHB and read at 100%, ZAB MIC50/90 values were 1/>32 mg/L. ZAB inhibited all ABC isolates at ≤1 mg/L (provisional breakpoint) when tested in CAMHB supplemented with HoS. Isolates were resistant to amikacin, imipenem, meropenem, and piperacillin-tazobactam (4-9% susceptible [S; CLSI/EUCAST]. Colistin (94% S [EUCAST]) and cefiderocol (94-99% S [CLSI/FDA]) comparator agents displayed activity against this isolate set.

Conclusions
ZAB demonstrated potent in vitro activity against recent ABC isolates collected from patients in hospitals in China. This agent may represent a potential option for treatment of infections caused by CRABC and further studies are needed to demonstrate its clinical effectiveness.

Table. Activity of zosurabalpin and comparator agents against 100 *Acinetobacter baumannii-calcoaceticus* complex isolates

	mg/L		% Susceptible [a]			
Antimicrobial Agent	MIC_{50}	MIC_{90}	CLSI	EUCAST	FDA	% inhibited at 1 mg/L[b]
Zosurabalpin (10% Serum)	0.25	0.5				100.0
Zosurabalpin (20% Serum)	0.25	0.5				100.0
Zosurabalpin (SR)	0.25	0.5				98.0
Zosurabalpin (100%)	1	>32				57.0
Cefiderocol	0.25	1	99.0		94.0	94.0
Amikacin [d]	>8	>8		9.0 [c]		0.0
Colistin	0.5	1		94.0		93.0
Imipenem	>32	>32	6.0	6.0	6.0	6.0
Meropenem	>32	>32	6.0	6.0 [e]	6.0	6.0
Piperacillin-tazobactam	>128	>128	4.0		4.0	1.0
Tigecycline	2	4				30.0

[a] Criteria as published by CLSI (2024), EUCAST (2024), and US FDA (2024).
[b] Provisional breakpoint for zosurabalpin
[c] For infections originating from the urinary tract. For systemic infections, aminoglycosides must be used in combination with other active therapy.
[d] Amikacin was tested below CLSI and FDA breakpoint criteria
[e] Using meningitis and non-meningitis breakpoints.
Abbreviations: **CLSI**, Clinical and Laboratory Standards Institute; **EUCAST**, European Committee on Antimicrobial Susceptibility Testing; **FDA**, Food and Drug Administration; **HoS**, heat-inactivated horse serum; **MIC**, minimum inhibitory concentration; **SR**, substantial reduction, **US**, United States.

RES-163: Genomic Epidemiology of Carbapenem-Resistant Escherichia coli From Hospitalized Patients from Five Public/Private Hospitals Across India

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Background
This study characterized carbapenem-resistant Escherichia coli (CR E. coli) isolates collected in a multicenter, prospective, observational study conducted in patients being treated for serious bacterial infections (SBI) from five public/private Indian hospitals from March 2023 to July 2024.

Method
Non-duplicate CR E. coli isolates obtained from clinically relevant sites had their whole genome sequenced (WGS) on Illumina platform and annotated using AMRFinderPlus and CARD. We determined multi-locus sequence types (MLST) and antimicrobial resistance genes.

Results
Overall, 37 CR E. coli isolates from complicated urinary tract infection (n=18), acute bacterial skin and skin structure infection (n=3), complicated intra-abdominal infection (n=6), hospital acquired pneumonia (n=6) and blood stream infection (n=5) were characterized. Wide intraspecies diversity was observed, with16 different STs distributed across the five hospitals. Most common STs included the high-risk clonal lineages ST 167 (9/37) and ST410 (6/37). All isolates harboured genes that confer resistance to multiple antibiotic classes. Aminoglycoside resistant genes were found in 23 isolates, with 13 isolates carrying the rmtB 16S RNA methylase gene. Carbapenemase genes were found in 32 isolates, with blaNDM-5 being the most prevalent (24/37), followed by blaOXA-48-like (16/37). All isolates exhibit four amino acid insertion in the PBP3 protein and in the quinolone resistance-determining regions (QRDRs) of the parC and gyrA genes.

Conclusions
High prevalence of genes conferring resistance to multiple classes of antibiotic in CR E. coli resulted in few therapeutic options for the clinical management of these patients. Access to new approved antibiotics with activity against carbapenem-resistant pathogens is critical for this region.

RES-164: Awareness of Antimicrobial Resistance Among Other Occupations when Compared with Healthcare Workers: A Systematic Review

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Background
Research on the prevalence of awareness of antimicrobial resistance (AMR) among various occupational groups compared to healthcare workers in India has emerged as a critical area of inquiry due to the escalating global health threat posed by AMR and its significant impact on morbidity, mortality, and healthcare costs. Since the discovery of antibiotics, misuse and overuse have accelerated resistance development, with India identified as the largest consumer of antibiotics among BRICS nations, exhibiting a 37% increase in per capita usage over the last decade.

Method
Based on the search strategy in PubMed, Google Scholar, Web of Science, Scopus and Embase, we found 1274 articles, out of which 186 were excluded (duplicates). 911 articles were excluded based on title and abstract screening. Subsequent to full text screening we included 67 articles for final data extraction.

Results
Across 40 studies, healthcare workers generally showed higher awareness of antibiotics than laypersons and non-healthcare groups. Awareness was lower among veterinary professionals, farmers, and rural populations often below 50%, but improved with targeted interventions. Pharmacists and community drug dispensers often lacked awareness, leading to inappropriate antibiotic dispensing.

35 studies reported significant knowledge gaps, particularly among nurses, pharmacists, and non-healthcare workers. While doctors and medical students had better knowledge, gaps remained in stewardship and resistance patterns. Misconceptions about antibiotic use and resistance were widespread.

Gaps and Further research priorities given in the table.

Conclusions
Healthcare workers show better AMR awareness than others, though gaps persist. Non-health groups, especially in rural areas, exhibit low awareness and widespread misconceptions.

Gap Area	Description	Future Research Directions	Research Priority	Occupational Groups Involved (Study Type Coverage)
Knowledge-Practice Gap in Healthcare Workers	Healthcare workers show high awareness but poor practice compliance	Longitudinal intervention studies to assess stewardship and behavior change	**High**	**Doctors**: 7 QS, 3 QI, 1 IS, 6 KAP **Nurses**: 5 QS, 2 QI, 1 IS, 4 KAP
Limited Awareness in Non-Healthcare Groups	Farmers, laypersons, and community pharmacists have low awareness and misconceptions	Tailored education programs with rural and semi-urban focus	**High**	**Laypersons**: 2 QS, 1 QI, 2 KAP **Agricultural/ Environmental Workers**: 1 QS, 1 QI, 1 KAP
Pharmacists' Role Underexplored	OTC antibiotic dispensing, poor awareness, commercial influences	Evaluate training, incentives, and regulatory interventions	**High**	**Pharmacy Staff**: 4 QS, 3 QI, 3 KAP
Informal Healthcare Providers Neglected	Prescribing without proper knowledge, under-researched group	Mixed-methods studies to design inclusive stewardship programs	Medium	**Informal Providers**: Overlaps with Pharmacy Staff data above
Lack of Standardized KAP Tools	Heterogeneous tools limit data comparability	Develop and validate culturally adapted KAP instruments	Medium	Applicable across all groups mentioned
Poor Long-Term Impact Evaluation	Few studies assess sustainability of interventions	Longitudinal follow-up studies to measure behavior change	Medium	Present only for Doctors and Nurses
Occupational Exposure Factors Underexplored	Influence of exposure and training on AMR practices is unclear	Assess how job roles shape risk perception and practice	Medium	**Veterinary, support staff** (included in Environmental Workers)
Socioeconomic & Cultural Barriers	Cultural norms and low education affect behavior but rarely addressed	Context-sensitive intervention frameworks through mixed methods	**High**	Predominantly affects **laypersons, informal providers, rural groups**
Rural/Semi-Urban Gaps	Lower awareness and poor practices; underserved in research	Community-based participatory research and tailored campaigns	**High**	**Laypersons, Agricultural Workers**
Policy Implementation Evaluation Lacking	Stewardship policies are poorly evaluated and inconsistently applied	Implementation science to assess adoption and impact	**High**	Cross-cutting; applies to **all groups**

Abbreviations: QS – Quantitative Survey, QI – Qualitative Interview, IS – Intervention Study, KAP – Knowledge, Attitude, Practice Assessment

RES-165: Prevalence of ESBL-producing Gram-negative Bacteria in Residents of a Long-term-care Health Facility in Japan

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Background
The prevalence of extended-spectrum β-lactamase (ESBL)-producing gram-negative bacteria has been increasing in medical institutions in Japan. However, the extent of ESBL-producing gram-negative bacteria colonization in elderly long-term care (LTC) facility residents remains largely unknown. This study investigated the carriage rate of ESBL-producers in elderly residents of a LTC facility in Japan.

Method
Between May 2024 to March 2025, used disposable diapers and urine were collected from non-symptomatic elderly, LTC residents. Bacterial isolates were identified using conventional urine culture methodology. Antimicrobial susceptibility testing was performed by CLSI agar dilution method. The CLSI disk test was used to detect ESBL production of an isolate. Clonal relatedness was analyzed by PFGE and ESBL genotyping by PCR.

Results
Of the 332 isolates from 127 residents, 191 were Enterobacterales isolates with the following distribution: 102 (53.4%) Escherichia coli isolates, with 49 (48.0%) ESBL-producers; 36 (35.3%) Klebsiella pneumoniae isolates, with 8 (22.2%) ESBL-producers; and 34 (33.3%) Proteus mirabilis isolates with no ESBL-producers. Of the 49 ESBL-producing E. coli isolates, 41 (87.3%) showed resistance to fluoroquinolones. CTX-M9 group was the most prevalent CTX-M group gene in ESBL-producing E. coli.

Conclusions
A high carriage rate of ESBL-producers was observed. A significant proportion of ESBL-producing E. coli were fluoroquinolone resistant highlighting the importance of infection control measures and affecting antimicrobial treatment strategies.

RES-167: Intensive Care Patient Outcomes of Multidrug-Resistant Ventilator-Associated Pneumonia: A Single Center Retrospective Cohort Study

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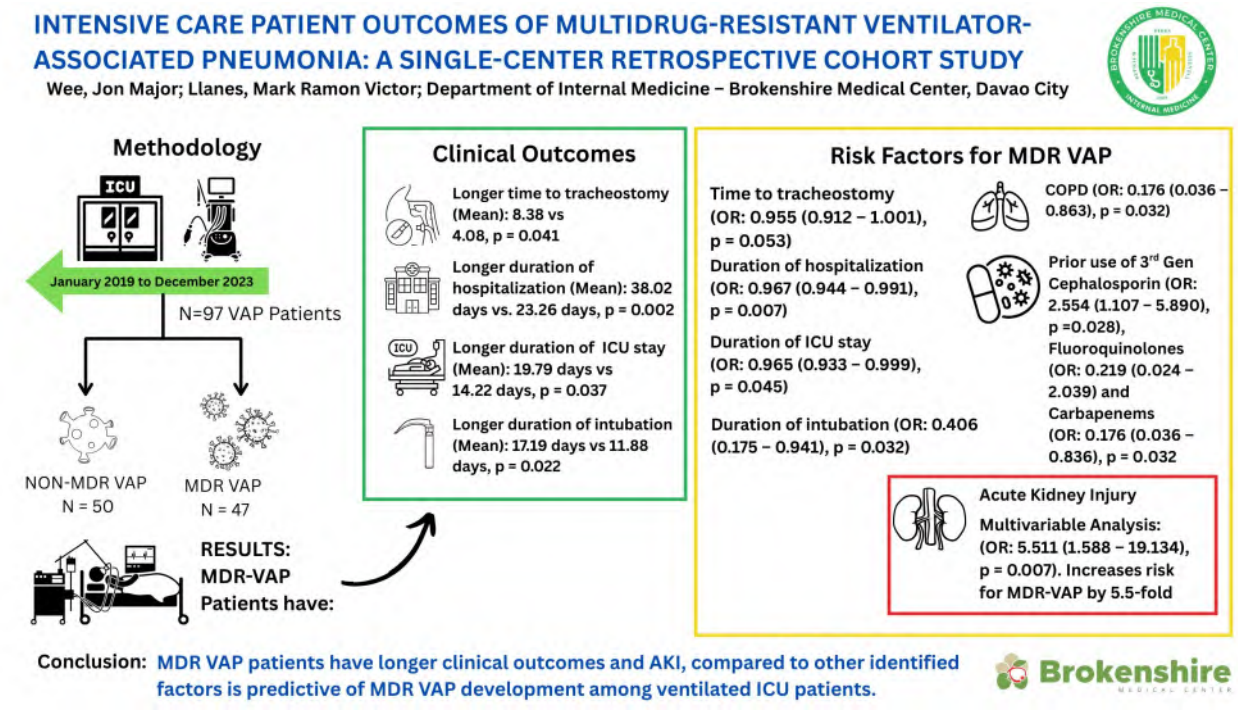
Background
In the Philippines, current literature has amply documented the risk factors of MDR-VAP patients. Also, no known local papers studied their correlation with hospital outcomes.

Method
Our study is a retrospective single-center cohort study that included VAP Patients in the ICU at Brokenshire Medical Center from January 2019 to December 2023. We compared the outcomes of MDR and Non-MDR VAP patients in terms of clinical characteristics and in-hospital outcomes, and determined significant risk factors for DR-VAP.

Results
97 patients were included in the study. 47 were classified as MDR-VAP, and the remaining 50 patients were Non-MDR VAP. MDR-VAP patients had longer time before tracheostomy insertion, stayed longer in the hospital, had longer ICU stay, and had longer intubation days compared to Non-MDR VAP patients. Risk factors for MDR-VAP include: COPD (OR: 0.176 (0.036 – 0.863), p = 0.032), Presence of Acute Kidney Injury (OR: 3.120 (1.293–7.529), p-value= 0.011), Time to tracheostomy (OR: 0.955 (0.912 – 1.001), p-value=0.053), the Duration of Hospitalization (OR: 0.967 (0.944 – 0.991), p-value=0.007), Duration of ICU Stay (OR: 0.965 (0.933 – 0.999), p-value= 0.045), Duration of Intubation (OR: 0.406 (0.175 – 0.941), p-value= 0.032), the use of third-generation Cephalosporins (OR: 2.554 (1.107 – 5.890), p-value=0.028), Fluoroquinolones (OR: 0.219 (0.024 – 2.039), p-value= 0.182), and Carbapenems use before MDR-VAP (OR: 0.176 (0.036 – 0.836), p-value 0.032). Multivariable analysis shows AKI (OR: 5.511 (1.588 – 19.134), p-value= 0.007) is predictive of MDR-VAP.

Conclusions
MDR VAP has longer clinical outcomes, and AKI is predictive of MDR VAP development in ventilated ICU patients.



RES-168: Propagation of blaIMP Within IncHI1 in Escherichia Coli from a Tertiary Referral Hospital of India

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Background
A significant issue facing the world today is beta-lactam antibiotic resistance. Multidrug resistant organisms, particularly pathogens that harbor beta-lactamases, pose a significant threat to global public health, leading to increased rates of morbidity and mortality. Imipenemase, also known as IMP-type metallo-β-lactamase (MBL), was first identified in Japan in the 1990s and since then has gained increased reporting, particularly in Asia. The current study characterizes the presence of blaIMP producing Escherichia coli of multidrug resistant phenotype.

Method
70 clinical isolates were subjected to susceptibility testing against different and the antibiotic susceptibility test results were interpreted as per CLSI, 2024 guidelines. The isolates were then screened to check the presence of blaIMP gene by PCR assay. blaIMP positive isolates were further checked for horizontal gene transferability by transformation and the plasmid incompatibility typing of the transformant was also performed to check the incompatibility typing associated with the carriage of blaIMP gene.

Results
PCR assay revealed that five (5) multidrug resistant Escherichia coli isolates were found harboring the blaIMP gene. The blaIMP positive isolates were horizontally transferred by transformation in the 0.25µg/mL Imipenem stress plates and the plasmid isolation was done for the transformants to check the plasmid incompatibility typing. The IncHI1 plasmid was identified with the carriage of blaIMP gene for all the isolates.

Conclusions
The study highlighted the occurrence of blaIMP producing Escherichia coli and IncHI1 type plasmid have the potential to be the primary vector facilitating the spread of the blaIMP genes within a single study centre in India.

RES-169: Expansion of Multiple Virulence Determinants Harboring Escherichia Coli Within a Clinical Setting of North-East India

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Background
An evolutionary route to pathogenicity is considered to be provided by the acquisition of virulence genes. Presence of specific virulence gene combinations in Escherichia coli is linked to various infections. One major public health concern is the presence of pathogenic Escherichia coli in the clinical settings as they are the most common organism causing nosocomial infections. Therefore, this study aimed at investigating the occurrence of different virulence determinants harboring Escherichia coli isolates in a tertiary referral hospital in the North-Eastern part of India.

Method
In this study, a total of 61 clinical Escherichia coli isolates were obtained from Silchar Medical College and Hospital, Silchar that were received for routine culture and sensitivity testing. The isolates were subjected to PCR for 12 different types of Escherichia coli virulence genes. Antibiogram profiling of the isolates was determined by Kirby-Bauer disc diffusion method. Furthermore, clonal analysis by enterobacterial repetitive intergenic consensus (ERIC) PCR was performed.

Results
Out of the tested 61 Escherichia coli isolates, 25 isolates were harboring different virulence genes. Seven different types of virulence genes namely chuA, arpA, yjaA, iutA, fyuA, fimH and papC were detected within the tested clinical Escherichia coli. Highest resistance pattern against Ampicillin followed by Imipenem and Ceftriaxone were observed. ERIC PCR revealed sixteen different haplotypes of Escherichia coli.

Conclusions
This study revealed the presence of multidrug-resistant, multiple virulence gene harboring Escherichia coli isolates highlighting the risk of dissemination of these virulence determinants causing a grave concern for infection control and prevention in the clinical settings.

RES-170: Ear Canal Carriage of Staphylococcus aureus Associated with Earphone Usage in Healthcare Workers

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Background
Remote work increased in healthcare workers during and after the COVID-19 pandemic. As earphones adhere closely to the ear canal, there is concern that increased humidity and temperature increases bacterial growth. Ear canal carriage of Staphylococcus aureus in healthcare workers using earphones was studied to determine the association between S. aureus carriage and duration of earphone use.

Method
Between August 2022 to August 2024, ear canals and earphones of healthcare workers were swabbed. Samples were cultured on mannitol salt agar to determine the presence of S. aureus. Duration of earphone usage per day over the past 7 days was recorded.

Results
S. aureus was detected in 20 (34%) of 59 subjects, of which 10 isolates were detected only in the ear canal, 5 in the earphone only, and 5 in both the ear canal and earphone. Sccmec type Ⅳ MRSA was isolated from 2 ear canal samples. The remaining isolates were MSSA. The average duration of earphones usage was 8.0 hours per day in the 20 S. aureus positive subjects compared to 5.8 hours per day in the 39 S. aureus negative subjects. Of the 43 samples collected from earphone users, S. aureus was detected in 19 (44%) subjects using earphones prior to sample collection, but only in 1 (6%) of the 16 subjects not using earphones.

Conclusions
Earphone usage duration was longer when S. aureus was detected in the ear canal. Prolonged use of earphones can increase ear canal carriage leading to potential spread to the healthcare environment.

RES-171: Real-World Usage, Efficacy, and Microbiological Features of Ceftazidime-Avibactam in Clinical Practice in China

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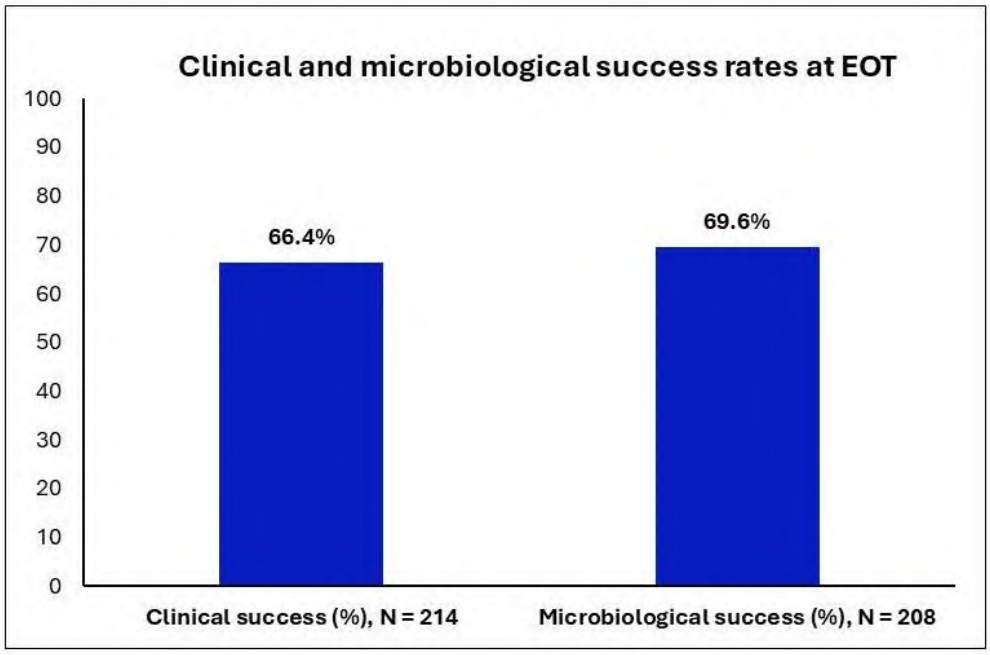
Background
Ceftazidime-avibactam has been increasingly used in treating infections caused by multidrug-resistant (MDR) bacteria. This study was conducted to characterize the real-world usage of ceftazidime-avibactam in China.

Method
This multicenter prospective observational study enrolled hospitalized patients who received ≥1 dose of ceftazidime-avibactam. Clinical and microbiological outcomes were evaluated among patients with ≥72 hours of treatment at end of treatment (EOT).

Results
Of the 220 adult patients enrolled, the mean age was 62.4 (±16.73) years. The most common ceftazidime-avibactam indications were pneumonia (64.5%), followed by complicated intra abdominal infection (16.8%) and bloodstream infection (7.3%). Overall, 227 pathogens were isolated, wherein 95 were delivered and analyzed at the central laboratory. K. pneumoniae (129 isolates, 56.8%) was the most identified pathogen, followed by P. aeruginosa (33 isolates, 14.5%). Among 116 K. pneumoniae isolates tested, 101 (87.1%) were resistant to meropenem; among 25 P. aeruginosa isolates tested, 18 (72.0%) were resistant. 51 out of 52 carbapenemase-producing K. pneumoniae isolates carried Serine-β-lactamase gene (one remained undetermined), and 6 of them co-harbored Metallo-β-lactamase genes. 75% of patients received definitive therapy of ceftazidime-avibactam, while 25% received empiric therapy. Overall, 214 patients with ≥72 hours of ceftazidime-avibactam were included in the clinically evaluable analysis set. The average duration of ceftazidime-avibactam use was 13.7 days. The all-cause in-hospital mortality was 9.8%. At EOT, clinical and microbiological success was achieved in 66.4% and 69.6% of patients, respectively (Figure).

Conclusions
This study provides valuable data on real-world usage of ceftazidime-avibactam in China, highlighting its role as an effective treatment for MDR pathogens.

Figure: Clinical success rate (clinically evaluable analysis set, N = 214) and microbiological success rate (microbiologically evaluable analysis set, N = 208) at EOT



EOT = End of treatment.
The clinically evaluable (CE) analysis set included all patients with at least 72 hours use of ceftazidime-avibactam and at least 1 non-missing clinical evaluation outcome.
The microbiologically evaluable (ME) analysis set included all patients with at least 72 hours use of ceftazidime-avibactam and at least 1 non-missing microbiological evaluation outcome.

RES-172: Drainpipe Thermal Disinfection Unit: A Practical Solution for Controlling Bacterial Contamination in Existing Sink Plumbing Systems

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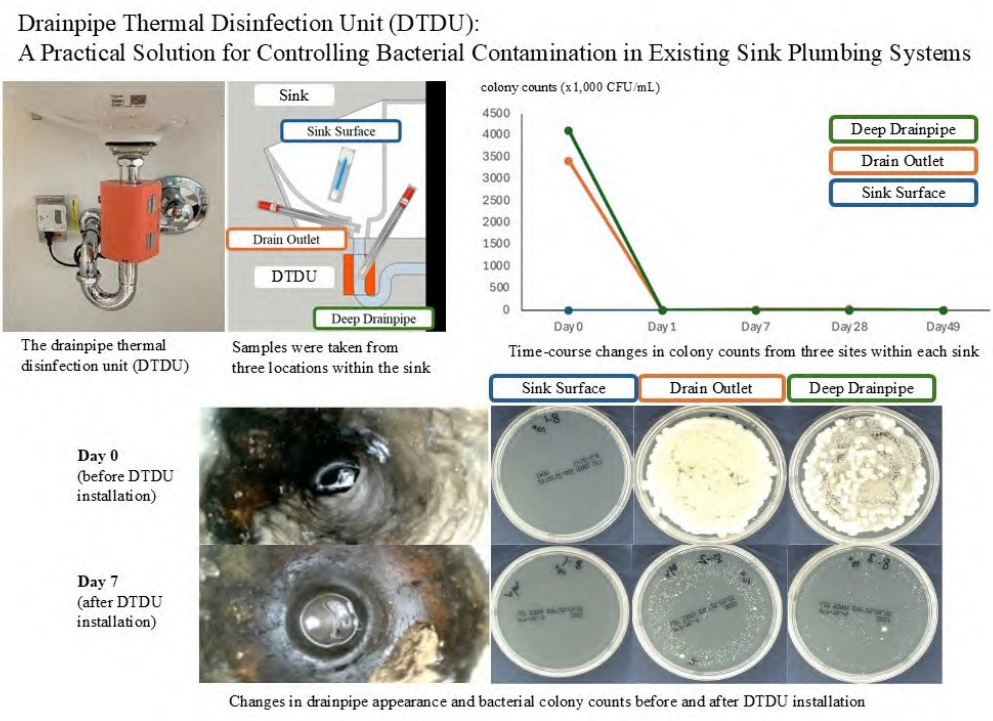
4Nagoya University Hospital

Background
Sink environments in healthcare settings serve as reservoirs and transmission sources for pathogens, including multidrug-resistant organisms. Bacteria in inner drainpipes migrate upward to the sink outlet, and splashes during handwashing contaminate surrounding areas or workers. This study evaluated the effectiveness of a Drainpipe Thermal Disinfection Unit (DTDU) in controlling bacterial contamination in sink plumbing without replacing existing pipes.

Method
DTDUs were installed on three sinks in the surgical ICU of a university hospital in Japan. Each unit was programed to heat the pipes to ≥100°C for 40 minutes every 6 hours. Samples were collected on Days 0, 1, 7, 28, and beyond. A fiberscope was used to observe the inner pipe surfaces. Swabs from the sink surface, outlet, and deep drainpipe were cultured at 37°C overnight. Bacterial species were identified, and colony counts were performed. Metagenomic analyses were performed as well. The sinks remained in routine clinical use and were cleaned daily with ethanol wipes.

Results
At baseline, Enterobacterales and glucose-non-fermenting Gram-negative rods were detected in the inner drainpipes. The bacterial load on sink surfaces was low, and the DTDU reduced colony counts in drainpipes by more than 99.9% within one week. Indeed, intraluminal structures, including microbial biofilms and trace metals, were visibly detached. No bacterial regrowth, leakage, or damage to the drainpipes occurred during long-term use.

Conclusions
DTDU installation significantly reduced bacterial colonization in existing drainpipes and demonstrated sustained antimicrobial effects. This engineering-based intervention represents a practical and effective measure for controlling microbial reservoirs in the sink environment.



RES-173: Methicillin-resistant Staphylococcus aureus Occurrence on Mobile Phones: Knowledge, Attitudes, Practices, and Its Transmission Among Healthcare Interns in Dumaguete City

Francine Marianne Caseres, Kemrick Tiu, Gian Deihl Oril, Maria Christine Gillana, Maired Baguinaon, Jamie Mariell Esquilla, Gin Paul Flores, Bdelle Flev Fajardo, Merah Franz Gutib, Mariella Felisse Cubero, Dominique Alojado

Silliman University

Background
The methicillin-resistant strain of Staphylococcus aureus (mrsa), is found on skin, mucous membranes, and frequently touched surfaces like mobile phones, which are vital in both communication and disease research. Due to this, investigating the link between mrsa and mobile phones is important due to their role in disease transmission.

Method
Using a descriptive correlational-comparative design, the study explored the mrsa contamination on mobile phones of 124 healthcare interns from Silliman University's Institute of Clinical Laboratory Sciences, Institute of Rehabilitative Sciences, College of Nursing, and School of Medicine. Data collection was through unannounced mobile phone swabbing and a Knowledge, Attitudes, and Practices (kap) questionnaire, ensuring data confidentiality and all procedures following guidelines.

Results
Results showed that Physical Therapy interns had the highest mrsa contamination (46.7%). Additionally, despite high overall kap scores—Medicine led in knowledge, Nursing in attitude, and Medical Technology in practice—one in six phones still tested positive for mrsa (16.9%). Despite this, infection control practices did not significantly influence mrsa occurrence on mobile phones, as revealed by Point-Biserial analysis. Furthermore, while no significant difference in knowledge was found among students from different health courses ($p = .184$) through Kruskal-Wallis and One-Way Anova tests, there were significant differences in attitude ($p = .46$) and practice scores ($p = .32$).

Conclusions
Thus, interns' attitudes and practices vary depending on their courses even when they generally possess consistent knowledge about mrsa. Despite strong awareness and good practices, the persistence of mrsa contamination emphasizes the need for more effective institutional hygiene protocols.

RES-174: Prevalence and Distribution of Multidrug-Resistant Organisms in Selected Units of a Tertiary Care Centre in South India: A Cross-Sectional Study

Arya Shaji Kumar, Meera Susan John, Shreya H.

Amrita Institute of Medical Sciences & Research Centre

Background
Multidrug-resistant organisms (MDROs), including CRE, CRAB, CRPA, MRSA, and VRE, are major contributors to healthcare-associated infections, especially in high-risk settings such as intensive care units. These organisms are linked with increased morbidity, limited treatment choices, and prolonged hospitalizations. This study was undertaken to determine the prevalence and distribution of MDROs in critical care units and their corresponding wards at a tertiary care centre in South India. It forms part of an ICMR-funded extramural project on antimicrobial resistance surveillance.

Method
A prospective cross-sectional study was conducted at Amrita Institute of Medical Sciences, Kochi, between October 2023 and March 2025. Clinical culture data from selected specimens (blood, urine, respiratory samples, tissue, and pus/abscess) were collected from two surgical ICUs, one medical ICU, and their respective wards. MDROs, including CRE, CRAB, CRPA, MRSA, and VRE, were identified based on final microbiology reports and analyzed by sample type and source (ICU vs ward).

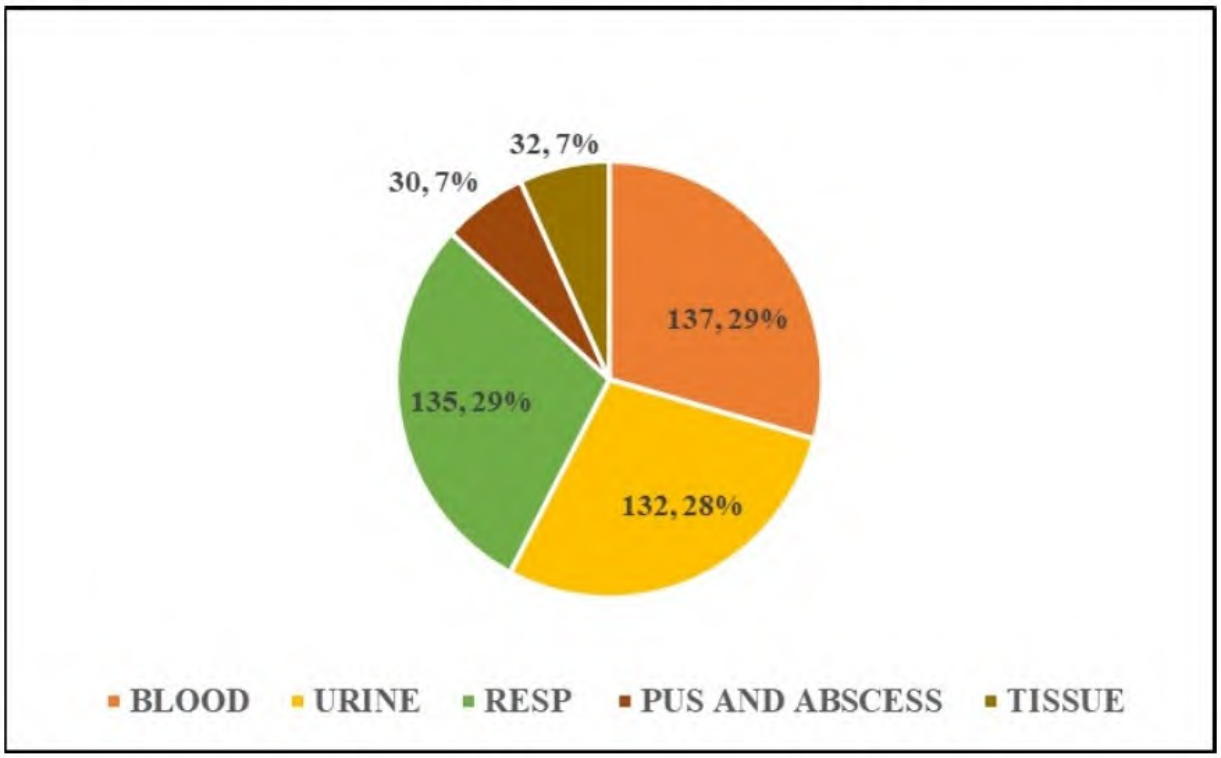
Results
Of 7,682 samples processed, 2,065 (26.88%) showed growth. Among 466 carbapenem-resistant isolates, Klebsiella pneumoniae (53%) predominated, followed by E. coli (18.66%), Acinetobacter baumannii (13.7%), and Pseudomonas aeruginosa (12%). Of 54 S. aureus isolates, 46.29% were MRSA; of 81 Enterococcus spp., 2.22% were VRE. Blood samples showed the highest carbapenem resistance. Most resistant isolates (74.2%) were from ICUs.

Conclusions
The study highlights a significant MDRO burden in ICUs, stressing the need for sustained surveillance, antimicrobial stewardship, and infection control measures to improve patient outcomes.

Table 1: Prevalence of Carbapenem-Resistant and Other Multidrug-Resistant Organisms Across Selected ICUs and Wards

Distribution of Multidrug-Resistant Organisms		
Category	**Total**	**Percentage (%)**
Total Carbapenem Resistant isolates	466	22.5
CRE (E coli, Klebsiella pneumoniae, Serratia, Citrobacter, Enterobacter)	346	74.24
CRAB	64	13.7
CRPA	56	12
MRSA	25	46.29
VRE	18	22.22
Distribution of Carbapenem-Resistant Isolates by Unit and Specimen Type		
Specimen Type	**ICU(n,%)**	**Ward(n,%)**
Total CR isolates	**346 (74.24%)**	**120 (25.75%)**
Blood	120 (34.68%)	17 (14.16%)
Urine	77 (22.25%)	55 (45.83%)
Respiratory	112 (32.36%)	23 (19.16%)
Pus and abscess	18 (5.2%)	12 (10%)
Tissue	19 (5.49%)	13 (10.83%)
MRSA Distribution by Unit and Specimen Type		
Total MRSA isolates	**15 (60%)**	**10(40%)**
Blood	5 (33.33%)	1 (10%)
Urine	2 (13.33%)	0 (0%)
Respiratory	6 (40%)	1 (10%)
Pus and abscess	2 (13.33%)	5 (50%)
Tissue	0 (0%)	3 (30%)
VRE Distribution by Unit and Specimen Type		
Total VRE isolates	**13(72.2%)**	**5(27.77%)**
Blood	7 (53.84%)	2 (40%)
Urine	5 (38.46%)	3 (60%)
Respiratory	0 (0%)	0 (0%)
Pus and abscess	1 (7.69%)	0 (0%)
Tissue	0 (0%)	0 (0%)

Figure 1. Distribution of Carbapenem-Resistant Isolates by Specimen Type



RES-175: Methicillin-Resistant Staphylococcus aureus (MRSA) Bacteremia in a Tertiary Care Hospital in Kerala

Arya Shaji Kumar, Shreya H., Radhika T. K.

Amrita Institute of Medical Sciences & Research Centre

Background
Methicillin-resistant Staphylococcus aureus (MRSA) remains a major contributor to both hospital- and community-acquired infections globally, with substantial impacts on patient morbidity, mortality, and healthcare burden. In India, MRSA prevalence among S. aureus isolates varies by geography and time, but long-term regional data, particularly from Kerala, are limited.

Method
This retrospective observational study was conducted at Amrita Institute of Medical Sciences, Kochi, Kerala. A total of 330 patients with blood culture-confirmed MRSA bacteremia from January 1998 to December 2024 were included. Data on demographics, comorbidities, clinical risk factors, treatments, and outcomes were collected and analyzed using Wilcoxon rank-sum and Pearson's Chi-squared tests in R software (v4.3.0).

Results
MRSA was isolated in 330 cases from 270,000 blood cultures (1.22/1000). Males comprised 73% of patients, with a median age of 51 years. Diabetes (41%), hypertension (34%), and chronic kidney disease (17%) were common comorbidities. Coronary artery disease significantly correlated with mortality ($p = 0.008$). Community-acquired infections accounted for 59% of cases. Key risk factors included prior hospitalization (76%), antibiotic use (62%), and invasive devices (86%). ICU admission occurred in 42%, with 26% requiring prolonged ICU stay. Vancomycin, Linezolid, and Teicoplanin were commonly used. Microbiological cure was achieved in 66%, while overall mortality was 21.8%, with strong associations to sepsis, AKI, and MODS.

Conclusions
This study highlights the persistent burden of MRSA bacteremia in Kerala, with a notable prevalence of community-acquired cases, underscoring the need for sustained surveillance and infection control strategies.

RES-176: Reducing Caesarean Section Surgical Site Infection Rates in a Tertiary Care Hospital in India: A Quality Improvement Initiative

Arya Shaji Kumar, Nimi Mohan, Radhika T. K.

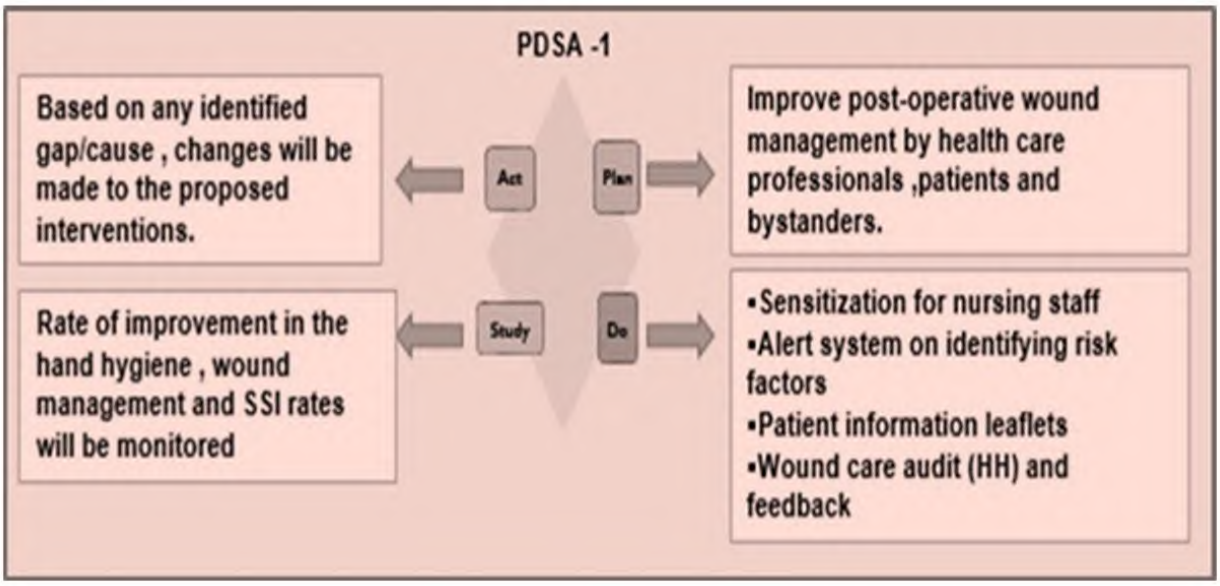
Amrita Institute of Medical Sciences & Research Centre

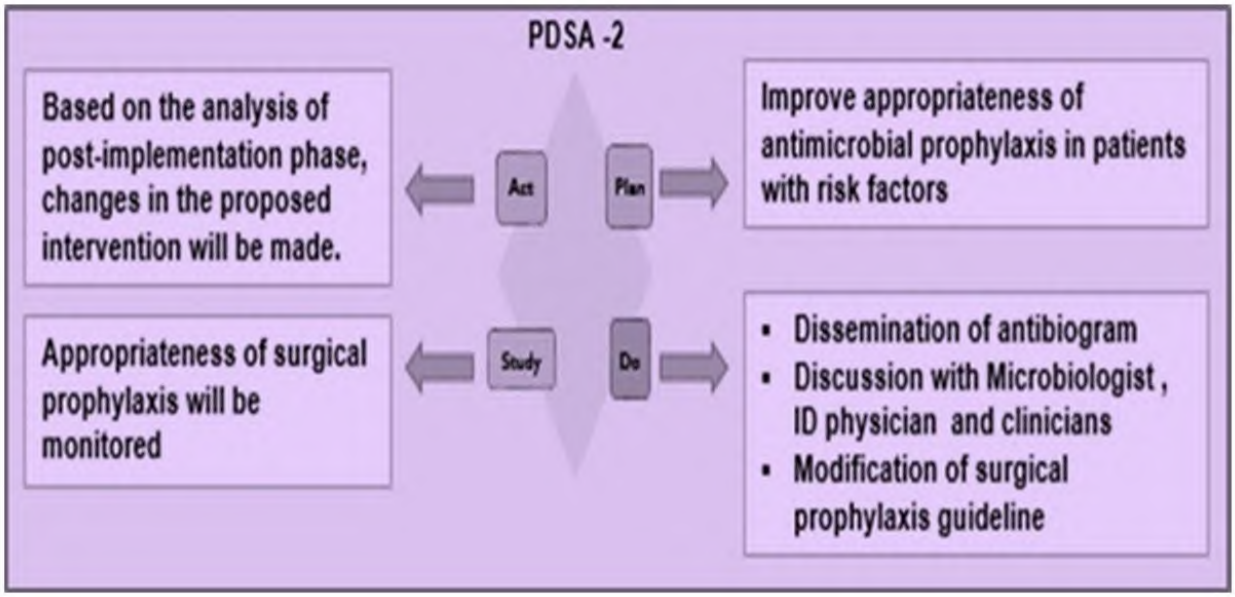
Background
Surgical Site Infections (SSI) are a significant healthcare concern, particularly in patients undergoing clean Lower Segment Caesarean Section (LSCS) surgeries. SSIs can lead to severe complications, extended hospital stays, and increased healthcare costs.

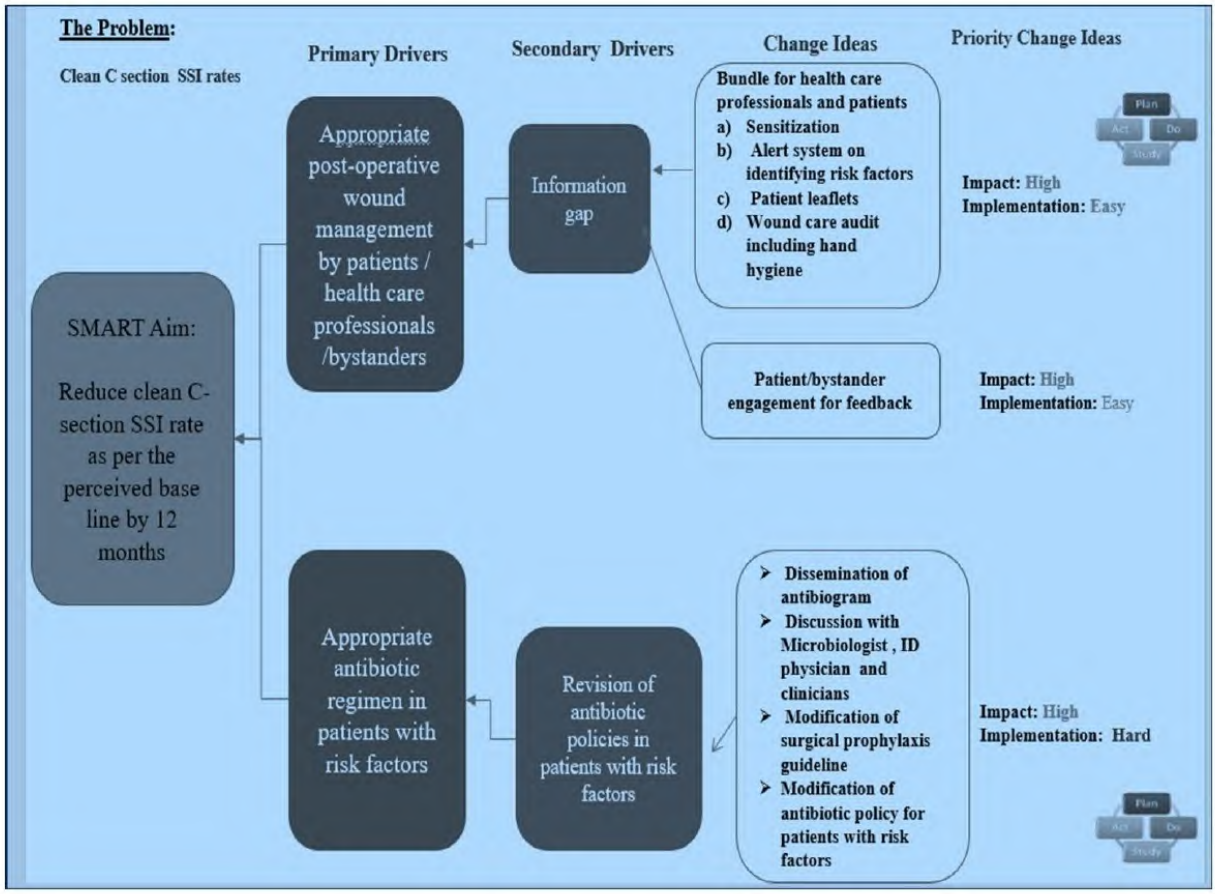
Method
A multidisciplinary quality improvement team utilized the PDSA model to design and implement strategies aimed at reducing SSIs in LSCS surgeries. They designed two quantitative interventions comprising a care bundle for healthcare professionals, bystanders, and patients, as well as interventions for appropriate surgical prophylaxis and antibiotic regimens for patients with risk factors. The key components of this care bundle include sensitization sessions for nursing staff, an alert system for identifying risk factors, patient leaflets, and wound care audits focusing on hand hygiene.

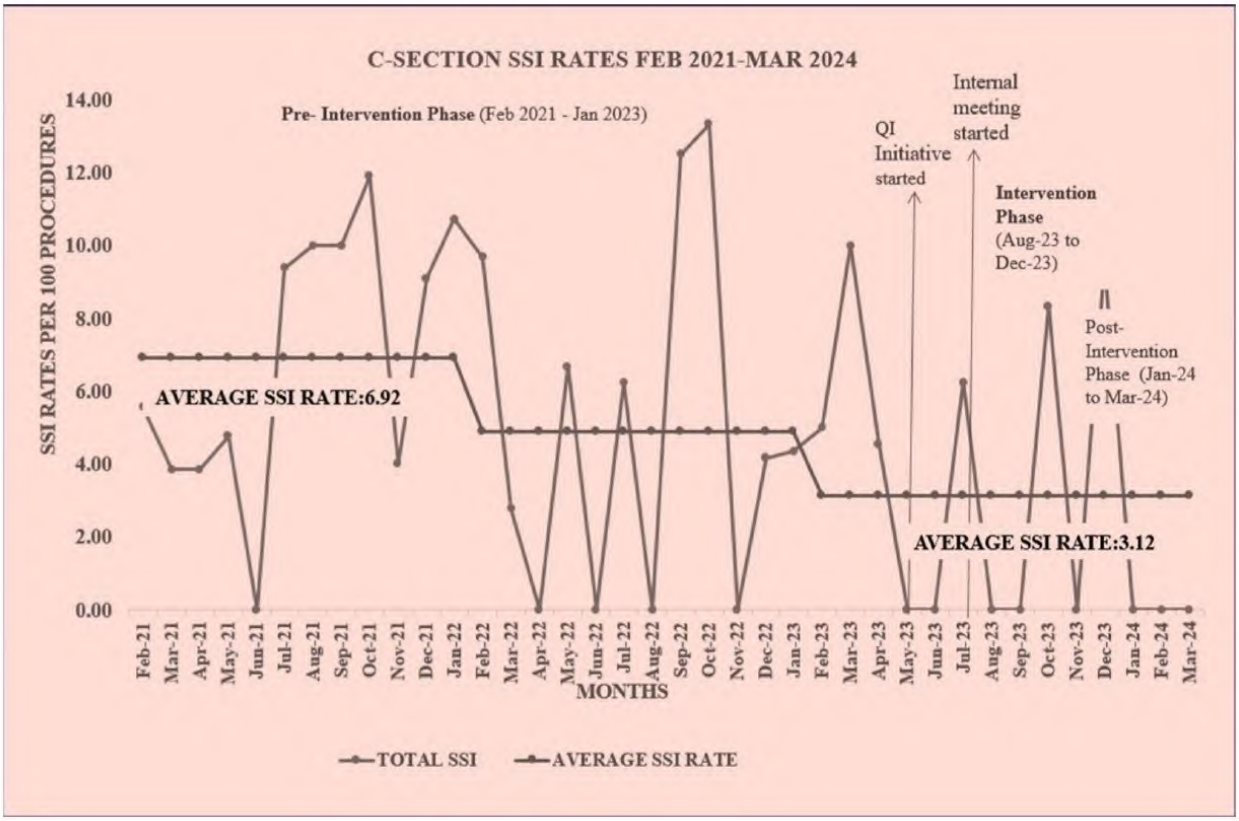
Results
The implementation of care bundle and targeted interventions led to significant reduction in the rate of SSI following caesarean surgery. The rate decreased from 6.69% (from February 2021 to January 2023) to 3.12% within 12 months.

Conclusions
This initiative underscores the preventability of SSIs through evidence-based interventions. Key to success were the comprehensive training and sensitization of healthcare staffs, patient and bystander education, and the implementation of standardized prophylactic measures. Sustained quality improvement efforts are vital for maintaining these gains and further enhancing patient outcomes in a tertiary care setting.




PDSA -2
Based on the analysis of post-implementation phase, changes in the proposed intervention will be made.
Act
Plan
Improve appropriateness of antimicrobial prophylaxis in patients with risk factors
Appropriateness of surgical prophylaxis will be monitored
Study
Do
Dissemination of antibiogram
Discussion with Microbiologist , ID physician and clinicians
Modification of surgical prophylaxis guideline


The Problem:
Clean C section SSI rates
Primary Drivers
Secondary Drivers
Change Ideas
Priority Change Ideas
SMART Aim:
Reduce clean C-section SSI rate as per the perceived base line by 12 months
Appropriate post-operative wound management by patients / health care professionals /bystanders
Information gap
Bundle for health care professionals and patients
a) Sensitization
b) Alert system on identifying risk factors
c) Patient leaflets
d) Wound care audit including hand hygiene
Impact: High
Implementation: Easy
Patient/bystander engagement for feedback
Impact: High
Implementation: Easy
Appropriate antibiotic regimen in patients with risk factors
Revision of antibiotic policies in patients with risk factors
Dissemination of antibiogram
Discussion with Microbiologist , ID physician and clinicians
Modification of surgical prophylaxis guideline
Modification of antibiotic policy for patients with risk factors
Impact: High
Implementation: Hard


C-SECTION SSI RATES FEB 2021-MAR 2024
SSI RATES PER 100 PROCEDURES
14.00
12.00
10.00
8.00
6.00
4.00
2.00
0.00
Pre- Intervention Phase (Feb 2021 - Jan 2023)
QI Initiative started
Internal meeting started
Intervention Phase (Aug-23 to Dec-23)
Post-Intervention Phase (Jan-24 to Mar-24)
AVERAGE SSI RATE:6.92
AVERAGE SSI RATE:3.12
Feb-21 Mar-21 Apr-21 May-21 Jun-21 Jul-21 Aug-21 Sep-21 Oct-21 Nov-21 Dec-21 Jan-22 Feb-22 Mar-22 Apr-22 May-22 Jun-22 Jul-22 Aug-22 Sep-22 Oct-22 Nov-22 Dec-22 Jan-23 Feb-23 Mar-23 Apr-23 May-23 Jun-23 Jul-23 Aug-23 Sep-23 Oct-23 Nov-23 Dec-23 Jan-24 Feb-24 Mar-24
MONTHS
TOTAL SSI
AVERAGE SSI RATE

RES-177: Mitochondrial Function is Involved in Hyphal Invasion and Virulence in Candida albicans

Chenru You, Chinghsuan Lin, Hsiaoyen Tsai
National Taiwan University

Background
Candida albicans is an opportunistic human fungal pathogen that preferentially infects immunocompromised individuals, causing various adverse conditions such as candidemia. It possesses numerous virulence factors, including morphological polymorphism, adhesion, and biofilm formation. Our previous studies have shown that a gene in the mitochondrial electron transport chain (ETC), essential for normal mitochondrial function in C. albicans, is involved in hyphal invasion and virulence. Therefore, the aim of this study is to evaluate the role of each ETC complex in invasive hyphal growth and virulence.

Method
Mutants of mitochondrial ETC-related genes were evaluated for invasive hyphal growth and virulence using both ex vivo and in vivo models.
Results

We found that mutants of specific genes associated with ETC complexes exhibited impaired invasive hyphal formation and reduced virulence in mice. Further analysis revealed that mitochondrial dysfunction does not impair glycerol synthesis or accumulation, yet still leads to defective invasive hyphal growth.

Conclusions
Our results suggest that mitochondrial function regulates invasive hyphal development by modulating intracellular reactive oxygen species (ROS) levels or other mechanisms in C. albicans.

RES-178: Expansion of Antimicrobial Stewardship (AMSP) And Infection Control Program (ICP) of ICMR in Secondary Care Hospitals

Arya Shaji Kumar, Radhika T. K.

Amrita Institute of Medical Sciences & Research Centre

Background
Antimicrobial resistance (AMR) is a growing public health threat, especially in healthcare settings where antibiotics are frequently misused. While antimicrobial stewardship programs (AMSP) and infection control practices (ICP) have been successfully implemented in tertiary care hospitals, secondary care facilities often lag due to inadequate resources, limited infrastructure, and lack of trained personnel. Strengthening AMSP and ICP in these settings is vital for reducing healthcare-associated infections (HAIs) and improving antibiotic use.

Method
A quasi-experimental, multicenter study was conducted from August 2021 to August 2023 in seven secondary care hospitals (four mid-level and three small-level) in Kochi, Kerala. The project was mentored by Amrita Institute of Medical Sciences in collaboration with the Indian Council of Medical Research (ICMR) and Pfizer. It included three phases: pre-implementation, implementation, and post-implementation. Baseline data on antibiotic use and staff knowledge were collected. AMSP and ICP committees were formed in each hospital, and staff received hybrid training sessions. Antibiotic prescribing audits, hand hygiene monitoring, and infection control assessments were conducted throughout the project.

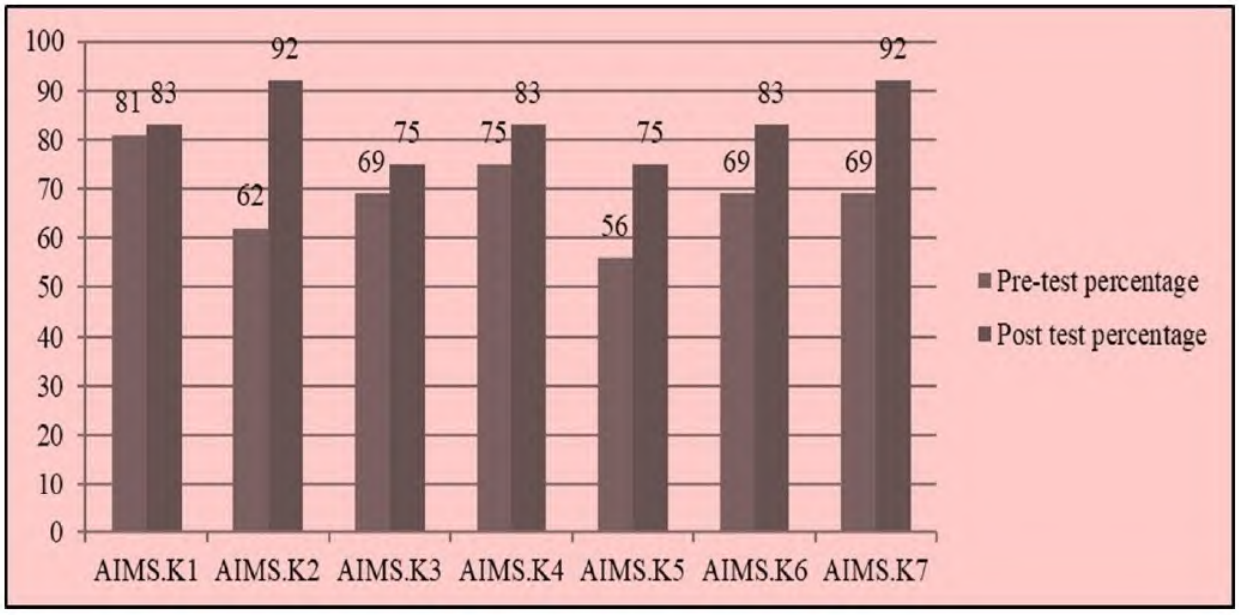
Results
Post-implementation, all hospitals showed improved antibiotic prescribing and infection control compliance. Two hospitals achieved full AMSP implementation, while others progressed partially due to staffing and logistical constraints. Significant reductions in HAIs and irrational antibiotic use were

Conclusions
The study demonstrates that AMSP and ICP can be effectively implemented in secondary care settings with appropriate mentorship and training. Continued institutional support, capacity building, and monitoring are essential for sustaining these gains and combating AMR at the secondary care level.

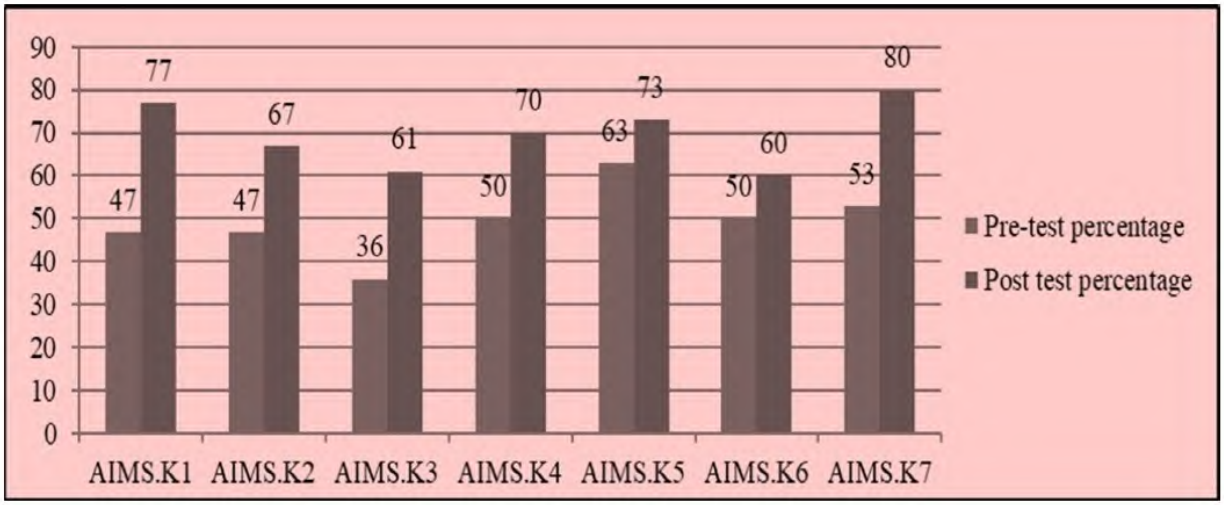
Profile of the hospitals

Name of the Hospital	Bed Strength	NABH	Rural/ Urban	Microbiology profile	
				In house /outsourced	Culture & sensitivity method
AIMS.K1	136	Entry level	Urban	In-house lab	Manual
AIMS.K2	120	Nil	Semi Urban	In-house lab	Manual
AIMS.K3	180	Entry level	Urban	In-house lab	Manual
AIMS.K4	95	Nil	Urban	Outsourced to DDRC lab	Vitek
AIMS.K5	50	Nil	Urban	In-house lab	Manual
AIMS.K6	70	Nil	Urban	In-house lab (from October 2021), before it was outsourced	Manual
AIMS.K7	275	Yes	Semi Urban	In-house lab	Vitek

AMSP pre and post-test percentage assessments



IPC pre-test and post-test percentage assessments



RES-179: The Interplay Between Social Behaviours and Acute COVID-19 Infection – Findings from a Longitudinal Cohort Study

Laysee Ong[2], Alexius Soh[1], Brenda Ong[1], Mark Chen[2]

[1]NCID
[2]TTSH

Background
While social behaviors pre-dispose individuals to COVID-19 infections, there is need to study social behavior changes post-infection, especially if re-infections can occur.

Method
Using longitudinal-cohort of community-dwellers, we examined COVID-19's effects on social-distancing behavior changes in peri-infection period, using two questionnaire-study-waves (Wave34: May-June; Wave36: August - September), when Omicron-variants predominated Singapore. Participants reported initial COVID-19 infection-date and social-distancing behavior within lookback-periods (28-days before study-wave initiation till study-participation-date). Behavior change was difference between Wave34 and Wave36, averaged across six social-distancing behaviors. Using mixed-effects regression, we investigated if infection-status was associated with change in social-distancing behavior, controlling for demographics and perceived-infection-risk.

Results
We included 942 participants (Mean age=49.3years, SD=13.9; 59.1% female). Based on infection-dates and lookback-period, there were: (Group1) 443 participants without reported infection, (Group2) 212 participants infected before Wave34's lookback-period, (Group3) 94 participants infected during Wave34's lookback-period, (Group4) 152 participants infected after Wave34 but before Wave36's lookback-period, and (Group5) 41 participants infected during Wave36's lookback-period.

Overall, social-distancing behaviors decreased across time. Mixed-effects regression model adjusted for demographics, perceived-infection-risk and Group, was statistically significant (Wald$\chi^2(19)=68.1$, $p<0.001$). Compared to Group1 (no infection), change in Group2's social-distancing was not significantly different ($\beta=-0.05$, $p=0.10$). However, relative to Group1, Group3 showed greater decrease in social-distancing ($\beta=-0.28$, $p<0.001$), while Group4 and Group5 showed increased social-distancing ($\beta=0.28$, $p<0.001$; $\beta=0.27$, $p<0.001$ respectively).

Conclusions
Findings suggest increased social-distancing during acute COVID-19 infection, but decreased social-distancing post-infection. The former may reflect physiological limitations during infection and socially responsible behaviors; latter may indicate reduce perceived vulnerability to future infections, decreasing effectiveness of social-distance interventions in preventing re-infections.

RES-181: Emergence and Transmission of Quinolone-Non-Susceptible Haemophilus Influenzae in a Geriatric Hospital in Japan

Fujiko Mitsumoto-Kaseida[1], Mika Murata[2], Daisuke Sasaki[2], Norihito Kaku[1], Kosuke Kosai[1], Hiroo Hasegawa[1], Katsunori Yanagihara[1]

[1]Nagasaki University Graduate School of Biomedical Sciences
[2]Nagasaki University Hospital

Background
Quinolone exhibit potent antimicrobial activity against Haemophilus influenzae (H. influenzae), with over 90% of isolates in Japan reported as susceptible. However, a persistently high prevalence of quinolone-non-susceptible H. influenzae was observed in a geriatric hospital, raising concerns about nosocomial transmission. Therefore, we conducted an investigation to assess clonal spread.

Method
Whole-genome sequencing was performed on 52 H. influenzae strains isolated between November 2018 and March 2020. Core genome multilocus sequence typing (cgMLST) was carried out using Ridom SeqSphere+.

Results
All 52 isolates were non-typeable H. influenzae (NTHi), and 28 (53.8%) were non-susceptible to ciprofloxacin or levofloxacin. These belonged to three sequence types (STs): ST2876 (16 strains), ST164 (8), and ST2874 (4). All 28 strains carried amino acid substitutions in GyrA (Ser84Leu, Asp88Asn) and ParC (Gly82Asp, Ser84Arg). Additionally, mutations in penicillin-binding protein 3 (PBP3), specifically Asn526Lys and Ser385Thr, were identified, consistent with β-lactamase-negative ampicillin-resistant (BLNAR). ST164 and ST2874 were isolated from single wards, while ST2876 appeared in multiple wards and suggested nosocomial spread by cgMLST. Patients with quinolone-non-susceptible strains were older (82.6±13.7 vs. 75.3±11.8 years, p=0.023) and more often required daily sputum suctioning (85.7% vs. 41.7%, p=0.001).

Conclusions
Unrecognized in-hospital transmission of quinolone-non-susceptible H. influenzae occurred in a geriatric setting. Reinforcement of infection control practices, including review of sputum suctioning procedures, is essential.

RES-183: Colonization and Environmental Transmission of Staphylococcus aureus from the Nasal Cavities of Nurses

Misato Enomoto, Masahiro Morita, Seiko Ono, Izumo Kanesaka, Akiko Kanayama Katsuse, Intetsu Kobayashi

Toho University/ Faculty of Nursing

Background
Long-term nasal colonization of Staphylococcus aureus in healthcare workers can potentially lead to transmission to the healthcare setting through hand contact. The objective of this study was to longitudinally monitor and characterize S. aureus detected in the nasal cavities, hands and surrounding environment of nurses.

Method
From May 2024 to April 2025, the nasal cavities, hands and frequently used devices such as medical phones of 58 nurses working in the general wards of a university hospital were sampled monthly.

Results
The data reflects 48 nurses who were sampled 2 or more times. S. aureus was detected in the nasal samples of 35 nurses. Of these 35 nurses, S. aureus was consistently detected in 10 nurses and intermittently detected in 25 nurses. MRSA was continuously detected in 3 nurses for 4–5 months while MSSA was continuously detected for 4–9 months in 31 nurses. In one nurse, MRSA was initially detected, followed by a 6-month clearance and detection of MSSA at 8 months. S. aureus, including MRSA, was detected on the hands and surrounding environment of 34 nurses. While environmental S. aureus detection was not continuous, the isolates matched those from the nasal cavities in some cases.

Conclusions
Persistent colonization of identical S. aureus strains in the nasal cavities of nurses was observed. It was shown that some environmental and hand isolates were genetically related to isolates in the nasal cavities of nurses which suggests possible transmission from the nasal site to the surrounding environment.

RES-184: Host Recognition Mechanism of EHEC Phage ECP52 and Expanding its Host Range by Phenotypically Shuffled Tail Fiber Proteins

Yoshimitsu Masuda, Yuki Matsuo, Yuzuki Yamada, Takahisa Miyamoto, Ken-ichi Honjoh

Kyushu University

Background
Lytic bacteriophages are effective tools for controlling bacterial infections including AMR bacteria, although there are still some challenges such as their narrow host ranges. This study aimed to expand phage host range by introducing random multiple tailfibers into a single phage particle without genetic modification in phage genome.

Method
First, we constructed the host strains which heterologously express the structural genes of long tailfibers (LTF) of enterohemorrhagic E. coli (EHEC) phage PE37. Then, EHEC phage ECP52 were converted into multi-tailfiber (MTF) phages by infecting the LTF expressing host strains. Finally, the lytic activity constructed MTF ECP52s against planktonic or biofilm cells were evaluated using EHEC host or non-host strains. In addition, to clarify the host recognition mechanism, putative receptor binding proteins of ECP52 were fused with fluorescent protein mCherry and used for host binding assay against single gene knockout mutants.

Results
Several ECP52-MTFs were constructed and such as ECP52-LTFr, -LTFe or -LTFre which involves the PE37 LTF protein locating at the root connection with main tail structure, LTF protein locating at the edge side of LTF structure, or both LTF proteins, respectively. Surprisingly, all ECP52-MTFs showed significant lytic activities against strain No. 166, which cannot be infected by ECP52, but still did not form any plaques on agar plate. ECP52-LTFre especially exhibited remarkable activity as strong as by PE37 which can originally infect strain No. 166.

Conclusions
This study demonstrated the potential of MTF phage approach to expand the host range of phages.

RES-185: Analysis of the Reasons and Factors for Not Being Vaccinated with Pneumococcal Vaccines: A Questionnaire Survey in Miyazaki Prefecture, Japan

Moeka Honda[2], Tomoyuki Fujii[2], Makoto Sumiyoshi[2], Yasuhiro Yamanari[2], Yuuki Yokoo[2], Kensuke Setoguchi[2], Akiko Kitamura[2], Yasuharu Oda[2], Hironobu Tsubouchi[2], Shigehisa Yanagi[2], Yasutoshi Hirabara[1], Ichiro Takajo[2], Taiga Miyazaki[2]

[1]Department of Pharmacy, University of Miyazaki Hospital, Miyazaki, Japan
[2]Division of Respirology, Rheumatology, Infectious Diseases and Neurology, Department of Internal Medicine, Faculty of Medicine, University of Miyazaki, Miyazaki, Japan

Background
Miyazaki Prefecture, located in the southern part of Japan, has an aging population and a lower rate of pneumococcal vaccination than the national average. The aim of this study was to analyze the characteristics of the unvaccinated population and clarify the reasons and factors for not being vaccinated.

Method
Between September and November of 2023, we conducted a cross-sectional, paper-based questionnaire survey for prefectural residents and physicians in the same area.

Results
Of the forms handed out to the general public, 3,148 were distributed, and 2,931 were analyzed. Among physicians, 83 questionnaires were distributed, and 81 were analyzed. The overall vaccination rate was 42% (783/1,845), with a median age of 72 (range 18–97). Among those aged 64 and under with underlying diseases who were recommended to receive the pneumococcal vaccine, the vaccination rate was 4% (16/401). For those aged 65 and over, the vaccination rate was 53% (n = 767/1,444). Among the unvaccinated group in the prefectural residents, the most frequent reason for not being vaccinated was "unawareness of the existence of the pneumococcal vaccine." Among physicians, the most frequent reason for not recommending pneumococcal vaccination was "failure to remember." Patients who visited pulmonologists had the highest vaccination rate, at 55%. Those with a history of influenza and/or the COVD-19 vaccines had higher pneumococcal vaccination rates.

Conclusions
This multifaceted approach enabled us to understand the key factors contributing to the low vaccination rate and clarify our next steps to improve pneumococcal vaccination in our aging community.

RES-186: Prevalence, Characterization, and Antimicrobial Resistance of Non-Typhoidal Salmonella Isolated from Chicken Meat in Fukuoka, Japan

Khin Zar Linn, Takahisa Miyamoto, Ken-ichi Honjoh, Yoshimitsu Masuda

Kyushu University

Background
Non-typhoidal Salmonella (NTS) is a zoonotic pathogen transmitted through contaminated food, and antimicrobial-resistant strains of NTS pose a global public health threat. Furthermore, the presence of virulence factors and the ability to form biofilms in NTS present serious risks to public health. This study examined the prevalence, serotype diversity, virulence genes, biofilm formation, and antimicrobial resistance of NTS in Fukuoka, Japan from 2023 to 2024.

Method
NTS was isolated from 50 chicken samples purchased from various supermarkets in Fukuoka using conventional methods and confirmed by PCR. Serotyping was performed with both an antisera kit and PCR. The isolates were tested for virulence genes (hilA, spiC, ssrB, spvC) and biofilm formation. Their susceptibility to 25 antimicrobials was assessed using broth microdilution and disk diffusion methods.

Results
Out of 50 samples examined, 32 (64%) were positive for Salmonella spp. and 32 strains were isolated. The isolates included 3 serotypes, with Schwarzengrund being predominant (25/32, 78.1%), followed by Thompson (5/32, 15.6%) and Oranienburg (2/32, 6.3%). All the isolates possessed hilA, ssrB, and spiC genes, but not spvC. Both S. Schwarzengrund and S. Thompson isolates showed varying biofilm formation. All the isolates of S. Thompson and S. Oranienburg were susceptible to all the antimicrobials tested. However, S. Schwarzengrund isolates were resistant to kanamycin (88.5%), tetracycline (76.9%), sulfamethoxazole/trimethoprim (42.3%), streptomycin (30.8%), minocycline (19.2%), and nalidixic acid (11.5%), with 38.5% of the isolates being multidrug resistant (MDR).

Conclusions
MDR S. Schwarzengrund in chicken highlighted a significant risk to food safety and public health.

RES-187: Challenges with the Evolving Diagnostic Landscape for MBL-Producing Gram-Negative Infections: Insights from Healthcare Professionals

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Pfizer

Background
Metallo-β-lactamase (MBL)-producing Gram-negative infections are an escalating global health concern, particularly in regions with variable access to diagnostic infrastructure. Rapid diagnostic tests (RDTs) offer the potential to accelerate detection and guide early, targeted treatment, yet their adoption remains inconsistent.

MBL prevalence is highest in India and Brazil, with rising rates in China and Saudi Arabia. The emergence of double-carbapenemase infections further complicates treatment selection and reduces the utility of single-target diagnostics.

Method
This study assessed diagnostic readiness and test availability across Brazil, China, India, Mexico, Saudi Arabia, and Taiwan. Conducted between November 2024 and January 2025, the research included 42 qualitative interviews with infectious disease experts, microbiologists, ICU physicians, and laboratory directors. It explored diagnostic workflows, technology use, and systemic barriers to access and adoption in both public and private healthcare settings.

Results
Findings revealed significant disparities in diagnostic access and challenges to adoption. Advanced tools like MALDI-TOF and syndromic panels are largely confined to tertiary hospitals. While lateral-flow assays and syndromic panels are valued for their speed and comprehensiveness, their use is limited by high costs and inadequate reimbursement. Infrastructure gaps, restricted lab hours, and lack of reimbursement for tests further hinder equitable access to rapid diagnostics.

Conclusions
To fully leverage the benefits of RDTs, cross-sectoral collaboration is essential. Strategic investments in diagnostic infrastructure, workflow optimization, policy advocacy for pricing and reimbursement, and a focus on education and awareness will be critical to ensure access to RDTs that can unlock timely, appropriate treatment of MBL-producing infections.

RES-188: Cytomegalovirus IgG Seropositivity in the Adult Population of Korea: A Cross-Sectional Study

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[3]Seoul Clinical Laboratories

Background
Cytomegalovirus (CMV) is a prevalent viral infection worldwide. Although South Korea has historically shown high CMV IgG seropositivity (>95%), recent declines have been reported. This study aimed to assess current CMV IgG seropositivity and analyze current trends in the Korean population.

Method
Residual samples from individuals undergoing regular health checkups were analyzed. CMV IgG was measured in two institutions using a commercial immunoassay (Alinity i CMV IgG Reagent Kit, Abbott), following the manufacturer's instructions. Results were interpreted as “Reactive” when the concentration of CMV IgG was ≥ 6.0 arbitrary unit (AU)/mL, and “Nonreactive” when CMV IgG was <6.0 AU/mL. Seropositivity was compared by sex and across age groups (20 – 29, 30 – 39, 40 – 49, and 50 – 59 yrs).

Results
A total of 1,978 samples (859 men and 1,041 women) were measured, where age group distribution was relatively balanced. Overall CMV IgG seropositivity was 89.9% (1,778/1,978), which was significantly higher in males (91.7%, 859/937) than females (88.3%, 919/1,041) (difference 3.4%, 95% confidence interval 0.8% – 6.0%, P = 0.012, Chi-square test). No significant gender difference was found within each age group. Seropositivity increased with age, from 76.3% (347/455, 20 – 29 yrs) to 99.8% (448/449, 50 – 59 yrs) (P for trend <0.001), consistent in both genders.

Conclusions
CMV IgG seropositivity in the general Korean population was 89.9%, higher in males. Due to lower seropositivity in younger adults, continued monitoring and further education are essential for CMV control and prevention.

RES-190: Performance Evaluation of RPIP: A Next-Generation Sequencing Platform for Pathogen Detection in Cerebrospinal Fluid

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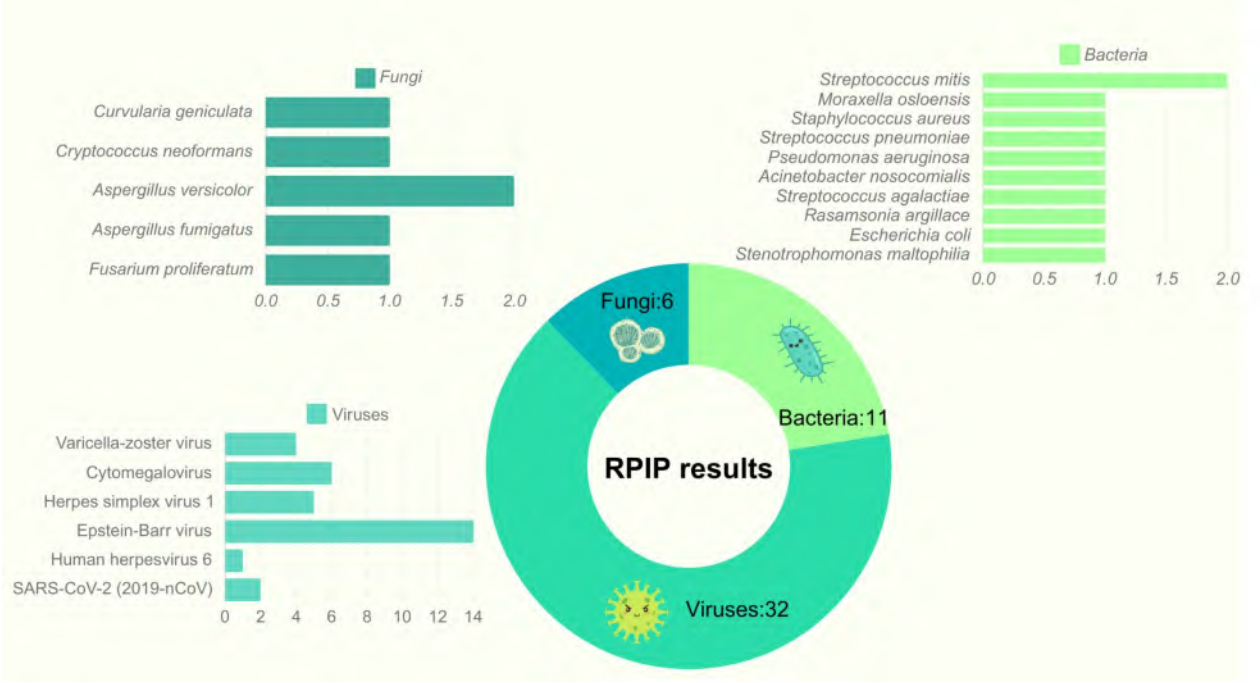
Background
Meningitis is a serious inflammation of the brain and spinal cord membranes, typically caused by infection. Conventional diagnostic tools such as Gram stain offer rapid results but have limited sensitivity, while culture methods are more accurate yet time-consuming. At our hospital, we use FilmArray Meningitis/Encephalitis (ME) panel, a rapid molecular diagnostic assay that identifies 14 pathogens in cerebrospinal fluid (CSF) within 2 hours. When FilmArray ME results are negative but clinical suspicion remains high, we perform additional testing using the Illumina RPIP panel—a next-generation sequencing (NGS) platform that detects a broader range of pathogens and antimicrobial resistance genes from minimal sample volumes.

Method
In this study, 104 residual CSF samples previously tested with FilmArray ME were analyzed using the Illumina RPIP and results were compared.

Results
FilmArray ME yielded 23 positive results, each identifying a single pathogen. RPIP detected 33 positives, including multiple pathogens per sample: 22 with one target, 7 with two, 3 with three, and 1 with four. Comparative analysis showed: 7 samples had identical results, 7 had partial overlap with additional RPIP findings, 7 were positive only by FilmArray ME, 17 only by RPIP, 2 had discordant targets, and 64 were negative by both. Overall concordance was 75% (78/104).

Conclusions
While RPIP offers broader pathogen detection through NGS, its multiple amplification steps may increase the risk of noise, especially in low-cell CSF samples. Therefore, RPIP results should be interpreted with caution and validated with clinical context and additional data analysis.



RES-192: Whole Shotgun Metagenomic Analysis of the Effect of Maternal Macronutrient Intake and Vegetarian Diet on Diversity, Relative Abundance of Taxa, and Pathway Abundance in the Breastmilk Microbiome of Indian Mothers

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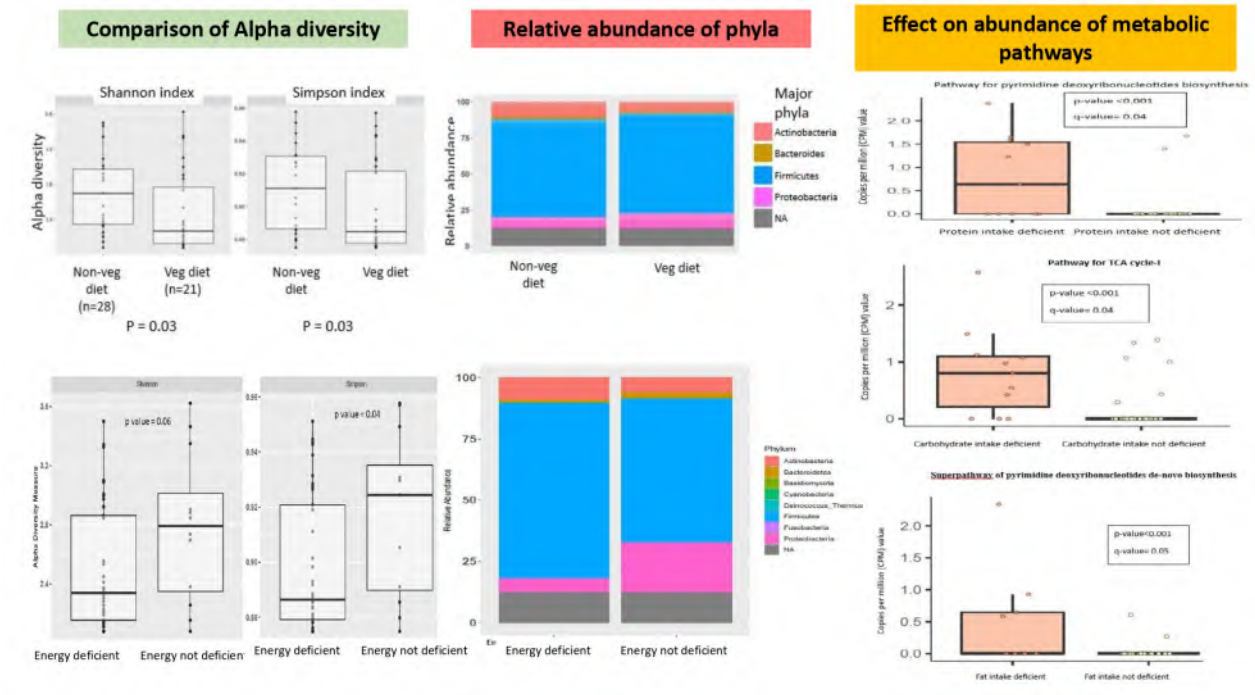
Background
There is paucity of data on the impact of maternal diet and macronutrient intake on breastmilk microbiome using whole shotgun metagenome sequencing (WSMG). Our study assessed how maternal dietary patterns influence breastmilk microbiome diversity, composition, and functional pathways.

Method
49 mothers were enrolled at a tertiary care center. Based on a 24-hour dietary record, subjects were classified (based on recommended dietary allowances) into “deficient” versus “no deficient” intake of various macronutrients. Breastmilk was collected 3–10 days postpartum, processed, and stored at –80 °C. DNA was extracted (DNeasy PowerSoil Kit, Qiagen), sequenced (Illumina), and analyzed for taxonomy/diversity MetaPhlAn, Phyloseq), pathways (HUMAnN 2.0).

Results
Mean (SD) maternal age was 27.92 (4.45) years, postpartum days at sample collection 6.96 (2.83) days, and BMI 22.88 (3.28). Energy-intake deficient mothers (n=37) showed significantly lower alpha-diversity (p=0.04) with increased Firmicutes, compared to non-deficient mothers. There were no significant differences in abundance of metabolic pathways. Protein-intake deficient (n=11) and carbohydrate-intake deficient (n=11) groups showed lower alpha-diversity (not significant) and increased abundance of pyrimidine biosynthesis and TCA Cycle-I, respectively [p<0.001]. Fat-intake-deficient (n=9) mothers had higher pyrimidine biosynthesis abundance (p<0.001) without diversity change. Non-vegetarians (n= 21) had higher alpha-diversity than vegetarians [p=0.03], phyla abundances were similar. Vegetarians showed more abundant pentose phosphate, Calvin–Benson–Bassham, homolactic fermentation pathways [all q<0.05].

Conclusions
Decreased dietary intake of energy and certain macronutrients were associated with reduced alpha-diversity and differences in abundance of functional gene pathways in breastmilk. Vegetarianism is associated with lower diversity, influences specific bacterial pathways in the breastmilk microbiome, suggesting diet influences breastmilk microbiome composition.



RES-193: Gram-Positive Organisms in Pyelonephritis: Risk Factors and Empirical Therapy

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Background
The risk factors for pyelonephritis caused by gram-positive organisms remain unclear, and guidance on when empirical therapy should target these pathogens is lacking.

Method
We conducted a retrospective study at a 358-bed community teaching hospital in Japan, reviewing records of adult inpatients diagnosed with pyelonephritis and positive blood cultures from October 2016 to December 2019. Data collected included urine gram stain results, urine and blood culture findings, causative organisms, empirical antibiotic therapy, and clinical outcomes.

Results
Among 241 cases of pyelonephritis (mean age 77.8 years; 30.3% male), gram-positive cocci (GPC) and bacilli (GPR) were identified as causative organisms in 21 cases (8.7%, 95% CI: 5.5–13.0%). The isolated pathogens included Streptococcus spp. (mainly β-hemolytic, n=8), Staphylococcus spp. (n=6), Enterococcus spp. (n=5), Aerococcus spp. (n=4), and Actinotignum schaalii (n=1), with some cases involving multiple organisms. Significant risk factors identified by Fisher's exact test included male sex (p=0.002), hydronephrosis (p=0.003), benign prostatic hyperplasia (p=0.010), ureteral stones (p=0.003), and ureteral catheter (p=0.016). Cox regression analysis identified male sex (odds ratio 4.32, 95% CI: 1.40–13.40, p=0.011), ureteral stones (odds ratio 6.09, 95% CI: 2.11–17.60, p<0.001), and ureteral catheter (odds ratio 8.69, 95% CI: 1.67–45.40, p=0.010) as independent predictors. Inappropriate empirical antibiotic therapy was significantly more common in gram-positive cases compared to gram-negative bacilli cases (23.8% vs. 2.7%, p=0.001).

Conclusions
Gram-positive cocci are more likely to cause pyelonephritis in specific populations, in whom inappropriate empirical therapy is frequent. Urine gram stain may help guide appropriate empirical antibiotic selection in these higher-risk groups.

RES-195: Analysis of False-Positive Urinary Pneumococcal Antigen Results at a Secondary Care Hospital in Japan

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Background
Streptococcus pneumoniae remains a leading cause of community-acquired pneumonia. Urinary antigen testing is widely used due to its rapid, non-invasive nature. However, false positives may result from cross-reactivity or colonization. We aimed to assess false-positive results in urinary pneumococcal antigen testing.

Method
This retrospective study was conducted at a secondary-care hospital in Shizuoka, Japan, between Jan 2022 and May 2025. Patients who tested positive for urinary pneumococcal antigen were categorized into an isolated group (those with S. pneumoniae isolated from sputum, urine, or blood cultures) and a non-isolated group. Cross-reactivity was assessed by isolating α-hemolytic streptococci.

Results
Among the 60 urinary antigen-positive patients, 15 were classified into the isolated group: all had Streptococcus pneumoniae detected in sputum cultures (14 with Geckler grades 3–5, 1 with Geckler grade 1–2/6), and two also had positive blood cultures. In the non-isolated group, α-hemolytic streptococci were isolated from good-quality sputum (Geckler grades 3–5) in 11 cases and from poor-quality sputum (Geckler grades 1–2) in 21 cases; in 13 cases, no pathogen was detected.

Conclusions
Only approximately 25% of urinary antigen-positive cases were confirmed to have S. pneumoniae isolated from clinically significant specimens. Among cases without S. pneumoniae isolation, α-hemolytic streptococci were identified in about 53% of cases. These findings suggest that urinary pneumococcal antigen positivity may reflect cross-reactivity or past infection, and interpretation of results should be made in conjunction with clinical findings.

RES-196: Efficacy and Safety of Using Inhaled Amikacin for Treatment of Pulmonary Non-Tuberculous Mycobacteria

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Background
Pulmonary non-tuberculous mycobacterium (NTM) infections are often resistant to multiple drugs and require combination antibiotic therapy. Intravenous (IV) amikacin is commonly used but limited by nephrotoxicity and ototoxicity. Inhaled amikacin may be a viable alternative. We aim to evaluate the efficacy and safety of inhaled amikacin in treating pulmonary NTM infections.

Method
We conducted a retrospective analysis of patients treated with inhaled amikacin (injectable formulation) for pulmonary NTM at Singapore General Hospital from January 2021 to December 2024.

Results
Eighteen patients received inhaled amikacin: 12 (66.7%) with Mycobacterium abscessus, 1 (5.6%) with Mycobacterium fortuitum, 2 (11.1%) with Mycobacterium avium complex, and 3 (16.7%) with mixed growth. The median treatment duration was 11.5 months (IQR 6-12), with a median dose of 500 mg once daily. Sputum culture clearance was achieved in 6 of 11 patients (54.5%), 9/18 (50.0%) had improvement in symptoms and 9/18 (50.0%) showed radiological improvement. Sixteen patients who had random amikacin levels tested had levels of <1.0. No patient developed nephrotoxicity. Hearing loss occurred in 4 of 11 patients (36.4%), of whom 3 had prior IV amikacin exposure and 3 had prior or concurrent use of azithromycin. One (5.6%) patient experienced vertigo, and 2 (11.1%) reported pre-existing tinnitus. Five (27.8%) patients discontinued treatment due to adverse effects, including hearing loss, vertigo, oral thrush, and itch.

Conclusions
Inhaled amikacin appears to be a viable treatment option for pulmonary NTM, particularly in patients with limited alternatives. It was generally well tolerated, though monitoring for ototoxicity remains important.

Table 1: Summary of cases and outcomes

Case	NTM Species	Smear positivity	Macrolide sensitivity	Radiological form	Antibiotic regimen prior to inhaled amikacin	Duration of treatment prior to inhaled amikacin (Weeks)	Antibiotic regimen with inhaled amikacin	Duration of inhaled amikacin (Months)	Dose of inhaled amikacin	Clearance culture	Symptomatic outcomes	Radiological outcomes	Adverse effects
1	Abscessus	Yes	No	NB	TGC, AMI, AZI	3	AZI	12	500mg OD	Not done	Improved	Improved	No
2	Abscessus	No	No	NB	IMI, AMI, LZD	2	CFZ	6	500mg BD	Not done	Stable	Improved	No
3	Abscessus, Fortuitum	No	Mixed	NB	CFX, AMI, AZI, CFZ	19	LZD, CFZ	12	500mg OD	Yes	Stable	Improved	No
4	MAC	Yes	No	NB	NA	NA	RMP, EMB, CFZ	12	500mg OD	Not done	Improved	Stable	No
5	Abscessus	No	Yes	NB	CFX, AMI, AZI	12	AZI, LFX	12	500mg OD	Yes	Stable	Improved	No
6	Abscessus	No	Yes	NB, C	ERV, CFX, CFZ	4	CFZ, LFX	12	500mg OD	Not done	Improved	Stable	No
7	Fortuitum	No	No	NB	NA	NA	ERV, CFZ	2	500mg BD	No	Stable	Stable	Oral thrush
8	Abscessus	No	No	NB, C	CFZ	10	CFZ, MFX	16	500mg OD	No	Worsened	Worsened	No
9	Abscessus	Yes	No	NB	CFX, AMI, AZI, DOX	13	CFZ	9	500mg OD	Yes	Improved	Mixed	Palpitations, hearing loss, tinnitus
10	MAC	Yes	Yes	NB, C	RMP, EMB, AZI, AMI	4	RMP, EMB, AZI	2	500mg OD	Not done	Improved	Improved	Vertigo
11	Abscessus	No	No	FC	CFX, AMI, LZD, CFZ	25	CFZ, LFX, DOX	6	500mg OD	No	Worsened	Improved	Hearing loss
12	Abscessus	Yes	Yes	NB	AMI, CFX, AZI, CFZ	18	AZI	4	500mg OD	Yes	Improved	Stable	Hearing loss
13	Abscessus	No	Yes	NB	IMI, AZI, LZD	2	AZI	3.5	250mg OD	Not done	Stable	Stable	Hearing loss
14	Abscessus	Yes	Mixed	NB, C	CFX, ERV, CFZ	6	CFZ, AZI	13	500mg OD	Not done	Improved	Improved	No
15	Abscessus	N	N	NB	CFX, AMI, CFZ	6	CFZ	14	500mg OD	No	Worsened	Mixed	No
16	Abscessus, Kansasii, MAC	N	N	NB, C	CFX, AMI, CFZ, RMP, AZI, EMB	6	CFZ, RMP, AZI, EMB	11	500mg OD	Yes	Improved	Improved	Chest tightness
17	Abscessus, Fortuitum	N	N	NB, C	ERV, AMI, CFZ	6	CFZ, CIP	12	500mg OD	Yes	Improved	Stable	No
18	Abscessus	N	Y	NB	CFX, AZI, AMI	3	CFX, AZI	6	250mg OD	No	Improved	Improved	Itch

MAC Mycobacterium avium complex; NB Nodular bronchiectatic; C Cavitary; TGC Tigecycline; AMI Amikacin; AZI Azithromycin; IMI Imipenem; LZD Linezolid; CFX Cefoxitin; CFZ Clofazimine; ERV Eravacycline; RMP Rifampicin; EMB Ethambutol; DOX Doxycycline; LFX Levofloxacin; MFX Moxifloxacin, CIP Ciprofloxacin

RES-197: Deep Learning for Early Bacterial Colony Identification through Time-Lapse Imaging

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[2]International University of Health and Welfare

Background
Accurate and rapid identification of bacterial species is crucial for timely diagnosis and effective treatment of infectious diseases. Traditional microbiological methods often rely on colony morphology and biochemical tests, which are time-consuming and labor-intensive.

Method
This study investigates the potential of deep learning for automated and early bacterial colony identification using time-lapse imaging. We cultured 6 types of Enterobacteriaceae species and collected colony images of developing colonies from initial inoculation to mature growth every 8 hours. ResNet architecture model was applied to deep learning. The original image set for AI training consisted of 320 images (Training: 80%, Validation: 20%). The data augmentation process was applied to the original image, and transfer learning or fine-tuning was performed on the AI models. We evaluated the agreement with AI classification.

Results
The AI recognition accuracy at each culture time point is shown in Table 1. The AI model with the highest accuracy in holdout validation showed a total accuracy of 1.000, average recall of 1.000, average precision of 1.000, and average F-1 score of 1.000.

Conclusions
This deep learning-based approach offers a non-invasive, high-throughput solution for automated bacterial identification, potentially reducing turnaround time in clinical microbiology laboratories and improving patient outcomes. Further research will focus on expanding the dataset, validating the model with diverse strains, and integrating it into an automated diagnostic platform.

		16 hour	24 hour	32 hour	40 hour	48 hour
Total accuracy		0.954	0.984	1.000	1.000	0.968
Average F1-score		0.938	0.987	1.000	1.000	0.956
Recall	*Escherichia coli*	0.625	1.000	1.000	1.000	0.875
	Klebsiella pneumonia	1.000	1.000	1.000	1.000	1.000
	Serratia marsescens	1.000	1.000	1.000	1.000	1.000
	Hafnia alvei	1.000	0.929	1.000	1.000	1.000
	Enterobacter cloacae	1.000	1.000	1.000	1.000	1.000
	Proteus mirabilis	1.000	1.000	1.000	1.000	1.000
Precision	*Escherichia coli*	1.000	1.000	1.000	1.000	1.000
	Klebsiella pneumonia	1.000	1.000	1.000	1.000	1.000
	Serratia marsescens	0.929	0.917	1.000	1.000	1.000
	Hafnia alvei	0.818	1.000	1.000	1.000	0.666
	Enterobacter cloacae	1.000	1.000	1.000	1.000	1.000
	Proteus mirabilis	1.000	1.000	1.000	1.000	1.000

RES-198: Expression of blaoxa-58 Is Enhanced Against Subinhibitory Concentration of Carbapenems

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Background
The blaOXA-58 gene in E. coli (Escherichia coli) is a rare but clinically significant β-lactamase determinant that confers resistance to certain β-lactam antibiotics via the OXA-58 oxacillinase, typically acquired by horizontal gene transfer. This study aimed to characterize blaOXA-58 in clinical E. coli isolates and analyzed its transcriptional response to sub-inhibitory carbapenem exposure.

Method
The total 264 clinical isolates of E. coli were obtained from Silchar Medical College and Hospital, Silchar, Assam, India, as secondary sources. Carbapenem susceptibility and minimum inhibitory concentration were determined by Kirby-Bauer disc diffusion and agar broth per CLSI 2022 guidelines. Carbapenemase production was assessed using the Rapidec® Carba NP test (Biomerieux, France). PCR (Polymerase Chain Reaction) targeting blaOXA-58 was performed followed by investigation of horizontal gene transferability of blaOXA-58 and plasmid based replicon typing (PBRT). Transcriptional expression of blaOXA-58 in wild condition (without carbapenem exposure) and under sub-inhibitory carbapenem stress (0.5 and 1µg/ml) were investigated by Quantitative Real-time PCR.

Results
Among 264 isolates, 46 isolates exhibited resistance towards carbapenems and are detected in Rapidec® Carba NP test. Four isolates among them were identified harbouring blaOXA-58 gene within transferable IncFIB and IncFREPB plasmids. The transcriptional response of blaOXA-58 in with or without subinhibitory concentration of carbapenems, and that revealed that the expression of blaOXA-58 gene was enhanced under imipenem & meropenem exposure.

Conclusions
This study highlights that both imipenem and meropenem exposure increase the blaOXA-58 expression. IncFIB and IncFREPB plasmids can act as a genetic vehicle for this carbapenem resistant determinant.

RES-202: Prevalence of and Factors Associated with Sarcopenic Obesity in People Living with HIV

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Background
Sarcopenic obesity (SO) is a metabolic condition defined by increased fat mass combined with reduced muscle mass and function, driven by aging and chronic inflammation. People living with HIV(PLWH) are at increased risk of SO. Prevalence and associated factors of SO are scarce in Thailand.

Method
Between September 2024 and May 2025, a cross-sectional study was conducted to determine the prevalence and factors associated with SO in PLWH at Siriraj hospital. PLWH aged 20-79 years and had been diagnosed HIV for at least 12 months were included. Hand grip strength and five-time sit-to-stand test were assessed. Body composition was measured using bioelectrical impedance analysis (BIA).

Results
Of 312 PLWH, median age was 53 years (IQR 44–60), 54.3% were male and median duration of HIV was 18 years (IQR 11-22). The prevalence of SO was 7.3% (95% CI: 4.87–10.81%). No significant associations were observed in initial multivariable analysis. However, dose–response analysis revealed associations between cumulative exposure to specific ART drugs and SO. A significant trend was noted with protease inhibitors (PIs) and abacavir(ABC), while stavudine (d4T) and ABC showed threshold effects at higher quartiles of exposure.

Conclusions
Prolonged exposure to certain antiretroviral drugs, especially PIs, d4T, and ABC, may contribute to SO in PLWH. These findings highlight the importance of personalized drug selection and support the need for future prospective study to assess causal relationship of factors associated with SO and health outcomes in this population.

Table 1: Dose–response relationship between cumulative antiviral therapy (by quartiles) and sarcopenic obesity

	Quantitative ART use							
	Q1 (reference)	Q2		Q3		Q4		P for trend
	OR (95%CI)	OR (95%CI)	p-value	OR (95%CI)	p-value	OR (95%CI)	p-value	
PIs		N/A	0.999	0.292 (0.034-2.532)	0.264	0.583 (0.058-5.844)	0.144	0.043
d4T		2.100 (0.432-10.212)	0.358	0.933 (0.174-5.007)	0.936	6.300 (1.745-22.743)	0.005	0.191
ABC		2.407 (0.322-17.979)	0.392	9.630 (1.028-90.164)	0.047	1.204 (0.105-13.838)	0.882	0.047

RES-203: Swineherds' Knowledge, Practices, and Quinolone-Resistant Escherichia coli in Selected Small-Scale Swine Farms

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Background
The overuse of quinolones in livestock, such as in swine farms, raises public health concerns in the Philippines due to its contribution to the emergence of quinolone-resistant Escherichia coli (QREC). These resistant microorganisms can spread through direct animal contact or the food chain, posing zoonotic risks.

Method
This study correlated the quinolone resistance profile of Escherichia coli (QRPEC), and the swineherds' demographics, knowledge, and practices among selected small-scale swine farms (SSfs). The study also compared swineherds' knowledge and practices in SSfs with and without the presence of QREC. Fecal swabs (n=90) were collected within SSf pigpens, and swineherds (n=30) were interviewed via questionnaire. Antimicrobial susceptibility tests were applied for QREC identification. A single PCR assay was applied to identify four common quinolone-resistant genes.

Results
Among the fecal swabs, 66 isolates were E. coli, of which 6 were QREC, showing variable resistance to ciprofloxacin, norfloxacin, and levofloxacin. Moreover, gyrA and parC genes were revealed, which may contribute to quinolone resistance. A significant relationship was found between knowledge and disuse of antibiotics in disease prevention (rs=.405, p=.026) and growth promotion (rs=.466, p=.009) in swine. Likewise, a significant difference was observed in using combination therapy between SSfs with and without QREC presence (U=27.500, p=.018).

Conclusions
While QREC was found in selected farms, no strong statistical link was observed between its presence and swineherds' knowledge or practices. However, a correlation exists between individual knowledge levels and certain antibiotic use practices, and a difference existed between SSfs with and without QREC in using combination therapy to treat swine.

RES-204: Knowledge, Attitude, and Practices Towards Human Immunodeficiency Virus (HIV) Pre-Exposure Prophylaxis (PreP) Among Health Care Workers in a Tertiary Hospital

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Background
Human Immunodeficiency Virus (HIV) remains a major global health issue, causing high morbidity and mortality rates. Traditional prevention methods have not been sufficiently effective in reducing new infections. To improve prevention, strategies like Pre-Exposure Prophylaxis (PrEP) have been introduced. However, in the Philippines, PrEP is underutilized due to limited awareness, social stigma, and other barriers.

Method
This study examines the knowledge, attitudes, and practices (KAP) of healthcare workers, including doctors, nurses, and allied health practitioners, at a tertiary hospital in Southern Mindanao regarding PrEP use in HIV-negative individuals. From January to June 2025, we conducted a cross-sectional descriptive study with 218 health professionals from St. Elizabeth Hospital Inc., using questionnaires to assess their KAPs on PrEP.

Results
Results showed that among 218 health professionals, 116 respondents (53.2%) were unaware of PrEP as a prevention strategy, indicating limited specialized knowledge on HIV. Despite this, healthcare workers generally had a positive attitude towards PrEP and were willing to learn more about it. A significant barrier to PrEP integration was the lack of knowledge about government agencies providing it.

Conclusions
Our findings reveal significant gaps in knowledge and awareness about PrEP, despite a generally positive attitude towards its use as an HIV prevention strategy, highlighting the urgent need for targeted educational initiatives and professional development programs to enhance understanding and promote safe practices related to PrEP. The study also identified significant impediments to PrEP prescription and referral. However, the participants demonstrated positive attitudes toward PrEP and a strong interest in learning more about it.

RES-205: The Role of EQA in Laboratory Testing for Biological Threats in Australia

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Background

A strong public health system is the foundation of an effective defence against biological threats and provides the framework to reduce the impact and transmission of disease outbreaks. External quality assessment (EQA) programs play a key role in enhancing and maintaining laboratory performance, thereby strengthening Australia's health system.

Method

In 2008, the Australian Government established the Security Sensitive Biological Agents (SSBA) Regulatory Scheme. Subsequently, funding was made available to establish the Biosecurity program at the Royal College of Pathologists of Australasia Quality Assurance Programs (RCPAQAP) to provide EQA for detecting SSBAs, other potential agents, and emerging disease threats. Rapid advancements in biotechnology and emerging disease threats have driven RCPAQAP to evolve and adapt its EQA programs to address the changing landscape of biosecurity threats.

Results

A diverse suite of EQA programs has been offered, covering over 25 different SSBAs and other pathogens to help strengthen laboratory competency and outbreak response, especially in early detection, identification, and notification. A biosecurity system that incorporates EQA ensures laboratories have the necessary skills, knowledge and technologies to detect a biological threat and identify the incident as natural or intentional.

Conclusions

The provision of EQA programs remains a key priority in enhancing and maintaining laboratory performance to respond effectively to SSBA incidents, where the stakes of accurate identification are high. The program is integral to state and national efforts to prepare, respond to and mitigate potential threats concerning natural or human-enabled disease outbreaks.

RES-206: Pitfalls in AWaRe-based Evaluation of Antimicrobial Use by Prescription Duration: An Analysis Using a National Database in Japan

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National Center for Global health and Medicine, Japan Institue for Health Security / AMR Clinical Reference Center

Background
The WHO-AWaRe classification aims to promote appropriate antimicrobial use (AMU), targeting 60% from the “Access” category. However, it does not account for clinical situations or treatment duration, which may lead to inappropriate evaluations. Some long-term regimens used for prophylaxis or chronic infections are appropriate but are classified as “Watch”. This study aimed to analyze AMU by prescription duration and examine how it affects AWaRe-based assessment.

Method
We analyzed oral outpatient AMU from 2013 to 2021 using a nationwide claims database in Japan. AMU was measured as defined daily doses per 1,000 inhabitants per day (DID). Prescriptions were classified as either short-term (<14 days) or long-term prescriptions (LT-prescriptions, ≥14 days).

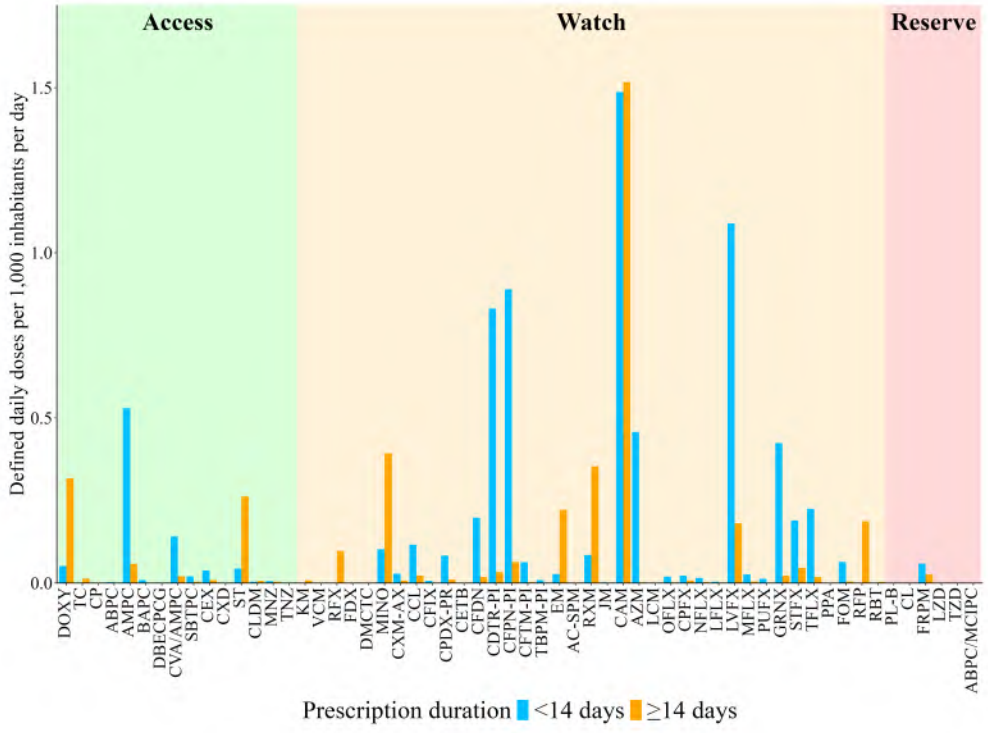
Results
The median total DID from 2013 to 2021 was 11.6 [IQR:9.9-12.3]; Among these, the median DID for LT-prescriptions was 3.5 [IQR:3.5-3.8]. LT-prescriptions accounted for approximately 30% of the total. A detailed analysis of 2019, unaffected by COVID-19 pandemic, revealed that the “Access” rate was 13.9%.

LT-prescriptions were frequent for clarithromycin (“Watch”), a standard treatment for nontuberculous mycobacteriosis (NTM), for minocycline (“Watch”) and for sulfamethoxazole-trimethoprim (“Access”), as shown in the Figure.

Each LT-prescription had 1.5, 0.4 and 0.3 DID, which accounted for 50.5, 85.7 and 79.3% of the total.

Conclusions
These findings highlight the fact that LT-prescriptions significantly affect the AWaRe-based assessment.

LT-prescriptions, especially clarithromycin (e.g., treatment for NTM), are sometimes appropriate but reduce “Access” rates, hindering the >60% goal. To promote appropriate AMU, a comprehensive assessment that considers not only the AWaRe classification but also the diseases and treatment duration is required.



RES-207: Effective Daily Sink Drain and Drainpipe Disinfection

Itaru Nakamura, Asami Okugawa, Tomohide Shimodaira, Yuri Miura, Hidehiro Watanabe

Tokyo Medical University Hospital

Background
Pathogenic microorganisms that colonize hospital sinks can cause healthcare-associated infections. These pathogens contaminate sink drains by growing up from the drainpipe and can infect patients, medical staff, and medical equipment through water splashback during sink use. We conducted a study on the microbial suppression effect of daily drain and drainpipe disinfection.

Method
From October 2023 to July 2025, 24 sinks used daily in the intensive care unit in Tokyo Medical University Hospital (Tokyo, 905beds) were targeted. Sinks were divided into five groups based on the intervention used (70% alcohol, 1% hypochlorous acid solution, 0.5% hypochlorous acid foam, acetic acid, and a drain heater). The effect was evaluated by monthly culturing the drain surface to detect pathogenic microorganisms (Enterobacteriaceae, Pseudomonas aeruginosa, Staphylococcus aureus, and Enterococcus faecalis), before each intervention and then every month after the daily disinfection was started. The drain surface's appearance was also observed.

Results
Total number of cultures was 379. The detection rate before intervention was 68% (12/19). After intervention, the detection rates for 70% alcohol, 1% hypochlorous acid solution, 0.5% hypochlorous acid foam, acetic acid, and the drain heater were 60% (25/42), 12% (11/90), 53% (55/103), 43% (15/35), and 69% (62/90), respectively. Only 1% hypochlorous acid solution significantly reduced the pathogens. It was also the only intervention with which rust was observed on the drain surface.

Conclusions
1% hypochlorous acid solution was effective for sink drain disinfection but caused metal corrosion. When choosing ideal disinfection methods, the longevity of the drain metal must also be considered.

RES-208: Utilization of Stepwise Initial Therapy Evaluation by AST Pharmacists for Appropriate Vancomycin Use

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Background
Our hospital has promoted antimicrobial stewardship (AS) by revising antibiotic notification forms and conducting in-hospital conferences. To further improve AS and standardize vancomycin use, a stepwise assessment by antimicrobial stewardship team (AST) pharmacists was introduced at the start of therapy.

Method
From January to December 2024, patients administered vancomycin were classified using a five-step assessment. Evaluations from January to June (pre-intervention) were retrospective; those from July to December (post-intervention) were prospective. Appropriate use was defined as ① agreement with use, or ② agreement with agent but dose adjustment needed. Inappropriate use included ③ need to confirm necessity of MRSA coverage, ④ pathogen already identified, and ⑤ no cultures or unclear indication. Process indicators such as days of therapy, rate of culture specimen submission, therapeutic drug monitoring, and duration of antimicrobial administration were compared.

Results
No significant changes were seen in assessment classifications or process indicators. However, 87% of inappropriately assessed cases had discontinued vancomycin within seven days, indicating timely collaboration. Most inappropriate cases involved respiratory infections from a single department, with no MRSA isolation or history.

Conclusions
The structured, objective assessment supported standardized evaluation of vancomycin use. It helped prioritize issues requiring pharmacist–physician collaboration and improved communication. Stepwise evaluation may be an effective tool for advancing AS activities by identifying targets for intervention.

RES-209: Utility of DNA Sequencing Analysis of Fungi Derived from Airway Secretions in Patients with Refractory Asthma in the Diagnosis of Allergic Bronchopulmonary Mycosis

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Background
Allergic bronchopulmonary myosis (ABPM) is a chronic airway disease characterized by progressive destruction of the bronchi due to an allergic reaction to fungi inhaled into the trachea. ABPM is often caused by Aspergillus spp.; other fungi are rare. However, identification of this fungus is often difficult. The diagnosis of ABPM is important because patients with refractory asthma may develop this disease.

Method
We retrospectively selected patients with refractory asthma who visited our Hospital between September 2024 and June 2025 and evaluated the proportion of those with ABPM. Refractory asthma was defined based on the Japanese Respiratory Society (JRS) Guidelines for the Management of Refractory Asthma as asthma patients who require high-dose inhaled steroid therapy. We used DNA sequencing of the internal transcribed spacer (ITS) region and of the D1–D2 region to identify the fungi.

Results
The analysis included 42 patients with refractory asthma. We studied 42 patients (69% women) with a median age of 63 years. Two of the 42 patients were diagnosed with ABPM. Their sputum contained a filamentous fungus that was difficult to identify, and contamination was considered possible; however, DNA sequence analysis enabled the diagnosis of ABPM (Fusarium sp. and Penicillium spp.). In both cases, the mucus plugs that were present at the time of initial diagnosis disappeared, and asthma control was excellent.

Conclusions
The diagnosis of ABPM is important in refractory asthma. DNA sequencing is useful for identifying the causative organisms of ABPM.

RES-210: A Genomic Data Mining Study of Nine Major Non-Polio Enterovirus Serotypes

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Background
This study aimed to elucidate the evolutionary characteristics of nine major non-polio enterovirus serotypes (CVA2, CVA4, CVA6, CVA10, CVA16, CVB3, CVB5, EV-A71, and EV-D68) through genomic data mining, focusing on their spatiotemporal distribution and evolutionary dynamics.

Method
We employed a data mining framework integrating programming, phylogenetic analysis, Bayesian evolutionary modeling, and selection pressure assessment. Over 40,000 genomic sequences from GenBank were analyzed to reconstruct temporal phylogenies, estimate evolutionary rates, and characterize amino acid variability in the capsid protein. Seasonal decomposition and spatial-temporal trend modeling were applied to evaluate epidemic patterns across six WHO regions.

Results
This study yielded several key findings that include: (1) Distinct biennial/triennial epidemic cycles for EV-D68 and seasonal peaks for HFMD-associated serotypes; (2) The novel “60% to transcend” theory: when the cumulative VP1 nucleotide mutations reach 60%, the cumulative non-synonymous amino acid mutations begin to exceed 60%, particularly in antigenic loops; (3) Episodic positive selection at critical VP1 codons, suggesting immune-driven evolution; (4) The relative genetic diversity trends, with EV-A71, CVA16 and CVA6 have shown sustained expansion, while CVB5 and EV-D68 diversity has plummeted.

Conclusions
This study provides a data-driven framework for global pathogen spectrum monitoring and informs public health strategies against enterovirus threats.

RES-211: Correlation Analysis of Peripheral Blood Composite Inflammatory Indices in Differentiating SARS-CoV-2 Infected Patients with and without Pneumonia

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Background
With the emergence of various SARS-CoV-2 variants, the clinical manifestations of COVID-19 have become increasingly diverse. This study aimed to evaluate whether peripheral blood composite inflammatory indices—namely the neutrophil-to-lymphocyte ratio (NLR), platelet-to-lymphocyte ratio (PLR), monocyte-to-lymphocyte ratio (MLR), C-reactive protein-to-lymphocyte ratio (CLR), eosinophil-to-lymphocyte ratio (ELR), systemic immune-inflammation index (SII), systemic inflammation response index (SIRI), aggregate index of systemic inflammation (AISI), and multi-inflammatory index (MII)—can differentiate between patients with and without pneumonia in confirmed COVID-19 cases.

Method
This retrospective study included hospitalized patients with COVID-19 confirmed by RT-PCR from nasopharyngeal swabs, admitted via the emergency department between January 1 and June 30, 2022. Peripheral blood composite inflammatory indices—including NLR, PLR, MLR, CLR, ELR, SII, SIRI, AISI, and MII—were derived from complete blood count parameters. Receiver operating characteristic (ROC) curve analysis was performed to assess the diagnostic ability of each index.

Results
Of the 287 patients enrolled, 162 (56.4%) had pneumonia confirmed by chest radiography and computed tomography. The pneumonia group exhibited significantly higher levels of NLR, PLR, MLR, CLR, SII, SIRI, AISI, and MII ($P < 0.05$). ROC analysis showed that NLR (AUC = 0.710), SIRI (0.705), CLR (0.702), SII (0.701), and MII (0.701) effectively distinguished pneumonic from non-pneumonic cases.

Conclusions
Given the cost-effectiveness and widespread availability of complete blood count (CBC) testing, peripheral blood inflammatory indices such as NLR, CLR, SIRI, SII, and MII have demonstrated potential in identifying COVID-19-related pneumonia. These indices may facilitate early triage, clinical risk stratification, and optimal resource allocation in emergency settings, thereby improving patient management.

Table 2. ROC analysis of derived blood composite inflammatory indices.

Biomarker	Cut-off	Sensitivity (%)	Specificity (%)	AUC	95% CI	p-value	Youden's Index	Odds Ratio
CRP	0.460	88.3	38.4	0.649	0.586–0.711	<0.001	0.267	4.69
PCT	2.110	53.1	85.6	0.688	0.623–0.748	<0.001	0.387	6.73
NLR	3.228	85.8	50.4	0.710	0.650–0.768	<0.001	0.362	6.14
PLR	142.31	71.6	49.6	0.613	0.550–0.675	<0.001	0.212	2.48
CLR	0.501	85.8	46.4	0.702	0.644–0.759	<0.001	0.322	5.23
MLR	0.215	86.4	30.4	0.587	0.521–0.650	<0.001	0.168	2.78
ELR	0.132	27.8	80.8	0.535	0.469–0.597	0.0968	0.086	1.62
SII	901.24	70.4	64.8	0.701	0.638–0.760	<0.001	0.352	4.37
SIRI	2.318	73.5	64.0	0.705	0.643–0.765	<0.001	0.375	4.92
MII	5.903	72.8	57.6	0.701	0.642–0.758	<0.001	0.304	3.64
AISI	485.72	55.6	64.0	0.597	0.528–0.662	0.001	0.196	2.22

NLR (Neutrophil to lymphocyte ratio) = Neutrophil count / lymphocyte count

PLR (Platelet to lymphocyte ratio) = Platelet count / lymphocyte count

MLR (Monocyte to lymphocyte ratio) = Monocyte count / lymphocyte count

ELR (Eosinophil to lymphocyte ratio) = Eosinophil count / lymphocyte count

CLR (C-reactive protein to lymphocytes ratio) = C-reactive protein (CRP) / lymphocyte count

SII (Systemic inflammatory index) = Neutrophil count × PLR

SIRI (Systemic inflammation response index)=Neutrophil count × monocyte count / lymphocyte count

MII (Multi-inflammatory index) = NLR × CRP

AISI (Aggregate index of systemic inflammation) =Neutrophil count × monocyte count × platelet count / lymphocyte count

RES-212: Whole-Genome Characterization of Shiga Toxin-Producing Escherichia coli Isolated from Ghanaian Livestock

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[2]Noguchi Memorial Institute for Medical Research

Background
Shiga toxin-producing Escherichia coli (STEC) is a zoonotic pathogen of significant public health concern, requiring a One Health approach to clarify its transmission and distribution. However, its prevalence and genomic characteristics in livestock animals remain underexplored in low-income countries. Here, we investigated the prevalence and genomic features of STEC in Ghanaian livestock, representing the first genomic report of STEC in the country.

Method
A total of 97 fecal samples were collected from goats, sheep, dogs, and a cat at the Effia Nkwanta Regional Hospital of Ghana in 2023. STEC was screened using CHROMagar STEC media and multiplex PCR targeting stx1 and stx2 genes. Whole-genome sequencing analysis were performed for the STEC isolates.

Results
STEC was detected in 12.1% of goat and sheep samples, but not in dogs or the cat. Whole-genome sequencing identified serotypes O38:H26, O43:H2, and O157:H7. The stx1c and stx2b genes were detected in O38:H26 and O43:H2, whereas stx2c and key virulence genes (chuA, eae, esp, nle, tir, and toxB) were exclusively found in O157:H7. Phylogenetic analysis revealed that O38:H26 isolates form a cluster closely related to clinical strains from the UK. O43:H2 isolates exhibited diverse stx profiles, linking animal, environmental, and clinical strains from North America and the UK. O157:H7 isolates were genetically similar to European clinical and food-derived strains.

Conclusions
Detection of diverse STEC serotypes and virulence genes in Ghanaian goats and sheep highlights their role as reservoirs for human infection, providing data for public health risk assessment and informing One Health-based control strategies.

RES-213: The Dynamic Changes of Tetracycline Resistance Using Oxytetracycline as a Pig Feed Additive and the Impact of Co-Administering Clostridium butyricum MIYAIRI 588

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[3]Miyarisan Pharmaceutical Co., Ltd.
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Background
Antimicrobial use is the major driver for AMR in humans and animals in general. In this study, we examined the alteration of antimicrobial resistance organism (AMO) and/or antimicrobial resistance genes (ARGs) during antibiotic use in fattening piglets and possible effectiveness of probiotic treatment.

Method
A total 20 of LWD piglets (13-14 weeks old with approximately 20kg) were randomly allocated into 2 groups with only basal diet as control group and CBM group that contains probiotic strain of Clostridium butyricum MIYAIRI588 with >2.5X10^8CFU/kg of feed. All piglets received 400mg/kg feed of oxytetracycline (OTC) for 1 week after 3 weeks taming. Then, fecal samples were collected weekly and Enterobacteriaceae and tetracycline related genes (TRG) were quantified by culture and qPCR, respectively.

Results
The rate of OTC resistance of isolated Enterobacteriaceae increased from 60% at baseline to 100% after 1 week OTC treatment. It is possible that selection pressure was observed clearly by OTC administration. In addition, the number of OTC resistant Enterobacteriaceae increased approximately 1,000 times by OTC treatment. On the other hand, only 10 time-increase was detected in CBM treated group. Interestingly, tetA, tetW and tetX gradually decreased after discontinuation of OTC treatment but tetM was persistently identified in the fecal specimens and thus, TRG pattern might have some variation in the pig intestinal tract.

Conclusions
These results demonstrated that antimicrobial treatment induced more abundance of AMO as well as ARGs but probiotic treatment might interfere with these concerns.

RES-214: Examination of the Efforts of the Antimicrobial Stewardship Team and Their Impact on the Appropriate Use of Antimicrobials

Hiroshi Kimura[1], Yukiro Kurokawa[1], Takaaki Yano[1], Yuichi Murakami[2], Koichiro Suemori[2], Noriaki Hidaka[1], Hisamichi Tauchi[2], Mamoru Tanaka[1]

[1]Department of Pharmacy, Ehime University Hospital
[2]Division of Infection Control, Ehime University Hospital

Background
In Japan, a reimbursement incentive for Antimicrobial Stewardship Team (AST) activities was introduced with the 2018 revision of the national medical fee schedule. At Ehime University Hospital, an AST has been active since April 2018, including a full-time pharmacist. The team monitors the use of broad-spectrum antimicrobials, positive blood culture results, and intravenous antifungal agents. Weekly conferences are held to review consultations and discuss individual cases. This study aimed to evaluate the impact of AST interventions on antimicrobial utilization.

Method
We evaluated the number of AST consultations, the acceptance rate of recommendations, pharmacist involvement, blood culture sampling practices—including positivity rates and the proportion of two-set collections—as well as antimicrobial use indicators: antimicrobial use density (AUD), days of therapy (DOT), and the AUD/DOT ratio.

Results
The number of AST consultations increased from 207 in 2018 to 720 in 2024, with recommendation acceptance rates consistently around 90%. Pharmacist involvement rose from 86 to 174 cases. Blood culture sets increased from 3,026 (2018) to 4,083 (2023), with a stable two-set collection rate of 95%. Meropenem AUD declined from 2.21 (2018) to 1.62 (2024).

Conclusions
These findings suggest that AST activities have played a significant role in promoting appropriate antimicrobial use, as reflected by the increased volume of consultations, high acceptance rates of recommendations, improved blood culture practices, and reduced use of broad-spectrum antimicrobials.

RES-215: Predictive Values of Neutrophil-To-Lymphocyte, Neutrophil-To-Platelet, and Platelet-To-Lymphocyte Ratios for In-Hospital Mortality in Patients with Bacterial Bloodstream Infections

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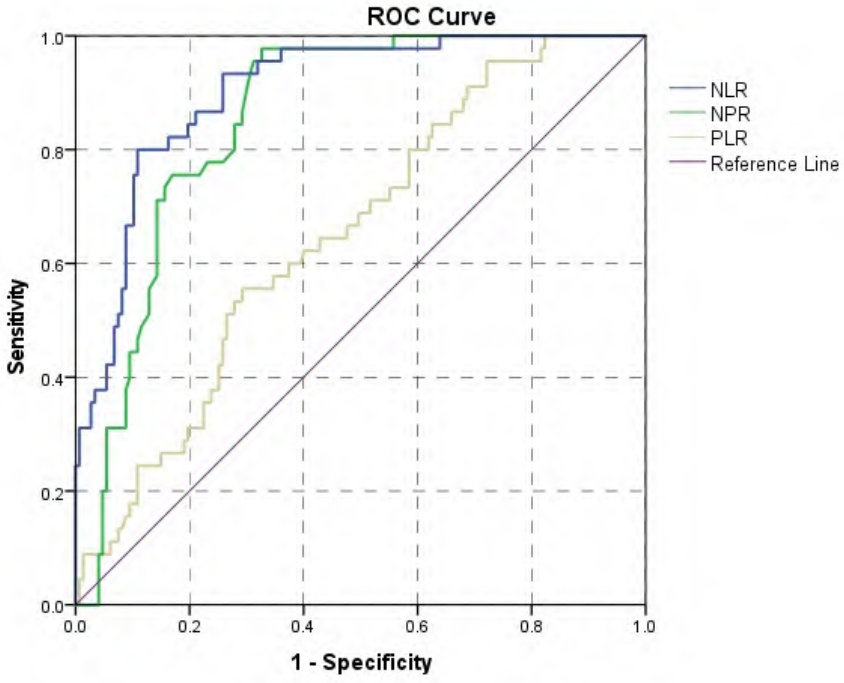
Background
Patients with bacterial bloodstream infections (BSIs) are associated with high morbidity and mortality. We aimed to investigate the early prognostic values of neutrophil-to-lymphocyte ratio (NLR), neutrophil-to-platelet ratio (NPR), and platelet-to-lymphocyte ratio (PLR), as well as determine their performance to predict in-hospital mortality in this population.

Method
This retrospective cohort study analyzed adult patients diagnosed with BIs during hospitalization at a tertiary hospital in Hanoi, Vietnam, between June 2024 and June 2025. Ratios from complete blood count data, including NLR, NPR, and PLR, were obtained on the day of admission. Additional data on demographics, laboratory results, microbiology, and clinical interventions were extracted from electronic medical records. The prognostic value and predictive performance of these ratios were assessed using logistic regression and receiver operating characteristic (ROC) curve analysis, respectively.

Results
Among the 192 patients included, the in-hospital mortality rate was 23.4% (45), with non-survivors exhibiting significantly higher levels of NLR, NPR, and PLR compared with the survivors. Escherichia coli and Klebsiella pneumoniae were the predominant pathogens of BIs. Multivariate logistic regression analysis demonstrated that elevated levels of NLR (aOR= 1.11, 95%CI= 1.070-1.153, p<0.001), NPR (aOR=14.484, 95% CI= 2.402-49.628, p=0.007), or PLR (aOR=1.003, 95% CI=1.001-1.004, p=0.012) were independently associated with increased risk of mortality. Of the three ratios, the performance of NLR in predicting in-hospital mortality was highest (AUC=0.902), followed by NPR (AUC=0.854) and PLR (AUC=0.650).

Conclusions
Our study revealed that NLR, NPR, and PLR could serve as early prognostic indicators of in-hospital mortality in adult Vietnamese patients with Bis.



RES-216: Microbiological Characteristics of Acute Cholangitis with Biliary-Enteric Anastomosis or Biliary Intervention

Yuta Kuhara, Hiroki Kitagawa, Norifumi Shigemoto, Yuki Kaiki, Masahide Miyata, Hirofumi Doi, Kensuke Shimbara, Ikki Nakashima, Kosuke Yoshimura, Shinnosuke Uegami, Shinya Takahashi, Hiroki Ohge

Hiroshima University Hospital

Background
We aimed to investigate the microbiological characteristics of pathogens isolated from blood cultures of patients with acute cholangitis (AC) after biliary-enteric anastomosis and biliary interventions. Based on these characteristics, we also investigated the appropriate antibiotic selection for these AC patients.

Method
A retrospective analysis was conducted on 366 patients diagnosed with AC and bacteremia between January 2015 and December 2024. Patients were categorized into three groups: AC after biliary-enteric anastomosis (A), AC associated with biliary interventions such as internal biliary stents or endoscopic sphincterotomy (B), and AC without any biliary procedures (C). Clinical characteristics of patients and microbiological characteristics of pathogens isolated from blood cultures were analyzed.

Results
The incidence of liver abscesses was significantly higher in group A (23%, $P < 0.001$). The most frequently isolated pathogens were Escherichia coli and Klebsiella spp. in all groups. ESCPM spp. (Enterobacter spp., including Klebsiella aerogenes, Serratia marcescens, Citrobacter freundii complex, Providencia spp., and Morganella morganii) were more frequently isolated in group A and B (A vs. C: 10% vs. 1.9%, $P = 0.047$; B vs. C: 15% vs. 1.9%, $P < 0.001$).The isolation rate of anaerobic bacteria showed no significant differences among the groups ($P = 0.073$).

Conclusions
Based on the isolation patterns of ESCPM spp., the history of biliary-enteric anastomosis or biliary interventions should be considered when determining the treatment strategy for acute cholangitis. For acute cholangitis with such a history, cefepime may be a better antibiotic option, particularly in severe cases.

RES-217: Weekly Antimicrobial Prophylaxis for Recurrent Symptomatic Urinary Tract Infections: A Randomized Controlled Trial

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Background
Background: Long term antimicrobial prophylaxis (AP) for recurrent symptomatic urinary tract infections (R-UTIs), is generally discouraged, given increased antimicrobial resistance (AMR). Beside AMR, complicated R-UTIs in adult patients with co-morbidities and/or indwelling urethral catheters, are associated with hospitalization, morbidity and mortality. The efficacy of once weekly AP to reduce R-UTIs, hospitalization, and emergence of antimicrobial resistance in Thailand, remain unclear.

Method
Methods: The randomized (1:1), open-label controlled trial of one weekly AP (intervention group, n=19) versus no AP (control group, n=19), was conducted in medical or surgical patients with catheter or noncatheter associated R-UTIs for 6 months. The primary outcome was the incidence of R-UTIs. Secondary outcomes included total and UTI-related hospitalization and incidence of emergent multidrug-resistant (MDR) uropathogen.

Results
Results: Baseline characteristics of eligible patients were comparable between groups. Incidence rate of overall R-UTIs and total hospitalization in the intervention group were significantly lower than those in the control group, 4.1 (2.4–7.0) versus 8.1 (5.6–11.9) episodes per 1,000 patient-days (95% CI), P = 0.03, and 7 versus 14 days, P = 0.03, respectively. Incidence rates of emergent MDR isolates were not significantly different between groups, (1.9 versus 3.6 episodes per 1,000 patient-days; P = 0.22), respectively. The AP agents were safe and well-tolerated.

Conclusions
Conclusion: Once weekly antimicrobial prophylaxis effectively reduces recurrent symptomatic catheter or noncatheter associated urinary tract infections and hospitalization without increased antimicrobial-resistance in medical or surgical patients. Further large-scale study on long-term efficacy and safety is warranted.

Primary outcome

Table 2. Overall and stratified UTI incidence rates of the study participants.

Category	Group	Total Episodes	Incidence Rate (per 1,000 patient-days)	95% CI	P-value
Overall UTI	Intervention	13	4.1	2.4 - 7.0	0.03*
	Control	26	8.1	5.6 - 11.9	
Lower tract UTI	Intervention	10	3.1	1.7 - 5.8	0.06
	Control	20	6.2	4.0 - 9.7	
Upper tract UTI	Intervention	3	0.9	0.3 - 2.9	0.31
	Control	6	1.9	0.8 - 4.2	

*p-value = < 0.05

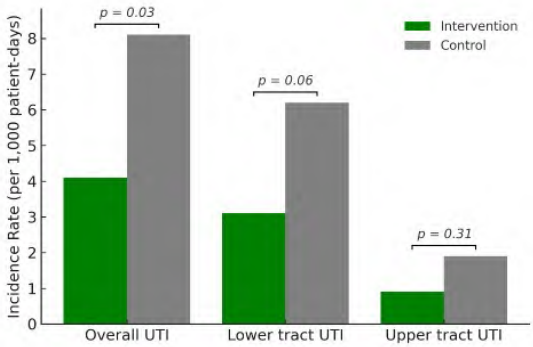

Figure 2. Overall and stratified UTI incidence rates of the study participants

RES-218: Achievement of Clinical Decision Support Systems (CDSS) on Optimizing Antibiotic Usage and Reducing Medication Costs in a Tertiary Hospital in Thailand

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Sunpasitthiprasong Hospital

Background

Sappasitthiprasong Hospital, a tertiary hospital in Thailand, reported that 54.5% of bloodstream infections involved drug-resistant pathogens, and 54.84% of Tigecycline prescriptions were inappropriate. To address this, a multidisciplinary team implemented a Clinical Decision Support System (CDSS) in September 2022 to optimize antibiotic use, particularly Tigecycline. The platform integrates guidelines, monitoring tools, and dosing calculators to support Antimicrobial Stewardship (AMS) decisions.
Objectives:
1. Compare monthly defined daily doses (DDD) of Tigecycline per 100 patient-days before and after CDSS
2. Assess AMS intervention rates and cost impact

Method

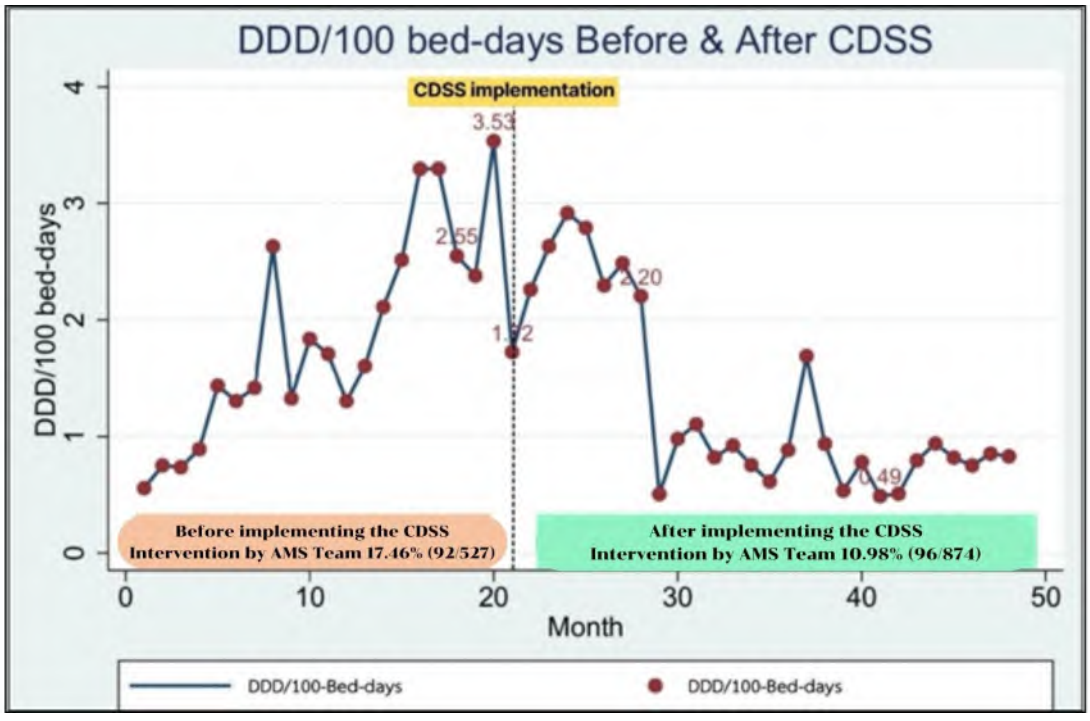
A retrospective study (Jan 2021–Dec 2024) using Interrupted Time Series Analysis and linear regression assessed trends in Tigecycline use and AMS interventions.

Results

Before CDSS, Tigecycline use rose by 0.13 DDD/month; after implementation, it declined by 0.07 DDD/month ($p < 0.001$). This reflected a 6.99% monthly increase pre-CDSS and a 5.47% decrease post-CDSS. An immediate 51.27% reduction was observed ($p < 0.001$). Over 28 months, cumulative use declined by 1.97 DDD per 100 patient-days ($p < 0.001$). AMS interventions fell from 17.46% to 10.98% ($p = 0.001$) [Picture 1]. Monthly Tigecycline costs dropped by ~88,129 THB (~2,415 USD), with average savings of 584,953 THB/month (~16,027 USD).

Conclusions

CDSS implementation improved antibiotic appropriateness, reduced AMS workload, and generated substantial cost savings. Local adaptation and user engagement are key to sustainability.



RES-221: Epidemiology of Healthcare-Associated Infections, Antimicrobial Resistance Patterns, and Hospital Antimicrobial Consumption in the Republic of Kazakhstan: Results of a Pilot Study

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Nazarbayev University School of Medicine

Background
Healthcare-associated infections (HAIs) are an emerging global health threat. Common HAIs include surgical site infections, urinary tract infections, pneumonia, and bloodstream infections. Although numerous studies have investigated the prevalence of HAIs worldwide, there is a paucity of data from post-Soviet countries. This study aims to fill this gap by presenting findings from a pilot study on the epidemiology of HAIs, associated resistance patterns, and antimicrobial use in four acute care hospitals in Kazakhstan.

Method
The study followed the methodology developed by the European Centre for Disease Prevention and Control and included 701 patients. Patient files were reviewed to extract information on antimicrobial use and HAIs. Data were analyzed using SPSS (version 24).

Results
The overall rate of HAIs was 3.8%. The highest rate was observed in intensive care units (ICUs) (48.1% of all HAI cases), followed by surgical departments (40.7%). Pneumonia was the most common type of HAI followed by urinary tract infection. Pseudomonas aeruginosa was the most frequently isolated pathogen, followed by Enterococcus faecalis. Resistance to carbapenems was the most commonly observed, followed by resistance to glycopeptides and third-generation cephalosporins. Of the 701 patients, 268 (38.2%) were prescribed antimicrobials, with up to four antibiotics prescribed simultaneously to some patients. In ICUs, antimicrobials were prescribed to 80.2% of patients. Ceftriaxone was the most commonly administered antibiotic, followed by cefazolin.

Conclusions
The findings of this study provide important insights into the current burden of HAIs in Kazakhstan and may help inform national strategies for HAIs prevention and antimicrobial stewardship.

RES-222: Implementation and Prospective Evaluation of a Machine Learning-based Early Warning System for Multidrug-resistant Organisms

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Background
While retrospective prediction of multidrug-resistant organisms (MDROs) is well documented, prospective evidence remains limited. This study implemented and evaluated a machine learning-based system to prospectively identify patients at risk of MDRO colonization or infection before microbiological confirmation.

Method
The MDRO detection system (Figure 1) was deployed at a 1200-bed university hospital in Thailand, integrated in real-time with the electronic health records (EHR). It was trained on historical data (1/1/2023-31/8/2024; 39,223 admissions) to predict 7-day risk of colonization/infection with extended-spectrum β-lactamase (ESBL)-producing Enterobacterales, carbapenem-resistant Enterobacterales (CRE), carbapenem-resistant A. baumannii or P.aeruginosa (CRAB/CRPA), methicillin-resistant S. aureus (MRSA), and vancomycin-resistant Enterococci (VRE). Prospective data collection began 1/9/2024 using live EHR feeds (microbiology, pharmacy, admissions) to generate daily predictions, which were evaluated against available microbiological results.

Results
Predictive performance post-training remained robust for CRE, VRE, and CRAB/CRPA (AUC-ROC >0.82), with CRE at 0.89 (Figure 2). The CRE model's performance dropped marginally from 0.92 to 0.89 in AUC-ROC. Key CRE predictors included catheter days, contact with CRE patients, and hospital stay duration (Figure). MRSA and ESBL performance was lower (0.70 and 0.65 AUC-ROC), likely due to the absence of a local screening program.

Conclusions
This proof-of-concept deployment demonstrates that machine learning can provide early MDRO warnings in acute care. Daily predictions allow up to 7-day foresight for high-risk patients, enabling proactive infection control. Future steps include extended evaluation and validation in previously non-screened cohorts.

Figure 1. Overview of the MDRO early detection system. Real-time data feeds from the electronic health record (EHR)—including laboratory, pharmacy, admission, and device data—are used to generate daily predictions of patient-level risk of colonisation or infection with multidrug-resistant organisms (MDROs). The system provides a 7-day risk forecast to enable earlier investigation and targeted infection control interventions.

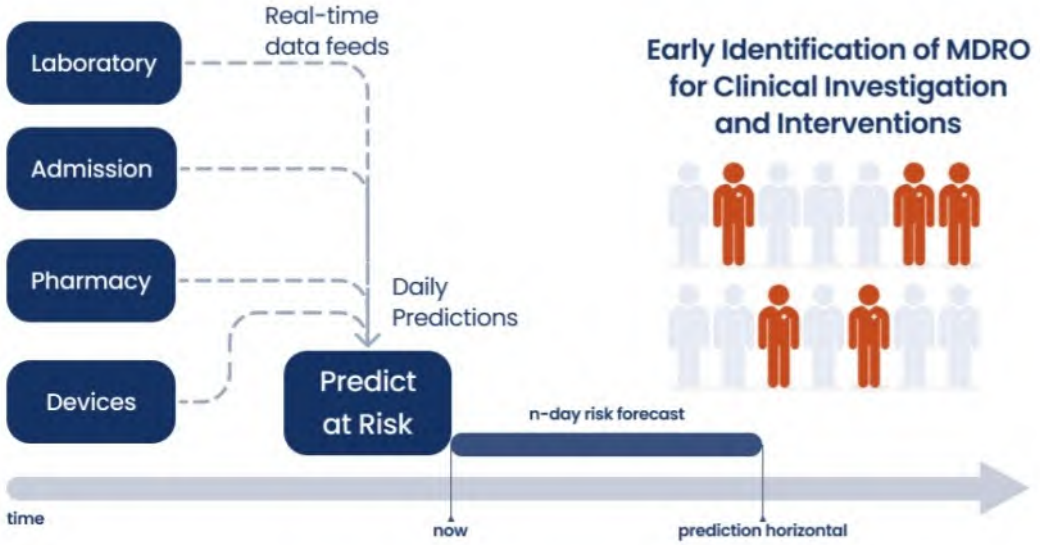

Table 1. Predictive performance of the MDRO detection system during the training (1/1/2023–31/8/2024) and prospective testing period (post 1/9/2024), reported as AUC-ROC. CRE, VRE, and CRAB/CRPA maintained strong generalisability in prospective evaluation (AUC-ROC ≥ 0.83), while ESBL and MRSA showed reduced performance due to the absence of a routine surveillance programme.

Condition Label	**Training Period (1/1/2023–31/8/2024)** **AUC-ROC (2dp)**	**Testing Period (post 1/9/2024)** **AUC-ROC (2dp)**	**Generalisability to Future** **Decrease in AUC-ROC (2dp)**
CRE	0.92	0.89	0.03
VRE	0.94	0.85	0.09
CRPA/CRAB	0.88	0.83	0.05
ESBL	0.84	0.71	0.13
MRSA	0.85	0.65	0.20

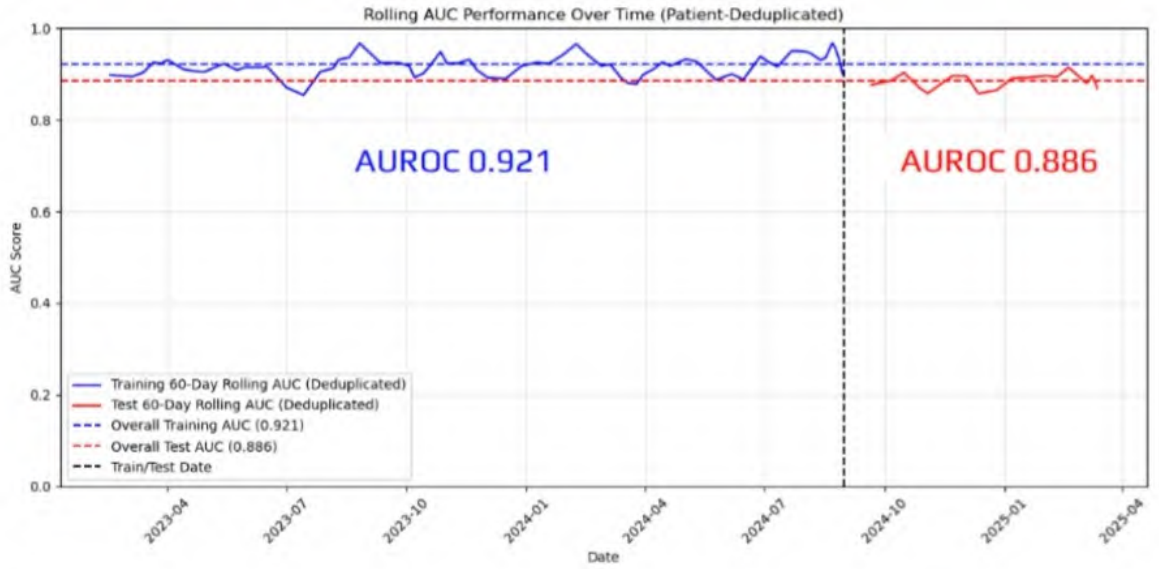

Figure 2. Rolling 60-day AUC-ROC for CRE prediction using the MDRO detection system. Model performance remained stable during training (AUC-ROC 0.921) and generalised well during the prospective evaluation period (AUC-ROC 0.886). The slight decline highlights a consistent, high-performing model across both retrospective and real-time collection settings.

RES-223: Association of HIV-1 Drug Resistance Mutations and Clinical Outcomes Among Patients with First-Line Antiretroviral Therapy Failure in the Philippines

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Research Institute for Tropical Medicine

Background
HIV drug resistance mutations affect antiretroviral therapy (ART), leading to disease progression and the development of opportunistic infections.

Method
This retrospective cohort study involved 142 adult patients with treatment failure to first-line antiretroviral therapy. Sociodemographic, clinical, laboratory, and genotypic data were abstracted. HIV subtypes and drug resistance mutations were identified via Sanger sequencing. Associations between resistance status, occurrence of any infection, and mortality were then examined using chi-square tests and multivariate logistic regression, adjusting for confounders.

Results
Of 142 patients with first-line ART failure, CRF01_AE subtype predominated (73%), consistent with the local epidemiologic shift. 52.8% harbored at least one HIV drug resistance mutation. NNRTI resistance was most frequent (94.7%), followed by NRTI (76.0%) and PI (9.3%) resistance. Dual-class resistance (NRTI + NNRTI) occurred in 66.7%. Opportunistic infections were more common among those with drug resistance (50.6% vs. 22.3%; OR 3.56, $p < 0.001$), with pulmonary tuberculosis most prevalent (29.3% vs. 7.4%; OR 5.84, $p < 0.001$). Mortality among resistant patients was higher than non-resistant patients, aligning with analyses showing that drug resistance significantly increases HIV/AIDS-associated mortality. The K65R mutation was associated with significantly lower odds of PTB (OR 0.16; $p = 0.007$) and OIs on multivariate analysis (OR 0.27; $p = 0.013$). Dual mutations involving M184V, K103N, and K65R were most commonly observed.

Conclusions
Dual-class resistance driven by M184V, K103N, and K65R dominated first-line ART failures and was strongly associated with opportunistic infections—particularly tuberculosis—and mortality. This highlights the need for routine viral-load monitoring, subtype-aware resistance testing, TB integration, high-barrier regimens, and adherence support.

Table 1. Association between HIV Drug Resistance and clinical outcomes

Clinical Outcome	With Resistance (n=75)	Without Resistance (n=67)	p-value	OR (95% CI)
Any Infection	53 (70.6%)	24 (35.82%)	< 0.001	4.32 (2.13-8.73)
Opportunistic Infections	38 (50.6%)	15 (20%)	< 0.001	3.56 (1.71-7.4)
CMV Retinitis	6 (8.0%)	2 (2.99%)	0.213	2.83 (0.55-14.51)
Pneumocystis Pneumonia	7 (9.33%)	4 (5.97%)	0.458	1.62 (0.45-5.80)
Pulmonary TB	24 (32%)	5 (7.46%)	< 0.001	5.84 (2.08-16.38)
Tuberculous Adenitis	8 (10.67%)	3 (4.48%)	0.181	2.55 (0.65-10.03)
Other Co-Infection	15 (20.0%)	9 (12.0%)	0.21	1.61 (0.65-3.97)
All-Cause Mortality	7 (9.33%)	2 (2.99%)	0.141	3.35 (0.67-16.70)
Absence of Opportunistic Infection and Other Co-Infection	15 (20.0%)	41 (61.19%)	< 0.001	0.16 (0.07-0.34)

RES-224: Clinical Diagnostic Performance of Digital PCR for Pathogen Detection in Patients with Klebsiella pneumoniae Bloodstream Infections

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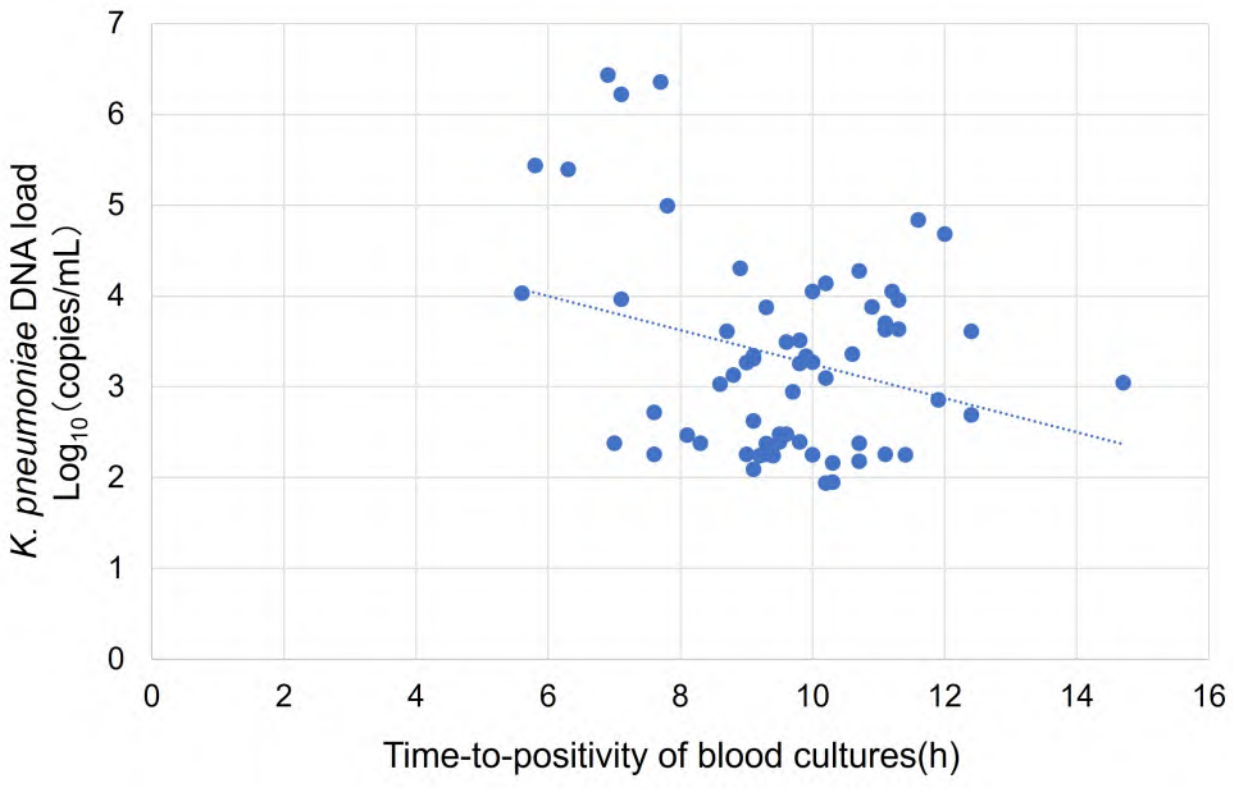
Hiroshima University Hospital

Background
This study aimed to examine the sensitivity and specificity of digital PCR (dPCR) and the association between bacterial DNA load in whole blood and the time-to-positivity (TTP) of blood cultures (BCs) in patients with Klebsiella pneumoniae (KP) BSIs.

Method
This study included adult patients with KP BSIs confirmed using BCs treated at our hospital from June 2023 to June 2025. The KP DNA load in whole blood was evaluated using dPCR. The KP specific primers and probes and primers and probes targeting CTX-M gene were used for dPCR. Whole blood samples from 50 patients with BC positive for pathogens other than KP (n=25) and BC negative (n=25) were also evaluated using dPCR.

Results
Of the 72 patients with KP BSIs, dPCR detected KP DNA in 63 (87.5%). The results of dPCR for KP had a sensitivity of 87.5% (95%CI 77.9-93.3), specificity of 100% (95%CI 92.8-100). Patients with positive dPCR results had significantly shorter TTP than those with negative results (median, 9.6 h vs. 10.4 h, p=0.046). Among dPCR-positive patients, patients with septic shock (n=11) had higher KP DNA load in whole blood (median, 98,932 copies/mL vs. 983 copies/mL, p < 0.001) and shorter TTP (median, 7.1 h vs. 9.8 h, p=0.004) compared with patients without septic shock. Among dPCR-positive patients, all patients with ESBL positive KP BSIs were positive for CTX-M gene.

Conclusions
Overall, dPCR effectively detected KP DNA in the whole blood of patients with KP BSI with a relatively short TTP. A higher KP DNA load is associated with septic shock.



RES-225: Mechanistic Insights into (p)ppGpp Mediated Survival of Neisseria meningitidis Under Nutrient Stress

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Background
Invasive meningococcal disease caused by Neisseria meningitidis is associated with a high mortality rate. The bacterial response to environmental stress is a critical factor in the infection process. One of the well-known bacterial stress adaptation systems in bacteria is the stringent response, mediated by the second messenger (p)ppGpp. However, many aspects in N. meningitidis remain unrevealed. This study aimed to investigate how (p)ppGpp contributes to the survival of N. meningitidis under amino acid starving conditions.

Method
N. meningitidis strain MC58 was used as a parental strain. A (p)ppGpp synthase gene deleted mutant (ΔrelA), a double mutant lacking both the synthase and hydrolase genes (ΔrelAΔspoT), and a ΔrelA complemented with relA+ strain (ΔrelA-relA+) were constructed. Growth kinetics and intracellular ppGpp levels were analyzed under amino acid starving conditions. To identify (p)ppGpp-responsive genes and metabolic pathways under amino acid starving conditions, transcriptomic analysis was performed.

Results
Both ΔrelA and ΔrelAΔspoT mutants exhibited growth defects and significantly reduced ppGpp levels under amino acid starving conditions. Transcriptomic analysis revealed 541 and 567 differentially expressed genes in the ΔrelA and ΔrelAΔspoT mutants, respectively. Gene Ontology (GO) enrichment analysis showed significant enrichment of protein translation-related GO terms (e.g., cellular component, ribosome GO:0005840) in both mutants. KEGG pathway analysis also identified enrichment of the ribosome pathway (ko03010), partially consistent with the GO results.

Conclusions
These findings suggest that N. meningitidis modulates metabolic processes via (p)ppGpp-dependent regulation of protein translation during amino acid starvation to promote survival.

RES-226: Clinical Manifestations, Laboratory Characteristics, and Outcomes of COVID-19 and Influenza in Hospitalized Patients at the Hospital for Tropical Diseases, Thailand

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Background
Seasonal influenza and COVID-19 are leading causes of severe respiratory disease and hospitalization worldwide, yet comparative data from developing countries remain limited. We evaluated clinical, laboratory, and outcome differences between the two infections in a tertiary care setting in Thailand.

Method
We performed a retrospective review of medical records for hospitalized patients with laboratory-confirmed COVID-19 (n = 215) and influenza (n = 53), admitted from January 2020 to June 2024 at the Hospital for Tropical Diseases, Bangkok. Demographics, comorbidities, symptoms, laboratory values, complications, intensive care unit (ICU) admission, length of stay, and mortality were analyzed.

Results
Influenza patients were significantly older and had a higher prevalence of underlying comorbidities. Although symptom profiles overlapped, fever, abdominal pain, and nausea/vomiting were more common in influenza. Laboratory and chest x-ray did not demonstrate the difference significantly. Complication and ICU-admission rates did not differ significantly, but COVID-19 patients had a longer median hospital stay and higher in-hospital mortality.

Conclusions
In this cohort, influenza more frequently presents with fever and gastrointestinal symptoms, while COVID-19 is associated with prolonged hospitalization and increased mortality despite similar levels of complications. These findings support targeted resource allocation and strengthen clinical differentiation strategies in settings with overlapping viral respiratory epidemics.

RES-231: Impact of Epstein–Barr Virus Genomic Alterations in Human Diseases and Oncogenesis

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Department of Virology, Nagoya City University Graduate School of Medical Sciences

Background
Epstein–Barr virus (EBV) infects over 90% of the global population and contributes to a broad range of human pathologies. Although its oncogenic potential is well established, the biological significance of EBV genomic alterations, particularly structural variants and mutations involved in immune evasion, remains still unclear. To address this, we comprehensively characterize EBV genomic variations across multiple disease contexts and evaluate their functional significance in oncogenesis.

Method
We conducted genomic profiling of 990 EBV genomes derived from EBV-associated diseases across diverse geographical regions. Both single nucleotide variants (SNVs) and structural variations (SVs) were systematically characterized, and relevant alterations were functionally validated using EBV-transformed B cell lines.

Results
Phylogenetic analysis revealed distinct geographical clustering of EBV SNVs. Convergent mutations were more frequently observed in EBNA2, EBNA3B and LMP1 with patterns suggesting immune-mediated selective pressure. Notably, a previously unrecognized immunogenic epitope within EBNA3B (amino acid 198–206) was identified as a recurrent mutation hotspot in Japanese samples, with strong binding to HLA-B35:01, suggesting host-specific immune selection. In parallel, structural variations, particularly large intragenic deletions, were enriched in haematological malignancies and uncommon in epithelial tumors or benign infections. Among these, EBNA3B emerged as one of the most frequently deleted regions. Functional studies revealed that EBNA3B knockout resulted in the downregulation of human tumor suppressor genes such as, PTEN and RB1, thereby supporting its role as a viral tumor suppressor.

Conclusions
Our study reveals EBV genomic alterations reflect immune pressure and disease context. A novel EBNA3B epitope highlights immune-driven evolution, while deletions support its tumor suppressive and therapeutic relevance.

RES-232: Single-Cell Metagenomic Profiling of Antimicrobial Resistance in Escherichia coli from the Densu River, Ghana

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[2]Department of Molecular Microbiology and Immunology, Graduate School of Medicine and Dental Science, Institute of Science Tokyo, Japan

Background
River water is a natural reservoir for antimicrobial resistance (AMR) genes, posing a growing threat to public health, particularly in developing countries where environmental surveillance is limited.

Method
In this study, we applied single-cell metagenomic analysis to investigate aquatic AMR profiles in bacterial strains isolated from the Densu River in Ghana.

Results
Following antimicrobial selection, 16S rRNA amplicon sequencing revealed a predominance of the genus Escherichia-Shigella. Single-cell metagenomic analysis uncovered strain-level diversity in Escherichia coli, including variants producing CTX-M-15 extended-spectrum β-lactamase. Pan-genomic analysis using Anvi'o identified 4,814 gene clusters, of which 2,264 were accessory genes and 605 were singletons. Phylogenetic reconstruction using the maximum likelihood method classified the isolates into three clades. Functional annotation using Cluster of Orthologous Genes revealed differences in gene function distributions.

Conclusions
These findings demonstrate that single-cell metagenomics enables ultrahigh-resolution characterization of AMR and virulence traits, surpassing the limitations of conventional bulk metagenomic approaches. This method provides a powerful tool for monitoring environmental AMR in regions with limited infrastructure and may contribute to the development of targeted strategies for AMR mitigation. Our approach lays the groundwork for establishing a robust surveillance system for AMR pathogens in aquatic ecosystems, particularly in under-resourced settings.

RES-233: The Impact of COVID-19 Pandemic on H. Influenzae Disease in One Community Hospital

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[2]Chia-Yi Hospital

Background
H. influenzae (HI) are important pathogens between toddler and elderly patients. Our hospital works as a community one and takes care of elderly patients. During the year of 2019 and 2024, the epidemics of COVID-19 infection are rise and flow. It might change the pattern of disease and ecology of bacteria. So, we want to investigate the trend and change of these effect.

Method
From Datong Collaboration System, we can obtain the HI patients from positive culture of clinical specimens during 2019 and 2024. Later, we seek whether other accompanying bacteria or not. Then, we collect the demographic and outcome of these patients. Finally, we would compare the impact of COVID-19.

Results
1. During the six years, there are 846 HI infection included. The infection sites are more at sputum (89.2%).
2. Male to female is 1.6 to 1. The distribution of age are more at elderly (>65y/o, 86%).
3. The outcome of these patients are maybe-discharge (65.7%), died (29.2%), hospitalized (2.6%) and others (2.5%).
4. There are 411 (48.6%) HI patients with accompanying bacteria.

Conclusions
1. HI are important pathogens in the hospitalized patients. The prevalence rate are higher at elderly, especial with men.
2. The crude mortality rate at our hospital are 29.2%. The mortality rate of male are higher than female.
3. There are 48.6% HI patients with accompanying bacteria. It might be due to HI need factor V, X for growth.

RES-235: Closing Diagnostic Gaps in Respiratory Infections: A 40-Target Multiplex PCR Assay for Comprehensive Pathogen Detection

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Background
Respiratory tract infections (RTIs) remain a leading global health burden, with upper RTIs accounting for approximately 12.8 billion cases annually and lower RTIs causing over 2.4 million deaths worldwide. The emergence of pathogens such as SARS-CoV-2, influenza A/B, and novel variants, along with frequent bacterial co-infections, highlights the urgent need for rapid and comprehensive diagnostics to support clinical decision-making and antimicrobial stewardship.

Method
We developed the Respiratory Pathogens Panel 40 (RPP-40), a high-throughput multiplex PCR assay combining quantitative melting curve analysis with dual-reaction detection of 40 respiratory pathogens: 19 viruses, 13 bacteria, and 8 fungal or atypical organisms. The assay was integrated into a fully automated, sample-to-result platform suitable for point-of-care testing. Analytical validation established the 95% limits of detection (LOD) for each target. Clinical performance was assessed using 1,039 diverse specimens, including sputum, oropharyngeal swabs, and bronchoalveolar lavage fluid (BALF), with results compared against metagenomic next-generation sequencing (mNGS).

Results
The RPP-40 assay delivers results within 2.5 hours from raw clinical samples with minimal hands-on time. All targets demonstrated LODs below 500 copies/mL. In clinical evaluation, RPP-40 showed superior sensitivity and specificity compared to mNGS, with findings validated by independent real-time PCR assays.

Conclusions
The RPP-40 assay fills critical gaps in respiratory diagnostics by offering a robust, rapid, and scalable solution for comprehensive detection of respiratory pathogens. Its automation-ready design and high diagnostic accuracy make it well-suited for both routine clinical use and outbreak-response scenarios, aligning with global priorities for enhanced RTI management and evidence-based antimicrobial prescribing.

RES-236: Antimicrobial Stewardship: Knowledge, Attitude and Practices of Healthcare Providers in Tertiary- Care Hospitals in Pakistan

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National Institute of Health Pakistan

Background
Antimicrobial resistance is a critical global threat, driven by antibiotic misuse and overuse in humans, animals and agriculture. Healthcare providers (HCPs) are pivotal in stewardship efforts to combat the AMR crisis. The study aims to strengthen Antimicrobial Stewardship Program (AMS) in hospitals of Pakistan to optimize antimicrobial use (AMU). Unchecked use of antibiotics is predicted to cost more than 10 million deaths annually by 2050 and place an ever-growing burden on the economy.

Method
A cross-sectional study was conducted among 386 Healthcare Providers (HCPs) to assess the Knowledge, Attitude and Practice (KAP) on Antimicrobial Stewardship (AMS) in public and private hospitals of Sialkot and Islamabad, Pakistan (07/23–12/23). A pre-tested semi-structured questionnaire was administered using systematic random sampling. Descriptive and inferential statistics of KAP survey data were performed using SPSS.

Results
Among 386 HCPs, mean scores show leadership (2.92, $p = 0.041$), accountability (3.05, $p = 0.012$), pharmacy expertise (2.95, $p = 0.056$), education practices (3.02, $p = 0.018$), antimicrobial use and tracking (3.01, $p = 0.023$, 3.27, $p < 0.001$) respectively. A significant difference in AMS knowledge (62.1%, $p < 0.01$), attitude (42.0%, $p = 0.045$), and practice (26.7%, $p = 0.012$) was observed. In addition, a remarkable association was found between accountability and tracking in private hospitals ($p = 0.028$).

Conclusions
This study highlights gaps in knowledge, inconsistent attitudes, and suboptimal AMS practices among HCPs. It identifies the need for strong leadership and policy implementation, targeted educational interventions and trainings to strengthen AMS practices in HCPs of Pakistan.

RES-237: Is Empiric Antipseudomonal Therapy Needed in Culture-Negative Hospital-Acquired Pneumonia?

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Background
Hospital-acquired pneumonia (HAP) is commonly caused by gram-positive and gram-negative bacteria, including Pseudomonas aeruginosa. Broad-spectrum antibiotics should be de-escalated once improvement is observed and resistant pathogens are not isolated to reduce antibiotic selection pressure and adverse events. However, sputum samples often have poor yield. With limited guidance on de-escalation therapies, this retrospective study compared the efficacy and safety of adjunct oral ciprofloxacin plus amoxicillin-clavulanate with oral amoxicillin-clavulanate monotherapy in de-escalation therapy for culture-negative HAP.

Method
This study included patients initiated on intravenous piperacillin-tazobactam for culture-negative HAP between August 2022 and January 2023 who were de-escalated to the oral regimens of interest. The primary outcome was 30-day mortality. Multivariate logistic regression was used to determine the effect of independent variables on 30-day mortality. Secondary outcomes were clinical cure, pneumonia recurrence, adverse events and multidrug-resistant organism acquisition.

Results
Of 175 patients included, 71 patients (40.6%) received adjunct ciprofloxacin whereas 104 patients (59.4%) received amoxicillin-clavulanate monotherapy. Baseline characteristics were comparable but amongst those receiving adjunct ciprofloxacin, there was a higher proportion of patients with late-onset HAP and a lower proportion with complicated pneumonia and intensive care unit admissions compared with those on monotherapy. Thirty-day mortality did not differ significantly between both groups (12.67% vs 12.50%, p-value = 0.97). Secondary outcomes were also comparable. Oral amoxicillin-clavulanate monotherapy was not associated with 30-day mortality (adjusted odds ratio: 0.92, 95% confidence interval: 0.34 – 2.49).

Conclusions
Efficacy and safety outcomes were comparable between both groups. Adjunct ciprofloxacin may not be necessary in empiric step-down oral therapy for culture-negative HAP.

Table 1. Comparison of efficacy and safety outcomes between patients who received oral amoxicillin-clavulanate monotherapy and oral amoxicillin-clavulanate with adjunct ciprofloxacin for culture-negative HAP

Outcome	Oral amoxicillin-clavulanate and ciprofloxacin (n=71)[a]	Oral amoxicillin-clavulanate (n=104)[a]	p-value
Mortality	9 (12.67)	13 (12.50)	0.97
Clinical cure	58 (81.69)	87 (83.65)	0.74
Recurrence	19 (26.76)	21 (20.19)	0.31
Adverse events	4 (5.63)	10 (9.62)	0.34
Multidrug-resistant organism acquisition	3 (4.23)	3 (2.88)	0.69

[a]Expressed as number (%)

Table 2. Univariate and multivariate analysis of 30-day mortality in patients who received oral amoxicillin-clavulanate monotherapy versus oral amoxicillin-clavulanate with adjunct ciprofloxacin for culture-negative HAP

	Univariate analysis		Multivariate analysis	
	Adjusted odds ratio (95% confidence interval)	p-value	Adjusted odds ratio (95% confidence interval)	p-value
Monotherapy (Oral amoxicillin-clavulanate)	0.98 (0.40 – 2.44)	0.97	0.92 (0.34 – 2.49)	0.86
Age	1.01 (0.98 – 1.05)	0.48	0.99 (0.95 – 1.04)	0.80
Chinese	1.86 (0.41 – 8.49)	0.42	1.46 (0.29 – 7.33)	0.64
Complicated pneumonia	1.85 (0.62 – 5.55)	0.27	1.44 (0.44 – 4.72)	0.54
Chronic obstructive pulmonary disease	2.21 (0.66 – 7.44)	0.20	2.27 (0.58 – 8.87)	0.24
Bronchiectasis	2.09 (0.41 – 10.75)	0.38	2.01 (0.34 – 12.00)	0.44
Late-onset	1.54 (0.49 – 4.83)	0.46	1.77 (0.52 – 6.06)	0.36
Use of intravenous antimicrobials within past 90 days	0.71 (0.28 – 1.80)	0.47	0.67 (0.25 – 1.79)	0.42
Charlson's Comorbidity Index score	1.28 (1.06 – 1.55)	0.01	1.32 (1.06 – 1.63)	0.01

RES-238: Microbiological Epidemiology and Clinical Outcomes of Carbapenem-Resistant Enterobacterales and Pseudomonas Aeruginosa Infections in Adult Patients Admitted to Intensive Care in India: A Multicenter Observational Study

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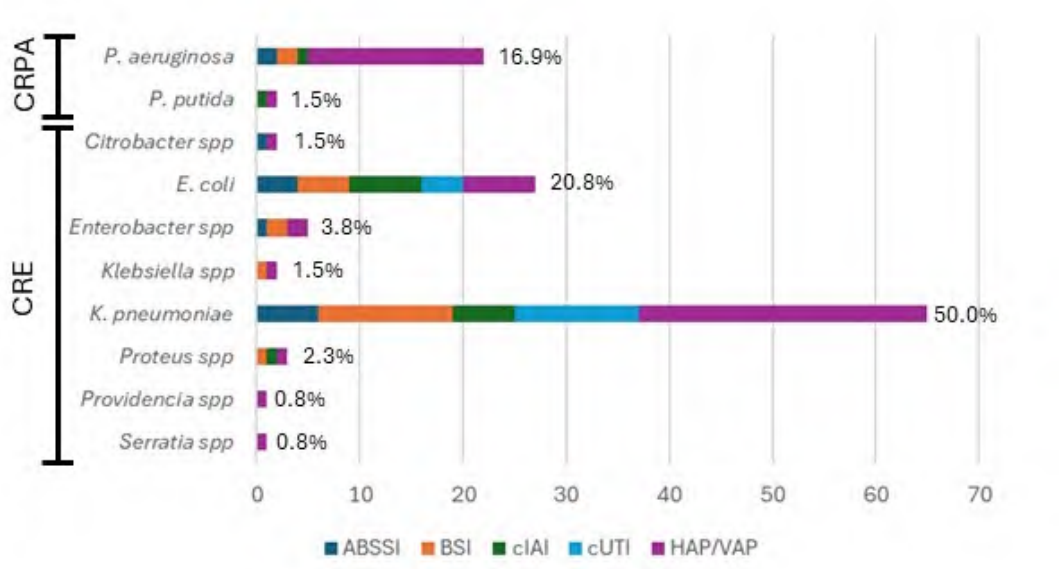
Background
There is a scarcity of studies understanding the epidemiology and management of carbapenem-resistant Enterobacterales (CRE) and P. aeruginosa (CRPA) infections in India. This study assessed the microbiological epidemiology, treatment patterns and clinical outcomes of adult patients with confirmed CRE/CRPA infections across five Indian tertiary care centers.

Method
From January 2023 to July 2024, adult patients admitted to the intensive care unit with confirmed CRE/CRPA infections were enrolled and followed for 28 days. Non-duplicate isolates underwent in vitro susceptibility testing at participating centres. Data on clinical characteristics, microbiological epidemiology, antimicrobial treatment, and patient outcomes were collected.

Results
A total of 106 patients were enrolled and the most common diagnosis was hospital or ventilator associated pneumonia (Figure 1). Among 119 isolates, Klebsiella pneumoniae was the most prevalent species (67), followed by Escherichia coli (26) and P. aeruginosa (16). In addition to carbapenem resistance, resistance to fluoroquinolones (97%) was very high among 105 isolates tested. Susceptibility to Amikacin was low in K. pneumoniae (7/64 tested; 10.9%), but modest for E. coli (11/25 tested; 44%). Resistance to colistin was observed in 13% K. pneumoniae (4/30 tested) isolates. The most commonly administered treatment was meropenem (n=68), predominantly administered empirically. The next most common were polymyxin B (n=50), ceftazidime/avibactam +/- aztreonam (n=49) and teicoplanin (n=35). The 28-day mortality rate was 34.9% and clinical success at test of cure was 60.8%.

Conclusions
CRE/CRPA infections are an increasing problem in India and despite introduction of new therapies, treatment options remain limited. Access to novel treatments is urgently needed.



RES-239: Molecular Analysis of Macrolide Resistance in Mycoplasma pneumoniae Among Children with Respiratory Infections in Jakarta, Indonesia, 2024

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Background
Mycoplasma pneumoniae is a key contributor to pediatric community-acquired pneumonia (CAP), with increasing global concerns about macrolide resistance. Limited data exist on its prevalence and resistance patterns in Indonesia. This study investigated M. pneumoniae prevalence, CAP etiology, and macrolide resistance mutations in children with acute respiratory infections (ARI) in Jakarta.

Method
From August 2024 to June 2025, a prospective study collected 51 nasopharyngeal/oropharyngeal swabs from children aged 0–18 years with ARI across five Jakarta healthcare facilities. Polymerase chain reaction (PCR), targeting the P1 adhesin gene, identified M. pneumoniae. The Respiratory Flow Chip Hybridization Molecular Panel screened 32 severe cases for 21 viruses and 3 atypical bacteria. Whole-genome sequencing (WGS) examined 23S rRNA (A2063G, A2064G, C2617G), L4 (codon 65–70), and L22 (codon 92–94) for resistance mutations.

Results
M. pneumoniae was found in 1.96% (1/51) of samples from a 2-year-old girl with bronchopneumonia co-infected with enterovirus. The panel detected pathogens in 46.88% (15/32) of samples, including respiratory syncytial virus A (RSV A), influenza A H1N1 2009, and adenovirus. WGS revealed no macrolide resistance mutations. Most patients were female (57%) and hospitalized (60%).

Conclusions
Low M. pneumoniae prevalence and predominant viral etiology emphasize the value of molecular diagnostics in Jakarta. No resistance mutations were detected, suggesting macrolide efficacy, but continuous monitoring is vital for effective CAP management.

RES-240: Functional Characterization of a Class A Carbapenemase CAE-1 in Carbapenem-Resistant Pseudomonas Aeruginosa Clinical Isolates

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Background
Two carbapenem-resistant Pseudomonas aeruginosa (CRPA) isolates were collected which lacked known carbapenemases, but produced a beta-lactamase CAE-1. CAE-1 was recently found in Comamonas aquatica and conferred resistance to penicillins and cephalosporins. In this study, we purpose to know whether CAE-1 was responsible for the carbapenem resistance in the CRPA isolates and its enzyme hydrolyzing characteristics.

Method
The blaCAE-1 and blaKPC-2 were cloned and expressed in Escherichia coli DH5a and P. aeruginosa PAO1, respectively, to test the resistance phenotypes. Steady-state kinetic assays were performed with KPC-2 as a comparator to determine the catalytic efficiency of CAE-1. The dissemination of blaCAE-1 were investigated through WGS and genomic analysis.

Results
Expression of blaCAE-1 in P. aeruginosa PAO1 resulted in resistance or intermediate susceptibility to piperacillin, ceftazidime, cefepime, aztreonam with minimal inhibitory concentrations 64 to 256 mg/L, and meropenem (4 mg/L) and ertapenem (8 mg/L), but susceptible to imipenem, exhibiting a broader resistance spectrum than that in E. coli DH5a. Kinetic studies showed CAE-1 had catalytic efficiency against all beta-lactams tested. CAE-1 demonstrated lower catalytic efficiency against most antibiotics than KPC-2, except for ceftazidime and cefepime. WGS revealed blaCAE-1 was located on an integrative and conjugative element approximately 120 kbp in size. Eleven clinical P. aeruginosa isolates harboring blaCAE-1 were identified in the P. aeruginosa genome database. Subsequent cgMLST identified two distinct clonal transmission clusters: one comprising 10 ST463 isolates, and the other involving 2 ST360 isolates from this study.

Conclusions
The CAE-1 confers carbapenemase activity in P. aeruginosa and has been disseminated among P. aeruginosa.

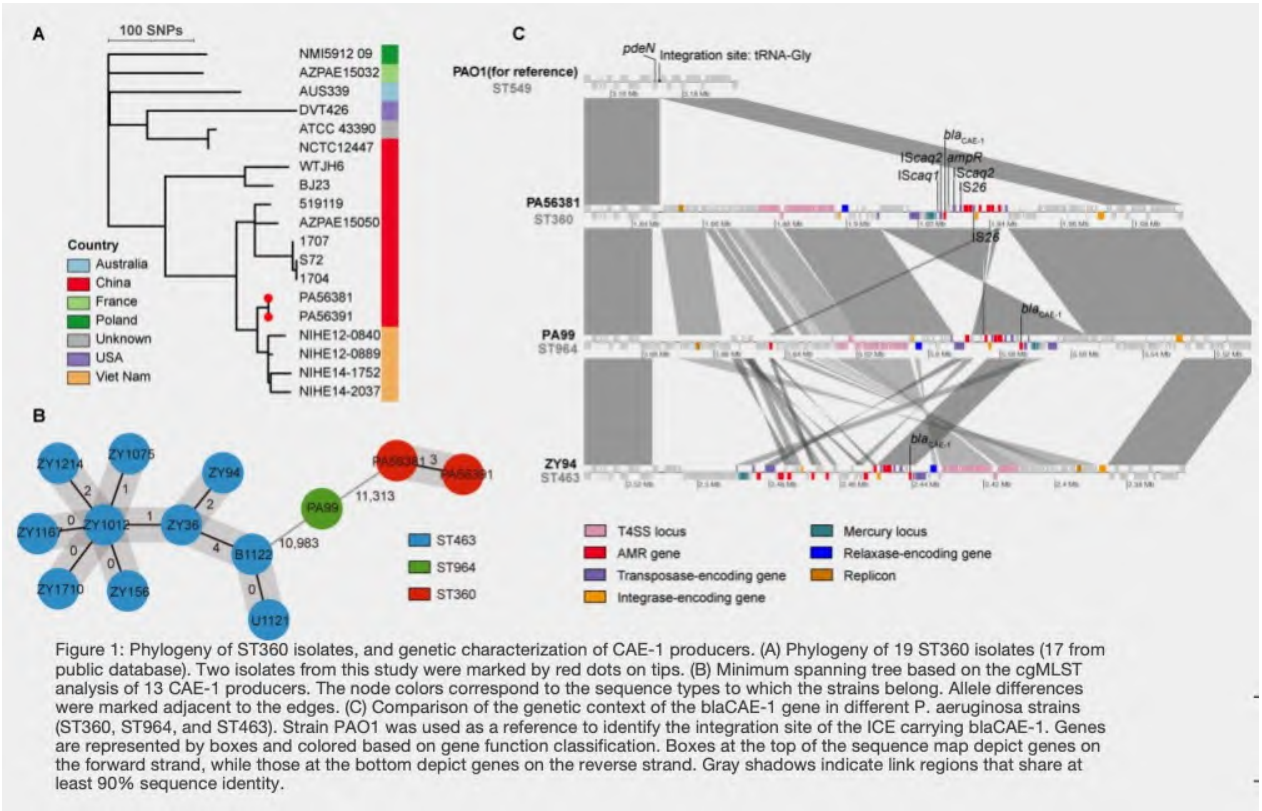

Figure 1: Phylogeny of ST360 isolates, and genetic characterization of CAE-1 producers. (A) Phylogeny of 19 ST360 isolates (17 from public database). Two isolates from this study were marked by red dots on tips. (B) Minimum spanning tree based on the cgMLST analysis of 13 CAE-1 producers. The node colors correspond to the sequence types to which the strains belong. Allele differences were marked adjacent to the edges. (C) Comparison of the genetic context of the blaCAE-1 gene in different P. aeruginosa strains (ST360, ST964, and ST463). Strain PAO1 was used as a reference to identify the integration site of the ICE carrying blaCAE-1. Genes are represented by boxes and colored based on gene function classification. Boxes at the top of the sequence map depict genes on the forward strand, while those at the bottom depict genes on the reverse strand. Gray shadows indicate link regions that share at least 90% sequence identity.

Table 1. In-vitro antimicrobial susceptibility for clinical isolates and recombinant strains producing CAE-1 and KPC-2

Antibiotic	MICs (mg/L)							
	P. aeruginosa (PA56381)	*P. aeruginosa* (PA56391)	*E. coli* DH5α (pUCP24)	*E. coli* DH5α (pUCP24-bla_{CAE-1})	*E. coli* DH5α (pUCP24-bla_{KPC-2})	*P. aeruginosa* PAO1 (pUCP24)	*P. aeruginosa* PAO1 (pUCP24-bla_{CAE-1})	*P. aeruginosa* PAO1 (pUCP24-bla_{KPC-2})
Piperacillin	64	64	<4	128	256	<4	256	512
Piperacillin-tazobactam	16/4	16/4	<2/4	4/4	128/4	<2/4	128/4	>256/4
Ticarcillin-clavulanate	256/2	>512/2	<4/2	<4/2	256/2	8/2	>512/2	>512/2
Ceftriaxone	NA	NA	<0.25	16	8	NA	NA	NA
Ceftazidime	16	16	<0.125	0.25	4	1	64	64
Ceftazidime-avibactam	1/4	1/4	0.06/4	0.125/4	0.06/4	1/4	1/4	2/4
Cefepime	16	16	<0.06	<0.06	2	1	128	>128
Cefoperazone-sulbactam	16	16	<0.25	2	8	2	128	256
Aztreonam	16	16	<0.25	<0.25	32	2	128	512
Imipenem	8	8	<0.06	0.25	4	1	1	64
Meropenem	8	8	<0.016	0.03	1	0.5	4	>32
Ertapenem	32	32	<0.03	<0.03	1	4	8	>64
Levofloxacin	0.25	0.5	<0.125	<0.125	<0.125	0.25	0.25	0.25
Amikacin	4	4	<1	<1	<1	2	2	2
Polymyxin B	1	1	0.25	0.5	0.5	1	1	1

Note: NA, not applicable.

Table 2. Kinetic parameters of CAE-1 and KPC-2

Antibiotic	CAE-1			KPC-2		
	*K*m (μM)[a]	*k*cat (s^{-1})[a]	*k*cat/*K*m($\mu M^{-1}s^{-1}$)	*K*m (μM)[a]	*k*cat (s^{-1})[a]	*k*cat/*K*m($\mu M^{-1}s^{-1}$)
Meropenem	23.53±3.74	0.35±0.02	0.02	7.91±1.78	4.90±1.16	0.66
Ertapenem	24.27±3.82	1.71±0.67	0.07	22.07±6.35	11.85±2.00	0.56
Imipenem	30.52±9.34	0.23±0.05	0.01	63.05±7.39	80.51±10.36	1.28
Ceftazidime	138.72±6.63	3.56±0.38	0.03	61.15±21.75	0.69±0.19	0.01
Cefepime	104.83±10.08	20.07±1.24	0.19	173.53±18.23	17.35±1.57	0.10
Piperacillin	167.38±3.56	95.29±15.36	0.57	21.26±4.61	13.51±2.39	0.64
Aztreonam	42.07±7.50	8.14±0.73	0.20	92.13±22.95	57.86±16.69	0.62

[a] k_{cat} and K_m values were calculated as the mean+SD of three independent measurements with three different enzyme purifications

RES-241: Whole Genome Sequencing of Methicillin-Resistant Staphylococcus Aureus (MRSA) Bacteraemia Strains Delineating Changing Lineages Associated with Specific Drug Resistance in Hong Kong, 2009-2024.

Ruiqi Zheng[1], Jun Yang[1], Carmen Li[1], Alfred Lee[2], Liu-Yue Yang[1], Rita Ng[1], Mingjing Luo[3], Sishuo Wang[1], Margaret Ip[1]

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[3]SIAT, Chinese Academy of Sciences, Shenzhen

Background
Methicillin-resistance Staphylococcus aureus (MRSA) is endemic in Hong Kong hospitals. MRSA infections complicate treatment options and associate with high morbidity/mortality and healthcare costs.

Objective: To characterize the sequence type structure and temporal dynamics of MRSA bloodstream

Method
Whole genome sequencing was performed on single-patient MRSA strains causing bacteraemia in hospitalized patients in a 1350-bed teaching hospital from 2009 to 2024. SA strains were stored in agar slants or glycerol/BHI at -80ºC. They were sub-cultured on conventional media and the identity confirmed with MALDI-TOF (Bruker), prior to DNA extraction (QIAamp 96 DNA QIAcube HT kit, Qiagen). DNA library was prepared following the manufacturer's protocol (Twist 96-Plex Library Prep Kit, Twist Bioscience) and sequenced (NextSeq 500 high-output platform, Illumina).

Results
Findings: A total of 1183 MRSA genomes for the 16-year period were analyzed. The median age of the patients was 78 years and 69.3% were male. Multi-locus sequence typing (MLST) analysis revealed four major sequence types: ST22, ST45, ST1774, and ST1047, accounting for 81.7% of all isolates. ST22 and ST45 were the most prevalent and persisted throughout the entire study period, while ST1047 demonstrated an increasing trend and ST1774 declined over time. Resistance rates were highest with moxifloxacin and erythromycin, while mostly susceptible to cotrimoxazole, mupirocin, daptomycin and vancomycin. Interestingly, an association between high gentamicin resistance rate in ST45 (82.2%) and fusidic acid resistance rate in ST1047 (17.1%) was noted.

Conclusions
Predominant and changing lineages of MRSA types associated with specific antibiotic resistance were observed in patients with MRSA bacteraemia.

RES-242: E. coli as a Living Nanofactories to Optimize Nanoparticle Synthesis for Enhanced Biomedical Applications

Awantika Singh, Hemant Ritturaj Kushwaha

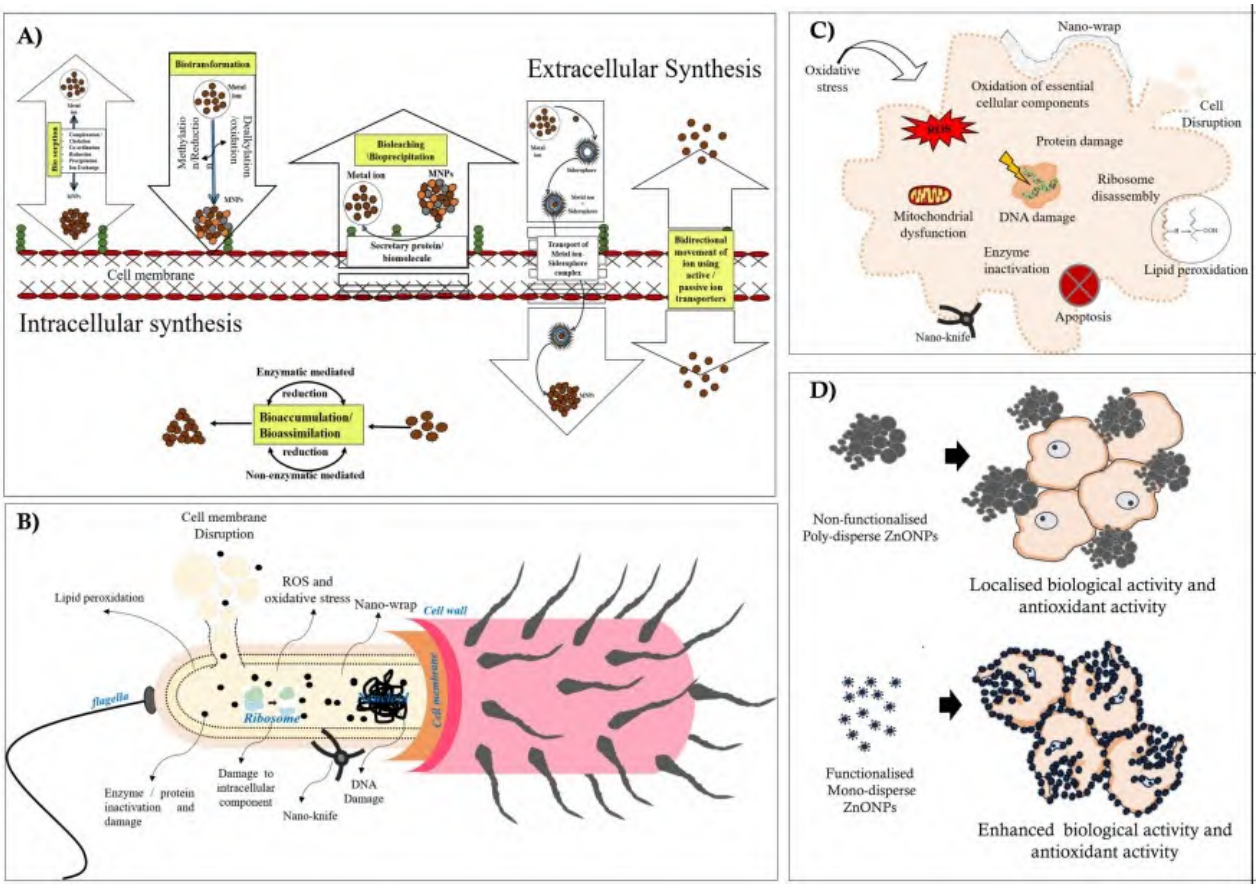
Jawaharlal Nehru University

Background
In the world of emerging alternatives to conventional antibacterial agents, the nanoparticles synthesized via bacterial nanofactories have shown immense potential as they are cost-effective, eco-friendly, simple, and less hazardous approaches. The bacterial nanofactories used in past research work are mostly pathogenic or difficult to culture; therefore, this study focuses on non-pathogenic Escherichia coli as a microbial nanofactory for the biosynthesis of zinc oxide nanoparticles (ZnONPs) with enhanced biomedical applications.

Method
The microbial engineering of the bacterial nanofactories was carried out to fine-tune the physiochemical properties of the synthesized nanoparticles. After that, the synthesized nanoparticles were characterized via various analytical techniques, and their biomedical applications were evaluated for antibacterial, anticancer, and antioxidant properties.

Results
The X-ray diffractometer (XRD) spectrum suggests that pure, crystalline, hexagonal, wurtzite-type ZnONPs were formed when treated with zinc salt precursor concentrations (40 and 80 mM). The high-resolution transmission electron microscopy (HR-TEM) images showed the synthesis of spherical nanoparticles (26-39 nm range) was formed. The SEAD pattern also confirms the formation of polycrystalline ZnONPs at higher concentrations, validating XRD results. Biological entities on the surface play a significant role as reducing and stabilizing agents in nanoparticle formation and its antioxidant properties. The antibacterial activity of ZnONPs is noteworthy against gram-positive and gram-negative pathogenic bacteria at 50 µg/mL. Similarly, the significant anticancer activity against lung cancer A549 cells was also observed at 50 µg/mL of ZnONPs.

Conclusions
This research highlights the potential of E. coli-based engineering for the sustainable and self-regulating synthesis of advanced biomaterials for enhanced biomedical applications.



RES-243: A Unified Platform for Rapid Pathogen Detection, Species Identification, and Antimicrobial Resistance Mutation Profiling

Qingge Li

Xiamen University

Background
The escalating threat of emerging and drug-resistant pathogens exacerbated by climate change highlights the urgent need for diagnostic platforms that are rapid, accessible, and cost-effective. Precise species identification and resistance mutation profiling are essential for effective treatment and long-term surveillance. Although sequencing technologies have accelerated pathogen discovery, their clinical utility remains limited by high costs and operational complexity.

Method
We developed MeltArray, a high-throughput, multiplexed amplification platform that integrates pathogen detection, species-level identification, and antimicrobial resistance (AMR) mutation profiling. MeltArray was evaluated in critical care settings using samples from 298 hospitalized patients.

Results
MeltArray enabled simultaneous detection of 62 sepsis-causing pathogens and 98 AMR mutations within 3 hours, directly from whole blood. It demonstrated high analytical sensitivity (as low as 1–5 CFU/mL) and broad sample compatibility across 32 body fluid types, including cerebrospinal fluid, bronchoalveolar lavage fluid, sputum, urine, ascites, bile, joint fluid, and abscess fluid, covering diverse infection sites. Compared to conventional diagnostics, MeltArray significantly reduced turnaround time while offering superior sensitivity, broader pathogen coverage, and comprehensive resistance profiling.

Conclusions
MeltArray represents a powerful and practical platform for infectious disease diagnostics and antimicrobial stewardship. Its speed, accuracy, and versatility position it as a valuable tool for timely clinical decision-making and enhanced pathogen surveillance at the point of care.

RES-244: Usefulness of Presepsin as a Biomarker for Sepsis: A One-year Clinical Diagnosis

Kyoung Ho Roh

National Health Insurance Service Ilsan Hospital

Background
Sepsis remains a critical cause of morbidity and mortality worldwide, rapid and accurate diagnostic tools to guide timely intervention. Presepsin, a soluble subtype of the CD14 receptor, has shown promise as an early biomarker for sepsis, offering faster kinetics compared to conventional markers such as procalcitonin (PCT) and C-reactive protein (CRP). This study aimed to assess the clinical performance and diagnostic utility of presepsin testing over a one-year period at a teaching hospital in Korea.

Method
The PATHFAST Presepsin assay (PHC Corporation, Japan), approved by the Ministry of Food and Drug Safety (MFDS), was analytically validated prior to clinical implementation, including assessments of detection limits and precision. Presepsin levels were stratified as negative (<300 pg/mL), equivocal (300–500 pg/mL), or positive (>500 pg/mL). From July 2024 to June 2025, test results were retrospectively analyzed alongside patient demographics, clinical departments, and sepsis-related diagnostic outcomes.

Results
A total of 3,885 tests were performed (1,961 males; 1,924 females; mean ages: 70.6 and 73.9 years, respectively). Most of the testing (91.1%) originated from the emergency department. Presepsin results were positive in 1,843 cases, equivocal in 947, and negative in 1,095. Sepsis-related diagnoses were documented in 10.0% of positive cases, compared to 2.8% and 1.9% in the equivocal and negative groups, respectively. Applying elevated cutoffs (700 and 1,000 pg/mL) further increased the proportion of sepsis diagnoses to 11.3% and 12.5%.

Conclusions
Presepsin demonstrated clinical utility as a supportive biomarker for early sepsis detection, particularly in emergency settings. Use of a higher cutoff may enhance diagnostic specificity without compromising identification.

RES-247: Lpp20 is a Key Player in Helicobacter pylori - Induced Platelet Aggregation and Activation

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Background
Helicobacter pylori (H. pylori) infection is implicated in various extra-gastric diseases, including acute coronary syndrome (ACS), and we have reported that its outer membrane lipoprotein Lpp20 may bind to and induce platelet aggregation. This study aimed to elucidate the mechanism of H. pylori-induced platelet activation by comprehensively analyzing Lpp20-mediated platelet aggregation and activation.

Method
Platelet-rich plasma (PRP) from four healthy volunteers (20s, male/female) and purified His-tagged Lpp20 protein were used. The lpp20 gene was cloned from H. pylori strain 26695, and an Lpp20-His fusion plasmid was constructed. The protein was expressed in E. coli BL21, followed by cell homogenization and protein extraction. The protein was then recovered by Ni-affinity chromatography and further purified by ultrafiltration. Lpp20-induced platelet aggregation was assessed by aggregometry and microscopic observation. Platelet-produced Thromboxane B2 (TXB2) and cyclic AMP (cAMP) were measured by ELISA. The expression of platelet activation markers, including CD62P (reflecting P-selectin release), PAC-1 (indicating activated GPⅡb/Ⅲa conformational change), and CD61 (a marker for platelet identification), was evaluated by flow cytometry.

Results
Lpp20 dose-dependently increased maximal platelet aggregation, and platelet aggregates were microscopically observed. In Lpp20-treated platelets, TXB2 production increased, cAMP production decreased, and expression of CD62P and PAC-1 was observed in a subset of platelets.

Conclusions
We demonstrated that the H. pylori membrane-associated protein Lpp20 dose-dependently induces platelet aggregation and activation, potentially through the arachidonic acid cascade and/or cAMP pathway. Thus, H. pylori-induced platelet aggregation and activation likely contribute to thrombotic disease pathogenesis, including ACS.

RES-248: Possible Cross Protection Between Influenza and COVID-19: Evidence from a Pilot Review of National Surveillance Data

Smeetha Nair, Prakash Priyanka, Muhammad Aqmal Bin Mohamad Haris, Paul Anantharajah Tambyah

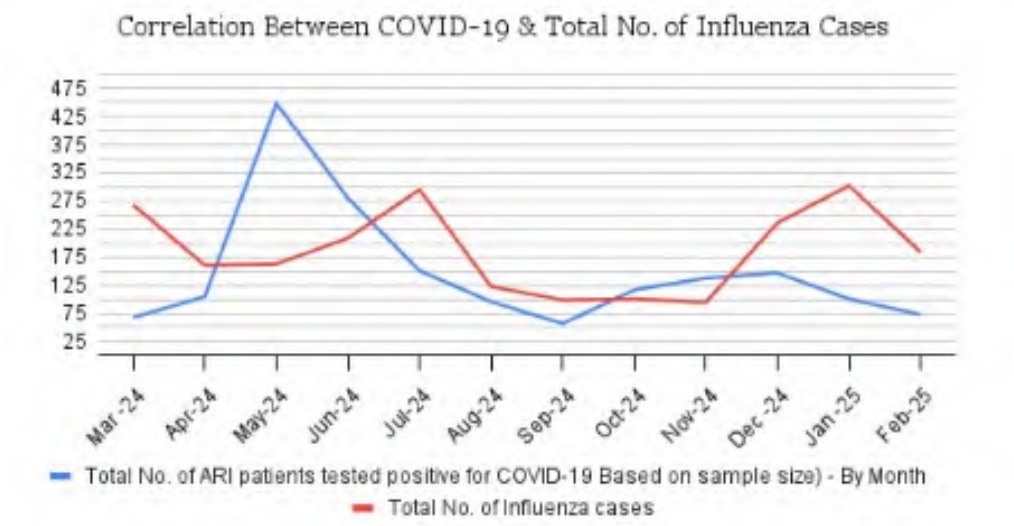
National University Hospital (NUH)

Background
Influenza disappeared worldwide during the first two years of the COVID-19 pandemic. Although this was widely believed to be due to social distancing, mask use and other non-pharmaceutical interventions, other respiratory viruses were not similarly suppressed. Recently, intriguing data from trials of combined influenza and COVID-19 mRNA vaccines have suggested a synergistic effect in terms of immune protection. We investigated possible viral interference between COVID-19 and influenza infections based on publicly available surveillance data from Singapore, an equatorial country without a well-defined influenza season.

Method
We analysed monthly reported cases of influenza and COVID-19 from the Singapore Ministry of Health (MOH) sentinel surveillance and notification systems from March 2024 to June 2025. The data were plotted on graphs in EXCEL. The study was granted a "review not required" approval by the National University of Singapore Institutional Review Board (NUS-IRB-2024-568).

Results
There were an average of 159.8 ± 80.7 cases of Influenza A, H3N2, H1N1 and Influenza B and 153.3 ± 106.3 cases of COVID-19 infection each month detected by the MOH surveillance systems. The monthly distribution is shown in the graph below.

Conclusions
It does appear that influenza and COVID infections peaked at different periods. Whether this is due to interference is not clear. This would require large epidemiological as well as mechanistic studies to evaluate if this is real. If it is, it would have significant public health implications.



RES-249: Impact of VIRTUO Blood Culture System Installation on Workflow Efficiency and Reporting Timeliness in the Emergency Laboratory

Jeongsoo Park, Dong Woo Shin, Woo Jin Shin

Seoul National University Bundang Hospital

Background
Timely detection and reporting of bloodstream infections (BSIs) are critical for early intervention, especially in emergency and intensive care settings. The VIRTUO® blood culture system was installed to replace BacT/ALERT 3D (BA3D) and BACTEC FX systems in our emergency laboratory. This study evaluates its impact on incubation delays, reporting times, and overall laboratory efficiency.

Method
We retrospectively analyzed blood culture data from 2018 (prior to installation) and 2021 (after installation) using laboratory information systems. Sampling times, incubation delays, and time to positivity were compared between systems. In particular, we focused on samples collected during night shifts (20:00–07:00), which accounted for 31.6% of total tests (13,211/41,746). Comparative analysis included time to incubation and time to positive result reporting.

Results
- After installation of the VIRTUO system, average incubation delay during night shift sampling was significantly reduced.
- Specifically, mean incubation time decreased from 7,666 minutes (BA3D, Feb 2, 2018) to 7,301 minutes (VIRTUO, Feb 2, 2021), representing a reduction of approximately 360 minutes.
- Reporting time for positive cultures was up to 6 hours earlier with VIRTUO compared to the previous FX system.
- Positivity rate trends remained stable, but early detection improved, particularly in ER and ICU samples.

Conclusions
The implementation of the VIRTUO blood culture system significantly reduced incubation delays and enabled earlier reporting of positive blood cultures, particularly during the night shift. These improvements enhance the timeliness of clinical decision-making in critical care settings.

RES-250: Analysis of Fluoroquinolone Resistance in Extended-Spectrum Beta-Lactamase-Producing Escherichia coli: Genetic Determinants and Prevalence in Clinical Samples from Toyama University Hospital

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Background
ESBL-producing Escherichia coli represents a major cause of resistance to β-lactam antibiotics and fluoroquinolones in hospital settings. This study examined CTX-M gene groups, chromosomal mutations conferring quinolone resistance, plasmid-mediated resistance genes (PMQR), and their link to patient characteristics using PCR and whole-genome sequencing (WGS).

Method
A total of 41 ESBL-producing E. coli isolates were analyzed. PCR and WGS were used to detect CTX-M groups, chromosomal mutations and PMQR genes. Patient data (age, sex, prior antibiotic use, hospitalization) were investigated for associations with resistance profiles.

Results
WGS confirmed all isolates carried at least one CTX-M gene. CTX-M-27 (41.1%) and CTX-M-14 (12.2%) were predominant in CTX-M-9 group; CTX-M-15 (29.3%) and CTX-M-55 (12.2%) in CTX-M-1 group. No isolates carried CTX-M-2. PCR and WGS showed discrepancies in CTX-M-1 group ($p < 0.0001$) but were more consistent for CTX-M-9 group ($p = 0.196$). Chromosomal mutations were frequent: gyrA (87.5%), parC (75.6%), and parE (78.0%). Significant co-occurrence was observed between gyrA-parC and gyrA-parE ($p < 0.0001$). Only two isolates carried aac(6')-Ib-cr with CTX-M-15, and one carried OqxA/B with CTX-M-27. Five isolates had neither PMQR genes nor chromosomal mutations.

No significant associations were found with patient demographics. CTX-M-1 was more frequent in patients with recent antibiotic use than CTX-M-9, though not statistically significant ($p = 0.53$).

Conclusions
No clinical differences were observed between CTX-M-1 and CTX-M-9 groups. Their silent transmission is commonly missed without nucleic acid-based analyses. WGS offers greater accuracy by overcoming PCR's potential detection limitations. Frequent and co-occurring chromosomal mutations further underscore the complexity of quinolone resistance mechanisms.

RES-251: Screening of Bacteriophages from Environmental Samples and Multidrug-Resistant Helicobacter pylori Strains

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Universiti Kebangsaan Malaysia

Background
The increasing prevalence of multidrug-resistant (MDR) Helicobacter pylori has significantly hindered eradication efforts, highlighting the need for alternative therapies. Phage therapy offers a promising strategy to overcome antibiotic resistance by utilizing bacteriophages as targeted antibacterial agents. This study aims to screen bacteriophages from environmental sources and MDR H. pylori strains.

Method
Environmental samples were collected from hospital sewage, household septic tanks, seawater, river, pond, drain, and four algae sources. Phage particles were extracted and tested against 25 MDR H. pylori strains using growth inhibition and spot tests. Additionally, prophage induction was assessed in 12 MDR H. pylori strains using UV radiation (exposure time between 30–120 s).

Results
Initial screening indicated that six lysates (hospital sewage, household septic tank, river, pond, drain, and algae B) reduced optical density growth values compared to controls, while seawater and other algal lysates showed higher OD values. Spot tests revealed that five samples (hospital sewage, household septic tank, river, pond, and drain) produced lysis against seven H. pylori strains, with lysis zones ranging from 1–10 mm. For prophage induction, four strains showed positive spot tests following UV exposure: strains 19005, 19033, 19046, and 21041 exhibited lysis at 120 s, 90 s, 30 s, and all exposure times, respectively.

Conclusions
These findings suggest wastewater is a promising source of therapeutic phages, and certain MDR H. pylori strains harbor inducible prophages, which may serve as candidates for isolating lytic phages. In conclusion, this study supports the potential of phage therapy as an alternative approach for combating MDR H. pylori infections.

RES-252: Gut Microbiome Restoration Through Phytocompounds: A Novel Approach to Treat Inflammatory Bowel Disease

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Background

Inflammatory bowel disease (IBD) is a lifelong, chronic condition affecting over 5 million people globally, with cases increasing especially in developed countries. While the exact cause of IBD remains unclear, compositional and functional alterations of the gut microbiome are recognized as key contributors to IBD pathogenesis. There is no cure for IBD, natural compounds with anti-inflammatory properties are increasingly explored as potential therapeutic options for IBD. This study investigates the impact of two novel plant-compounds on microbiome regulation in a 2,4,6-Trinitrobenzene sulfonic acid (TNBS)-induced colitis mouse model.

Method

A TNBS-induced colitis model was used to evaluate therapeutic efficacy. Disease severity was assessed through clinical and macroscopic scoring. Microbiome composition and functional pathway changes were analyzed using PacBio HiFi full-length 16S rRNA gene sequencing of colon tissue.

Results

TNBS administration resulted in significant weight loss, inflammation, and disrupted gut microbiota, with increased Acutalibacter muris, Monoglobus pectinilyticus, and Streptococcus pneumoniae, and decreased Staphylococcus ureilyticus and Mailhella massiliensis. Treatment with comps 4 and 6 restored microbial balance and improved clinical outcomes, with comp 4 showing substantial efficacy. Functional pathways such as peptidoglycan biosynthesis and the Bifidobacterium shunt, downregulated during colitis, were upregulated with post-treatment, supporting gut barrier integrity and reducing pro-inflammatory IL-6.

Conclusions

This study provides insights into IBD pathogenesis and highlights the therapeutic potential via restoring gut dysbiosis and immune dysregulation with natural compounds. Our findings underscore the promise of comps 4 and 6 as effective agents for IBD management, paving the way for future clinical applications.

RES-254: Oropharyngeal Microbiota and Mycobacterium tuberculosis Carriage Among Migrant Workers in Klang Valley

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Background
Malaysia receives many economic migrants annually, primarily from Indonesia, Bangladesh, and Nepal - nations with a high incidence of tuberculosis (TB). These migrants often reside in suboptimal accommodations, increasing their vulnerability to respiratory tract infections and TB. This study aimed to investigate Mycobacterium tuberculosis (Mtb) carriage and characterize the oropharyngeal (OP) microbiota of migrant workers working in Klang Valley, Malaysia.

Method
From March till May 2024, 258 sputum samples were collected from healthy Indonesian, Bangladeshi and Nepalese study participants at the North South Initiative office and from Hospital Canselor Tuanku Muhriz. Demographic data were collected, samples cultured on Lowenstein-Jensen medium and colonies subjected to PCR for Mtb detection. DNA extracted from sputum samples were used for 16S rRNA next-generation sequencing (16SNGS) on the Illumina NovaSEQ6000 to profile OP microbiota. Association between OP microbiota abundance and demographic variables were investigated.

Results
No active TB infection was detected in the study participants. Interestingly, 16SNGS revealed a stable OP microbiota for all participants dominated by Rothia spp., Streptococcus vestibularis and Granulicatella adiacens; these bacteria are usually prevalent in healthy adults. The only notable difference in investigated parameters was Beta diversity differences in OP microbiota composition between domestic and non-domestic workers (PERMANOVA, $p = 0.006$); living conditions or antibiotic use did not appear to affect OP microbiota diversity.

Conclusions
Stringent pre-employment health screenings could have contributed to negative TB transmission among the studied migrant population. The stability of the OP microbiota indicates resilience to external factors such as living conditions and antibiotic use.

RES-256: Effect of Carbapenem Exposure on the Fitness of Extended Spectrum Beta-Lactamase (ESBL)-Producing Escherichia coli Strains Isolated from Migrant Communities Working in the Klang Valley, Malaysia

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Background
Silent carriage of Extended Spectrum Beta-Lactamase (ESBL)-producing Escherichia coli (ESBLEC) is a risk factor for onward dissemination of the bacteria and host future infections. In this study, we investigated the effect of carbapenem exposure on the fitness of ESBLEC strains isolated from economic migrants of the Klang Valley, Malaysia.

Method
Between January and March 2024, 258 participants were recruited into the study. Demographic data were collected, rectal swabs were cultured on CHROMagar ESBL, and antimicrobial susceptibility testing was performed using the Vitek 2 system. Strains identified as ESBLEC were then assayed for ESBL genes, and ERIC-PCR was conducted to identify clusters. The dominant genotypes were then subjected to different (i) concentrations and (ii) duration of exposure to carbapenems (imipenem, ertapenem, and meropenem). Post-exposure, fitness (growth curves and desiccation survival) of ESBLEC strains was determined.

Results
ESBLEC carriage was found in 26.0% of participants (n = 67), with highest positivity in Bangladeshi migrants. Domestic and manufacturing workers were most affected. All strains were resistant to third-generation cephalosporins and 68.7% (n = 46) were ciprofloxacin-resistant. The most prevalent ESBL gene was blaCTX-M-1. ERIC-PCR revealed two major ESBLEC clusters. Dominant genotypes survived exposure to imipenem and ertapenem better than to meropenem. Interestingly, no significant difference in growth or desiccation tolerance was observed post-carbapenem exposure in all tested strains, suggesting phenotypic stability.

Conclusions
These findings underscore the presence of robust ESBLEC strains among migrant communities working in Klang Valley, Malaysia. The risk for onward ESBLEC dissemination into the community remains to be investigated.

RES-257: Retrospective Analysis of Antibiotic Resistance Genes in Pseudomonas aeruginosa Clinical Isolates from a Tertiary Medical Centre

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Background
Pseudomonas aeruginosa is a Gram-negative pathogen often associated with healthcare-associated infections, especially in immunocompromised patients. Its capacity to develop resistance complicates treatment. This study aimed to determine the distribution of antibiotic resistance genes in P. aeruginosa clinical isolates collected from a tertiary medical center between April and November 2017.

Method
Forty-six clinical isolates were collected from Universiti Malaya Medical Centre in 2017. DNA was extracted and conventional PCR was used to detect 16 resistance genes, including porin (oprD), efflux pump regulators (nfxB, mexT, mexR), beta-lactamases (TEM, OXA, CTXM, VIM, GES, VEB, DIM, AmpC), and carbapenemases (IMP-A, IMP-B, IMP-C, NDM). Ethical approval was obtained (MREC ID NO: 2021331-10012).

Results
All 46 isolates (100%) carried nfxB, mexT, and AmpC. mexR and oprD were detected in 89.1% and 34.8% of isolates, respectively. VIM and OXA were found in 4.3% and 2.2%, while no isolates harbored TEM, CTX-M, GES, VEB, DIM, or any of the carbapenemase genes tested.

Conclusions
This study provides a molecular overview of the distribution of antibiotic resistance genes in P. aeruginosa clinical isolates collected prior to 2019. The high prevalence of intrinsic regulatory genes and AmpC suggests the widespread presence of resistance-related genetic elements before increased surveillance efforts in recent years. Unlike studies published from 2020 onwards, molecular data on P. aeruginosa earlier isolates at this center remain limited. These findings serve as a reference point for tracking evolution of resistance mechanisms in P. aeruginosa in Malaysian healthcare settings. This study was funded by Fundamental Research Grant Scheme grant FP017-23 (FRGS/1/2023/SKK10/UM/02/10).

RES-258: Effect of Vancomycin Exposure on Fitness of Methicillin-Resistant Staphylococcus aureus (MRSA) Isolated from Klang Valley, Malaysia

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Background
Vancomycin remains the first-line treatment for methicillin-resistant Staphylococcus aureus (MRSA) infections. Prolonged exposure to vancomycin may impose a fitness cost on MRSA, affecting its growth and stress tolerance. We investigated the effect of vancomycin exposure on the fitness (growth and desiccation tolerance) of representative MRSA strains circulating in Klang Valley, Malaysia, between December 2023 and May 2024.

Method
MRSA strains tested in this study were HM57, HM52, HM4, ID147, BD10 and BD51. Minimum inhibitory concentrations (MICs) of the tested strains towards vancomycin were determined using VITEK-2 system. Strains were then subjected to vancomycin exposure under two approaches: (i) ½X MIC exposure for 24, 48, and 72 hours; and (ii) 1X MIC and 2X MIC exposure for 24 hours. The strains' growth curves and desiccation tolerance (enumeration of surviving colonies) post-vancomycin exposure was then determined.

Results
All tested strains had a vancomycin MIC of < 2mg/L and survived sub-MIC vancomycin exposure across all timepoints. ID147, BD10 and HM57 survived increasing concentrations of vancomycin exposure up to 2X MIC. Vancomycin exposure (both time and concentration) resulted in slower growth for strains ID147, BD51, HM52 and HM4; whereas BD10 and HM57 showed no noticeable changes. On the other hand, desiccation tolerance remained unaffected in most strains, except for ID147, which showed a reduction (also for both time and concentration exposure) in number of surviving colonies.

Conclusions
Our preliminary findings showed that MRSA strains exhibited different fitness response following vancomycin exposure, potentially influenced by strain background. Further studies are needed to confirm these associations.

RES-259

Antifungal Development with Molecular Biology

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Japan

Background
As drug-resistant fungal infections surge globally, Candida glabrata stands out as a major clinical threat due to its intrinsic azole resistance. Yet, antifungal drug development has stagnated for decades. What if we could systematically reveal its hidden vulnerabilities? By building the first genome-scale mutant platform in C. glabrata, we aimed to uncover novel, lethal drug targets—starting with the ergosterol biosynthesis pathway.

Method
We constructed a genome-wide conditional mutant library in Candida glabrata using a tetracycline-repressible system. Gene repression phenotypes were assessed to identify essential genes. Cross-species comparison with S. cerevisiae accounted for gene redundancy. We then analyzed 27 ergosterol pathway genes for essentiality.

Results
A total of 939 essential genes were identified in C. glabrata, with 94.9% overlap with S. cerevisiae when gene redundancy was considered. Among 27 ergosterol pathway genes analyzed, ERG25, encoding C-4 methyl sterol oxidase, induced the most rapid and irreversible cell death upon repression. Chemical screening identified compound 1181-0519, a selective ERG25 inhibitor with strong antifungal activity and minimal toxicity to mammalian cells. Further screening of plant extracts revealed several candidates with selective growth inhibition of C. glabrata, suggesting the potential for natural product–based ERG25 inhibitors.

Conclusions
We developed a genome-wide mutant library in C. glabrata and identified ERG25 as a highly promising antifungal target. A selective inhibitor was discovered, and plant-derived screening is ongoing. This platform enables rational discovery of fungal-specific drug targets and represents a valuable resource for developing new therapies against resistant fungal infections.

RES-262: Characterization of Th1/Th2/Th17/Treg Cytokine Profiles In COVID-19: A Cross-Sectional Study on Children

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Background
Early research on COVID-19 highlighted the occurrence of cytokine storms in some children a condition marked by excessive immune activation. This hyperinflammatory response, characterized by the overproduction of cytokines, can cause severe damage to host tissues, particularly the lungs, contributing to COVID-19 severity. This study aimed to characterize the cytokine profiles of Th1, Th2, Th17, and Treg cells (IFN-γ, IL-12, IL-4, IL-6, IL-17A, IL-23, IL-10, and TGF-β) at different stages of COVID-19 infection and to evaluate their correlation with disease severity in children up to 18 years of age.

Method
A cross-sectional study was conducted involving 30 healthy individuals (control group) and 50 COVID-19 patients admitted to the hospital. The patients were categorized into three groups based on disease severity: mild, moderate, and severe. Serum samples were collected from all participants, and cytokine levels were quantified using enzyme-linked immunosorbent assay (ELISA).

Results
Dynamic expression patterns were observed for all cytokines in the COVID-19 group. Among these, IL-6 levels showed a statistically significant elevation, particularly in patients with severe COVID-19, compared to the control group. However, the levels of other cytokines (IFN-γ, IL-12, IL-4, IL-17A, IL-23, IL-10, and TGF-β) did not demonstrate a consistent correlation with disease severity across the mild, moderate, and severe groups.

Conclusions
This study provides critical insights into the cytokine response in COVID-19 patients, emphasizing the role of IL-6 in disease progression. The findings suggest that cytokines IL-6, could serve as potential therapeutic targets and biomarkers for disease severity, thereby contributing to the understanding of COVID-19 pathophysiology and guiding treatment strategies.

RES-263: Class 1 DISARM System Prevents Klebsiella pneumoniae Sequencing Type 23 from Conjugative carbapenemase-encoding plasmids

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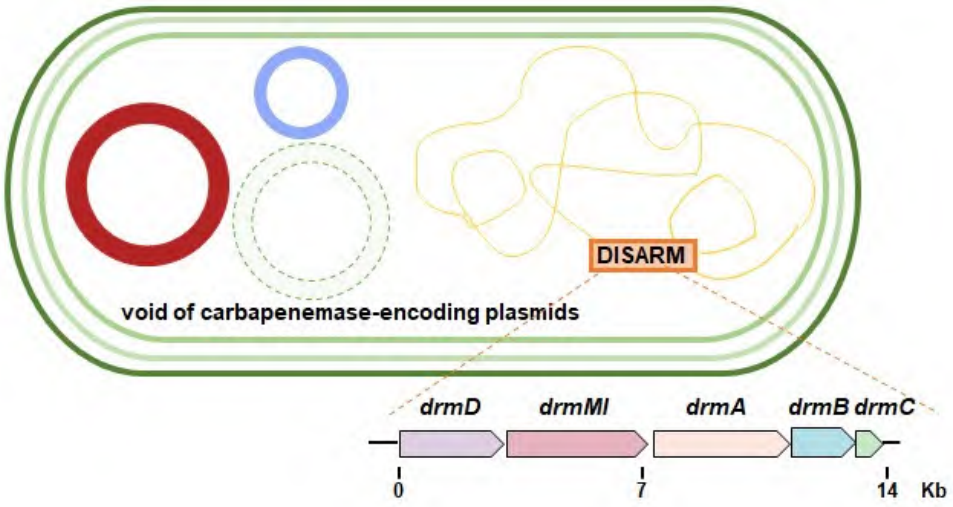
Background
Canonical hypervirulent sequencing type 23 (ST23) Klebsiella pneumoniae causes severe infections, while it generally maintains susceptibility to a broad spectrum of antibiotics, yet the molecular basis of this phenotypic characteristic remains poorly understood. The purpose of this study was to investigate whether the presence of the DISARM system defenses carbapenemase-encoding plasmids invasion in K. pneumoniae.

Method
The distribution of DISARM system was analysed in silico, and its methylation motifs were charaterized using PacBio single-molecular real-time sequencing. Further, plasmid transformation and conjugation assays were applied to investigate whether the presence of the DISARM system prevent from carbapenemase-encoding plasmid invasion.

Results
Here, we demonstrate that the DISARM system was widespread in ST23 K. pneumoniae, modifying host 5'-GRACRAC-3' motifs which were distributed in all conjugative plasmids in K. pneumoniae. The transformation efficiency of plasmid pCOLADuet-MTmotif with the methylated cognate site was marginally reduced compared with the plasmid pCOLADuet-1 without the site in a ST23 DISARM-positive strain KP2613. Moreover, Class 1 DISARM could effectively hinder the antimicrobial resistance (blaKPC-2, blaNDM-1 and blaNDM-5) plasmids invasion with conjugation efficiency reduced by ranging from 12- to 117-fold in KP2613 and 4.55- to 15.67-fold in BL21. Systematic deletion of individual DISARM genes (drmA, drmB, drmC, drmD, and drmMI) revealed that disruption of any single gene did not fully abolish DISARM-mediated defense.

Conclusions
Overall, our study demonstrated that Class 1 DISARM provides robust protection against antimicrobial-resistant plasmids, which may be a potential factor underlying the high antimicrobial susceptibility of ST23 hypervirulent K. pneumoniae.



RES-265: Genomic Surveillance Uncovers High Diversity and Regional Resistance in Streptococcus uberis from Dairy Cows

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Background
Antimicrobial resistance (AMR) is a global health threat requiring coordinated One Health surveillance across human and veterinary medicine. Streptococcus uberis, a major cause of bovine mastitis, leads to economic losses in dairy production and is often treated with broad-spectrum antimicrobials critical to human medicine. Despite its importance, genomic data on S. uberis from East Asia, particularly Japan, are scarce. This study aimed to characterize the genomic and antimicrobial resistance features of Japanese S. uberis isolates in comparison with global strains.

Method
Thirty-seven S. uberis were isolated in Japan. Antimicrobial susceptibility testing was done. The genomes of our 37 strains combined with 180 strains worldwide were analyzed.

Results
Phylogeny of strains with those worldwide was analyzed. The regional clustering (i.e., Japan, Asia, Europe, Oceania, North America) was overall observed in the multilocus sequence typing and core genome analysis. Moreover, AMR genes were investigated. The principal coordinate analysis (PCoA) of AMR genes showed a distinct Japanese pattern, with aadE, tet(O), and erm(B) predominating-correlating with the observed antibiotic susceptibility of oxytetracycline at 35%, lincomycin at 32%, and erythromycin 27% among the tested strains. Furthermore, virulence genes were analyzed. The PCA of virulence genes also showed regional patterns, however differential abundance analysis did not identify Japan-specific virulence markers. Thus, S. uberis isolates from Japan exhibit distinct AMR gene profiles compared to global strains.

Conclusions
These findings highlight the need for region-specific genomic surveillance to guide targeted mastitis control and inform One Health strategies for AMR mitigation.

RES-267: BCG Vaccination as a Predictor of In-Hospital Mortality in Non-HIV Tuberculous Meningitis

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Background
Tuberculous meningitis (TBM) is the most severe form of tuberculosis infection, carrying up to 50% mortality and a high risk of permanent neurological disability. Indonesia has implemented routine Bacille Calmette–Guérin (BCG) vaccination since 1973 to prevent severe TB, However, BCG's protective effect declines over time of vaccination. Data on the specific efficacy of BCG against TBM among adult patients is limited.

Method
This retrospective cohort study included 366 non-HIV TBM patients: 283 with a BCG scar and 83 without a BCG scar. A BCG scar on the upper arm indicated prior vaccination. Clinical, laboratory, radiological, and outcome data were collected systematically and analyzed using Chi-square and Mann–Whitney tests, with multivariate analysis via logistic regression. A p-value <0.05 was considered statistically significant.

Results
Patients without a BCG scar showed higher rates of decreased consciousness (89% vs. 74%), cranial nerve palsy (26% vs. 12%), and in-hospital mortality (41% vs. 24%) (all $p < 0.005$). In-hospital mortality was associated with decreased consciousness (96% vs. 70%), hydrocephalus (49% vs. 27%), severe TBM (33% vs. 11%), and absence of a BCG scar (34% vs. 19%). Multivariate analysis demonstrated that decreased level of consciousness and absence of BCG vaccination as independent predictors of in-hospital mortality.

Conclusions
Adult non-HIV tuberculous meningitis patients who receive the BCG immunization tend to present with less severe TBM and lower in-hospital mortality rates. Although TBM outcomes are influenced by multiple factors, these findings suggest that prior BCG vaccination may confer a protective effect against disease severity and death.

Table 1a. Comparison of Clinical, Laboratory, Radiological Features, and Outcomes in Tuberculous Meningitis Patients by BCG Vaccination Status

Variabel	BCG Vaccination History		p-value
	Yes	No	
	N (%)	N (%)	
Sex Male	163 (57.6)	38 (45.8)	0.076
Fever	217 (77.8)	60 (75.9)	0.849
Headache	232 (84.4)	65 (84.4)	1.000
Altered consiousnes	208 (73.5)	74 (89.2)	0.005*
Cranial Nerve Palsy	27 (11.5)	19 (26.4)	0.004*
Hemiparesis	166 (58.9)	53 (64.6)	0.417
TB Symptom	232 (82.0)	72 (86.7)	0.394
CSF Opening pressure (median [IQR])	12.00 [10.00, 15.00]	12.00 [10.00, 13.00]	0.542
CSF Leukocytes (median [IQR])	39.00 [4.50, 137.50]	51.00 [3.00, 140.50]	0.976
CSF Protein (median [IQR])	131.00 [57.00, 264.00]	150.10 [62.00, 265.00]	0.654
Predominant Monocyte	215 (76.0)	58 (69.9)	0.328
CSF Blood Glucose Ratio (median [IQR])	0.34 [0.20, 0.51]	0.33 [0.21, 0.49]	0.999
Hydrochepalus	94 (33.2)	26 (31.3)	0.850
Meningeal Enhancement	139 (49.1)	46 (55.4)	0.376
Tuberculoma	31 (11.0)	9 (10.8)	1.000
Infarct	47 (16.6)	15 (18.1)	0.884
Lungs TB	82 (29.0)	22 (26.5)	0.764
Lungs Extra TB	13 (4.6)	3 (3.6)	0.938
TBM Grade			
Grade 1	12 (4.3)	2 (2.5)	0.140
Grade 2	225 (80.9)	59 (73.8)	
Grade 3	41 (14.7)	19 (23.8)	
Marais score (median [IQR])	12.00 [11.00, 14.00]	12.00 [11.00, 14.00]	0.653
In-Hospital Mortality	67 (24.0)	34 (41.0)	0.004*
Total	283	83	

Table 1b Results of Multivariate Logistic Regression Analysis of In-Hospital Mortality in Patients with Tuberculous Meningitis

Variabel	OR (Odds Ratio)	95% CI	p-value
consciousness	10.70	3.39 – 52.26	0.0005
Hydrocephalus	1.67	0.98 – 2.84	0.058
TBM Grade 2	0.32	0.05 – 2.65	0.243
TBM grade 3	0.83	0.12 – 7.23	0.854
BCG Vaccination	0.52	0.29 – 0.92	0.024

RES-268: Clonal Spread of Non-Typable Haemophilus influenzae in Long-Term Ventilator Units: High Prevalence of blaROB-1 Without Ceftriaxone Resistance

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Background

Over the past two years, the repeated isolation of Haemophilus influenzae from respiratory and blood specimens in two long-term ventilator care units (RCW-A and RCW-B) of our hospital prompted an investigation into potential clonal dissemination. This study aimed to assess the genetic relatedness and antimicrobial resistance profiles of the isolates.

Method

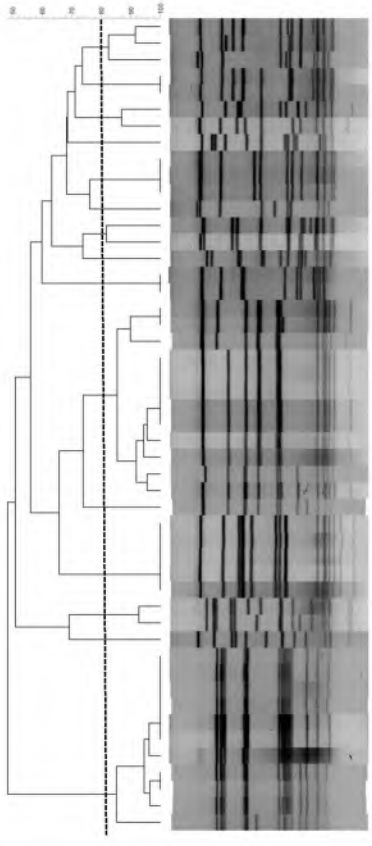
We analyzed 49 H. influenzae isolates: 24 clinical strains obtained from 22 patients (RCW-A: 3 patients; RCW-B: 2; other wards: 17) and 25 strains recovered through active respiratory screening of 49 ventilated patients (RCW-A: 21/31 (67.8%); RCW-B: 4/18 (22.2%). Species identification was performed using the Bruker MALDI-TOF MS system. Genotyping via pulsed-field gel electrophoresis. (PFGE) revealed 15 distinct pulsotypes.

Results

Notably, 23 of 24 isolates from RCW-A clustered into two dominant pulsotypes (Groups J and O), and 7 of 7 isolates from RCW-B clustered into Groups L and M, supporting localized transmission. In contrast, 18 isolates from other wards exhibited greater genetic diversity (10 pulsotypes). All isolates tested negative for bexA, classifying them as non-typable H. influenzae (NTHi). Resistance gene analysis showed a high prevalence of blaTEM-1 (89.8%) and a markedly higher rate of blaROB-1 carriage in RCW isolates (13/31; 41.9%) compared to non-RCW units (2/18; 11.1%). Importantly, all isolates remained susceptible to ceftriaxone (MIC range <0.016–0.38 μg/mL).

Conclusions

These findings suggest ongoing clonal transmission of NTHi in our long-term ventilator units, coupled with increased carriage of blaROB-1. Although ceftriaxone resistance was not observed, continued molecular surveillance and targeted infection control interventions are warranted to mitigate further spread.



PFGE Group	Units	Number	Date	Clinical or Surveillance	Sex	Age	Sample	Ceftriaxone MIC (μg/mL)	TEM-1	ROB-1
A1	ER	HI-36	2025.03.11	Clinical	Male	77	Sputum	<0.016	+	-
A2	ER	HI-40	2025.03.26	Clinical	Male	40	Blood	0.19	+	-
A3	Ward	HI-39	2025.03.21	Clinical	Male	71	Sputum	<0.016	+	-
B1	ER	HI-29	2025.02.03	Clinical	Male	90	Blood	<0.016	+	-
B1	ER	HI-35	2025.03.05	Clinical	Male	75	Sputum	0.19	+	-
C1	Ward	HI-38	2025.03.20	Clinical	Male	61	Sputum	0.094	+	-
C2	Ward	HI-45	2025.04.22	Clinical	Male	73	BAL	0.023	+	-
D1	Ward	HI-48	2025.05.08	Clinical	Male	68	Sputum	0.032	+	-
E1	ER	HI-31	2025.02.21	Clinical	Male	57	Sputum	<0.016	+	-
E1	Ward	HI-37	2025.03.17	Clinical	Male	91	Sputum	0.19	+	-
E1	ICU	HI-42	2025.04.07	Clinical	Male	91	Sputum	0.19	+	-
F1	ER	HI-44	2025.04.15	Clinical	Female	76	Blood	<0.016	+	-
G1	Ward	HI-30	2025.02.08	Clinical	Male	21	Blood	0.25	+	-
G2	Ward	HI-41	2025.03.31	Clinical	Female	38	Sputum	0.125	+	-
H1	ER	HI-49	2025.05.28	Clinical	Male	50	Blood	0.016	-	-
I1	ER	HI-28	2025.01.23	Clinical	Male	83	Blood	<0.016	+	+
I1	Ward	HI-34	2025.03.03	Clinical	Male	77	Sputum	0.125	+	-
J1	RCW-A	HI-32	2025.02.25	Clinical	Female	59	Sputum	0.125	+	-
J1	RCW-A	HI-33	2025.02.25	Clinical	Female	81	Sputum	<0.016	+	+
J2	RCW-A	HI-08	2025.02.12	Surveillance	Female	59	Sputum	0.094	+	-
J3	RCW-A	HI-15	2025.02.12	Surveillance	Male	64	Sputum	<0.016	+	-
J3	RCW-A	HI-16	2025.02.12	Surveillance	Male	67	Sputum	0.016	+	+
J3	RCW-A	HI-17	2025.02.12	Surveillance	Male	56	Sputum	<0.016	-	-
J3	RCW-A	HI-24	2025.02.12	Surveillance	Female	63	Sputum	0.023	-	+
J3	RCW-A	HI-25	2025.02.12	Surveillance	Female	82	Sputum	0.016	+	+
J4	RCW-A	HI-18	2025.02.12	Surveillance	Male	76	Sputum	0.016	+	-
J5	RCW-A	HI-27	2025.01.22	Clinical	Male	80	Blood	<0.016	+	-
J6	RCW-A	HI-04	2025.02.12	Surveillance	Female	86	Sputum	0.023	+	+
J7	RCW-A	HI-23	2025.02.12	Surveillance	Female	92	Sputum	0.016	+	+
K1	RCW-A	HI-10	2025.02.12	Surveillance	Male	81	Sputum	0.023	+	-
L1	RCW-B	HI-19	2025.02.12	Surveillance	Female	72	Sputum	<0.016	+	-
L1	RCW-B	HI-20	2025.02.12	Surveillance	Female	96	Sputum	<0.016	+	-
L1	RCW-B	HI-21	2025.02.12	Surveillance	Female	97	Sputum	<0.016	+	-
L1	RCW-B	HI-22	2025.02.12	Surveillance	Male	80	Sputum	<0.016	+	-
L1	RCW-B	HI-26	2025.01.13	Clinical	Male	66	Blood	<0.016	+	-
M1	RCW-B	HI-46	2025.04.28	Clinical	Male	66	Sputum	0.38	+	+
M2	RCW-B	HI-47	2025.05.01	Clinical	Male	58	Blood	0.25	+	+
N1	ICU	HI-43	2025.04.14	Clinical	Male	68	Sputum	0.25	+	+
O1	RCW-A	HI-01	2025.02.12	Surveillance	Male	71	Sputum	0.016	-	+
O1	RCW-A	HI-02	2025.02.12	Surveillance	Male	83	Sputum	0.016	+	+
O1	RCW-A	HI-03	2025.02.12	Surveillance	Female	76	Sputum	0.064	-	+
O1	RCW-A	HI-05	2025.02.12	Surveillance	Male	85	Sputum	0.016	+	+
O1	RCW-A	HI-12	2025.02.12	Surveillance	Female	96	Sputum	0.016	+	+
O1	RCW-A	HI-14	2025.02.12	Surveillance	Female	71	Sputum	<0.016	+	-
O2	RCW-A	HI-13	2025.02.12	Surveillance	Female	103	Sputum	0.023	+	-
O3	RCW-A	HI-07	2025.02.12	Surveillance	Male	32	Sputum	0.023	+	-
O3	RCW-A	HI-11	2025.02.12	Surveillance	Male	69	Sputum	0.016	+	-
O4	RCW-A	HI-09	2025.02.12	Surveillance	Female	81	Sputum	0.016	+	-
O5	RCW-A	HI-06	2025.02.12	Surveillance	Male	72	Sputum	<0.016	+	-

RES-270: Analysis of MDRO Infections on Clinical Outcomes: A Study of WHO Priority Pathogen List in Hospitalized Patients

Zinatul Hayati, Asyriva Yossa Dania

Universitas Syiah Kuala

Background
The incidence of multidrug-resistant organisms (MDROs) in healthcare settings poses a significant challenge to patient management and clinical outcomes. Notably, infections caused by MDRO pathogens have been reported to be associated with heightened morbidity and mortality among hospitalized patients.

Method
This study analyzed clinical outcomes related to infections caused by MDROs in hospitalized patients at dr. Zainoel Abidin General Hospital in Banda Aceh, Indonesia, using microbiological laboratory data collected throughout 2024. The researchers sorted the data to identify cases involving key MDRO pathogens and included the hospitalized patients from whom any of these pathogens were isolated. Additionally, they gathered demographic information, including age, sex, length of hospital stay, and patient outcomes. Chi-square was used to see the relationship between MDRO pathogenic bacteria and patient outcomes.

Results
There are four major MDROs bacteria isolated from 1436 hospitalized patients. Overall, there are 1745 clinical specimens which isolated the targeted MDRO, those are ESBL-producing Escherichia coli (75.5%), Methicillin-resistant producing Staphylococcus aureus (73.4%), ESBL-producing Klebsiella pneumoniae (52.5%), and Carbapenem-resistant Acinetobacter baumannii (20.4%). Male (52.9%) and people aged-over-60 years (34.6%) were more prevalent to get infected by MDROs bacteria. Most of the patients were hospitalized for not more than 30 days (90.8%). The crosstabulation analysis of outcomes and MDROs frequencies indicated that there was no statistically significant difference (p = 0.258); however, the prevalence of infections leading to mortality caused by MDROs were greater (61.7%) compared to those caused by susceptible bacteria.

Conclusions
The emergence of these resistant strains bacteria leads to increasing mortality compared to susceptible strains.

Table. Frequencies of MDROs Bacteria

Characteristics	MDRO	%	Non-MDRO	%	Total	p-value
Organisms						
Escherichia coli	466	75.5	151	24.5	617	
Acinetobacter baumannii	71	20.5	277	79.5	348	
Staphylococcus aureus	246	73.4	89	26.6	335	
Klebsiella pneumoniae	234	52.5	211	47.5	445	
Overall	1017	58.3	728	41.7	1745	
Patient's Age (years)						
≤ 30	147	55.7	117	44.3	264	
31 - 45	115	53.7	99	46.3	214	
46 - 59	298	64.6	163	35.4	461	
≥ 60	300	60.4	197	39.6	497	
Patient's Gender						
Male	442	58.2	318	41.8	760	0.156
Female	418	61.8	258	38.2	676	
Patient's Outcome						
Recovered	521	58.7	366	41.3	887	0.258
Death	339	61.8	210	38.3	549	
Patient's Length of Stay						
≤ 30 days	786	60.2	519	39.8	1305	0.405
> 30 days	74	56.5	57	43.5	131	

RES-271

Temperature-Dependent Synthesis of CuO-Based Nanocomposites with Glucose and GO: A Strategy to Combat Antimicrobial Resistance

Anu Singh, Hemant Ritturaj Kushwaha

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Background

Antimicrobial resistance (AMR) is a continuous threat as bacteria have generated various mechanisms to resist conventional antibiotics, such as enzyme inactivation, modified efflux pumps, decreased cell permeability, biofilm formation, etc. Metal and metal oxide nanoparticles have been studied extensively as antibacterials; however, in-depth knowledge of their physicochemical properties and interaction mechanisms with microorganisms needs to be explored.

Method

Three types of nanocomposites (i.e., glucose-capped copper oxide nanoparticles, GO-stabilized copper oxide nanoparticles, and GO-stabilized glucose-capped copper oxide nanoparticles) were synthesized at 35, 75, and 100°C.

X-ray powder diffraction analysis results were studied in terms of the effect of the composition and synthesis temperature.

Transmission Electron Microscopy and RAMAN analysis were performed to investigate the effect of composition and temperature on the shape and size of the nanoparticles.

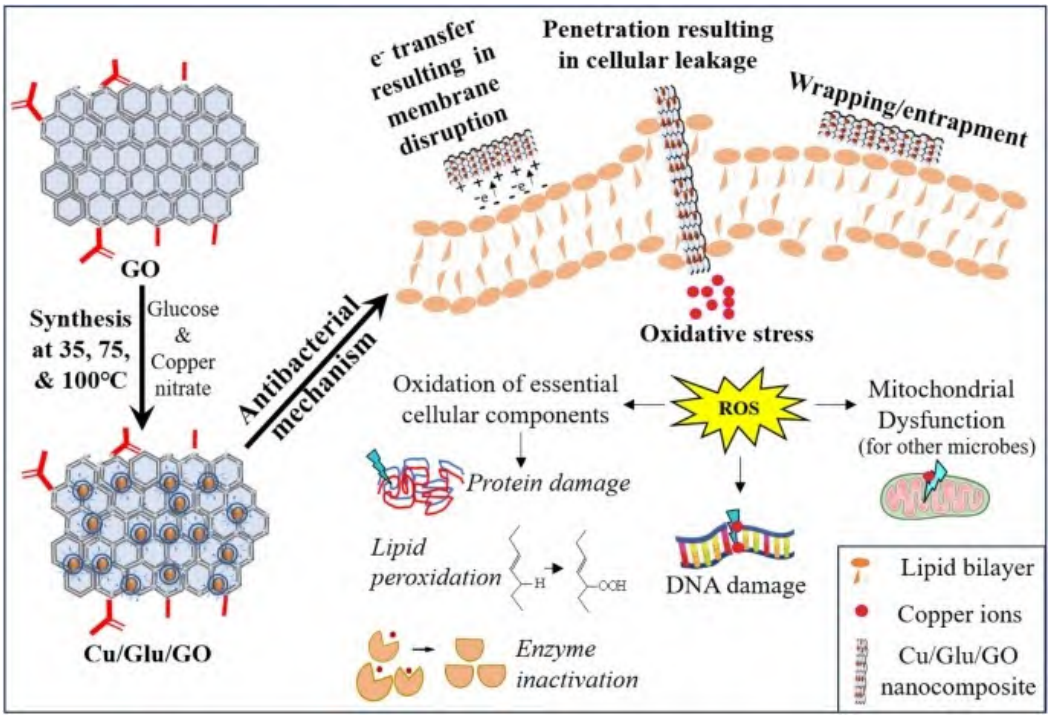
Antibacterial studies were also performed in terms of the effect of composition, temperature, and concentration.

Results

Structural studies revealed that copper-nanoparticles possess oxide forms, and the size of nanoparticles is reduced with increasing temperature. At the same time, chemical structure analysis of GO shows that it is also reduced with increasing temperature. It is observed that the shape of copper oxide-nanoparticles is successfully controlled by glucose. Antibacterial testing against laboratory strains of Escherichia coli and Bacillus anthracis shows that all the nanocomposites synthesized at 35°C possess better antibacterial activities compared to other nanocomposites and GO.

Conclusions

Specifically, 100 mg/mL of Cu/Glu/GO synthesized at 35°C can be used as an efficient alternative antibacterial agent; however, cytotoxicity analysis can help to explore its clinical usage.



RES-273: Characterisation of Genomic and Phenotypic Antimicrobial Resistance in Paediatric Streptococcus pneumoniae Carriage Isolates in Malaysia following Pneumococcal Conjugate Vaccine (PCV) Implementation (2021–2023)

Nurul Hanis Ramzi[2], Andrew Chun Hoong Tan[2], Nur Alia Johari[2], Anna Marie Nathan[5], Norhayati Aida Sulaiman[5], Cindy Shuan Ju Teh[5], Mohamad IkramIlias[8], Zakuan Zainy Deris[8], Siti Nur Haidar Hazlan[8], Nur Syafiqah Mohamad Nasir[8], Asrar Abu Bakar[3], Muhd Alwi Muhd Helmi[3], Wan Khairunnisa Wan Juhari[3], Norhidayah Kamarudin[3], Chun Wie Chong[4], David Cleary[6], Rebecca Anderson[7], Alexander Lister[7], Stephen Bentley[9], Lesley McGee[1], Stephanie Lo[9], Harry Hung[9], Stuart Clarke[7], Lokman Hakim Sulaiman[2]

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[2]IMU University
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Background
The persistence and evolution of multidrug-resistant (MDR) Streptococcus pneumoniae (Spn) in nasopharyngeal carriage remains emain critical for transmission and potential disease development. Following Malaysia's rollout of PCV10 (2020) and PCV13 (2023), limited data are available on antimicrobial resistance (AMR) trends among Spn carriage isolates in children under 5. We aimed to characterise genomic and phenotypic AMR profiles of Spn carriage isolates post-PCV implementation in Malaysian children <5 years, and identify Global Pneumococcal Sequence Cluster (GPSC)-associated MDR patterns and genotype–phenotype concordance.

Method
A total of 154 Spn isolates from MY-Pneumo (2021–2023) were analyzed. Serotyping was performed using CDC sequential multiplex-conventional PCR and the GPS WGS pipeline. AMR determinants were identified using AMRFinderPlus. Phenotypic resistance was assessed via BD Phoenix and disc diffusion. MDR was defined as resistance to ≥1 agent in ≥3 classes. Associations with GPSCs were analyzed using chi-square tests.

Results
Of the 140 pneumococcal isolates that passed quality control, WGS successfully resolved all non-typeable (NT) (12.3%) outcomes, particularly with serogroups 6, 15, and 23. Genotype–phenotype concordance exceeded 90% across key antibiotic classe. Fifty isolates (35.7%) were MDR, with GPSC16 and GPSC5 accounting for 38%. These were predominantly linked to serotypes 6A/6B and 23A/6C. Serotypes 6A and 6B are included in PCV13, while 23A and 6C are non-vaccine types (NVTs). These two lineages showed significantly higher proportions of MDR compared to other GPSCs ($p < 0.001$).

Conclusions
WGS offers high-resolution AMR and serotype profiling, supporting its integration into national pneumococcal surveillance strategies in the post-PCV era.

RES-274: Food-Derived Lactobacillus Cell-Free Supernatant Enhances Growth of Carbapenem-Resistant Acinetobacter baumannii

Frenzen Wyntha Requilino

Institute of Clinical Laboratory Sciences - Silliman University

Background
Fermented foods are known sources of Lactobacillus species with potential antimicrobial activity.

Method
This study examined whether cell-free supernatants (CFS) from Lactobacillus spp. isolated from tuba and apple cider vinegar could modulate the growth of Carbapenem-resistant Acinetobacter baumannii (CRAB) using Time-Kill and Checkerboard assays.

Results
While acidic (unadjusted) CFS demonstrated initial inhibitory activity, neutralization of pH abolished this effect. Notably, time-kill assays revealed a paradoxical increase in bacterial absorbance and regrowth of CRAB strains (ML and ATCC BAA-1605) when exposed to neutralized CFS, particularly beyond the 12-hour mark. Turbidity (at 600 nm) readings consistently showed enhanced growth rates of CRAB in the presence of neutralized CFS, suggesting a growth-promoting effect possibly due to metabolites remaining in the CFS after removal of viable Lactobacillus cells. Synergistic inhibition was not observed in checkerboard assays with meropenem or amikacin, further indicating that these CFS did not enhance antibiotic efficacy. Instead, a slight antagonistic effect was observed.

Conclusions
These findings raise concern that neutral pH Lactobacillus-derived byproducts may inadvertently provide favorable conditions for CRAB survival. These results underscore the complexity of probiotic-antibiotic-pathogen interactions and highlight the importance of pH and metabolic context when exploring fermented-food-derived probiotics as adjunct therapies. Further studies are warranted to elucidate the metabolic mechanisms involved in CRAB proliferation under exposure to neutralized probiotic supernatants.

RES-275: Siderophore-Mediated Cargo Delivery: Syntheses of Antibiotic Conjugates and Evaluation of their Uptake

Kalaiarasu Lakshminarayanan, Loganathan Rangasamy

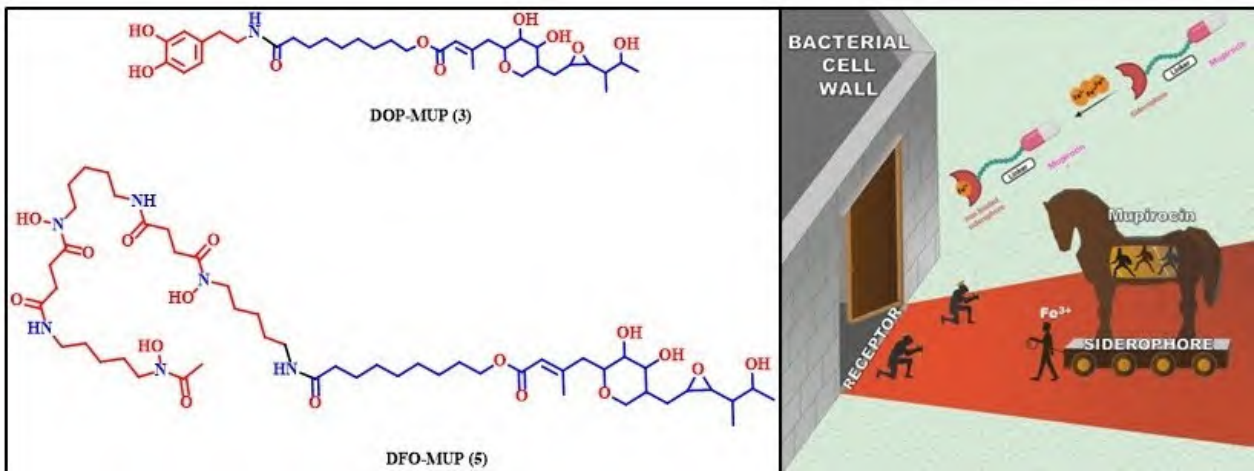
Vellore Institute of Technology

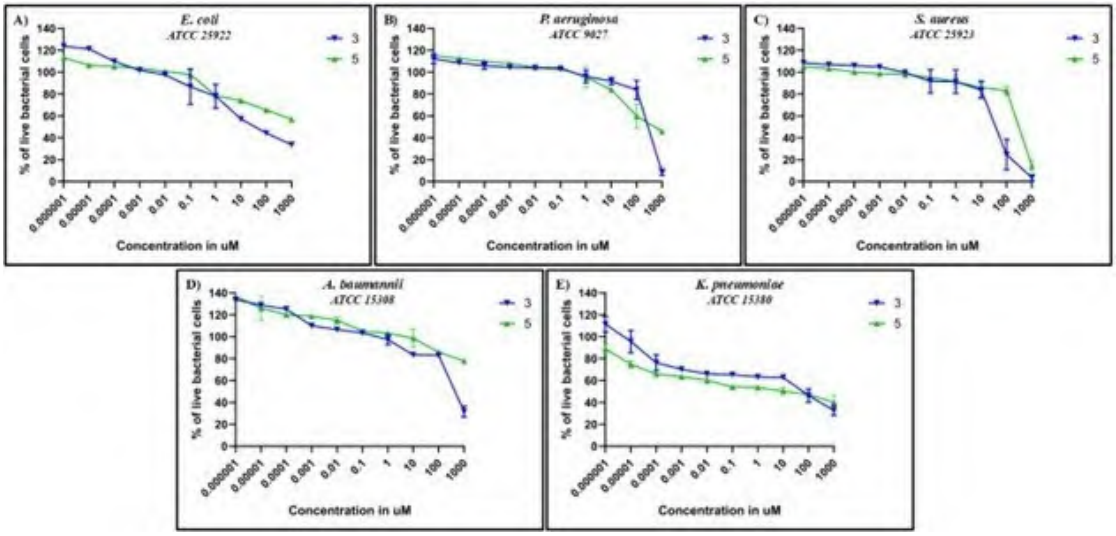
Background
Antimicrobial resistance (AMR) is a significant global health concern, particularly due to the ESKAPE pathogens, which are highly virulent and lead to substantial mortality worldwide, as recorded by the WHO. Therefore, the WHO declared AMR as one of the top 10 global public health threats to humanity. Hence, there is an urgent need to develop potent and selective antibiotic delivery strategies for these resistant bacteria.

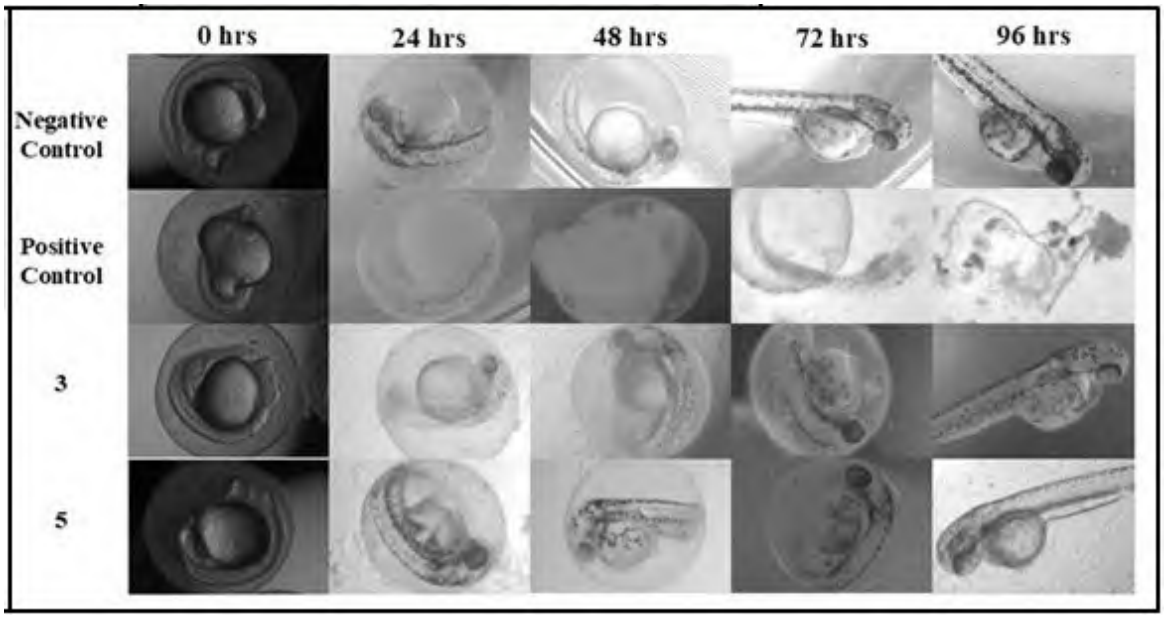
Method
This innovative project synthesized siderophore antibiotic conjugates using cutting-edge chemistry to ensure stable conjugation.

Results
The synthesized SAC showed an increase in antibacterial activity against pathogen strains like E. coli (ATCC 25922), S. aureus (ATCC 25923), P. aeruginosa (ATCC 9027), A. baumannii (ATCC 15308), and K. pneumoniae (ATCC 15380) with MIC values of 78.11 µM, 69.22 µM, 401.28 µM, 657.67 µM, and 86.51 µM compared to the parent antibiotic. A comparison with the parent antibiotic indicated that the SAC increases activity by 1.3-, 0.08-, 2.4-, 1.5-, and 2.2-fold against the respective bacterial strains. The cytotoxicity of SAC in the BRL 3A and HEK 293 cell lines indicates that it is non-toxic at concentrations greater than 100 µM. The in vivo cytotoxicity studies in zebrafish embryos confirmed the safety of the synthesized SAC at concentrations up to 300 µM for the 96 hpf (hours post-fertilization) period.

Conclusions
These study results suggest that the siderophore delivery would improve antibiotic internalization through the siderophore receptor against resistant pathogens. Therefore, SAC could be a promising candidate and potentially revolutionize treatment in the fight against antibiotic resistance, which contributes to AMR.




A)
E. coli
ATCC 25922
B)
P. aeruginosa
ATCC 9027
C)
S. aureus
ATCC 25923
D)
A. baumannii
ATCC 15308
E)
K. pneumoniae
ATCC 15380
% of live bacterial cells
Concentration in uM
3
5


0 hrs
24 hrs
48 hrs
72 hrs
96 hrs
Negative Control
Positive Control
3
5

RES-278: Targeting MDR E. coli with Bacteriophage–CNP Synergy: Antibiotic-Free Therapeutics Strategy in UTI Infections

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Shree Ramkrishna Institute of Computer Education and Applied Sciences, Sarvajanik University

Background

The rising prevalence of multidrug-resistant (MDR) E. coli in UTIs in India poses a serious challenge to infection control. Due to the pan drug resistance, antibiotics are increasingly ineffective against pathogens. Bacteriophages offer targeted antibacterial activity, and when combined with carbon nanoparticles (CNPs), may enhance therapeutic efficacy through synergistic action.

Method

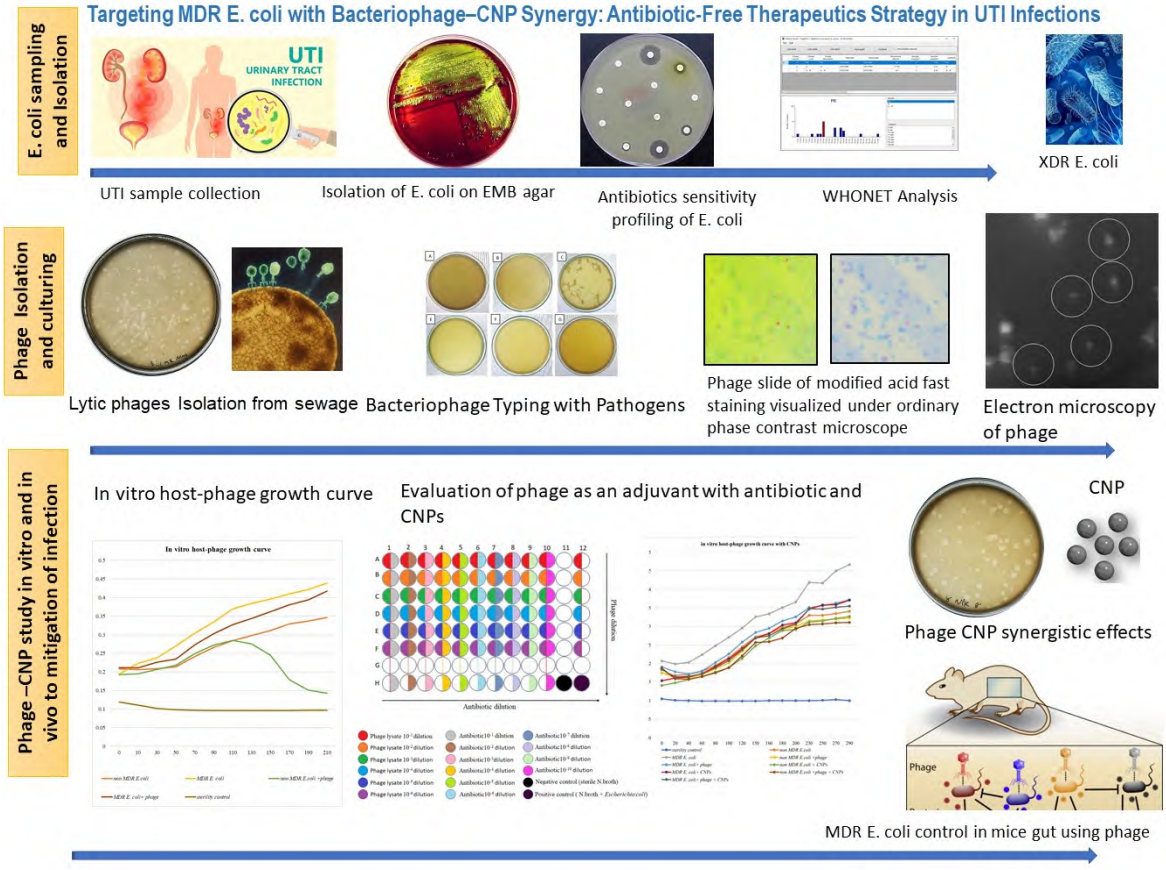
MDR E. coli strains were isolated female urine sample. Identification was performed using MALDI-TOF MS, followed by antibiotic susceptibility testing. Bacteriophages were isolated using a three-step enrichment and $ZnCl_2$ precipitation method. The lytic activity and host specificity of phages were assessed via plaque assays. Combination therapy using phage and CNPs was evaluated through in vitro growth inhibition assays (96-well plate checkerboard method), one-step growth curves, and electron microscopy.

Results

Phages demonstrated potent lytic activity against MDR E. coli, with no effect on non-target bacteria. Phage stability and viability at different pH and temperature was found remarkable. Combination therapy with CNPs significantly enhanced bacteriolytic effects and delayed regrowth in vitro. Scanning electron microscopy confirmed phage integrity and host interaction. The phage-CNP combination showed greater efficacy than individual treatments, indicating synergistic potential. Mice gut experiments suggest the MDR E. coli is totally killed by phage.

Conclusions

This study underscores the potential of phage-CNP combination therapy as a novel and translational approach to controlling MDR E. coli. The findings support the development of phage-based interventions along with CNP application as an adjuvant. The mice-based experiment suggests the possibilities to control the MDR E. coli without the antibiotics.



RES-279: Revisiting The Risk Factors for Catheter Related Bloodstream Infections (CRBSI) in ESRD Patients of a Tertiary Government Hospital in The Philippines from 2017 to 2021: A Retrospective Cohort Study

Jessmine Competente

Ospital ng Makati

Background
The estimated incidence of CRBSI among Filipino hemodialysis patients ranges from 0.6 to 6.5 episodes per 1,000 catheter-days. A review of the risk factors contributing to CRBSI in a tertiary government hospital was conducted to determine if they align with both international and local data. This study examined risk factors and bacteriologic profile in the development of CRBSIs in hemodialysis patients at Ospital ng Makati.

Method
The study included adult Chronic Kidney Disease inserted with central venous catheters (CVC) for hemodialysis at Ospital ng Makati from 2017 to 2021. Baseline demographic, clinical, laboratory, and microbiological data were collected retrospectively. Patient records were reviewed to monitor for occurrence of CRBSI within six months post CVC insertion.

Results
An incidence rate of 27% of CRBSI was recorded. Gram-positive bacteria were the most common pathogens (58%), predominantly Methicillin-resistant Staphylococcus aureus (25%). Among gram-negative bacteria (22%), Burkholderia cepacia (7%) was the most common. Thirty eight percent (38%) of the isolates were multi-drug resistant (MDR). Baseline risk factors such as leukocytosis ($p<0.01$), hypoalbuminemia ($p<0.01$), benign prostatic hyperplasia ($p<0.05$), ventricular hypertrophy ($p <0.05$), and sepsis ($p<0.05$) during hospitalization were clinically significant in development of CRBSI.

Conclusions
Gram-positive bacteria continue to be a common cause of CRBSI. There is a growing number of multidrug-resistant organisms isolated. Additionally, new risk factors have been identified as potential independent contributors to the development of CRBSI.

RES-280: Does Using Antibiotics in End-Of-Life Care Improve Outcomes? A Rapid Umbrella

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Background
The use of antibiotics in end-of-life (EOL) care is a complex and debated topic, with research exploring their impact on survival, symptom relief, quality of life, and broader public health concerns such as antimicrobial resistance. Evidence from systematic reviews and meta-analyses suggests that antibiotics are frequently prescribed to EOL patients, often with the intention of symptom management or prolonging life, but the benefits are inconsistent and context-dependent.

Method
Our search in PubMed, EMBASE, Web of Science and Google Scholar provided 40 results of existing reviews on topic of interest, and it included 8 duplicates. Further 22 articles were not appropriate and hence 10 studies were included. AMSTRAR 2 criteria was used to assess quality of Reviews. We assessed the consistency of findings across reviews and evaluated overlapping primary studies using the Corrected Covered Area (CCA) method.

Results
Antibiotic use in end-of-life or palliative care shows variable outcomes for symptom improvement and survival. While some studies indicate significant symptomatic relief for urinary tract infections (67% to 92% improvement), efficacy for other infections like pneumonia is often low or absent. Data on survival prolongation is inconsistent. Critically, antibiotics can cause adverse effects and may prolong hospital stays, potentially increasing discomfort.

Conclusions
Antibiotics are commonly used in end-of-life care, but their benefits for survival and symptom relief are limited and inconsistent, with potential harm including adverse effects and contribution to antimicrobial resistance. Decision-making should be individualized and guided by clear goals of care. There is a pressing need for more robust, patient-centered research to inform practice.

Outcome Measured	Advanced Dementia	Terminal Cancer	Mixed EOL Populations	Symptom Relief	Adverse Effects
Prevalence of Use	**3**	**2**	**4**	**GAP**	**GAP**
Survival Benefit	**2**	**2**	**1**	**GAP**	**GAP**
Symptom Relief	**1**	**1**	**2**	**3**	**GAP**
Adverse Effects	**GAP**	**GAP**	**1**	**GAP**	**2**
Antimicrobial Resistance	**GAP**	**GAP**	**1**	**GAP**	**1**

RES-281: Impact of Pharmacist-Driven Antimicrobial De-escalation on Resistance and Clinical Outcomes in Patients with Bloodstream Infections

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Sunprasitthiprasong Hospital

Background
Antimicrobial resistance (AMR) is a growing global threat, projected to cause 10 million deaths annually by 2050. To combat this, The Joint Commission mandates hospitals to implement Antimicrobial Stewardship Programs (ASP), and the CDC recommends pharmacist co-leadership. This study evaluates the impact of pharmacist-driven antimicrobial de-escalation on the emergence of resistance in patients with bloodstream infections (BSI).

Method
This retrospective study was conducted at Sunprasitthiprasong Hospital and included hospitalized adults (≥18 years) with positive blood cultures from July 2024 to March 2025. Patients with multidrug-resistant organisms at baseline were excluded.

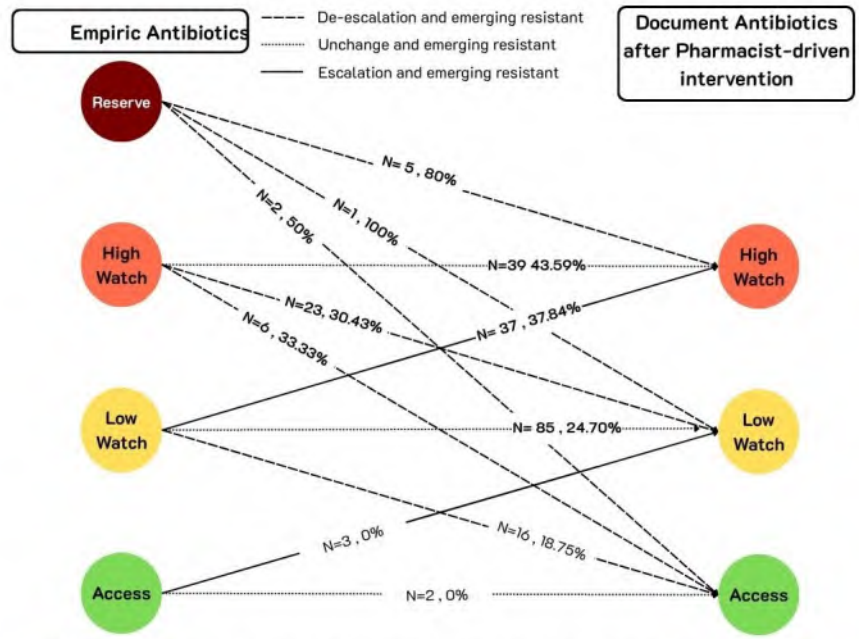
The primary outcome was the effect of pharmacist-recommended de-escalation on emerging resistance. Secondary outcomes included in-hospital mortality, length of stay, and hospitalization costs.

Results
Among 219 eligible patients, E. coli was the most commonly isolated pathogen (39.27%), followed by K. pneumoniae (11.87%). The predominant source of infection was primary bacteremia, followed by urinary tract infections.

A total of 62 patients (28.31%) received pharmacist-driven de-escalation. The emerging resistance rate was slightly lower in the de-escalation group (30.65%) than in the non-de-escalation group (32.48%), with no statistically significant difference (OR 0.91, 95% CI 0.45–1.84, P = 0.793). No significant differences were observed in 28-day mortality, hospital stay, or cost.

Conclusions
Pharmacist-driven de-escalation was not associated with increased resistance or adverse outcomes. It may be a safe and supportive strategy for antimicrobial stewardship. Further studies are warranted to confirm these findings.

Figure 1 : Antimicrobial category switching and percentage of emerging resistant in patient recieving de-escalation, unchanged or escalation therapy



Note : Acess and **Reserve** includes WHO Access and Reserve antibiotics. **Low watch** includes WHO second-line cephalosporins (e.g. Ceftriaxone, Ceftazidime) and fluoroquinolones. **High watch** includes antibiotics providing partial ESBL coverages and carbapenems (e.g. Piperacillin/tazobactam, Carbapenems)

RES-282: Reducing CAUTI Risk Through Biofilm Prevention: Evidence-Based Strategies for Urinary Catheter Management

Wani Devita Gunardi

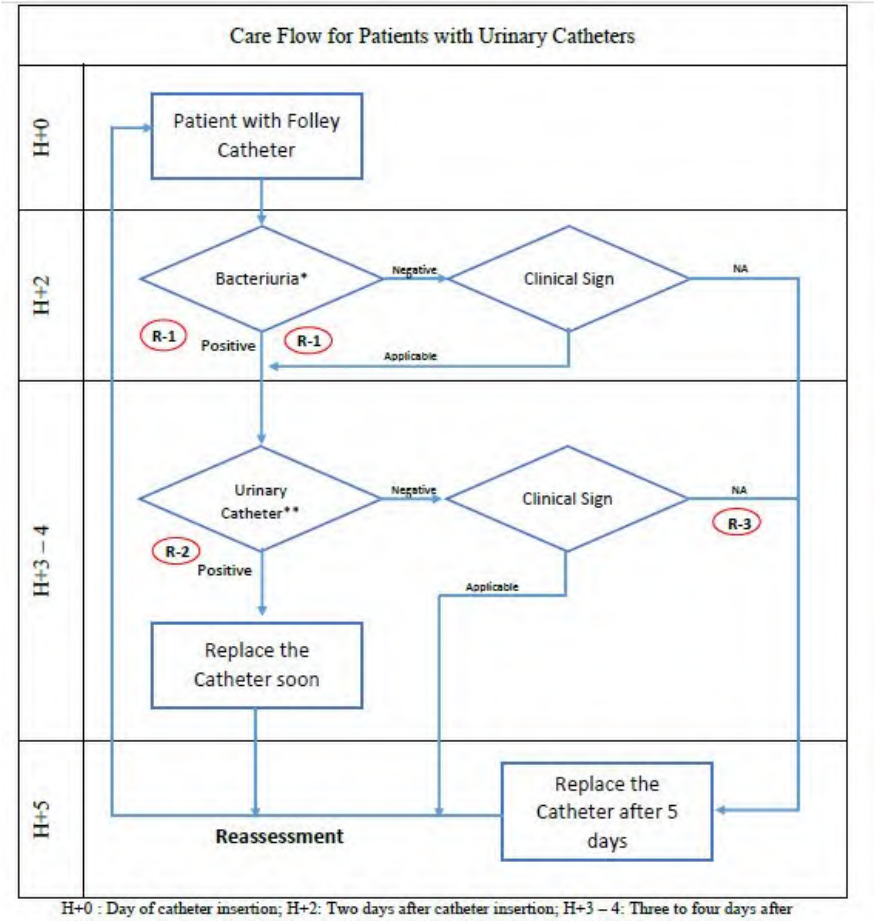
Krida Wacana Christian University

Background
Catheter-associated urinary tract infections (CAUTIs) are common healthcare-associated infections, mainly caused by biofilm formation on urinary catheters. Gender and catheter duration are key risk factors. Biofilms lead to recurrent infections and reduce antibiotic efficacy. Thus, evidence-based catheter management is vital to reduce CAUTI risk.

Method
This prospective observational study involved 109 adult patients undergoing urinary catheterization between September 2017 and January 2018. Patients with pregnancy, urinary tract abnormalities, malignancy, or HIV were excluded. Urine samples were collected twice: after catheter insertion and before removal. Bacteriuria was screened using flow cytometry and confirmed by culture. Removed catheters were cultured to assess biofilm. Isolates from urine and catheters were tested for biofilm-forming ability using Congo Red Agar.

Results
Participants were aged 18–88 years, predominantly female. The mean catheterization duration was 5.6 ± 2.1 days; most were catheterized ≥5 days. Diabetes was present in 22%, and 68.8% received antibiotics. Bacteriuria occurred in 34% post-insertion and 20% at removal, significantly associated with catheterization ($p = 0.029$). Antibiotics reduced bacteriuria (9.3% vs. 44.1%, $p < 0.001$; OR = 0.130) but not biofilm formation (73.4%, $p > 0.05$). CRA-positive isolates had 13.5 times higher biofilm potential. Biofilms developed by day 3 (62%) and bacterial dispersal occurred around day 5. Risk factors for biofilm included female sex, early bacteriuria, and catheterization >5 days ($p = 0.004$).

Conclusions
Early biofilm detection and catheter removal by day 5 are recommended to reduce CAUTI risk. Empirical antibiotics should be reserved for symptomatic cases with lab confirmation.



H+0 : Day of catheter insertion; H+2: Two days after catheter insertion; H+3 – 4: Three to four days after catheter insertion; H+5: Five days after catheter insertion; R-1: Empirical antibiotic recommendation; R-2: Definitive antibiotic recommendation; R-3: recommendation to stop theraphy; *: through flowcytometry test; **through identification, sensitivity test, and antibiofilm test (CRA).

RES-283: Geographic Patterns of Nontuberculous Mycobacteria Diversity in Southeastern China: Insights from a Multiplex PCR-Based Surveillance Study

Aijie Fang[2], Qingge Li[1]

[1]Xiamen University
[2]Zeesan Biotech

Background
Nontuberculous mycobacteria (NTM) are increasingly recognized as important causes of pulmonary disease globally. In China, where tuberculosis (TB) remains endemic, NTM infections are frequently underdiagnosed due to overlapping clinical and radiographic features. Accurate species-level identification is vital for effective treatment and public health decision-making.

Method
Between January and June 2025, over 11,000 clinical specimens were collected from patients with suspected TB in three coastal cities along southeastern China—Shanghai (n=2,873), Fuzhou (n=4,500), and Guangzhou (n=6,784). Specimen types included sputum, bronchoalveolar lavage fluid, pleural effusion, mycobacterial cultures, and other respiratory samples. All were tested using the MeltPro® Myco Identification Kit, a recently approved multiplex real-time PCR assay capable of detecting 19 clinically relevant NTM species in a single reaction.

Results
NTM were detected in all three regions, with a distinct geographic gradient in species diversity from north to south. Shanghai exhibited the lowest diversity, while Guangzhou showed the highest, including both common species (e.g., M. intracellulare, M. abscessus, M. avium) and rare species (e.g., M. scrofulaceum, M. chelonae). This trend suggests increasing environmental exposure and niche variability favoring NTM diversity in southern regions.

Conclusions
Our study reveals a clear regional pattern in NTM distribution along China’s southeastern coast. These findings underscore the value of species-level identification for accurate diagnosis and tailored treatment, especially in TB-endemic regions where NTM may be overlooked.

RES-284: Detection of Sexually Transmitted Infections Using Multiplex qPCR in Female Sex Workers in Yogyakarta, Indonesia: A Mixed-Methods Study

Eka Dian Ayu Agustina Fatem[2], Bombong Nurpagino[1], Tri Wibawa[3], Titik Nuryastuti[3]

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[2]Universitas Cenderawasih, Jayapura, Indonesia
[3]Universitas Gadjah Mada, Yogyakarta, Indonesia

Background
Female Sex Workers (FSWs) represent a key population at high risk for Sexually Transmitted Infections (STIs), including gonococcal and non-gonococcal urethritis, HIV, hepatitis B, and syphilis. This study aimed to determine the incidence of N. gonorrhoeae, C. trachomatis, M. genitalium, syphilis, and HIV, assess antibiotic resistance profiles of M. genitalium, and explore the role of local stakeholders in STI management among FSWs in Parangkusumo, Yogyakarta.

Method
We conducted a mixed-method study using an explanatory sequential design. Quantitative analysis involved detecting M. genitalium and antibiotic resistance, detecting N. gonorrhoeae, and C. trachomatis by quantitative polymerase chain reaction (qPCR) and serological screening for HIV and syphilis. Qualitative data were obtained from stakeholder interviews assessing the implementation of Indonesian Ministry of Health Regulation No. 23/2023 concerning HIV, AIDS, and STI control in Yogyakarta.

Results
M. genitalium was detected in 19.7% of endocervical swab specimens. Macrolide resistance-associated mutations were present in 84.6% of isolates, while parC gene mutations linked to fluoroquinolone resistance were identified in 92.3%. N. gonorrhoeae and C. trachomatis were detected in 18.2% of samples, with 7.6% showing co-infections. HIV and syphilis seroprevalence were 8.5% and 14.6%, respectively. Interviews revealed frequent unsupervised antibiotic use among FSWs and highlighted that, although STI control policies exist, greater support for community health workers is needed.

Conclusions
The high prevalence of macrolide-and fluoroquinolone-resistant M. genitalium underscores the urgent need to expand molecular diagnostic capacity for STIs. Incorporating STIs testing and strengthening collaboration with local community workers could enhance STI management in high-risk populations.

RES-285: Evaluation of Automated Fluorescent Immunoassay System for Detection of Norovirus in Stool Samples

Han-Sung Kim, Ho Young Kim

Hallym University Medical Center

Background
Antigen test are widely used for the detection of enteric adenoviruses. AFIAS Noro assay (Biotech Med, Korea) is an automated fluorescent immunoassay for detections of norovirus in stool samples. We evaluated the performance of detecting norovirus of this assay by comparing it to that of real-time PCR.

Method
AFIAS assay was performed in 24 norovirus-positive and 28 norovirus-negative stool samples. Real-time PCR was used as reference method.

Results
The sensitivity and specificity of AFIAS assay were 79.2% and 100%, respectively, in detecting norovirus when compared to real-time PCR. Nineteen samples were positive for both AFIAS assay and real-time PCR, while 28 samples were negative for both AFIAS assay and real-time PCR. Five samples were positive only for real-time PCR. The overall concordance rate between AFIAS assay and real-time PCR was 90.4%.

Conclusions
The AFIAS Noro assay showed high sensitivity, specificity and good correlation with real-time PCR and is likely to be as useful in detection of norovirus in stool samples.

RES-286: Streamlining Pathogen Surveillance: Evaluating Next Generation Sequencing as an Alternative to Phenotypic Serotyping and Antimicrobial Resistance Testing

Phakawat Chotejaruchaiya[1], Chayaporn Suphavilai[1], Patipan Boonsimma[1], Kar Mun Lim[1], Tongtong Liu[4], Wei Ern Ong[2], Yen Ee Tan[2, 3], Niranjan Nagarajan[1,5], Karrie Ko[1,3]

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Background
Phenotypic serotyping and antimicrobial resistance (AMR) testing are critical components of infectious disease surveillance, outbreak investigation, and vaccine development. However, these conventional methods are often labor-intensive, time-consuming, and limited in scalability. Next-generation sequencing (NGS) offers a promising alternative for streamlined serotype and AMR characterization. We assessed the performance of NGS-based bioinformatics tools for serotyping and AMR prediction using a diverse, multi-species in-house dataset, with conventional phenotypic methods as the reference standard.

Method
Over 300 clinical isolates of Streptococcus pneumoniae, Neisseria gonorrhoea, and Salmonella enterica were included in this study. All isolates underwent phenotypic testing and whole-genome sequencing to generate three comprehensive in-house datasets. We evaluated a range of publicly available AMR and serotyping bioinformatics tools including RASE, Pathogenwatch, AMRFinderPlus, SeroBA, SeroCall, SeqSero1, SeqSero2, and SISTR using Illumina and Nanopore reads and assembly, with predictions compared to phenotypic results. Tools' accuracy, speed and generalizability were assessed.

Results
AMR tools achieved F1 scores of 0.87–0.91 across three species, with reduced performance on N. gonorrhoeae compared to S. pneumoniae, and variability between read and assembly inputs. Serotyping tools showed over 90% concordance and were able to identify phenotypically non-typable S. pneumoniae samples. Turnaround times were also compared between phenotypic and NGS-based approaches to highlight improvement in turnaround time (TAT).

Conclusions
NGS-based bioinformatics tools for AMR and serotyping demonstrated improved TAT and high concordance with traditional phenotypic methods, supporting their potential for streamlining pathogen surveillance. However, continued refinement to ensure broader species coverage is crucial for scalable implementation.

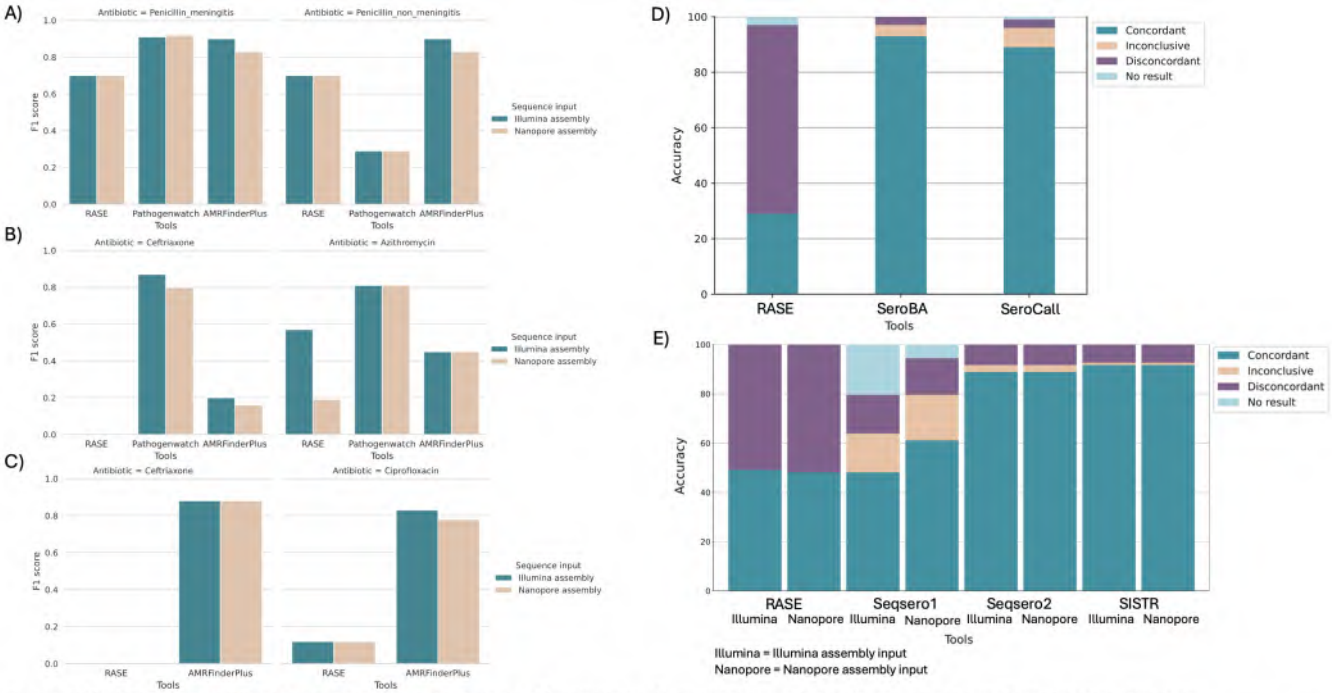


Figure 1. (A-C) AMR tools demonstrated high F1 scores in in-house datasets of *S. pneumoniae*, *N. gonorrhoeae*, and *S. enterica*, using Illumina and Nanopore assembly inputs. F1 score = A metric that balances precision (Of all isolates predicted as resistant, how many are truly resistant) and recall (Of all truly resistant isolates, how many did the tool predict correctly. (D-E) Serotype tools showed high concordance with traditional phenotypic results in in-house datasets of *S. pneumoniae* and *S. enterica*, using read and assembly inputs, respectively.

RES-287: Fungicidal Effect of Antimicrobial Agents Against Environmental Fungi by Broth Microdilution Method

Yordhathai Thongsri, Namthip Amonnitichoksakula, Paweena Pameea, Suchaya Taraporna, Kanchana Usuwanthim, Pachuen Potup, Sophit Khanthawong

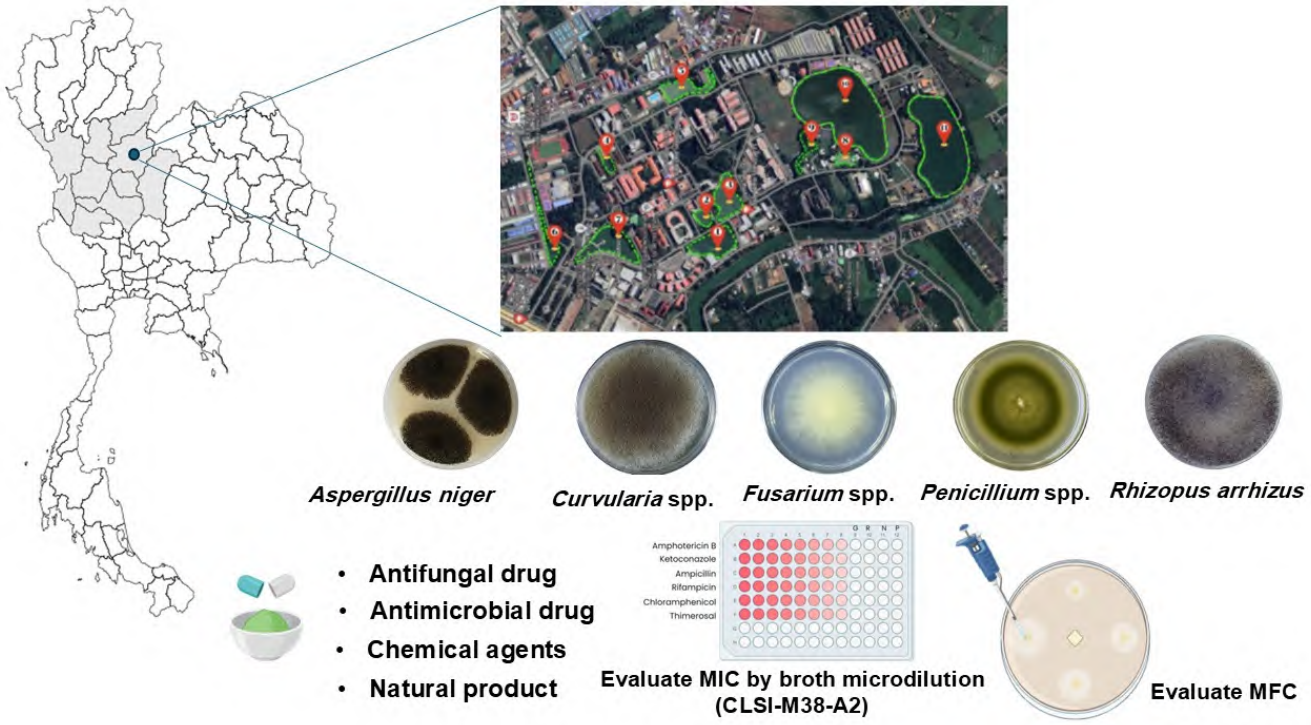
Naresuan University

Background
The World Health Organization (WHO) has published a report of nineteen fungal species highlighting the most critical pathogens. During the COVID-19 pandemic linked to an increased incidence of comorbid invasive fungal infections which high morbidity and mortality. Despite the growing concern, fungal infections receive little attention and resources, leading to a paucity of quality data on antifungal resistance patterns.

Method
Five fungal strains including of Aspergillus niger, Curvularia spp., Fusarium spp., Penicillium spp., and Rhizopus arrhizus, which isolated from environmental sources were evaluated with antimicrobial agents. Two antifungal drugs (amphotericin B and ketoconazole); three antimicrobial drugs (ampicillin, rifampicin, and chloramphenicol); the chemical agents (dimethyl sulfoxide (DMSO), methanol, ethanol, and thimerosal were tested. The antifungal activity was assessed by broth microdilution method referencing the Clinical and Laboratory Standards Institute (CLSI) M38-A2 guideline.

Results
The results of R. arrhizus were resistance to ampicillin, chloramphenicol, and rifampicin, with MIC values of >1,600, 800, and 50 µg/mL, respectively. It was susceptible to amphotericin B, ketoconazole, and thimerosal at a concentration of ≤ 12.5 µg/mL. The four remaining fungal species could not determine. Further evaluation by disk diffusion method showed ampicillin could inhibit 20% of all fungal isolates. Amphotericin B inhibited two fungal strains (40%) and Ketoconazole could inhibit 60%. Thimerosal could inhibit all five fungal species (MIC ≤ 12.5 to 100 µg/mL). All environmental fungal isolates exhibited 100% resistance to chloramphenicol and rifampicin.

Conclusions
This research shows the effect of antifungal agents against environmental fungi, which could provide a treatment strategies of fungal infections in the future.



RES-288: Explainable Machine Learning Framework: Mycobacterium Abscessus Complex Subspecies Classification and Antimicrobial Resistance Prediction

Phakawat Chotejaruchaiya[4], Patipan Boonsimma[4], Hatairat Yingtaweesittikul[3], Karrie Ko[5,2], Chayaporn Suphavilai[4], Niranjan Nagarajan[4], Suwatchareeporn Rotcheewaphan[1], Kanphai Wongjarit[1]

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Background
Mycobacterium abscessus, consisting of 3 subspecies: abscessus (MAB), bolletii (MBO), and massiliense (MMA), is a group of rapidly growing nontuberculous mycobacterium (NTM) implicated in chronic pulmonary and cutaneous infections. Accurate subspecies identification is important for guiding treatment, as MMA is typically macrolide-susceptible, while MAB and MBO often have inducible macrolide resistance. Phenotypic susceptibility testing is slow (14 days), and molecular detection of erm(41), rrl, and rrs mutations remains insufficient to optimize treatment regimens requiring ≥3 active agents. To overcome these limitations, we propose integrating whole-genome sequencing (WGS) with explainable artificial intelligence (XAI) to enable simultaneous subspecies identification, resistance prediction across multiple drugs, and discovery of novel genomic markers in an interpretable way.

Method
Seven ML/XAI models were trained on 432 publicly available genomes with phenotypic resistance profiles using 80/20 train-test split. Predictive performance was measured by F1 score and compared with WGS baseline tools. ML/XAI models explainability was evaluated using known markers. Subspecies were identified using k-mer-based approach. Gene alignments were performed.

Results
ML models achieved F1 scores of 0.88-0.97 for clarithromycin and 0.50-0.71 for amikacin, comparable to baseline tools. XAI captured 2 known markers and identified potential novel resistance determinants. Gene alignment showed heterogeneity in clarithromycin and amikacin resistance among MABC subspecies and potential sub-lineages.

Conclusions
Our ML/XAI models demonstrated comparable performance to current tools, while providing explainable outputs for detecting novel resistance markers and sublineages. This promising approach can be extended to other mycobacterial species, ultimately enabling faster diagnostics and therapy optimization.

A)

	F1 score	
Tools	**Clarithromycin**	**Amikacin**
Baseline tools		
NTM-profiler	0.97	0.00
Mab_ariba	0.97	Not Available
Random prediction	0.39	0.42
ML + target genes		
Logistic regression	0.97	0.50
Random Forest	0.96	0.50
XGboost	0.97	0.50
RuleFit	0.96	0.50
ML + extended genes		
Logistic regression	0.92	0.71
Random Forest	0.88	0.71
XGboost	0.91	0.71
RuleFit	0.97	0.71

B)

Methods	AMR phenotype inferance	Novel marker identification	Subspecies identification	Novel lineage identification	Turn around time
Antibiotic susceptiblity testing	✓				6 (Acquired) or 17 days (Inducible)
Line probe assay	✓		✓		1-2 days
WGS bioinformatics tools	✓		✓		4-5 days
Our framework	✓	✓	✓	✓	4-5 days

Acquired = acquired macrolide resistance, and other drugs
Inducible = inducible macrolide resistance

Figure 1. (A) Our four models trained from target genes and extended genes demonstrated comparable F1 scores to baseline tools NTM-profiler and Mab_ariba in predicting resistance in Clarithromycin and Amikacin. F1 score = A metric that balances precision (Of all isolates predicted as resistant, how many are truly resistant) and recall (Of all truly resistant isolates, how many did the tool predict correctly). (B) Comparison of our framework and existing methods, highlighting the key advantages. Turnaround time indicates the estimated total duration from patient sample collection to the delivery of the analysis result.

RES-289: Endometriosis vs Fusobacterium spp. – Microbiological and Molecular Analysis of Endometrial Tissue Samples of Endometrium Patients Vs Control

Maja Czerniachowska[3], Agnieszka Kiryszewska-Jesionek[2], Malgorzata Brauncajs[2], Adrian Bekier[2], Piotr Machnicki[2], Dorota Pastuszak-Lewandoska[2], Filip Franciszek Karuga[1], Dorota Kolasa-Zwierzchowska[1], Paulina Glogowiec[1], Krzysztof Szyłło[1]

[1]Clinic of Gynecology, Gynecological Oncology and Endometriosis Treatment
[2]Department of Microbiology and Laboratory Medical Immunology
[3]Medical Univesity of Lodz

Background
Endometriosis is a disease characterized by mild to severe pelvic pain and abnormal uterine bleeding, affecting approximately 10-15% of women of reproductive age. Although the exact pathogenesis is not yet fully understood, recent studies suggest that it may be influenced by the presence of bacteria in endometrial tissue, indicating a potential causal role.

Method
The study included 16 female patients: 7 diagnosed with endometriosis and 9 patients who underwent hysterectomy due to other reasons. From each patient, oral and cervical swabs were collected prior to surgery, and during surgery, peritoneal fluid and cyst wall samples were collected. Endometrial cyst wall sample and peritoneal fluid were put in a sterile container, while oral and cervical swabs were collected into a tube with Amies transport medium, and a sterile tube with no medium and frozen at -20°C. All samples were cultured with appropriate broth and agar medium and incubated in anaerobic conditions. Each sample underwent both molecular and microbiological analysis. DNA was isolated and amplified using PCR using FUSO1 and FUSO2.

Results
PCR analysis revealed the presence of Fusobacterium DNA in 14 out of 16 oral swab samples: 8 out of 9 in the control group and 6 out of 7 in the endometriosis group. There was no statistically significant difference between the groups. DNA analysis of other samples - cervical swabs, peritoneal fluid, and endometrial cyst walls yielded negative results. In microbiological analysis, no Fusobacterium colonies were cultured.

Conclusions
To draw final conclusions, further analysis based on a larger group of patients is necessary.

RES-290: Empiric Antibiotic Use in the Older Adult with Community-Acquired Pneumonia: A Retrospective Study on Guideline Adherence, Appropriateness of Therapy, and Clinical Outcomes at A Tertiary Hospital in the Philippines

Demver Gomez, Terrence Louis Carlos, Ma. Charmian Hufano, Divinagracia Estimada-Salonga

De Los Santos Medical Center

Background
Pneumonia remains a leading cause of hospitalization and death among older adults, with approximately 3 million deaths annually worldwide. In the Philippines, CAP guidelines are generalized for adults and lack age-specific recommendations, leading clinicians to often use broader-spectrum antibiotics. Local data on pathogen profiles and resistance patterns in older patients are limited.

Method
We conducted a retrospective cohort study of 129 patients aged ≥60 years admitted for moderate- to high-risk CAP in 2023 at a tertiary hospital. Clinical, microbiologic, and treatment data were collected. Outcomes were analyzed in relation to adherence to the 2020 Philippine CAP guidelines and culture-based appropriateness of empiric therapy using Fisher's exact test and logistic regression (<0.05).

Results
Of the 129 patients, 71% received guideline-adherent empiric antibiotics. In the non-adherent group, 68% received broader-spectrum agents with anti-Pseudomonal coverage. There were no significant differences in in-hospital mortality (9.9% vs 12.5%) or prolonged hospital stay (>7 days: 40.7% vs 37.5%) between adherent and non-adherent groups (p>0.05). Among 22 patients (17%) with positive cultures, only 31.8% received appropriate antibiotics based on susceptibility results. Predominant pathogens were Klebsiella pneumoniae, and Escherichia coli. Culture-based appropriateness was not associated with better outcomes.

Conclusions
Guideline-adherent empiric therapy was not inferior to broader-spectrum regimens in terms of mortality or hospital stay. These findings support the use of guideline-recommended antibiotics in older adults with CAP. The low diagnostic yield of cultures highlights the need for improved microbiologic testing.

RES-291: Observing the Trends of Echinocandin Resistance Patterns in Common Candida Species in a Tertiary Care Centre in the Himalayan Foothills

Sukriti Yadav[1], Imola Jamir[2]

[1]AIIMS Rishikesh
[2]Nagaland Institute of Medical Sciences and Research (NIMSR), Kohima, India

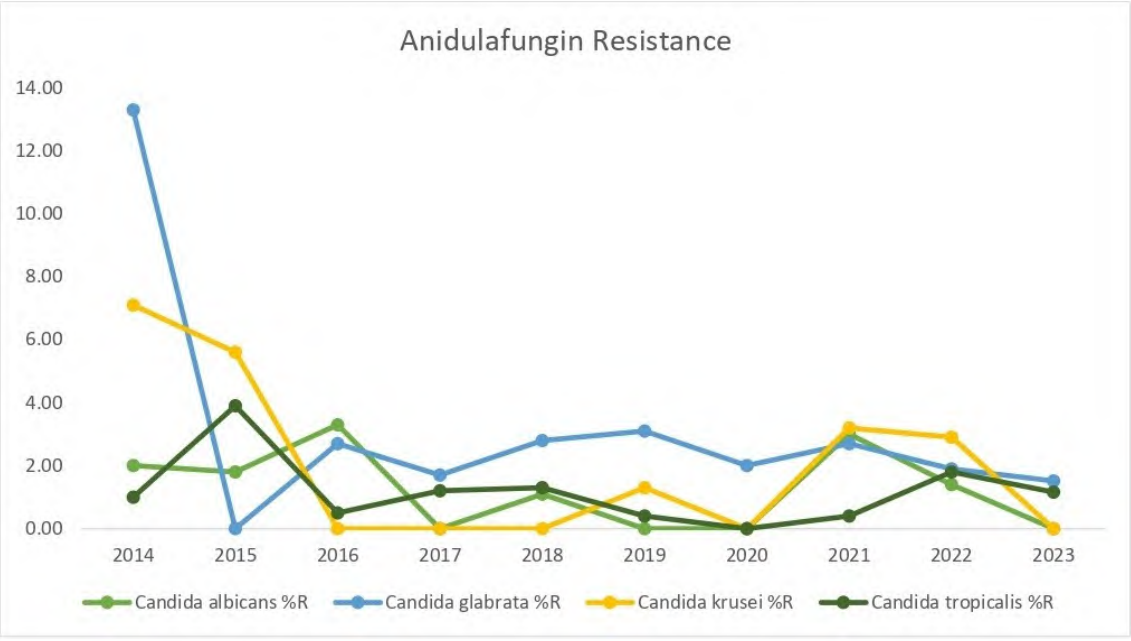
Background
Among fungal pathogens, Candida species are the predominant pathogenic agents. They are responsible for causing a range of infections from superficial mucocutaneous to invasive candidiasis. Traditionally, C. albicans has been the most frequently isolated species. However, there has been a notable epidemiological shift toward non-albicans Candida (NAC) species such as C. glabrata, C. tropicalis, C. krusei, etc., worldwide. Rapid, accurate identification of yeasts, along with antifungal susceptibility (AFST) profiling, is key for initiating targeted and timely therapy. In this study, we evaluated the trends of antifungal susceptibility of Candida species isolated from clinical samples for a decade.

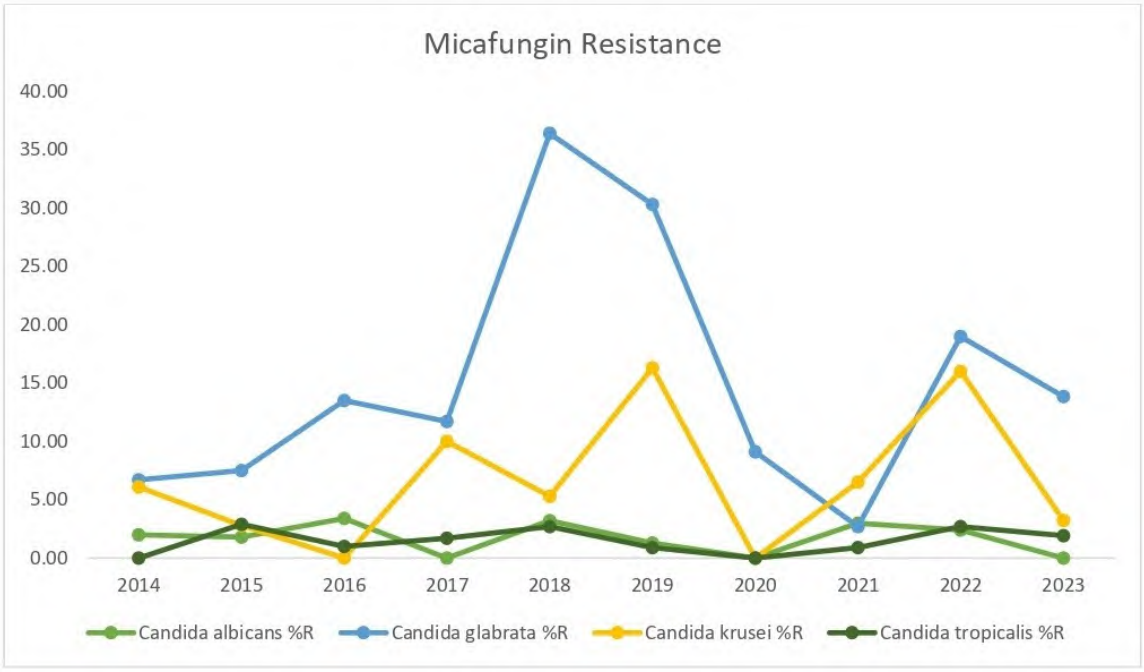
Method
Clinically Isolated strains were subjected to AFST for echinocandin – Anidulafungin, Caspofungin and Micafungin per the CLSI M27-A3 & interpreted per M60 & M27M44S guidelines. All results were compiled in MS Excel 2019 version, and AFST analysis was done using WHONET 2024.

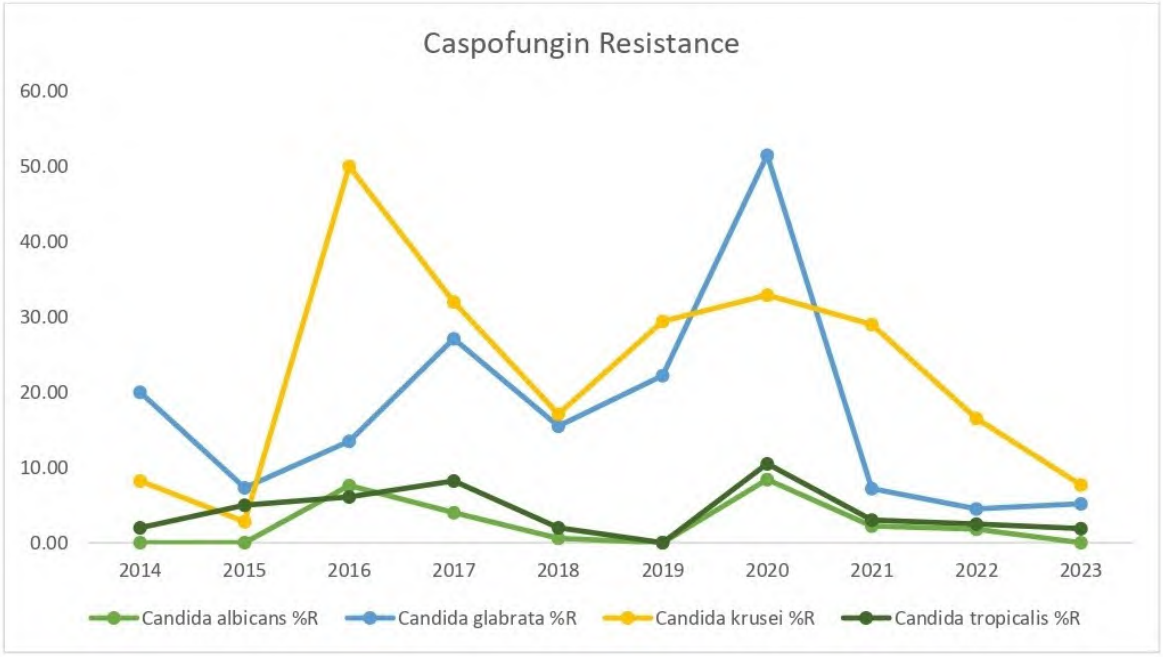
Results
Most commonly isolated species were C. tropicalis, C. albicans, C. krusei, and C. glabrata in descending order. A distinct pattern of decline in resistance during the study period was noted for Anidulafungin
C. albicans (2.0% to 0.03%)
C. krusei (7.1% to 0.01%)
C. glabrata (13.3% to 1.52%)

Caspofungin
C. tropicalis (2.0% to 1.19%)
C. krusei (8.3% to 7.6%)
C. glabrata (20.0% to 5.17%)
In the case of C. albicans, the change was noted from 2016 (7.6% - 0.01%).
(Graph attached)

Conclusions
There is a positive, clear, and distinct decrease in echinocandin resistance in a decade-long period. This information may be useful in future for reconsidering treatment guidelines of such infections.




Micafungin Resistance
40.00
35.00
30.00
25.00
20.00
15.00
10.00
5.00
0.00
2014
2015
2016
2017
2018
2019
2020
2021
2022
2023
Candida albicans %R
Candida glabrata %R
Candida krusei %R
Candida tropicalis %R


Caspofungin Resistance
60.00
50.00
40.00
30.00
20.00
10.00
0.00
2014
2015
2016
2017
2018
2019
2020
2021
2022
2023
Candida albicans %R
Candida glabrata %R
Candida krusei %R
Candida tropicalis %R

RES-293: Molecular Epidemiology of Drug-Resistant Mycobacterium tuberculosis Isolates from the Republic of Korea, 2021–2025

Seong Wook Pyo, Min Ji Lee, Youngmi Kim, Jeongsub Lee, Donghyeok Kim, Jaeil Yoo

Korea Disease Control and Prevention Agency (KCDA)

Background
Drug-resistant tuberculosis (DR-TB) remains a critical public health challenge due to its prolonged treatment regimen, lower cure rates, and potential for transmission. Molecular epidemiological analyses provide valuable insights into the dissemination and genetic diversity of DR-TB strains, which are essential for developing targeted intervention strategies.

Method
Between 2021 and 2025, a total of 304 drug-resistant Mycobacterium tuberculosis isolates were collected across the Republic of Korea. Of these, 81 were rifampicin-resistant (RR), 199 multidrug-resistant (MDR), 22 pre-extensively drug-resistant (pre-XDR), and 2 extensively drug-resistant (XDR). Lineages were determined by spoligotyping, and core genome multilocus sequence typing (cgMLST) based on 2,891 loci was employed to assess genetic relatedness.

Results
Spoligotyping revealed that the majority of isolates (89.8%, n=293) belonged to the East Asian lineage, followed by the Euro American (9.2%), East African Indian (0.7%), and Indo Oceanic lineages (0.3%). cgMLST analysis identified 293 unique complex types and nine clusters encompassing 20 isolates. Each cluster included 2 to 4 isolates, with time intervals between case notifications ranging from 3 to 34 months. Among these clusters, epidemiological links were confirmed in three cases (household, workplace, and relapse), while no epidemiological connections were found for the remaining six genetic clusters. Most isolates were genetically distinct and classified as singletons.

Conclusions
This study provides the current status of DR-TB transmission in the Republic of Korea. No evidence of large-scale transmission caused by a single genotype was identified. Continuous molecular epidemiological surveillance is necessary for national TB control.

RES-294: Comparison of Baseline Characteristics and Mortality Outcomes Between Carbapenem-Resistant and Non-Resistant Enterobacterales Bloodstream Infections: A Retrospective Study

Tipanong Gatechan, Korawan Pudpong, Praphatsorn Chaphakdee

Sunpasitthiprasong Hospital

Background
Bloodstream infection (BSI) due to carbapenem-resistant Enterobacterales (CRE) is emerging as an urgent public health threat worldwide, often leading to limited treatment options and poor outcomes. CRE bloodstream infections are an escalating global public health concern that demands urgent attention from healthcare systems worldwide. This study aimed to compare the clinical features and outcomes between patients with CRE and non-CRE BSI.

Method
A retrospective study was conducted in adult patients (aged ≥18 years) admitted to a tertiary hospital in Thailand from July 2024 to March 2025. All patients had bloodstream infection with microbiological confirmed by Enterobacterales. Patients were divided into CRE and non-CRE groups. Demographics; comorbidities; infection sources; microbial resistance patterns; treatment; and clinical outcomes were reviewed. Factors associated with 14-day all-cause mortality were assessed with univariate and multivariate logistic regression.

Results
Amount 147 patients were included, with 37.41% in the CRE group. Compared to the non-CRE group, CRE patients had significantly longer hospitalization (median 28 vs. 10 days, p<0.001) and higher hospital costs (median 8,179.21 vs. 1,608.10 USD, p<0.001). ICU admission was more frequent in CRE group (45.5% vs. 14.1%, p<0.001). The 14-day mortality in CRE was 20% versus 2% in non-CRE. On multivariate analysis, prolonged hospitalization [OR=0.95, 0.87-1.03] and ceftazidime-avibactam resistance [OR=1.2, 0.2-7.02] were found to be independently associated with mortality, although without statistical significance.

Conclusions
Patients with CRE bloodstream infections are more likely to require ICU care, have longer hospital stays, and incur higher treatment costs. These findings highlight the urgent need for diagnostic stewardship strategies to improve clinical outcomes.

Baseline characteristic (%)	CRE group	non CRE group
Patients (N)	55	92
Male	61.8	51.1
Age (mean, IQR)	60 (52.5-71.0)	63.5 (56.0-74.0)
Comorbidity		
Cardiovascular disease	38.2	32.6
Diabetes mellitus	27.3	31.5
Renal disease	18.2	29.3
Solid malignancy	10.9	17.4
Hematologic malignancy	16.4	5.4
Pathogens		
Escherichia coli	41.8	77.2
Klebsiella pneumoniae	58.2	22.8
Source of infection		
Primary Bacteremia	58.2	31.5
Catheter related infection	18.2	1.1
Urinary tract infection	14.5	41.3
Pneumonia	5.5	6.5
Intraabdominal infection	1.8	16.3
Appropriate empirical therapy	20	75
Appropriate document therapy	52.7	97.8
ICU admission	45.5	14.1
Ventilator use	47.3	38.0
Inotropic drug use	27.3	14.1
Last admission in 3 month ago	45.5	34.8
receive IV antibiotic in 3 month ago	41.8	25
14 day all cause mortality	20	2.2
Hospital cost [USD] (median, IQR)	8,179.21 (3,523.59 - 16,574.97)	1,608.10 (962.74 - 3,045.18)

RES-297: Limits of Single-Locus Barcoding in the Aspergillus Flavus Complex from Ocular Infections

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Background
Accurate identification of pathogenic Aspergillus within the A. flavus complex remains challenging.

Method
In our study, we evaluated single-locus DNA barcoding-internal transcribed spacer (ITS), β-tubulin (BenA), and calmodulin (CaM) for three ocular isolates morphologically identified as A. flavus. Their genomic DNA was extracted to perform PCR amplification and Sanger sequencing for each locus sequence. Each gene was combined with those of other Aspergillus spp. from GenBank for species identification by phylogenetic analyses.

Results
ITS analyses showed three strains were clustered with A. flavus, A. oryzae, A. fasciculatus, A. minisclerotigenes and A. aflatoxiformans at 100% similarity (corrected distance = 0.00 substitutions/site). BenA showed three strains were 99-100% similarity to A. flavus/A. oryzae. CaM showed 97-99% similarity to A. flavus, A. oryzae and A. fasciculatus. Trees from individual loci did not separate the isolates at species level.

Conclusions
In conclusion, single-locus barcoding with ITS, BenA and CaM did not resolve species boundaries within the A. flavus complex. For routine clinical reporting, designation as A. flavus complex is appropriate.

RES-300: Clinical Characteristics and Outcomes of Raoultella Bacteremia: A Retrospective Analysis of 32 Cases

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Department of General Internal Medicine, Kobe City Medical Center West Hospital

Background
Raoultella species are emerging opportunistic pathogens that can cause serious infections, yet comprehensive clinical data remain limited. This study aimed to describe the clinical and microbiological features of Raoultella bacteremia in hospitalized patients.

Method
We conducted a single-center, retrospective observational study including all patients with Raoultella bacteremia admitted between May 2015 and May 2025, collecting data on demographics, clinical characteristics, antimicrobial susceptibility, and outcomes.

Results
Of the 32 identified cases, 26 (81.3%) were R. planticola, 5 (15.6%) R. ornithinolytica, and 1 (3.1%) was a mixed infection. The median patient age was 77 years, and 62.5% were male. Most cases (84.4%) were community-acquired, while 15.6% were healthcare-associated. Indwelling devices were present in 18.8% of cases. Active malignancy and immunosuppressive therapy were observed in 9 (28.1%) and 2 (6.3%) patients, respectively. The most common source of bacteremia was the biliary tract (19 cases, 59.4%), followed by the urinary tract (7 cases, 21.9%) and the gastrointestinal tract (3 cases, 9.4%). All isolates were resistant to ampicillin, with one cefazolin-resistant AmpC producer; all remained susceptible to third- and fourth-generation cephalosporins, cefmetazole, carbapenems, aztreonam, and aminoglycosides. Resistance to fluoroquinolones and trimethoprim-sulfamethoxazole was observed in two isolates each. The in-hospital mortality rate was 6.3% (2 cases).

Conclusions
Raoultella bacteremia primarily affected elderly patients with biliary tract involvement and a notable proportion of malignancy. While species distribution, infection sources, and antimicrobial susceptibility patterns were consistent with previous reports, the proportions of coexisting malignancy and mortality differed, highlighting the need for further case accumulation and multicenter studies.

RES-301: Strengthening Antimicrobial Resistance (AMR) Surveillance and Response: The Fleming Fund in Asia (2016–2025)

Sittidech Surasri[3], Heidi Hopkins[5], Yu Nandar Aung[3], Manish Pathak[2], Jacob Wildfire[5], Neha Gulati[2], Ben Amos[1], Cyril Buehler[6], Emmanuel Azore[4], Stanley Fenwick[3], Toby Leslie[5]

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[2]Mott MacDonald, India
[3]Mott MacDonald, Thailand
[4]Mott MacDonald, Uganda
[5]Mott MacDonald, United Kingdom
[6]ORDiagnostics SA, France

Background
Antimicrobial resistance (AMR) threatens global health, particularly in areas with limited laboratory capacity and surveillance infrastructure. The United Kingdom's Fleming Fund addresses these gaps through investments in laboratories, workforce training, and data systems to strengthen AMR surveillance, taking a One Health approach integrating human, animal, and environmental health sectors.

Method
Program monitoring data (2016–2025) from Fleming Fund-supported countries in Asia were reviewed. Metrics included numbers of supported laboratories, infrastructure enhancements, equipment provision, trainings and fellowships, external quality assessment (EQA), data production, and contributions to WHO Global Antimicrobial Resistance and Use Surveillance System (GLASS) and national AMR strategies.

Results
By 2025, the Fleming Fund supported 201 laboratories across eleven Asian countries, comprising 64% human health, 32% animal health, and 4% environmental/food safety sites. Infrastructure strengthening covered refurbishment of laboratory premises and procurement of basic and advanced equipment (automated blood culture systems, susceptibility testing platforms, mass spectrometers). Workforce development included 27,110 training attendances and 186 fellowships. Supported sites processed approximately 3.75 million human clinical and 102,000 animal specimens. Of sites assessed in 2024-25, 116/127 (91%) demonstrated capacity improvement per standardized benchmarks, with 51 laboratories participating in EQA. At policy level, all eleven countries submitted AMR data to WHO GLASS, five updated their National Action Plans, and four have costed AMR surveillance strategies.

Conclusions
The Fleming Fund has markedly advanced AMR surveillance capacity in Asia, expanding laboratory infrastructure, workforce expertise, and data use for policy and stewardship. Sustaining these gains will require continued investment, national ownership, and integration across sectors.

RES-302: Hyperinflammatory Phenotypes May Be More Important Than Age and Co-Morbidities in Predicting Adverse Outcomes in Hospitalized Patients with Influenza A

Jinghao Nicholas Ngiam[1], Matthew Chung Yi Koh[1], Hidayat Lokman[2], Jickky Palmae Sarathy[2], Dinah Aziz[2], Yee Joo Tan[2], Paul Anantharajah Tambyah[1]

[1]National University Hospital
[2]National University of Singapore

Background
Influenza A virus (IAV) infection leads to a broad range of clinical outcomes, which may be influenced by the host's inflammatory response. Understanding distinct inflammatory phenotypes could help identify patients at higher risk for adverse outcomes and guide targeted treatment strategies.

Method
We conducted a prospective observational study of 41 hospitalized adult patients with laboratory-confirmed IAV infection. Baseline clinical and laboratory data were collected, including absolute neutrophil count (ANC) and platelet (Plt) count. Latent class analysis was performed to identify inflammatory phenotypes based on ANC and Plt levels. Patients were then stratified by classes, and the association between phenotype and adverse clinical outcomes (defined as intensive care unit admission, or prolonged hospital stay greater than 1 week), was assessed using logistic regression adjusted for age.

Results
Age and co-morbidities did not correlate with adverse outcomes (Table 1). The hyperinflammatory phenotype (35.8%, 15/41), was defined by elevated ANC (>7×10⁹/L) and Plt count (>450×10⁹/L), and had a 40% rate of adverse outcomes, compared with 15.4% in the normo-inflammatory group. After adjusting for age, the hyperinflammatory phenotype remained associated with higher odds of clinical deterioration (adjusted odds ratio 3.63, 95%CI 0.83 – 16.17, p=0.091), approaching statistical significance (Figure 1, Table 2).

Conclusions
A hyperinflammatory phenotype defined by elevated ANC and Plt was observed in a subset of hospitalized IAV patients and was associated with worse clinical outcomes. Further validation and exploration of the underlying mechanisms may inform future risk stratification and immunomodulatory interventions in severe IAV.

Table 1: Descriptive characteristics of hospitalised patients with influenza A virus infection

Parameter	Total (n=41)	Adverse outcomes (ICU or long hospital stay >7 days) (n=10)	No adverse outcomes (n=31)
Age (years)	61 (±12)	60 (±13)	61 (±12)
Total white cell count (x10⁹/L)	8.2 (±3.4)	11.0 (±4.4)	7.4 (±2.6)
Absolute neutrophil count (x10⁹/L)	6.3 (±3.1)	8.4 (±4.2)	5.6 (±2.4)
Platelet count (x10⁹/L)	232 (±106)	248 (±139)	228 (±96)
Haemoglobin (g/dL)	12.5 (±2.4)	12.4 (±2.8)	12.6 (±2.3)
Hospital length of stay (days)	5 (±3)	9 (±3)	4 (±1)
Required intensive care	4 (9.8%)	4 (40.0%)	0 (0.0%)

Table 2: Multivariable logistic regression, showing the association of inflammatory phenotype on adverse outcomes, adjusting for age

Parameter	Adjusted odds ratio (95% confidence interval)	P-value
Hyperinflammatory phenotype (Class 2)	**3.63 (0.83 – 16.17)**	**0.091**
Age (years)	1.00 (0.94 – 1.06)	0.918

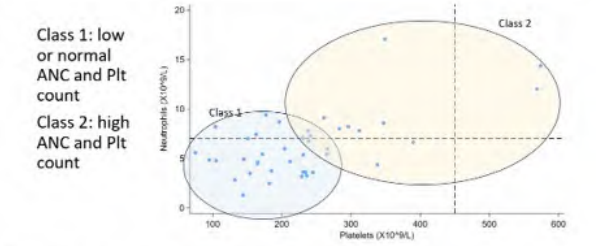

Figure 1: Latent class analysis identifying two distinct phenotypes: hyper-inflammatory (defined by elevated ANC and Plt) and the normo-inflammatory group

RES-303: Mapping Maternal Group B Streptococcus Colonization in Nepal: First Steps Toward Surveillance to Inform Vaccine Policy

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Background
Streptococcus agalactiae (Group B Streptococcus, GBS) is a major cause of neonatal sepsis, pneumonia, meningitis, and stillbirth. Early-onset disease typically results from vertical transmission during delivery. While maternal vaccination is a promising preventive strategy, regional data to guide implementation are limited. South Asia accounts for 25–30% of global pregnancies, yet data on GBS colonization remain scarce, including from Nepal.

Method
We enrolled 387 pregnant women presenting for delivery at two hospitals in Bhaktapur, Nepal. Recto-vaginal swabs were collected and cultured directly onto GBS chromogenic agar and then re-plated again after enrichment in LIM broth. Presumptive GBS colonies were confirmed biochemically, serotyped by multiplex PCR, and tested for antimicrobial susceptibility. Up to seven colonies per positive sample were analyzed for genotypic and serotype diversity.

Results
The prevalence of maternal GBS colonization was 4.4% (95% CI: 2.8–6.9). Serotype Ia was most common (41.2%), followed by VII, III, II (17.7% each), and Ib (5.9%). All isolates were penicillin-susceptible; 64.7% were non-susceptible to tetracycline. Median Minimum Inhibitory Concentrations (MICs) for ampicillin and flomoxef were 0.125 µg/mL and 0.25 µg/mL, respectively. Within-sample genetic diversity was seen in 41.2% of positive samples; one sample had two distinct serotypes. Cesarean sections accounted for 50% of deliveries. Broad-spectrum antibiotic use was high (81.1%), mostly ceftriaxone for prophylaxis.

Conclusions
Maternal GBS colonization was low, suggesting universal screening may not be feasible. High cesarean rates and antimicrobial use complicate GBS disease surveillance and underscore the need for context-specific approaches.

Figure 1: A representative RAPD PCR result for a GBS positive sample showing the presence of diverse genotypes with the same sample

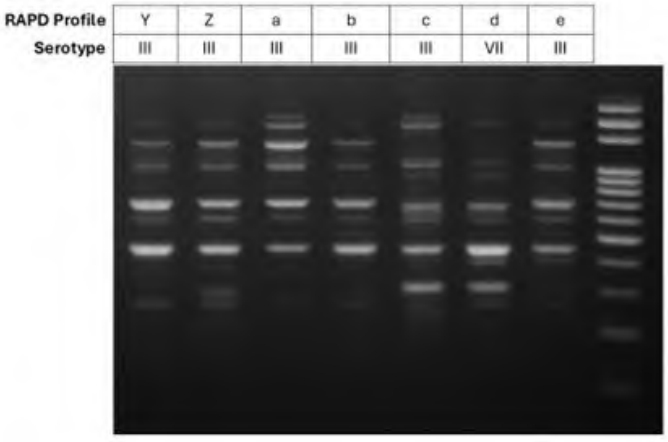
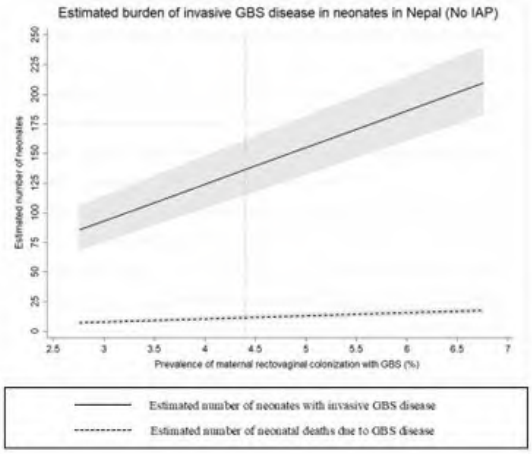


Figure 2. Estimated annual burden of invasive neonatal GBS disease in Nepal attributable to maternal rectovaginal colonization with *Streptococcus agalactiae* (prevalence: 4.4%)

If 50% of neonates acquire GBS through their colonized mother, 1% of the GBS colonized neonates develop invasive disease, and the case fatality rate for the neonates with the invasive GBS disease is 8.4%.



RES-306: ITS Barcoding Pythium Species Causing Eye Infection

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Background
Pythium spp., especially P. insidiosum is a fungus-like pathogen causing severe diseases of skin, eye, blood vessel, and can spread systemically to infect multiple organs which losing an infected organ or death is always an outcome. Rapid identification of the fungal species is important to decelerate the outcomes.

Method
In our study, 9 strains of Pythium species isolated from patients with eye infection were DNA-extracted for PCR-sequencing of internal transcribed spacer region (ITS). The 9-ITS sequences were combined with those of other species and closely related genera collected from GenBank. Phylogenetic analyses were performed to identify species.

Results
The results showed that 7 strains were P. insidiosum, and 2 strains were P. periculosum. Pythium periculosum is rare for eye infection. ITS analyses could produce barcoding gaps among Pythium species and closely related genera. Intraspecific distances of species in P. insidiosum complex i.e., P. insidiosum, P. periculosum and P. aphanidermatum, were lower than their interspecific distances.

Conclusions
Consequently, ITS barcoding would be an appropriate tool for use in routine as another gold standard method for Pythium species identification.

RES-308: Comparative Genomic and Molecular Characterisation of Hypervirulent and Classical Strains of Klebsiella pneumoniae from Clinical Isolates

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Universiti Putra Malaysia

Background
Klebsiella pneumoniae is a clinically significant pathogen in both healthcare and community settings. These species have evolved, acquiring resistance and virulence, enhancing their pathogenicity. Hypervirulent Klebsiella pneumoniae (hvKp) is recognized as a distinct strain associated with severe and invasive infections. Compared to classical Klebsiella pneumoniae (cKp), hvKp is often identified by elevated expression of virulence markers. Thus, this study aims to characterize hypervirulent and classical strains of Klebsiella pneumoniae via molecular genomic approaches.

Method
Clinical Klebsiella pneumoniae isolates were collected from two hospitals in Malaysia over two years. HvKp and cKp were defined based on the positive string test and presence of virulence genes. From the inclusion criteria, demographic and virulence genes distribution, susceptibility profile, molecular serotype, and sequence type were compared and analyzed for these strains.

Results
From 241 isolates, 60 (25%) were identified as hvKp, and 181 (75%) were cKp. HvKp was predominantly isolated from blood and associated with bloodstream infections. Meanwhile, cKp was mainly isolated from urine and linked to other infections. Both strains remained susceptible to antibiotics, though cephalosporin resistance was observed. HvKp demonstrated higher expression of rmpA2, iutA, and wcaG genes compared to cKp. Additionally, serotype analysis showed that hvKp was confined to K1/K2 serotypes, whereas cKp displayed diverse serotypes, including K5 and K54.

Conclusions
HvKp poses a serious clinical concern due to its ability to cause severe infections and confer hypervirulence compared to the classical strain. Continued surveillance and improved molecular diagnostics in healthcare settings are crucial to monitor the emergence and spread of hvKp.

RES-312: Epidemiology and Antibiogram of Burkholderia pseudomallei: An 8-Year Laboratory-Based Study

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International Islamic University Malaysia

Background
Melioidosis is a significant public health concern in Southeast Asia. This study aims to describe the distribution and antimicrobial susceptibility of its causative bacteria, Burkholderia pseudomallei, isolated from specimens received by a diagnostic microbiology laboratory located in Pahang, Malaysia.

Method
A retrospective analysis was conducted on 127 index B. pseudomallei isolated from early 2017 until mid-2025. The patients' demographics and the isolates' microbiological data were extracted from the laboratory information system. Chi-square tests were used to assess associations between specimen type, gender, and age groups of patients.

Results
76.4% isolates were obtained from male patients (male-to-female ratio 3.23:1). Adults (>18 years) constituted 98% of cases, with peak incidence observed in the 40-69 age group (69%). The mean age is 53.7 years. Across the study period, a seasonal clustering was observed in July and August. Blood was the predominant specimen type (59%). No significant association was found between specimen type and gender or age group ($p=0.9$ and $p=0.644$, respectively). High susceptibility rate was observed for ceftazidime (99%), doxycycline (98%), meropenem (96%), and amoxicillin-clavulanate (94%). The lowest susceptibility rate was seen for trimethoprim-sulfamethoxazole (SXT, 81%), followed by imipenem (IPM, 86%).

Conclusions
Melioidosis predominantly affects middle-aged males and frequently presents as bacteremia. The observed seasonal trend involving the inter-monsoon period (July and August) requires further investigation to elucidate the disease transmission risk in guiding the targeted public health interventions. Despite high susceptibility to key antibiotics, a relatively low susceptibility to SXT and IPM reinforces the need for continued antimicrobial resistance surveillance and monitoring in endemic settings.

RES-313: Clinical Outcomes of Early Consultation with Infectious Disease Physicians in Emergency Department Patients with Suspicion of Sepsis or Septic Shock

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[2]Mahasarakham Hospital

Background
Sepsis and septic shock are major causes of morbidity and mortality worldwide. Early consultation with infectious disease (ID) physicians have been associated with improved antimicrobial stewardship and potentially better patient outcomes.

Method
This quasi-experimental study at Srinagarind Hospital, Khon Kaen University, Thailand, enrolled adults (≥18 years) with suspected sepsis or septic shock presenting to the emergency department (ED). Two phases were compared: usual care (control) and mandatory early infectious disease consultation (intervention). The primary outcome was 30-day mortality; secondary outcomes included appropriateness of empirical antibiotics, antibiotic modification within 24 hours, antibiotic consumption, and hospitalization costs.

Results
A total of 300 patients were enrolled, 150 in each phase. Baseline characteristics were generally comparable, although patients in the intervention phase were older and had a higher prevalence of cerebrovascular disease. At ED presentation, patients in the intervention phase more often required mechanical ventilation (26.7% vs. 8.7%, $P < .001$) and ICU admission (32.0% vs. 12.7%, $P < .001$). They also received more appropriate empirical antibiotics (62.7% vs. 41.3%, $P < .001$), with fewer cases of unnecessary broad-spectrum use (30.7% vs. 44.0%) and inadequate therapy (6.7% vs. 14.7%). Antibiotic modification within 24 hours was also less frequent (6.0% vs. 20.0%, $P < .001$). However, 30-day survival did not differ significantly (98.0% vs. 96.7%, $P = .227$).

Conclusions
Early ID consultation in the ED improved the appropriateness of empirical antimicrobial therapy among patients with suspected sepsis or septic shock. Further studies are warranted to explore its impact on mortality and antimicrobial resistance.

RES-318: Purulent pericarditis in Thailand: A Comparative Analysis of Bacterial and Non-Bacterial Causes

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Mahidol University

Background
Purulent pericarditis is a rare, life-threatening neutrophilic effusion. This study investigates its clinical profile and pathogens in Thailand.

Method
This retrospective study of 55 adults with purulent pericarditis (2005–2021, Siriraj Hospital) categorized cases into bacterial (n=20) and non-bacterial (mycobacteria/fungi, n=35) groups.

Results
Of 55 patients with purulent pericarditis (67.3% male, median age 51 years), dyspnea (96.4%), fever and cough (70.9%) predominated. Bacterial cases exhibited more chest pain (80% vs. 54.3%, p=0.057), tamponade (70% vs. 40%, p=0.032), and associations with liver disease/malignancy, while non-bacterial cases were associated with HIV, jugular venous distention, hepatomegaly, edema, and prolonged symptoms (30 vs. 4 days, p<0.001). Bacterial cases exhibited marked neutrophilic leukocytosis. Imaging differences included opacities and low-voltage EKGs in non-bacterial cases, which also showed effusive-constrictive /thick pericardium features on echocardiography.

Pericardial fluid showed pus in bacterial cases (70%, p<0.001), serosanguinous in non-bacterial cases (48.6%, p=0.046), and cultures were positive in 60% overall (78.9% in bacterial cases). M. tuberculosis was the most common pathogen (56.4%), followed by Gram-positive (16.4%), Gram-negative (12.7%) bacteria, non-tuberculous mycobacteria (5.5%), Nocardia and mixed bacteria (each 3.6%), and fungi (1.8%). All patients received antimicrobials; steroids were predominantly used in non-bacterial cases. Surgery occurred in 52.7%. Bacterial group had higher in-hospital (50% vs. 8.6%, p=0.001) and 1-year mortality (60% vs. 28.6%, p=0.022).

Conclusions
Purulent pericarditis in Thailand displays distinct etiologies: bacterial cases are acute with higher mortality, while non-bacterial forms—mainly M. tuberculosis—follow a subacute course with serosanguinous effusions. Timely pericardial fluid analysis and targeted therapy are critical for favorable outcomes.

RES-319: A Nationwide, Multicenter Cross-Sectional Observational Survey Assessing Physicians' Perspectives on Antibiotic Utilization (Syrup/Tablets) in Paediatric and Adult Patients with Respiratory Tract Infections (RTIs)

Amitrajit Pal, Ajitkumar Gondane, Dattatray Pawar, Akhilesh Sharma

Alkem Laboratories Ltd.

Background
Respiratory tract infections (RTIs), including both upper and lower types, are among the most frequently encountered conditions across all age groups. Empirical antibiotic use remains common, with prescribing decisions influenced by age, comorbidities, and familiarity with agents like amoxicillin-clavulanate, cephalosporins, macrolides, and doxycycline. This study aimed to assess health care professionals' (HCPs) perspectives, prescribing behaviors, and clinical rationale for using different antibiotic & their formulations (syrup/tablets) in paediatric and adult RTIs, while identifying key challenges and factors influencing decision-making.

Method
A multicenter, cross-sectional, questionnaire-based observational study was conducted across India following ethics committee approval. A 12-item structured questionnaire was administered to HCPs. Responses were analyzed for completeness and validity.

Results
In the interim analysis, a total of 2,539 HCPs participated. Children aged 0–10 years were reported as the most affected group (26.9%). Common clinical presentations included acute otitis media (36.7%), bacterial sinusitis (21.9%), and community-acquired pneumonia (20.2%). Co-amoxiclav was selected as the first-line antibiotic by 94%, primarily for its efficacy (61.4%) and safety (25%). Guideline adherence influenced prescribing in 56.4%, and 62.4% utilized anti-microbial susceptibility testing. In treatment failures, dose escalation (45.8%) or switching to alternatives like high-dose co-amoxiclav (40.2%) or cefpodoxime (33.8%) was common. Dosing adjustments based on weight were reported by 75.9%, with diarrhoea being the most noted adverse event (17.8%).

Conclusions
Co-Amoxiclav continues to be the cornerstone of RTI management among health care professionals. The findings reflect a rational, guideline-aligned, and evidence-informed approach, reinforcing the importance of continued medical education and robust antibiotic stewardship practices.

RES-320: A Multicenter Retrospective Real-World Study Assessing the Clinical Effectiveness of Co-Amoxiclav in the Treatment of Upper Respiratory Tract Infections (URTIs)

Amitrajit Pal, Ajitkumar Gondane, Dattatray Pawar, Akhilesh Sharma

Alkem Laboratories Ltd.

Background
Upper respiratory tract infections (URTIs) are a leading cause of outpatient visits and antibiotic prescriptions globally. Co-Amoxiclav, a fixed-dose combination of amoxicillin and clavulanic acid, is widely used for its broad-spectrum activity, particularly against β-lactamase-producing pathogens. However, real-world evidence on its clinical effectiveness and safety remains limited. This study evaluated the real-world clinical effectiveness and safety of Co-Amoxiclav in managing adult URTI patients across varied healthcare settings, using both symptomatic and laboratory outcome measures.

Method
This multicenter, retrospective study analyzed electronic medical records of adult patients (≥18 years) diagnosed with URTIs and treated with Co-amoxiclav in outpatient and inpatient settings. Effectiveness was assessed by symptomatic resolution and changes in white blood cell (WBC) count and C-reactive protein (CRP) from Day 0 to Day 7 (if available). Safety was evaluated based on adverse event incidence during the treatment period.

Results
In the analysis, 30,258 records were reviewed (mean age: 39 years; 72.9% male). Undifferentiated URTI with fever and cough (81.5%) was most common diagnosis, followed by tonsillitis (6.4%), otitis media (4.9%), pharyngitis (3.5%), sinusitis (2.7%), and rhinitis (1.0%). Co-Amoxiclav 625 mg twice daily for five days was the main regimen (80.4%). Clinical cure was achieved in 93.6%, with 6.3% cases showing improvement. WBC decreased from 10,399/mm³ to 8,098/mm³, and CRP from 20.11 mg/L to 9.05 mg/L from Day 0 to 7. There were minimal adverse events reported.

Conclusions
This study affirms Co-amoxiclav's effectiveness and safety in real-world URTI management, supporting its empirical use and role in antibiotic stewardship.

RES-321: Unveiling Viral Co-infections in Paediatric Pertussis: A Retrospective Study from Sabah, Malaysia

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2University Malaysia Sabah

Background
Bordetella pertussis commonly known as whooping cough remains a significant public health challenge particularly in Southeast Asia, where its true burden is often underestimated. In Sabah Malaysia, pertussis continues to pose a serious threat to paediatric populations.

Method
This retrospective study conducted at the Sabah Women and Children Hospital aimed to identify the prevalence and patterns of B. pertussis co-infections among children. We analysed 1,469 respiratory samples collected from paediatric patients between May 2020 and June 2025. All samples were tested using the Qiagen QIAstat-Dx Respiratory Panel (QIAstat-Dx RP) to detect B. pertussis and 22 other respiratory pathogens directly from nasopharyngeal swab (NPS) specimens. Additionally, we collected data on patient demographics, history on oxygen requirement and intensive care unit (ICU) admissions.

Results
B. pertussis was detected in 3.9% (48/1,469) of cases with 81.3% (39/48) showing viral co-infections. Enterovirus/Rhinovirus (23/39), RSV (23/39) and Adenovirus (6/39) were most common co-infections. No bacterial co-infections (Legionella pneumophilia or Mycoplasma pneumoniae) were observed. Affected patients were predominantly infants below 1 year old (34/48, 70.8%) with 100% requiring oxygen support and 58.3% (28/48) admitted to the ICU.

Conclusions
Viral co-infections are highly prevalent in paediatric B. pertussis cases in Sabah and are associated with severe disease related to oxygen dependence and intensive care in most patients. These findings highlight the importance of having robust and rapid syndromic testing to allow early diagnostic, intervention and targeted treatments in order to mitigate the dual burden of B. pertussis and respiratory viral infections in high-risk populations.

RES-322: Molecular Subtypes of Blastocystis spp. Among Hospitalized Children with Acute Gastroenteritis in Kuala Lumpur, Malaysia

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[2]National University of Malaysia

Background
Blastocystis spp. is a genetically diverse intestinal protist increasingly recognized in gastrointestinal disorders. However, molecular subtype (ST) data on symptomatic children from urban populations remain scarce in Malaysia.

Method
A prospective, cross-sectional, single-center observational study was conducted between September 2024 and July 2025 at a tertiary hospital in Kuala Lumpur. Stool samples (n = 191) were collected from pediatric patients aged 2 months to 12 years, clinically diagnosed with acute gastroenteritis (AGE). Deoxyribonucleic acid (DNA) was extracted, and the small subunit ribosomal RNA (SSU rRNA) gene was amplified by polymerase chain reaction (PCR) using RD5 and BhRDr primers. Amplicons were sequenced using Sanger sequencing. Sequences were confirmed using the Basic Local Alignment Search Tool (BLAST) of the National Center for Biotechnology Information (NCBI) and submitted to the Public Multi-Locus Sequence Typing (PubMLST) 18S rRNA database for subtype and allele identification.

Results
A total of 7 out of 191 samples (3.7%) tested positive for Blastocystis spp. Subtype analysis identified ST3 in four samples (57.1%), while ST1, ST2, and ST15 were each found in one sample (14.3%). Allele 34 was the most frequently identified, presenting in three ST3 isolates. ST15, a rarely reported subtype in humans, was also detected, contributing to the spectrum of observed genetic diversity.

Conclusions
This study reports distinct Blastocystis subtypes among pediatric AGE cases in an urban Malaysian setting. The identification of ST15 in conjunction with the widely distributed ST3 highlights the need for broader subtype monitoring and the routine incorporation of Blastocystis testing in diagnostic protocols for pediatric gastroenteritis.

RES-323: A Laboratory-Initiated AFB Smear Protocol for Respiratory Samples that Reduces Waste and Saves Manpower Cost

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Ng Teng Fong General Hospital

Background
While World Health Organisation now recommends molecular methods as the initial diagnostic test for pulmonary TB and rifampicin resistance, many healthcare institutions continue to rely on conventional AFB smears for contact tracing and healthcare worker exposure management. This is despite Xpert® MTB/RIF Ultra (Xpert-TB)'s superior sensitivity over microscopy, studies which show robust correlation between Xpert-TB and AFB smear grading, and the labour-intensive nature of AFB smear preparation.

Method
Between November 2024 and April 2025, our laboratory performed reflex AFB smear testing only for respiratory samples with positive TB PCR by Xpert-TB. Samples with negative Xpert-TB results did not undergo AFB smear testing, or had existing requests cancelled.

Results
A total of 253 AFB smear requests from respiratory samples were received during the study period, where 172 (68%) were TB PCR-negative. Based on the proposed algorithm, 128 PCR-negative samples were excluded from AFB smear testing, while 44 were still tested due to workflow lapses such as staff unfamiliarity. All 44 AFB smears were negative, consistent with PCR results, demonstrating the redundancy of these tests. This workflow saved approximately 2,048 minutes of man-time related to smear processing and reading, resulting in significant cost and labor efficiencies.

Conclusions
While complete elimination of AFB smears in favor of TB PCR for infectivity assessment remains ideal, our protocol of reflex AFB smear testing only for PCR-positive respiratory samples serves as an effective compromise. This approach reduces waste and enables significant cost savings while providing infection control teams with necessary information for contact tracing decisions.

RES-325: Prevalence and Risk Factors of CRE Colonization in Long-Term Care Hospitals: A Prospective Study

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Background
Carbapenem-resistant Enterobacterales (CRE) in long-term care hospitals (LTCH) is increasing. This study aimed to investigate the prevalence and risk factors for CRE colonization among LTCH residents.

Method
From September 2022 to December 2024, rectal swab specimens were collected from current residents and newly admitted patients at four LTCHs. Samples underwent culture followed by immunochromatographic assay to detect carbapenemase-producing Enterobacterales (CPE). Patients who initially tested negative for CRE underwent weekly follow-up testing, up to a maximum of six times. If CRE was detected, active surveillance cultures were discontinued, and infection control interventions were implemented. A case-control study design was used to identify risk factors, and odds ratios were calculated.

Results
Among 140 asymptomatic patients, 34 (24.3%) tested positive for CRE, with a total of 35 CRE isolates identified. Of these, 27 (79.4%) were confirmed as CPE. Notably, 70.6% of CRE-positive patients were identified during the first screening. Among patients who initially tested negative, 8.6% (10 out of 116) converted to positive later. Multivariate analysis revealed that recent ICU admission within a year (OR, 2.98; 95% CI, 1.07–8.19; P = 0.02), use of invasive devices within a year (OR, 3.85; 95% CI, 1.42–9.75; P <0.01), and antibiotic use within the last three months (OR, 3.51; 95% CI, 1.42–8.86; P <0.01) were significant risk factors for CRE colonization.

Conclusions
The CRE positivity rate was higher among newly admitted patients compared to current residents. The conversion rate from CRE-negative to CRE-positive status was 8.6%. Active surveillance testing should be considered for high-risk patients upon admission.

RES-328: Antagonistic Activity of Bacteriocin-producing Strain Streptococcus salivarius K12

Vladislav Andreev, Vladislav Privolnev, Tatiana Kovalenko, Alexander Chernavin

R-Pharm

Background

One of the modern healthcare problems is increasing resistance of pathogenic microorganisms to antibiotics. The use of probiotics in clinical practice becomes promising direction in the prevention of bacterial infections caused by resistant microbes. One of the most promising probiotic is SsK12.

Method

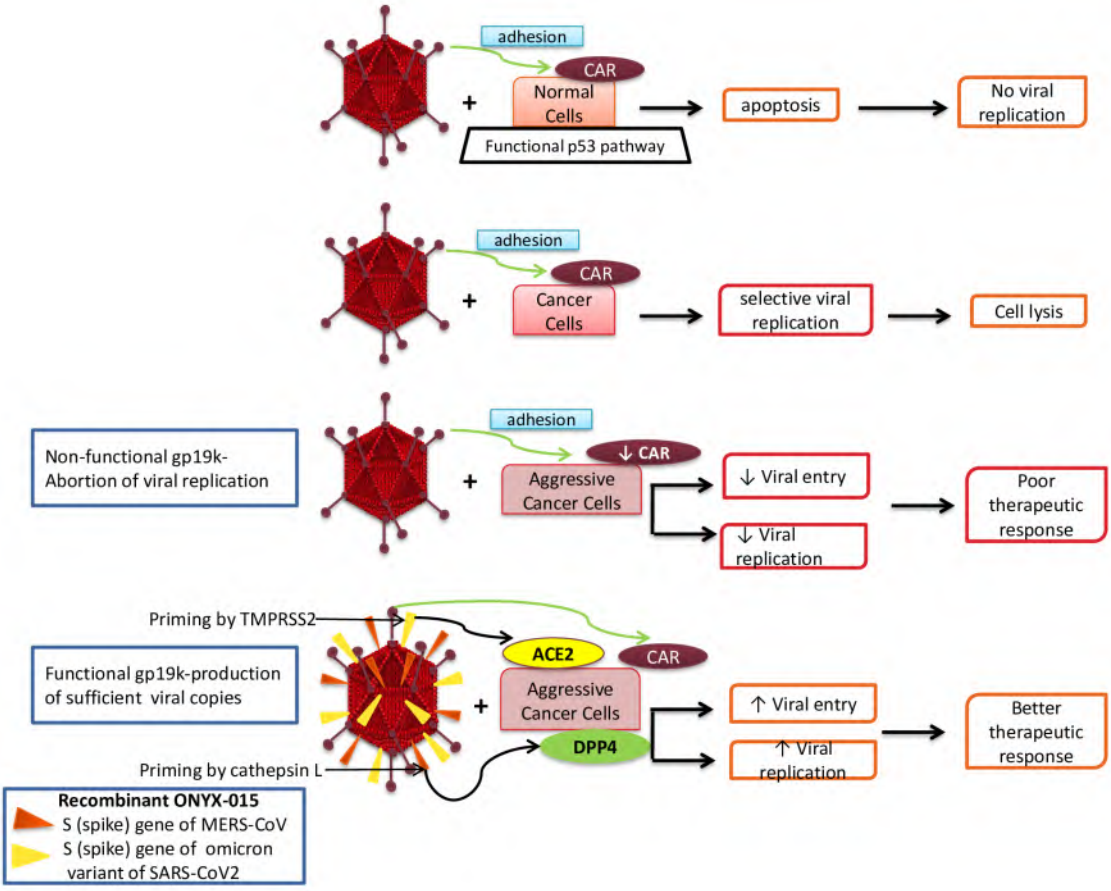
Aim- to evaluate antagonistic activity of SsK12 against S.pneumoniae, S.pyogenes, S.aureus; E.coli, P.aeruginosa, C.albicans. SsK12 was isolated from dietary supplement, containing 1×109 CFU/tablet. Tablet was dissolved in enrichment broth. The resulting suspension was seeded on 5% blood agar and incubated at 35°C in 4-6% CO2 for 48 hours. Raised culture was identified as SsK12 using MALDI-TOF mass spectrometry method. The evaluation of SsK12 antagonistic activity was carried out using perpendicular streak technique. Daily SsK12 culture was inoculated as heavy streaks with a loop at one side of Petri dish with Muller-Hinton agar (MHA) and incubated for 24 hours at 350C in anaerobic conditions. It was supposed that bacteriocins would diffuse over the whole area of the agar. On the next day clinical isolates of test cultures were streaked at clear side of MHA Petri dish. MHA Petri dish inoculated with SsK12, and test cultures streaked perpendicularly on the same day was used as control.

Results

No growth of S.pyogenes, a few S.pneumonia colonies and growth of all other pathogens were noted on the dish with SsK12 culture. Growth of all pathogens detected on the control dish.

Conclusions

SsK12 possesses antagonistic activity against S. pyogenes, S.pneumoniae, no activity against other pathogens. SsK12 can be used as probiotic for ENT infections prophylaxis.



RES-330: Carbapenem-Resistant Burkholderia cepacia Complex IsolatesCarrying blaNDM−1 and blaNDM−5 in Ventilator-AssociatedPneumonia Patients and Contaminated Ventilator Tubing

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[1]Allama Iqbal Medical College Lahore
[2]Doctors Institute of Medical & Emerging Sciences

Background
Ventilator-associated pneumonia (VAP) represents an important nosocomial infection, frequently encountered in intensive careunit (ICU) settings which results in prolonged hospital stays.

Method
This studyinvestigates the antimicrobial susceptibility patterns and mechanisms of carbapenem resistance among BCC bacteria from VAPpatients and the ventilator tubing. The blood and respiratory specimens from patients diagnosed with VAP were collected.In addition, the ventilators were also screened for the presence of BCC bacteria. The susceptibility profiling of BCC isolateswas performed against the various antimicrobial agents, and screening for acquired beta-lactamase enzymes was conducted bypolymerase chain reaction.

Results
Out of the total 134 patients with BCC-associated VAP, B. cepacia, Burkholderia multivorans, and Burkholderia cenocepacia was 68.7% (n = 92), 18.7% (n = 25), and 12.7% (n = 17). Overall, the BCC isolates showed varyingsusceptibility to different antibiotics: 76.9% were susceptible to chloramphenicol, 76.1% to minocycline, 69.4% to meropenem,60.4% to ceftazidime, 51.5% to trimethoprim-sulfamethoxazole, and 50% to levofloxacin. Resistance to ceftazidime (51/92, 55.4%) and meropenem (36/92, 39.1%) was exclusively observed in B. cepacia isolates, and all isolates of B. multivorans and B. cenocepaciawere found to be susceptible to both beta-lactam drugs. Among the 134 clinical isolates, 15 were found to harbor the blaNDMvariants, that is, blaNDM−1 and blaNDM−5. All carbapenem-resistant isolates from the ventilator tubing were identified as B. cepaciaand were found to harbor either the blaNDM−1 or the blaNDM−5 variants.

Conclusions
The observed increase in resistance and the emergence of acquired beta-lactamases among BCC isolates highlight a concerning trend that could potentially lead to serious outbreaks.

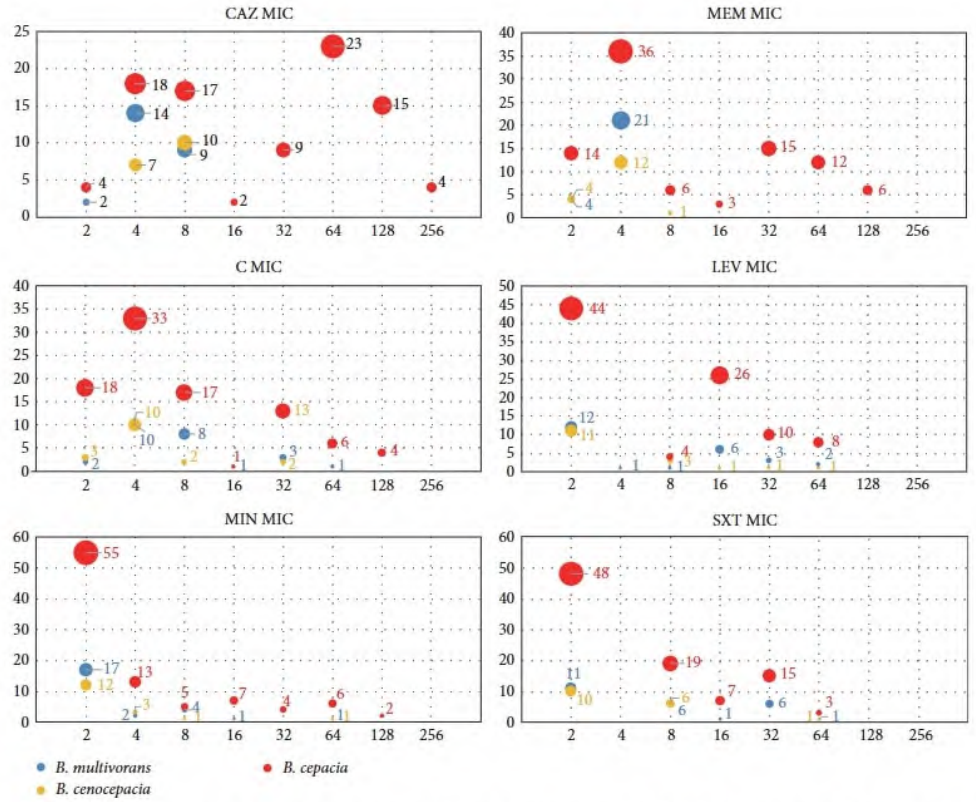

FIGURE 2: Bubble graph showing the distribution of minimum inhibitory concentrations (MICs) of various antimicrobial agents against BCC isolates from VAP patients. The *Y*-axis shows the number of isolates, while the *X*-axis shows the MIC values. CAZ, ceftazidime; MEM, meropenem; C, chloramphenicol; LEV, levofloxacin; MIN, minocycline; SXT, trimethoprim-sulfamethoxazole.

RES-332: Resurgence of Tularemia in Georgia, 2024: Continuing Trends and Emerging Patterns

David Chakhunashvili, David Tsereteli, Giorgi Chakhunashvili

National Center for Disease Control and Public Health

Background
Tularemia is a zoonotic disease caused by Francisella tularensis, capable of causing severe illness in humans. Clinical forms include ulceroglandular, glandular, and pneumonic types. In Georgia, tularemia surveillance began in 1946. Between 2018 and 2022, only 1-2 cases were reported annually. However, in 2023, a notable increase was observed, with 16 confirmed cases in eastern regions and mostly in spring through autumn. This study presents tularemia data from 2024.

Method
Tularemia is classified in Georgia as an especially dangerous pathogen requiring immediate reporting. Data was extracted from Electronic Integrated Disease Surveillance System (EIDSS). Probable cases had compatible symptoms and a positive micro-agglutination test (MAT); confirmed cases met additional laboratory and epidemiological criteria.

Results
In 2024, 20 confirmed tularemia cases were recorded (10 male, 10 female). The average age of the patients was 37.95 years, with a range from 13 to 62 years. Clinical presentations included ulceroglandular (70%), glandular (20%), and pneumonic (10%) forms. In all cases, exposure occurred in eastern part of the country; however, all patients were diagnosed in Tbilisi. Seasonal distribution was as follows: winter (25%), spring (60%), and summer (15%).

Conclusions
The continued rise in tularemia cases suggests a sustained epidemiological shift. Strengthening surveillance, public health preparedness, and intersectoral collaboration is essential. Further investigation into environmental sources and animal reservoirs is needed to better understand and mitigate ongoing transmission.

RES-333: Epidemiology and Antimicrobial Profiling of Extrapulmonary Nontuberculous Mycobacteria (NTM) at Srinagarind Hospital, Khon Kaen University

Chutipapa Sukkasem[3], Rungsima Methachaiphatkun[3], Waewta Kuwatjanakul[3], Arnone Nithichanon[1], Wantin Sribenjalux[2], Piroon Mootsikapun[2]

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Background
Nontuberculous mycobacteria (NTM) are environmental organisms capable of causing disease, particularly in immunocompromised hosts. Accurate species identification and antimicrobial susceptibility testing are essential to guide effective therapy.

Method
This retrospective study analyzed data from the Clinical Microbiology Laboratory of Srinagarind Hospital, Khon Kaen University, between January 2020 and December 2023. The aim was to determine the epidemiology and antimicrobial susceptibility profiles of NTM isolated from pulmonary and extrapulmonary specimens. Species identification and drug susceptibility testing were performed according to standard microbiological protocols.

Results
A total of 170 nontuberculous mycobacterial (NTM) isolates were included in the analysis. Among pulmonary samples (n = 93), Mycobacterium intracellulare accounted for 29.0% (27/93) and Mycobacterium abscessus complex for 28.0% (26/93). In extrapulmonary specimens (n = 77), M. abscessus complex was the most frequently identified species at 40.3% (31/77), followed by M. intracellulare at 26.0% (20/77). Pulmonary M. abscessus complex isolates demonstrated high susceptibility to amikacin (100%, 5/5) and clarithromycin (80%, 4/5), while extrapulmonary isolates showed 100% susceptibility to both agents (8/8). Pulmonary Mycobacterium fortuitum group isolates exhibited 100% susceptibility to amikacin, ciprofloxacin, moxifloxacin, and linezolid (4/4). M. intracellulare from pulmonary sources showed 87.5% (7/8) susceptibility to clarithromycin, while Mycobacterium avium showed 100% susceptibility to amikacin, moxifloxacin, and clarithromycin (1/1). In contrast, extrapulmonary M. intracellulare isolates had a lower clarithromycin susceptibility rate of 75.0% (3/4).

Conclusions
This study provides insight into species distribution and antimicrobial susceptibility of NTM isolated from diverse specimen types. The findings support clinicians in selecting appropriate treatments and contribute to improved NTM infection management.

Table 2 The results of the antimicrobial susceptibility test of NTM isolated by sample type.

Drugs (%S)	Pulmonary				Extrapulmonary			
	M. abscessus complex (n=5)	*M. fortuitum* group (n=4)	*M. intracellulare* (n=8)	*M. avium* (n=1)	*M. abscessus* complex (n=8)	*M. fortuitum* group (n=1)	*M. intracellulare* (n=4)	*M. avium* (n=0)
Cefoxitin	0	25	-	-	25	0	-	-
Imipenem	0	50	-	-	0	0	-	-
Amikacin	100	100	50	100	100	0	25	-
Ciprofloxacin	0	100	-	-	25	100	-	-
Moxifloxacin	0	100	50	100	50	100	0	-
Trimethoprim / sulfamethoxazole	20	75	-	-	37.5	100	-	-
Linezolid	40	100	37.5	0	75	0	0	-
Doxycycline	0	50	-	-	12.5	0	-	-
Clarithromycin	80	75	87.5	100	100	0	75	-
Tobramycin	0	25	-	-	12.5	0	-	-

RES-334: Carbapenem resistant Klebsiella pneumoniae in University Clinical Hospital Mostar, Bosnia and Herzegovina

Sanja Jakovac, Josipa Tomic, Tanja Petrovic, Doris Martinovic Rizikalo, Maja Kljakic

Universitiy Clinical Hospital Mostar

Background
The appearance of carbapenemases in enterobacteria is a major problem in clinical practice, due to the great diversity of enzymes and the fact that carbapenemases resistance can be spread by horizontal gene transfer.

Method
The study was conducted at the University Clinical Hospital (UCH) Mostar on 100 isolates of carbapenem-resistant (CR) K. pneumoniae collected during 2018, 2022-2025. Isolates were collected from different clinical samples of hospital patients regardless of age, gender and underlying disease. For all tested antibiotics (carbapenems, quinolones, trimethoprim/sulfamethoxazole and other beta-lactam antibiotics) except colistin and tigecycline, MIC was determined using Vitek 2 according to EUCAST (European Committee on Antimicrobial Susceptibility Testing) standards. MIC for colistin was determined by the method of microdilution in broth. MIC for tigecycline was determined by E test. The presence and type of carbapenemase was determined in vitro by rapid diagnostic test for the detection of OXA-163, OXA-48, KPC, NDM and VIM carbapenemases (RESIST – 5 O.O.K.N.V., Coris BioConcept).

Results
For all tested isolates, MIC for meropenem and imipenem was ≥ 8 mg. Some of the tested isolates were sensitive to amikacin and colistin. All tested isolates were sensitive to tigecycline. Most of the tested isolates possess carbapenemase OXA-48 as the dominant mechanism of resistance to carbapenems. 1 isolate from 2022, 2 isolates from 2024 and 1 isolate from 2025 possessed carbapenemase NDM.

Conclusions
These are the first multi-year data on the presence of CR K. pneumoniae with OXA-48 and NDM resistance mechanism within UCH Mostar.

RES-338: Comparison of DNA Extraction Protocols for Long-Read Sequencing of Clinical Pathogenic Fungi

Thitima Suwannasaeng, Suwalak Chitcharoen, Pratsanee Hiangrach, Pasinee Sangsiwarit

Khon Kaen University

Background
Accurate identification and genomic analysis of fungal pathogens are crucial for clinical management and surveillance. Conventional diagnostics often lack the sensitivity to distinguish closely related or cryptic species. Long-read sequencing technologies like Oxford Nanopore Technologies and PacBio sequencing offer species-level resolution and high-quality genome assemblies but require high-quality, high-molecular-weight DNA. Extracting such DNA is especially difficult from clinical fungal isolates due to their robust, polysaccharide-rich cell walls.

Method
Four extraction methods, Qiagen DNeasy UltraClean Microbial Kit, Qiagen DNeasy PowerSoil Pro Kit, Real Genomics Genomic DNA Extraction Kit (Mini Plant), and a Cetyltrimethylammonium Bromide (CTAB) extraction, were tested on fungi including Fusarium, Aspergillus, Pythium, Rhodotorula, Candida, Curvularia, and Bipolaris. Experimental modifications included varying bead size (0.5–3.0 mm) and incubation time. DNA yield and quality were assessed via Nanodrop and agarose gel electrophoresis.

Results
The Qiagen DNeasy UltraClean Microbial Kit consistently produced strong, high-molecular-weight DNA bands (>10,000 bp) with small smear band. Use of 0.5 mm glass beads improved mechanical lysis efficiency, especially for filamentous molds. Prolonged lysis incubation further enhanced DNA yield and integrity. The CTAB extraction method yielded DNA per Nanodrop but lacked visible bands, likely due to protein contamination or shearing. Both the Qiagen DNeasy PowerSoil Pro Kit and Real Genomics Genomic DNA Extraction Kit (Mini Plant) gave weak or inconsistent bands, likely due to ineffective bead lysis.

Conclusions
The Qiagen UltraClean Microbial Kit demonstrated superior performance in extracting high-quality fungal DNA suitable for long-read sequencing. These findings highlight the importance of method selection for optimized extraction in clinical mycology.

RES-339: Genomic Characterization and Transferability of blaCTX-M-55-Carrying Plasmids in Escherichia coli from Malawian Broiler Chickens

Pilirani Chisembe[3], Duc Trung Dao[3], Daraden Vang[3], Yohei Kobayashi[2,3], Masato Suzuki[4], Gilson Njunga[1], Joseph Nkhoma[1], Ryo Kinoshita-Daitoku[3], Eisuke Kuroda[3], Kouji Kimura[3], Keigo Shibayama[3]

[1]Central Veterinary Laboratory
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[3]Nagoya University
[4]National Institute of Infectious Diseases

Background
The global spread of extended-spectrum β-lactamase (ESBL)-producing Escherichia coli poses a growing public health concern. While poultry is recognized as a major reservoir of ESBLs, data on the mobility and genetic context of ESBL genes in African settings remain limited. This study investigated the genomic characteristics and transferability of E. coli isolates carrying blaCTX-M-55, a commonly detected ESBL gene globally, from Malawian broilers and compared their plasmids with those from other sectors.

Method
Whole-genome sequencing of 21 blaCTX-M-55-positive E. coli isolates in Malawi was performed using short-read sequencing. Eight of these isolates underwent long-read sequencing to resolve complete genome structures, including plasmids. Bacterial conjugation assays were performed to evaluate plasmid transferability using an E. coli recipient. Comparative genomic analyses were performed between plasmids in this study and reference plasmids from humans, animals, and the environment.

Results
Fifteen isolates were conjugative, including seven harboring blaCTX-M-55 on diverse plasmid types: IncFIB (n=1), IncFII (n=1), IncFII::IncN (n=2), IncHI2 (n=3). Plasmid sizes ranged from 46.8-331.3 kb (GC content: 46.8-52.9%). Several antimicrobial resistance genes (e.g., sul2, tetA, and floR) were frequently identified. Virulence factor genes (iro, fepA, and icsP/sopA) were exclusively detected in the IncFIB plasmid. Notably, conserved genetic structures flanking blaCTX-M-55 were observed across diverse plasmid types and sources: IS26-blaCTX-M-55-wbuC-blaTEM-1B-IS26 (IncFII::IncN), IS26-hp-blaCTX-M-55-wbuC-blaTEM-1B-IS26 (IncFIB), ISEcp1-blaCTX-M-55-wbuC-hp-Tn3 (IncHI2).

Conclusions
The observed similarities and transferability of poultry-derived plasmids indicate the potential for cross-sectoral transmission of blaCTX-M-55-carrying plasmids through horizontal gene transfer worldwide mediated by mobile genetic elements. These findings support the importance of the One Health approach in antimicrobial resistance surveillance.

RES-340: Trends in Carbapenem-resistant Enterobacterales and the In Vitro Activity of Aztreonam-avibactam Against Isolates Collected in the Asia/Pacific Region, 2019-2023 as a Part of the ATLAS Global Surveillance Program

Gregory Stone[2], Mark Estabrook[1], Henry Li[1], Katherine Perez[2], Dan Sahm[1]

[1]IHMA
[2]Pfizer

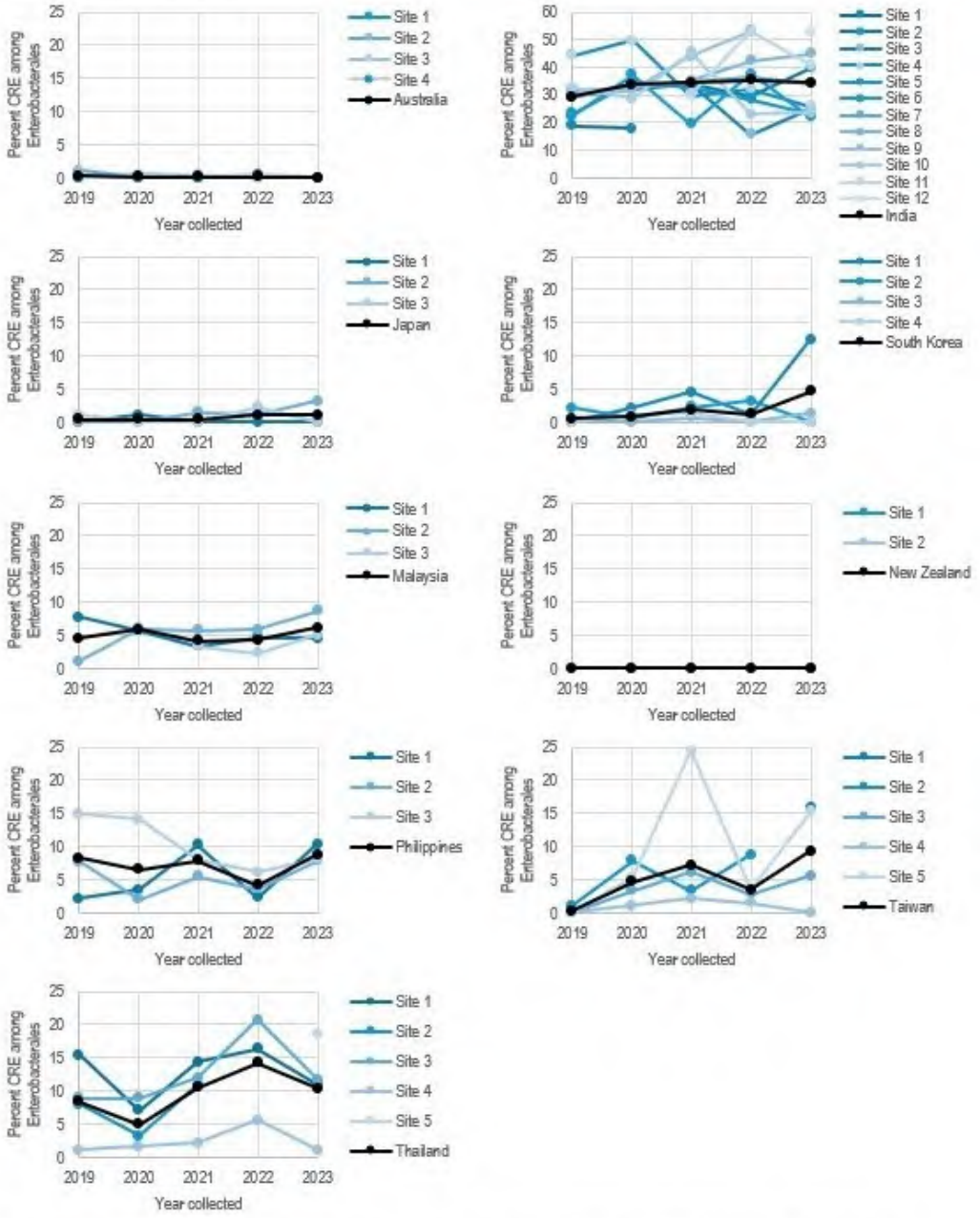
Background
Aztreonam-avibactam is an approved therapeutic in the United States and Europe. Aztreonam is stable to hydrolysis by metallo-β-lactamases (MBLs), while avibactam inhibits class A, C, and some class D β-lactamases, often co-carried by MBL-positive isolates. This study shows trends in carbapenem-resistant Enterobacterales (CRE) among isolates collected from 2019-2023 in Asia/Pacific (APAC). Also presented is the in vitro activity of aztreonam-avibactam against CRE.

Method
18718 isolates were collected from 41 sites in 9 countries in APAC that participated in five consecutive years of surveillance. Antimicrobial susceptibility was according to CLSI broth microdilution and CRE defined by meropenem-nonsusceptibility (CLSI). The number of each species submitted from each site was dictated by a protocol: 33% Klebsiella pneumoniae, 33% Escherichia coli, and 33% other Enterobacterales.

Results
CRE rates among collected isolates in Australia, Japan, and New Zealand remained ≤5% in 2019-2023. The greatest changes from 2019 to 2023 were seen in Taiwan (9.0 percentage point increase) and India (5.1 percentage point increase) (Figure). Overall rates in 2023 were highest in India (34.4%). ATM-AVI activity against CRE from 2019-2023 was [country (percent susceptible)]: India (92.6), Malaysia (100), Philippines (100), Taiwan, (99.1), and Thailand (98.3) (Table). Aztreonam-avibactam activity was comparable across years in each country except India, where 8.8 percentage points fewer CRE isolates were susceptible in 2023 compared to 2019.

Conclusions
Aztreonam-avibactam demonstrated potent in vitro activity against CRE, which is on the rise in many countries. Antimicrobial-resistance in India remains a unique challenge.

Figure 1. Rates of carbapenem-resistance among collected Enterobacterales isolates, by country, site, and year



An average of 105 isolates were collected per site, per year (standard deviation 36.3 isolates). Not every site participated in every year.

Table 1. *In vitro* activity of aztreonam-avibactam against CRE, by country and year

	Year, Number of CRE (percent susceptible to ATM-AVI)[a]					
Country[b]	**2019**	**2020**	**2021**	**2022**	**2023**	**All years**
India	247 (98.4)	432 (94.9)	434 (93.1)	412 (88.6)	356 (89.6)	1881 (92.6)
Malaysia	8 (8 of 8)	10 (100)	11 (100)	12 (100)	15 (100)	56 (100)
Philippines	22 (100)	18 (100)	21 (100)	11 (100)	25 (100)	97 (100)
Taiwan	1 (1 of 1)	18 (100)	39 (100)	19 (100)	33 (97.0)	110 (99.1)
Thailand	30 (96.7)	27 (100)	46 (97.8)	39 (97.4)	35 (100)	177 (98.3)

a. Percent susceptible using EUCAST 2025 breakpoints.

b. Only includes countries from which ≥10 CRE were collected from ≥4 years of collection.

RES-341: In Vitro Activity of Aztreonam-avibactam against Carbapenemase-producing Enterobacterales Isolates Collected in India as a part of the ATLAS Global Surveillance Study, 2019-2023

Gregory Stone[2], Mark Estabrook[1], Henry Li[1], Katherine Perez[2], Dan Sahm[1]

[1]IHMA
[2]Pfizer

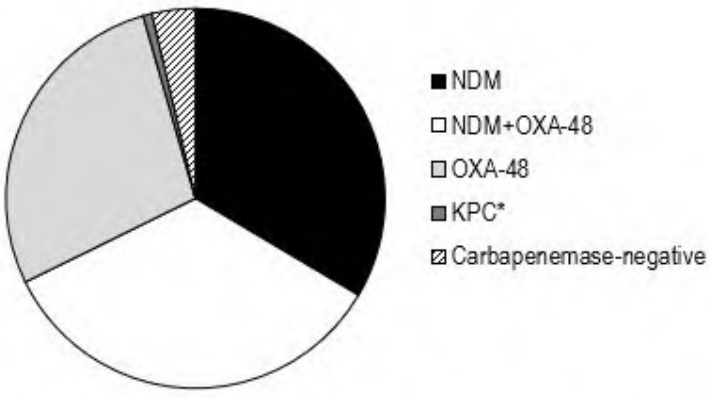
Background
Aztreonam-avibactam is an approved therapeutic in the United States, Europe, and India. Aztreonam is stable to hydrolysis by metallo-β-lactamases (MBLs), while avibactam inhibits class A, C, and some class D β-lactamases, often co-carried by MBL-positive isolates, that inactivate aztreonam. This study demonstrates the in vitro activity of aztreonam-avibactam against carbapenem-resistant Enterobacterales (CRE) isolates collected from 2019-2023 in India.

Method
5,596 Enterobacterales isolates were collected from 12 sites in India in 2019-2023. Broth microdilution was performed according to CLSI guidelines and aztreonam-avibactam susceptibility was interpreted according to EUCAST 2025 breakpoints. Meropenem-nonsusceptible isolates (CLSI breakpoints) were screened for β-lactamases by PCR.

Results
1881/5596 (33.6%) of isolates were meropenem-nonsusceptible and 1841 were available to characterize. Of characterized CRE, 34% carried a variant of NDM, 28% a variant of OXA-48-like, and exclusive of those, a further 34% carried both NDM+OXA-48-like carbapenemases (Figure). Of characterized CRE, 92.7% were susceptible to aztreonam-avibactam (MIC90 of 4 µg/mL) (Table). Isolates carrying different carbapenemases demonstrated susceptibility to aztreonam-avibactam [carbapenemase, number of isolates (percent susceptible)]: NDM, 617 (82.7%); OXA-48-like, 512 (99.0%); NDM+OXA-48-like, 630 (97.1%).

Conclusions
Aztreonam-avibactam demonstrated potent in vitro activity against isolates of CRE carrying NDM+OXA-48-like carbapenemases and isolates that carried OXA-48-like carbapenemases without detected MBLs.

Figure 1. Carbapenemases identified among 1841 CRE



*Includes two isolates that also co-carry OXA-48-like carbapenemases.

Table 1. *In vitro* activity of aztreonam-avibactam against CRE, by carbapenemase

		Aztreonam-avibactam MIC (µg/mL), cumulative percent inhibited													
Phenotype/Genotype	**n**	**≤0.015**	**0.03**	**0.06**	**0.12**	**0.25**	**0.5**	**1**	**2**	**4**	**8**	**16**	**32**	**64**	**>64**
Characterized CRE	1841	15	21	79	207	732	386	73	78	**115**	84	28	8	4	11
		0.8	2	6.2	17.5	57.3	78.2	82.2	86.4	**92.7**	97.2	98.8	99.2	99.4	100
NDM	617	12	19	64	93	104	50	31	61	76	**69**	23	7	3	5
		1.9	5	15.4	30.5	47.3	55.4	60.5	70.3	82.7	**93.8**	97.6	98.7	99.2	100
OXA-48-like	512	3		5	46	306	**125**	14	3	5	3	1			1
		0.6		1.6	10.5	70.3	**94.7**	97.5	98.0	99.0	99.6	99.8			100
NDM+OXA-48-like	630			7	59	287	195	**23**	10	31	11	4			3
				1.1	10.5	56	87	**90.6**	92.2	97.1	98.9	99.5			100
KPC*	14			1	2	4	3	2			**1**			1	
				7.1	21.4	50.0	71.4	85.7			**92.9**			100	

Abbreviations: MIC, minimum inhibitory concentration; CRE, carbapenem-resistant Enterobacterales

MIC_{90} values are in bold

*Includes two isolates that also co-carry OXA-48-like carbapenemases.

Characterized CRE consisted of: *Klebsiella pneumoniae* (n=1272), *Escherichia coli* (n=367), Morganellaceae (n=81), *Enterobacter* spp. (n=61), *Serratia marcescens* (n=26), *Klebsiella* spp. (n=20), *Citrobacter* spp. (n=11), and Others (n=3).

RES-342: In Vitro Activity of Aztreonam-avibactam against Carbapenemase-producing Enterobacterales Isolates Collected in China as a part of the ATLAS Global Surveillance Study, 2020-2022

Gregory Stone[2], Mark Estabrook[1], Henry Li[1], Katherine Perez[2], Dan Sahm[1]

[1]IHMA
[2]Pfizer

Background
Aztreonam-avibactam is an approved therapeutic in the United States, Europe, and China. Aztreonam is stable to hydrolysis by metallo-β-lactamases (MBLs), while avibactam inhibits class A, C, and some Class D β-lactamases, often co-carried by MBL-positive isolates, that inactivate aztreonam. This study examines the in vitro activity of aztreonam-avibactam against carbapenem-resistant Enterobacterales (CRE) isolates collected in China, 2020-2022.

Method
4,236 Enterobacterales isolates were collected from 20 sites in mainland China. Broth microdilution was performed according to CLSI guidelines. Meropenem-nonsusceptible isolates (CLSI breakpoints) were characterized by short-read whole genome sequencing.

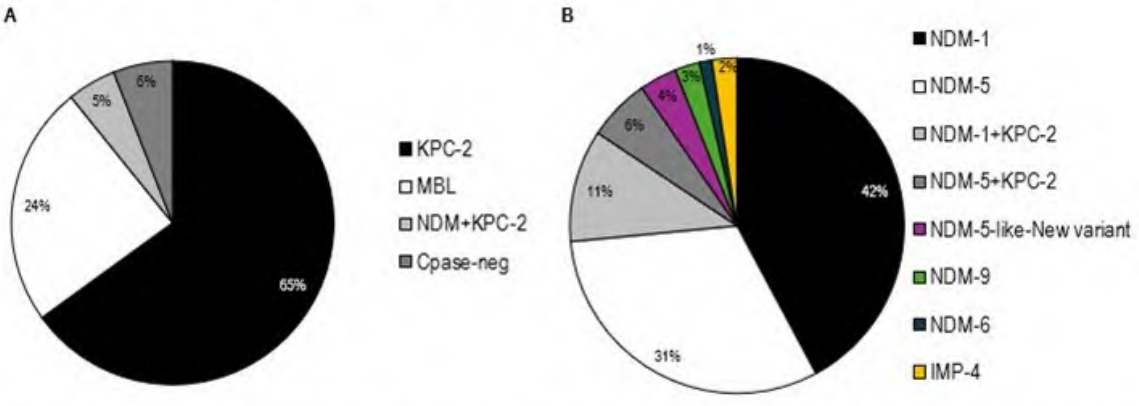
Results
351/4,236 (8.3%) of isolates were CRE, of which 286 were available for molecular characterization. Of characterized CRE, 65% carried KPC-2, 24% carried an MBL, or 5% a combination of NDM-1 or NDM-5 and KPC-2 (Figure 1). Among MBLs, the most common were NDM-1 (53%) and NDM-5 (37%). Other variants of NDM and IMP-4 accounted for the remaining 10%.

Of characterized CRE, 99% were aztreonam-avibactam-susceptible (MIC90 of 2 µg/mL). This was comprised of KPC-2-producing isolates (98.9% susceptible) and isolates that carried an MBL±other carbapenemases (100% susceptible) (Table 1).

A difference was observed in the MIC90 of aztreonam-avibactam against NDM-1- and NDM-5-positive isolates (0.5 and 4 µg/mL, respectively). Previously-described mutations in E. coli PBP3 were present in 0/35 NDM-1-positive isolates and 8/26 NDM-5-positive isolates (not shown).

Conclusions
KPC-2, NDM-1, and NDM-5 were the dominant carbapenemases among clinical Enterobacterales in China. Aztreonam-avibactam demonstrated potent in vitro activity against these isolates and presents a promising therapeutic option to treat infections caused by CRE.

Figure 1. Carbapenemases identified among CRE



A. Carbapenemases found in 286 characterized isolates. Abbreviations: MBL, metallo-β-lactamase; Cpase-neg, carbapenemase-negative.

B. Variants of carbapenemases found in 83 isolates that carried an MBL or NDM+KPC-2.

Table 1. *In vitro* activity of aztreonam-avibactam against CRE, by carbapenemase variant

		Aztreonam-avibactam MIC (µg/mL) and cumulative percent inhibited at concentration													
Phenotype/genotype	**n**	**≤0.015**	**0.03**	**0.06**	**0.12**	**0.25**	**0.5**	**1**	**2**	**4**	**8**	**16**	**32**	**64**	**>64**
Characterized CRE	286	3	4	9	39	40	79	66	**31**	12	1			1	1
		1.0	2.4	5.6	19.2	33.2	60.8	83.9	**94.8**	99.0	99.3			99.7	100
KPC-2	186			1	9	25	65	52	**26**	6	1			1	
				0.5	5.4	18.8	53.8	81.7	**95.7**	98.9	99.5			100	
MBL±others	83	3	4	7	28	10	8	14	**3**	6					
		3.6	8.4	16.9	50.6	62.7	72.3	89.2	**92.8**	100					
NDM-1	35	2	2	5	15	5	**5**			1					
		5.7	11.4	25.7	68.6	82.9	**97.1**			100					
NDM-5	26		2	1	8	4	1	3	3	**4**					
			7.7	11.5	42.3	57.7	61.5	73.1	84.6	**100**					
NDM-1+KPC-2	9					1		8							
						11.1		100							
NDM-5+KPC-2	5						2	3							
							40.0	100							
NDM-5-like-NV	3				3										
					100										
NDM-9	2			1	1										
				50.0	100										
NDM-6	1									1					
										100					
IMP-4	2	1			1										
		50.0			100										

Abbreviations: MIC, minimum inhibitory concentration; CRE, carbapenem-resistant Enterobacterales; MBL, metallo-β-lactamase; NV, novel variant (all three of which are the same variant).

MIC_{90} values are in bold for categories with ≥10 isolates.

Characterized CRE include: *Klebsiella pneumoniae* (n=212), *Enterobacter* spp. (n=23), *Escherichia coli* (n=23), *Citrobacter* spp. (n=12), Morganellaceae (n=6), other *Klebsiella* spp. (n=5), and *Serratia* spp. (n=5).

RES-343: In vitro Activity of Aztreonam-avibactam against Enterobacterales Isolates Collected from Patients in Intensive Care Units and General Wards, by Infection Source, ATLAS Surveillance Study, 2019-2023

Gregory Stone[2], Meredith Hackel[1], Katherine Perez[2], Dan Sahm[1]

[1]IHMA
[2]Pfizer

Background
Aztreonam (ATM) is a monobactam stable against hydrolysis by metallo-β-lactamases (MBLs), and avibactam (AVI) inhibits class A, class C, and some class D serine β-lactamases. ATM-AVI is being developed for use against infections caused by drug-resistant Enterobacterales, especially those co-producing MBLs and other β-lactamases. This study evaluated the in vitro activity of ATM-AVI and comparators against Enterobacterales collected in 2019-2023 as part of the ATLAS global surveillance program.

Method
21,638 isolates from patients in ICUs and 50,465 isolates from patients in general wards were collected from 225 medical centers and 56 countries excluding North America and China. Antimicrobial susceptibility was performed by broth microdilution according CLSI methods and interpreted using EUCAST 2025 breakpoints.

Results
Overall, ATM-AVI was the most active agent tested against Enterobacterales isolates collected in ICUs (99.4% susceptible; MIC90=0.25 mg/L) and general wards (99.7% susceptible; MIC90=0.25 mg/L), followed by meropenem (85.6% susceptible; MIC90=16 mg/L and 93.5% susceptible; MIC90=0.12 mg/L, respectively). Against carbapenem-nonsusceptible (CRE) isolates, ATM-AVI was also the most active agent, with >97% susceptible.

Conclusions
The in vitro activity of aztreonam-avibactam against Enterobacterales isolates from all infection sources in both ICU and general wards underscores its importance as a potential therapy for infections caused by these organisms, including CRE and MBL-positive isolates.

Organism	N	Agent											
		AZA		ATM		FEP		MEM		LVX		CST	
		MIC_{90}	%S	MIC_{90}	%S	MIC_{90}	%S	MIC_{90}	%S	MIC_{90}	%S	MIC_{90}	%S
ICU Ebac	21620	0.25	**99.4**	>64	60.2	>32	63.5	16	86.6	>8	64.5	>8	81.3
Blood	5435	0.25	**99.5**	>64	54.8	>32	57.2	>16	84.8	>8	60.2	>8	82.1
IA	2128	0.25	**99.4**	>64	62.1	>32	66.3	16	87.7	>8	65.8	>8	87.2
LRT	9756	0.25	**99.6**	>64	64.6	>32	68.7	16	88.1	>8	70.4	>8	80.7
SSS	2114	0.25	**99.1**	>64	59.1	>32	61.7	16	86.2	>8	60.8	>8	77.6
UT	2187	0.5	**98.2**	>64	53.3	>32	55.3	>16	83.4	>8	51.3	>8	79.9
CRE	2903	1	**97.0**	128	7.0	>32	0.5	>16	0	>8	7.1	>8	76.1
E. coli	4832	0.12	**97.8**	64	61.0	>32	63.3	≤0.06	**95.1**	>8	58.2	0.5	**99.7**
MBL-pos	214	8	72.4	>64	5.6	>32	0	>16	1.9	>8	5.6	0.5	**100**
K. pneumoniae	7965	0.25	**99.9**	>64	43.0	>32	42.9	>16	71.9	>8	47.3	1	**92.1**
MBL-pos	1018	0.5	**99.7**	>64	6.7	>32	0.2	>16	2.8	>8	5.7	8	79.2
Non-ICU Ebac	50430	0.25	**99.7**	>64	68.6	>32	71.9	0.12	**93.5**	>8	67.5	>8	81.5
Blood	11648	0.25	**99.8**	>64	67.2	>32	70.4	0.25	**93.2**	>8	67.8	>8	87.0
IA	8107	0.25	**99.7**	64	70.9	>32	75.5	0.12	**94.9**	>8	71.6	>8	88.1
LRT	7631	0.25	**99.8**	>64	69.9	>32	73.6	0.25	**92.9**	>8	71.4	>8	80.8
SSS	11088	0.12	**99.7**	64	71.1	>32	74.0	0.12	**93.9**	>8	68.3	>8	73.1
UT	11956	0.25	**99.6**	>64	65.2	>32	67.9	0.25	**93**	>8	61.2	>8	80.0
CRE	3263	1	**97.6**	128	7.7	>32	0.8	>16	0	>8	8.2	>8	82.1
E. coli	15971	0.12	**99.3**	64	66.5	>32	69.0	≤0.06	**97.9**	>8	59.0	0.5	**99.7**
MBL-pos	276	8	**81.5**	>64	5.8	>32	0	>16	2.9	>8	6.5	0.5	**100**
K. pneumoniae	14093	0.25	**99.9**	>64	53.9	>32	54.6	>16	83.2	>8	56.6	1	**96.2**
MBL-pos	979	0.5	**99.8**	>64	7.3	>32	0	>16	3.2	>8	5.5	8	87.0

Abbreviations: AZA, aztreonam-avibactam; ATM, aztreonam; FEP, cefepime; MEM, meropenem; LVX, levofloxacin; CST, colistin; %S, percent susceptible; MIC_{90} in mg/L; ICU, intensive care unit; Ebac, Enterobacterales; IA, intraabdominal; LRT, lower respiratory tract; SSS, skin/skin structure; UT, urinary tract; CRE, carbapenem (meropenem) nonsusceptible; MBL, metallo-β-lactamase

RES-344: In Vitro Activity of Ceftazidime-avibactam Compared to Ceftolozane-tazobactam Against Pseudomonas aeruginosa, ATLAS Global Surveillance Program, 2020-2023

Gregory Stone[2], Meredith Hackel[1], Katherine Perez[2], Dan Sahm[2], Paurus Irani[2]

[1]IHMA
[2]Pfizer

Background
Avibactam (AVI) is a β-lactamase inhibitor with potent inhibitory activity against Class A, Class C, and some Class D serine β-lactamases. The combination of ceftazidime (CAZ) with AVI has been approved for several indications caused by gram-negative bacteria. This study examined the in vitro activity of CAZ-AVI and comparators against Pseudomonas aeruginosa collected worldwide in 2020-2023 compared to the activity of ceftolozane-tazobactam (C/T).

Method
28,138 non-duplicate P. aeruginosa isolates were collected from 209 sites/55 countries worldwide (excluding North America and China) as part of the ATLAS surveillance study from 2020 to 2023. Susceptibility testing was done following CLSI broth microdilution and interpreted using CLSI 2025 breakpoints. Meropenem (MEM) MIC values >2 µg/mL triggered β-lactamase gene screening.

Results
Among all P. aeruginosa, CAZ-AVI showed good activity (89.7% susceptible, MIC90=16 µg/mL). When 428 MBL-producers were removed, the percentage susceptible to CAZ-AVI increased to 91.0% and the MIC90 decreased to 8 µg/mL. C/T showed similar activity to CAZ-AVI (88.6% susceptible, MIC90=8 µg/mL), with 21.9% of C/T nonsusceptible isolates susceptible to CAZ-AVI. Among all isolates, 24.5% were non-susceptible to meropenem, and of these, 61.6% were susceptible to CAZ-AVI.

Conclusions
CAZ-AVI demonstrated good in vitro activity against P. aeruginosa isolates. CAZ-AVI continues to be a useful therapeutic option for infections caused by P. aeruginosa, especially those not harboring MBLs.

Phenotype/ Genotype (n)	Drug													
	CAZ-AVI		CAZ		C/T		MEM		TZP		LVX		CST	
	MIC_{90}	%S	MIC_{90}	%S	MIC_{90}	%S	MIC_{90}	%S	MIC_{90}	%S	MIC_{90}	%S	MIC_{90}	%I[a]
All PA (28,138)	16	89.7	64	77.8	8	88.6	16	75.5	>64	74.2	>8	69.8	1	99.7
MEM NS (6,902)	>64	61.6	>64	38.8	>16	58.7	>16	0	>64	30.3	>8	26.6	1	99.5
All, no MBL (27,710)	8	91.0	64	79	8	90.0	16	76.6	>64	75.3	>8	70.8	1	99.8
All, CT NS (3,208)	>64	21.9	>64	4.7	>16	0	>16	11.1	>64	6.4	>8	12.1	1	99.2
All, CAZ-AVI R (2,910)	>64	0	>64	0.4	>16	13.8	>16	9.0	>64	4.5	>8	10.8	1	99.3

MIC_{90} in µg/mL; CAZ-AVI, ceftazidime-avibactam; CAZ, ceftazidime; C/T, ceftolozane/tazobactam; MEM, meropenem; TZP, piperacillin-tazobactam; LVX, levofloxacin; CST, colistin; PA, *Pseudomonas aeruginosa*: S = susceptible; NS = non-susceptible; MBL = metallo-β-lactamase; R = resistant
[a]As there is not a CLSI Susceptible category for colistin, percent Intermediate is shown.

RES-345: In Vitro Activity of Ceftazidime-avibactam and Comparator Agents Against Enterobacterales and Pseudomonas aeruginosa from Pediatric Patients in the Asia/Pacific Region: ATLAS Surveillance Program, 2019-2023

Gregory Stone[2], Mark Wise[1], Katherine Perez[2], Paurus Irani[2], Dan Sahm[1]

[1]IHMA
[2]Pfizer

Background
Antimicrobial resistance (AMR) is a major public health concern, including among pediatric patients. This study examined AMR among Enterobacterales and Pseudomonas aeruginosa collected from individuals <18 years of age in 11 Asia/Pacific countries as part of the ATLAS surveillance program from 2019-2023, focusing on the activity of ceftazidime-avibactam (CZA) and comparators.

Method
For ATLAS, 1604 Enterobacterales and 535 P. aeruginosa were collected from pediatric patients in 61 medical centers in 11 countries (Australia, China, Hong Kong, India, Japan, Malaysia, New Zealand, Philippines, South Korea, Taiwan, Thailand) from 2019-2023. Susceptibility testing was performed by broth microdilution following CLSI reference methodology and interpreted with CLSI 2025 breakpoints.

Results
Against the Enterobacterales (n=1581), CZA was the most active agent among comparators, inhibiting 92.9% of the isolates (Table). Meropenem (90.7% susceptible [S]) and ceftolozane-tazobactam (85.1% S) were also highly active. CZA inhibited 100% of the isolates from six countries (Australia, Hong Kong, Japan, New Zealand, South Korea and Taiwan), while isolates from India were the least susceptible to all antimicrobials. Against P. aeruginosa (n=531), CZA was the second most active agent among comparators (94.0% S). Regarding the individual countries, 100% of the isolates collected in New Zealand and South Korea were susceptible to CZA, while those from Thailand were the least susceptible (83.1% S to CZA and 83.3% S to ceftolozane-tazobactam).

Conclusions
CZA demonstrated potent in vitro activity against both Enterobacterales and P. aeruginosa from pediatric patients in Asia/Pacific. These data suggest CZA remains a prudent therapeutic choice to consider against these pathogens.

Activity of ceftazidime-avibactam and comparators against Enterobacterales and *P. aeruginosa* collected from pediatric patients in the Asia/Pacific region

Region/country (n)	% Susceptible					
	CZA	CAZ	MEM	TZP	C/T[a]	LVX
Enterobacterales						
All Asia/Pacific (1581)	92.9	66.6	90.7	80.4	85.1	65.8
Australia (164)	100	89.6	100	91.5	95.7	90.2
China (704)	95.9	68.9	93.6	83.8	88.0	61.8
Hong Kong (48)	100	81.3	100	93.8	93.0	79.2
India (213)	69.5	27.2	64.8	53.1	56.5	38.0
Japan (41)	100	87.8	97.6	85.4	88.2	80.5
Malaysia (79)	97.5	79.7	97.5	89.9	91.0	86.1
New Zealand (45)	100	86.7	100	91.1	95.5	97.8
Philippines (59)	89.8	67.8	88.1	83.1	85.7	72.9
South Korea (94)	100	71.3	100	87.2	93.0	72.3
Taiwan (14)	100	92.9	100	78.6	81.8	78.6
Thailand (120)	90.8	55.0	85.8	70.0	81.3	59.2
***P. aeruginosa*[b]**						
All Asia/Pacific (531)	94.0	83.6	83.8	81.5	95.5	81.0
Australia (74)	98.6	81.1	97.3	83.8	100	86.5
China (166)	97.6	83.7	80.1	78.3	98.6	82.5
India (81)	87.7	84.0	86.4	85.2	85.5	74.1
Japan (29)	86.2	82.8	72.4	72.4	100	82.8
Malaysia (38)	94.7	86.8	81.6	86.8	100	84.2
New Zealand (29)	100	93.1	93.1	96.6	100	79.3
South Korea (11)	100	81.8	90.9	72.7	100	81.8
Philippines (27)	96.3	92.6	85.2	88.9	94.7	77.8
Thailand (59)	83.1	76.3	74.6	78.0	83.3	76.3

Abbreviations: CZA, ceftazidime-avibactam; CAZ, ceftazidime; MEM, meropenem; TZP, piperacillin-tazobactam; C/T, ceftolozane-tazobactam; LVX, levofloxacin.
[a]C/T not tested in 2019 (Enterobacterales tested 2020-2023: n=1332; *P. aeruginosa* tested 2020-2023: n=425).
[b]Countries with ≤10 *P. aeruginosa* isolates from pediatric patients not shown (Hong Kong, n=10; Taiwan, n=7).

RES-346: In Vitro Activity of Ceftazidime-avibactam and Comparator Agents Against Enterobacterales from Bloodstream Infections in Asia/Pacific: ATLAS Global Surveillance Program, 2019-2023

Gregory Stone[2], Mark Wise[1], Katherine Perez[2], Paurus Irani[2], Dan Sahm[1]

[1]IHMA
[2]Pfizer

Background
The β-lactamase inhibitor avibactam (AVI) exhibits potent inhibitory activity against Class A, Class C, and some Class D serine β-lactamases and is approved for use with ceftazidime (CAZ) for several indications. This study evaluated the in vitro activity of CAZ-AVI and comparators against Enterobacterales isolated from the blood of infected patients in the Asia/Pacific region as part of the ATLAS surveillance program from 2019 to 2023.

Method
A total of 5569 non-duplicate clinically significant Enterobacterales isolates from bloodstream infections were collected in 11 countries in the Asia/Pacific region (Australia, China, Hong Kong, India, Japan, Malaysia, New Zealand, Philippines, South Korea, Taiwan, Thailand) from 2019-2023. Susceptibility testing was performed by broth microdilution following CLSI reference methodology and interpreted with CLSI 2025 breakpoints. Meropenem-nonsusceptible (MEM-NS) isolates (excluding those from China) were screened for the presence of β-lactamase genes.

Results
Overall, 92.3% of isolates were susceptible to CAZ-AVI (MIC90 = 2 µg/ml) an increase of >25 percentage points over CAZ alone (Table). CAZ-AVI was active against 78.0%, 67.3%, 55.6% and 83.4% of the CAZ-NS, piperacillin/tazobactam-NS, ceftolozane/tazobactam-NS and levofloxacin-NS isolates, respectively, in each case a higher percentage than comparators. Versus MEM-NS isolates, CAZ-AVI was able to inhibit the growth of 34.5%; however, considering only those MEM-NS isolates that were shown to be metallo-β-lactamase (MBL)-negative, the susceptibility rate increased to 92.4% (MIC90 = 4 µg/ml).

Conclusions
Based on these in vitro data, CAZ-AVI appears to provide a valuable therapeutic option for treating bloodstream infections caused by Enterobacterales, except those carrying MBLs.

Organism/Phenotype/Genotype (n)	Agent, [MIC_{90} (µg/ml), % Susceptible]											
	CZA		CAZ		MEM		TZP		C/T[a]		LVX	
	MIC_{90}	%S	MIC_{90}	%S	MIC_{90}	%S	MIC_{90}	%S	MIC_{90}	%S	MIC_{90}	%S
All Enterobacterales (5569)	2	92.3	>64	65.1	16	88.7	>64	76.9	>16	82.2	>8	57.9
CAZ-NS (1941)	>64	78.0	>64	0	>16	67.7	>64	41.2	>16	49.0	>8	22.2
TZP-NS (1287)	>64	67.3	>64	11.3	>16	51.4	>64	0	>16	24.3	>8	18.9
C/T-NS (800)	>64	55.6	>64	2.1	>16	36.9	>64	3.8	>16	0	>8	14.0
LVX-NS (2343)	>64	83.4	>64	35.6	>16	74.6	>64	55.4	>16	63.2	>8	0
MEM-NS (631)	>64	34.5	>64	0.8	>16	0	>64	0.8	>16	0.8	>8	5.9
MEM-NS, MBL-Neg[b] (132)	4	92.4	>64	2.3	>16	0	>64	0.8	>16	0.9	>8	3.0

Abbreviations: CZA, ceftazidime-avibactam; CAZ, ceftazidime; MEM, meropenem; TZP, piperacillin-tazobactam; C/T, ceftolozane-tazobactam; LVX, levofloxacin; NS, non-susceptible; MBL, metallo-β-lactamase.
[a] C/T not tested in 2019 (for 2020-2023, n=4499).
[b] MEM-NS isolates collected in China were not molecularly characterized and thus not included here.

RES-348: Antibiotic Prescribing Patterns for Acute Uncomplicated Cystitis in Outpatients: A Nationwide Analysis in Korea, 2019–2022

Yuri Seo[1], Yumi Seo[2]

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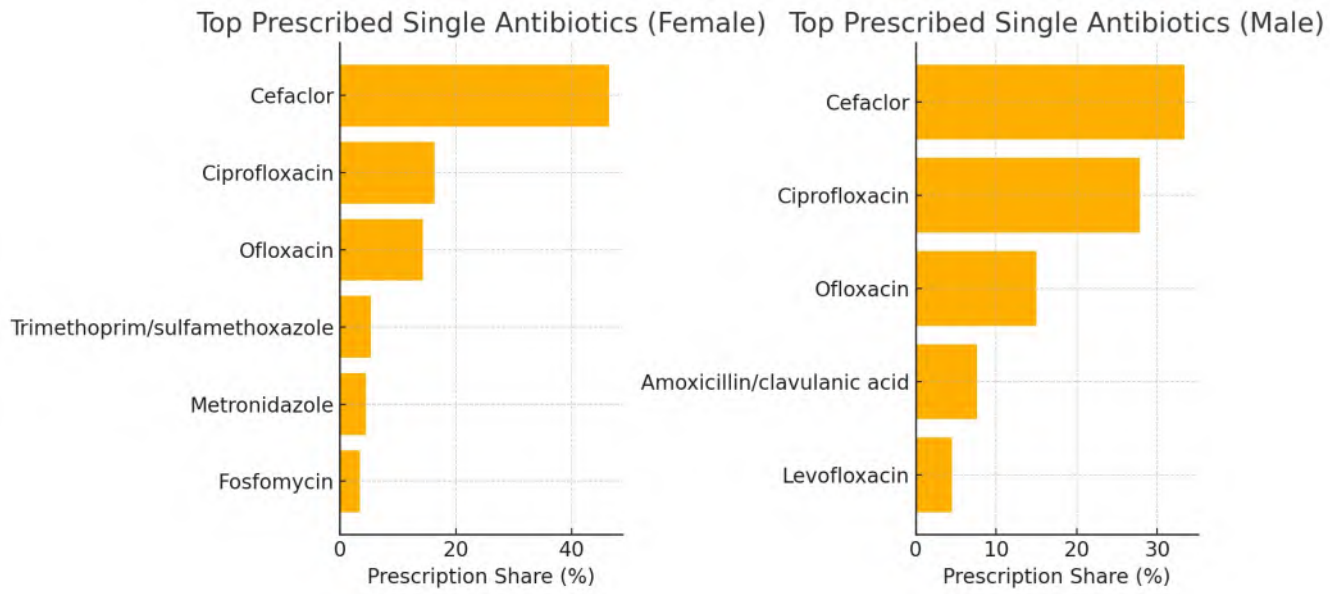
Background
Acute uncomplicated cystitis is common, affecting ~10% of women annually and up to 60% at least once in a lifetime. Escherichia coli is the predominant pathogen, accounting for 70–83% of acute uncomplicated cystitis. Empirical antibiotic selection should consider local resistance rates, cost, and treatment failure risk. Following safety warnings from the U.S. FDA, the Korean Ministry of Health restricted fluoroquinolone reimbursement as first-line therapy for uncomplicated cystitis. Korean guidelines (2018) recommend nitrofurantoin, fosfomycin, or pivmecillinam; however, limited availability necessitates frequent use of fluoroquinolones and cephalosporins.

Method
We analyzed Korea Health Insurance Review and Assessment Service data for adults (≥19 years) diagnosed with acute cystitis (ICD-11: N300) between January 2019 and December 2022. Patients with sexually transmitted infections, malignancies, congenital urogenital anomalies, or pregnancy were excluded. After excluding ineligible cases and those without antibiotic prescriptions, 2,534,322 patients were included (94,750 men [3.7%], 2,439,572 women [96.3%]).

Results
In women, the most prescribed single agents were second-generation cephalosporins (42.09%), fluoroquinolones (28.00%), and penicillins (10.34%); top agents included cefaclor (46.47%), ciprofloxacin (16.30%), and ofloxacin (14.29%). In men, fluoroquinolones (41.12%), second-generation cephalosporins (32.64%), and penicillins (8.74%) predominated; top agents included cefaclor (33.39%), ciprofloxacin (27.81%), and ofloxacin (14.97%). The most common combination therapies were cefaclor + metronidazole (48.69%) in women and metronidazole + levofloxacin (47.95%) in men.

Conclusions
Despite guidelines, fluoroquinolone use remains high in acute cystitis treatment, underscoring the need for ongoing education on antibiotic selection and duration to minimize resistance. The COVID-19 pandemic (2020–2023) may have influenced healthcare access and prescribing trends; continued monitoring is warranted.



RES-349: Electronic Device and Middleware Interface for Rapid Microbiological Report in Tertiary Hospitals and Data Channeling System for WHONET Surveillance

Kanakron Dechnithichanon[2], Anukoon Prato[2], Phisit Uirungroj[2], Chanwit Tribuddharat[1]

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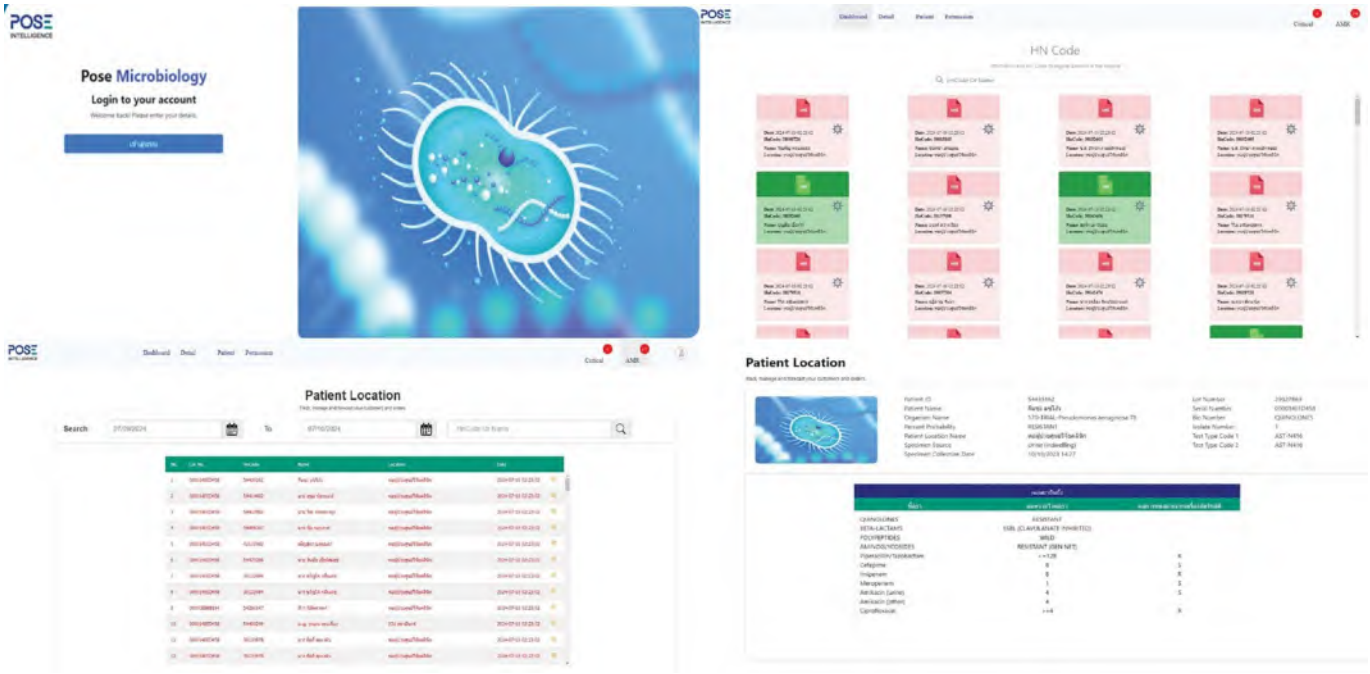
Background
Microbiological reports of pathogen and antibiogram are crucial for successful treatment. Rapid turnaround time can reduce morbidity and mortality in critically infected patients by early antibiotic treatment. Automated bacterial identification systems are now available in most hospitals; however, some do not get full capacity of such systems. We developed specialized electronic device and middleware interface to deliver real-time microbiology reports including parameters, such as organism name, specimen type, antibiotic resistance profile, to terminal end users (physicians or infection control nurses) throughout healthcare facility. Encrypted hexadecimal data in HL7 (Health Level Seven) format can be further sent as CSV file into WHONET software (Brigham and Women's Hospital in Boston, USA, Version: 25.7.18 for epidemiological report or outbreak surveillance.

Method
Once automated identification system, e.g., VITEX2, and antibiotic susceptibility results were available, data were transmitted through RS-232 port (inter-device operability with option for TCP/IP protocol over a network) using specialized electronic device. Data were compiled with HIS data from server (all needed patient demographic data were included) and encrypted data were delivered to terminal personal computers at designated location for easy access by authorized personnel (password secured access) in dashboard style showing alerts and critical events.

Results
(To be shown in Figure)

Conclusions
With automated real-time direct report delivery to end users throughout healthcare facility, hospital can improve patient care by early specific and appropriate antibiotic treatment. The system can reduce administrative burden, and automated data exchange can reduce manual data entry, free up workload. Data can be delivered to WHONET software directly.



RES-351: Prevalence of Disseminated Histoplasmosis in Newly Diagnosed HIV-positive Patients in Vientiane, Lao PDR – An Under-Recognised Opportunistic Infection

John Evans[3], Anousone Douangnouvong[3], Saykham Phaxayaseng[2], Valy Keoluangkhot[1], Davanh Sengdatka[5], Odith Keokanchan[2], Chaothao Chuefue[2], Othila Rasphone[1], Leeyounjera Yang[1], Ko Chang[1], Koukeo Phommasone[5], Sue J. Lee[4], Tamalee Roberts[3], Elizabeth Ashley[5]

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Background
Disseminated histoplasmosis is an opportunistic infection seen in advanced HIV infection. It is widespread, although not uniformly so, across the globe. Prevalence is unknown in many low-resource countries, but emerging evidence suggests it is common in southeast Asia. Diagnosis is challenging, partly due to limited access to validated diagnostic tests.

Method
In this pilot study of newly diagnosed HIV-positive adults in Vientiane, Laos, we estimated prevalence of Histoplasma antigenaemia using two Histoplasma antigen assays: a point-of-care urinary test (OIDx) and a serum assay (MiraVista) performed retrospectively at a reference laboratory once enrolment was closed.

Results
We recruited 229 patients (72% male), with a median age of 29 years (IQR: 24.5 – 36). The prevalence of histoplasmosis was 7% and 11% by serum and urinary antigen tests, respectively. Inpatient admission, night sweats, splenomegaly, and lower haemoglobin were significantly associated with a positive test result in both assays ($p < 0.05$).

The majority of patients with a positive urinary antigen test (15/26 (58%)) were treated with antifungals (itraconazole +/- amphotericin B deoxycholate), and one antigen-positive patient died during the follow-up period (median 34 days). Nearly a quarter (6/26 (23%)) with a positive urinary antigen test were treated empirically for tuberculosis, although they did not have any positive microbiological tests for this infection, raising the possibility of misdiagnosis.

Conclusions
Histoplasma infections are likely under-diagnosed in Laos. Therefore, testing should be integrated into clinical protocols when investigating immunosuppressed patients at risk of opportunistic infections. Local evaluation of novel assays is essential, ideally against a reference standard.

RES-352: Plasmid-Encoded Resistance in XDR Salmonella Typhi: A Growing Public Health Threat

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[2]Government College University Lahore, Pakistan
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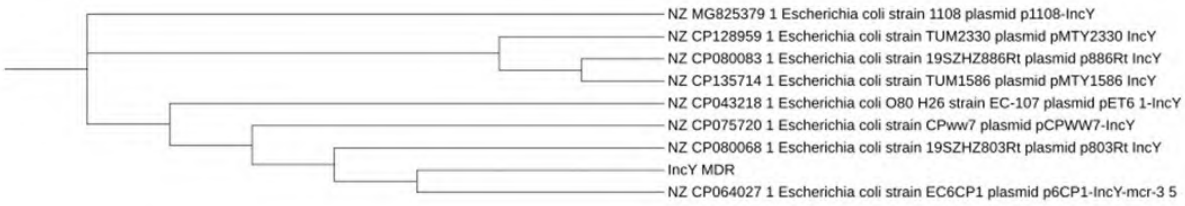
Background
Antimicrobial resistance and emergence of MDR and XDR S. typhi is a major threat in Pakistan. Failure of treatment with conventional antibiotics leads to importance of exploring alternative treatment plan. Therefore, the present study was done to checked the resistance pattern as well molecular basis of resistance among clinical isolates of S. typhi.

Method
384 clinical isolates of S. typhi were processed according to standard microbiological techniques. Antimicrobial sensitivity testing was performed by using VITEK-2 compact system. DNA was extracted and Gene specific PCR was done to confirm XDR S. typhi. Whole Genome Sequencing was performed and Plasmid finder software was used for plasmids identification.

Results
Among 382 S. typhi, males were predominant which accounted for 61.7% and 43.2% samples were from age group of less than 10 years. Carbapenems and azithromycin showed 100% sensitivity. XDR S. typhi accounted for 38% of total isolates. Most commonly found plasmids were IncQ1, IncY and IncC.

Conclusions
XDR Salmonella Typhi poses a significant challenge in the treatment of typhoid fever and serious threat for public health. Inheritance of plasmids from related species leads to emergence of XDR typhoid is a notable future concern.



Phylogenetic tree of IncY MDR plasmids from E. coli strains. In phylogenetic relationship among IncY plasmids associated with MDR phenotype shows contrasting IncY plasmids that unlike XDR groups, are quite disordered clusters with longer branch lengths, which indicates a greater genomic diversity and possibly different sources of acquisition for antimicrobial resistance genes.

RES-353: Potential Disinfecting Activity of Annona squamosa L., Durio zibethinus L., and Nephelium lappaceum L. Against Known Gram-Positive Bacterial Isolates

Mika Alexandrea Yangco[1], Dianne Keith Tabujara[1], Kyrelle Jace Uriarte[1], Jaybriel Andrei Uy[1], Elisse Andrea Villar[1], Maria Vanessa Yap[1], Florence Navidad[1], Reuel Bennett[2]

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Background
Fruit peels have begun demonstrating a myriad of potential beyond mere food waste, presenting possible de-escalation on the increasing prevalence of antibacterial resistance. On such premise, this study aims to explore the potential antimicrobial properties of methanol and ethanol extracts from three fruit peels, i.e., Durio zibethinus L. (durian), Nephelium lappaceum L. (rambutan), and Annona squamosa L. (sugar apple)—against gram-positive bacteria isolates, with reference to commonly isolated bacteria from gadgets.

Method
Determination of extract effectiveness using Kirby-Bauer disc diffusion revealed that 100% methanol rambutan extract (MR1) exhibited the highest average inhibition zone at 19.5 ± 0.9 mm, while methanol durian extracts showed minimal to no inhibition. Both methanol and ethanol rambutan extracts showed the lowest MIC value of 125 µg/mL, while MA, ER, and MR showed the lowest MBC value of 250 µg/mL, indicating bactericidal effect at lower concentrations.

Results
Generally, findings suggest methanol rambutan extract holds the most potential as a natural disinfectant. The positive findings of this study regarding the antimicrobial effects of ethanolic and methanolic extracts of the three fruit peels against known standardized bacterial isolates present a significant step towards finding environmentally safer alternatives to chemical disinfectants.

Conclusions
It is recommended to include a DMSO solvent control in future susceptibility tests and to use standard antibiotic disks for comparison. Future research may also explore the effects of fruit ripeness, the use of distilled water as solvent, and the activity of fruit peel extracts against gram-negative isolates, expanding the relevance of fruit peels as eco-friendly antimicrobial agents.

RES-354: From Hyphae to Zoospores: Optimizing zoospore induction in Pythium insidiosum

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Background
Pythium insidiosum is an oomycete pathogen causing pythiosis, a life-threatening disease affecting both humans and animals. The infective stage is characterized by asexual reproduction through zoosporangia, which release motile, biflagellate zoospores that attach to host tissues. To effectively mimic natural infection and investigate host immune responses, the use of motile zoospores is essential. The standard in vitro culture protocol involves culturing P. insidiosum on Sabouraud dextrose agar (SDA) or blood agar (BA) at 37°C for 24 h. Subsequently, the hyphae are transferred to cornmeal agar (CMA) supplemented with sterile blanket grass (Axonopus compressus) and incubated at 37°C for 48 h. The colonized blanket grass is placed into a zoospore induction medium containing calcium and magnesium ions (Ca^{2+} and Mg^{2+}) and incubated at 37°C for 18 h. However, motile zoospores rapidly encyst, resulting in reduced suitability for infection studies. We aimed to optimize the culture conditions to enhance high zoospore yield and minimize premature encystment.

Method
Two culture media (BA and SDA) and two incubation durations (16 and 18 h) were compared.

Results
The results demonstrated that BA, likely due to its higher iron content, supported superior fungal growth and a greater number of zoospores compared to SDA. Although no significant difference between the incubation times, the 16 h incubation consistently resulted in fewer encysted zoospores.

Conclusions
This study suggests that culturing P. insidiosum on BA followed by a 16 h incubation in induction medium enhances the production of motile zoospores. This optimized method is advantageous for future investigations into the pathogenesis of P. insidiosum.

RES-356: Tuberculosis Treatment Outcome Among Individuals with Hematologic and Solid Malignancies in High TB Burden Setting

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Background
The risk of tuberculosis (TB) reactivation due to immunosuppression from malignancy therapies is well recognized. This study aimed to evaluate TB treatment outcomes and factors associated with mortality among TB patients with hematologic and solid malignancies.

Method
We conducted a retrospective cohort study among adult patients diagnosed with active TB at Ramathibodi Hospital and Chakri Naruebodindra Medical Institute, Mahidol University, Thailand, between November 2014 and October 2024.

Logistic regression was used to determine the factors associated with mortality after TB treatment in TB patients with malignancy.

Results
A total of 3,453 TB patients, 625 (18%) patients who were diagnosed with malignancy [solid malignancy (n=512) and hematologic malignancy (n=113)] before TB diagnosis, and 2,828 (82%) without malignancy were analysed. The majority of them were male (51.5%), with a median age of 64.5 (IQR: 55.3-72.9) for malignancy and 53.3 (35.0-67.25) years for non-malignancy, respectively. TB patients with malignancy had a lower treatment success rate (75.8% vs 82.3%; p <0.001) and higher mortality rate (15% vs 3.5%; p <0.001) compared to non-malignancy. In TB patients with malignancy, male (aOR 1.72 (95%CI 1.04-2.84), P =0.032), BMI < 18.5 kg/m2 (aOR 2.13 (95%CI 1.32-3.45), P= 0.002), diabetes (aOR 2.17 (95%CI 1.28-3.68), p= 0.004) and receiving cytotoxic drugs (aOR 1.71 (95%CI 1.04-2.82), P= 0.034) were independently associated with death after TB treatment.

Conclusions
TB patients with hematologic or solid malignancy in Thailand had lower TB treatment success rates and higher mortality rates compared to TB patients without malignancy. Strategies for early diagnosis and preventive management in this population should be scaled up.

Table. Factors associated with mortality in TB patients with malignancy (n=625)

	Univariable		Multivariable	
	Odds ratio (95%CI)	P-value	Adjusted odds ratio (95%CI)	P-value
Age ≥ 60	1.72 (1.04-2.82)	0.032	1.57 (0.93-2.65)	0.391
Male	1.85 (1.14-3.00)	0.013	1.72(1.04-2.84)	0.032
BMI ≤ 18.5 kg/m^2	2.13 (1.34-3.37)	0.001	2.13 (1.32-3.45)	0.002
Disseminated TB	1.35(0.65-2.79)	0.417		
Co-morbidity				
• Diabetes	2.04(1.25-3.34)	0.004	2.17(1.28-3.68)	0.004
• Chronic kidney disease	1.77 (0.96-3.25)	0.063		
• Cardiovascular disease	1.38 (0.66-2.86)	0.379		
• COPD	2.31(1.07-4.96)	0.032	1.57(0.70-3.52)	0.267
Receiving cytotoxic drugs	5.20 (3.70-7.30)	<0.001	1.71 (1.04-2.82)	0.034
Receiving corticosteroids*	4.92(3.00-8.07)	<0.001	1.29 (0.71-2.35)	0.391

Abbreviation: BMI: Body mass index, COPD: Chronic obstructive pulmonary disease
* Corticosteroids equivalent dose ≥ prednisolone 20 mg/day

RES-358: High Seroprevalence of Antibodies to Salmonella typhi Protein Antigens HlyE and CdtB in Chandigarh, India: Evidence of Ongoing Community Transmission

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Background
Typhoid fever caused by Salmonella enterica serovar Typhi continues to impose a significant disease burden in South Asia. Conventional diagnostics such as Widal test and blood culture have limited sensitivity. Serological assays targeting Hemolysin E (HlyE) and Cytolethal Distending Toxin subunit B (CdtB) offer a robust alternative for capturing both recent and cumulative exposure.

Method
We performed an age-stratified, cross-sectional serosurvey in Chandigarh, India, analyzing 1,138 serum samples: 199 from Widal-positive cases, 770 from routine biochemistry submissions, and 169 from blood culture-confirmed typhoid patients. Serial follow-up samples were collected from culture-positive individuals to assess antibody persistence. IgG and IgM responses against purified HlyE and CdtB were quantified using in-house ELISAs. Seropositivity thresholds were established from negative controls, and age-related trends were evaluated.

Results
High IgG seropositivity was observed for both antigens, reflecting widespread prior exposure. IgM responses indicated recent infections. Antibody levels peaked in young adults (21–30 years), suggesting active transmission. Longitudinal follow-ups of culture-confirmed cases revealed sustained IgG responses over time, validating these antigens as markers of prior infection. Strong correlation between anti-HlyE and anti-CdtB IgG confirmed assay reliability.

Conclusions
High seroprevalence to HlyE and CdtB across multiple cohorts and persistence in follow-up samples demonstrate ongoing S. Typhi circulation in Chandigarh. These antigens provide superior resolution of exposure dynamics and support the integration of serosurveillance with typhoid conjugate vaccine strategies in endemic urban regions.

RES-359: Cost-Effectiveness Analysis of Dalbavancin in an Acute District Hospital in UK

Alice Liu

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Background
The unique mode of delivery of dalbavancin makes it ideal for OPAT and particular patient groups (e.g. non-compliance, PWID or difficulty with vascular access). However it is often treated as a last resort of antibiotic due to its high cost. This study is to analyze whether dalbavancin is a cost-effective drug from the health-economic perspective.

Method
The reasons for dalbavancin prescriptions and length of course were analyzed retrospectively in terms of its appropriateness for purpose. The healthcare cost was compared between inpatient settings and OPAT with dalbavancin.

Results
Sixty-three patients were prescribed dalbavancin in this study. Forty-one patients (65%) used in OPAT settings. 53(84%) used for unlicensed indications and 20(32%) started without identifiable causative pathogens. 104 treatments were delivered and the course duration (1-4 doses) varied against indications. Bone and Joint Infections were the most popular (20,32%) followed by osteomyelitis (9,14%) and septic arthritis (8,13%) respectively. The total drug expenditure was £18,7052.76; of which £122,690.50 (66%) was spent in OPAT. However, if the forty-one patients were treated as inpatients, it would cost the health authority 4 times as much in budget according to the cost-model of a 7-day inpatient stay against OPAT setting.

Conclusions
The study demonstrated a significant cost reduction in dalbavancin use in OPAT compared with the hospital stay with daily intravenous antibiotic. The benefits include reducing the need for intravenous vascular access facilities hence the risk of injection site infections; minimizing the operational cost such as overheads and staffing to run a daily OPAT service.

Dalbavancin for *routine* OPAT –Expensive? Can we afford?

Title: Cost-effectiveness analysis of dalbavancin in an acute district hospital in UK

Liu A

NHS Gloucestershire Hospitals NHS Foundation Trust

Background

Dalbavancin[1] is a new semisynthetic lipoglycopeptide which is widely used in OPAT settings to prevent hospital admission and facilitate early hospital discharge. Its unique mode of delivery makes it ideal for a particular type of patients (eg. non-compliance, PWID or difficulty with vascular access). However it is often treated as a ***last resort*** of antibiotic due to its high cost[1]. This study is to analyse whether dalbavancin is a cost-effective drug from the health-economic perspective.

Methods

The reasons for dalbavancin prescriptions and length of course were analysed retrospectively in terms of the appropriateness of the purpose. The healthcare cost was compared between inpatient settings and OPAT with dalbavancin.

Results

Sixty-three patients were prescribed dalbavancin in the study period; forty-one patients (65%) received dalbavancin either in OPAT or Day Case Units (Figure 1). 53 patients (84%) used dalbavancin for unlicensed indications and 20 patients (32%) started without identifiable causative pathogens. In total 104 treatments were delivered and the course duration (1-4 doses) varied against indications. Bone and Joint Infections were the most common users (20,32%) followed by osteomyelitis (9,14%) and septic arthritis (8,13%) respectively (Figure 2). The total drug expenditure on dalbavancin was £187,052.76; of which £122,690.50 (66%) was spent in OPAT. However, if the forty-one patients were treated as inpatients, it would cost the health authority 4 times as much in budget per week; ie. £348,013.33 according to the cost-model of a 7-day inpatient stay comparing with OPAT setting[2,3] (Figure 3).

Figure 1. Demographics of the Dalbavancin Prescriptions During The Study Period (11 months) at the Acute District Hospital in UK

Total number of patients (N):	63
Number of OPAT* patients:	41 (65%)
• Number of patients in Day Case units	15 (24%)
OPAT = discharge hospital within 24hours or no hospital admission*	
Number of Inpatients#:	22 (35%)
Inpatients# = stay in hospital > 24hours	
Number of patients starting dalbavancin due to other reasons (eg. no cannula access, ADR of other antibiotics): Note: except PWID	5 (8%)
Number of PWID patients:	10 (16%)

Figure 2. The indications, dosage and number of courses of dalbavancin use during the study period

Infection Types	Number of patients	Number of Empirical Use of dalbavancin	Dosage and Number of courses received by the patients (pt)
SSTIs	7	3	5pts- 1500mg stat; 1pt- 1500mg x 2; 1 pt – 500mg x 2
Discitis	4	3	1 pt – 1500mg stat; 3 pts – 1500mg x 2
Osteomyelitis	9	3	3 pts – 1500mg stat; 6 pts – 1500mg x 2
Septic arthritis	8	1	4 pts – 1500mg stat; 4 pts – 1500mg x2
Bone and Joint Infections	20	5	5 pts – 1500mg stat; 13 pts – 1500mg x 2; 1 pt (infected dislocated R THR with open relocation, debridement and insertion of stimulant beads) – 1500mg x 3 on D1, D8, wk4; 1pt (infected L TKR) – 1500mg x 4 on D1, D8, wk4 and wk5
Abscess (groin, liver, spine)	3	1	3 pts – 1500mg x 2
Endocarditis	4	1	2 pts – 1500mg stat; 2 pts – 1500mg x 2
Diabetic foot infection	2	0	1 pt – 1500mg stat; 1 pt – 1500mg x 2
Septicaemia/ bacteraemia	2	0	1 pt – 1500mg stat; 1 pt (renal impairment)- 750mg D1 then 375mg D8
CAP	1	1	1 pt – 1000mg stat
Sacral and leg ulcers	3	2	3 pts -1500mg stat
Total:	63	20 (32%)	26 patients received 1 course, 35 patients received 2 courses 1 patient received 3 courses, 1 patient received 4 courses

Figure 3. The Healthcare Cost between inpatient and OPAT settings for a 7-day treatment — OPAT with Dalbavancin = 24% of Inpatient Cost

	Inpatient Stay (7-day treatment)	OPAT with Dalbavancin
Medicine Cost (Conventional daily antibiotic treatment vs dalbavancin)	£1,420.00	£2,011.32
Infusion material costs (e.g. diluents, disposable infusion pumps, consumables such as venflon cannula)	£171.19	£12.00
Nursing costs (Agenda for change NHS Pay Bands 2024/25 for a band 6 nurse)	£60.93	£13.79
Hospital Bed-Day Costs (NHS Tariff 2023/25)	£6,832.00	£0.00
Blood analyses	£4.00	£4.00
Grand Total	**£8,488.13**	**£2,041.11**

Conclusions

The study demonstrated a significant cost reduction in dalbavancin use in OPAT compared with the hospital stay with daily intravenous antibiotic. Dalbavancin treatment has recently been extended widely to other unlicensed indications especially in orthopaedic infections which are often hard to treat and require prolonged hospital stay if there are no suitable oral antibiotics. Dalbavancin provides an alternative antibiotic option to facilitate hospital discharge, reducing the need for intravenous vascular access facilities and reducing the risk of injection site infections. Moreover it does not incur the high operational cost such as overheads and staffing to run a daily outpatient intravenous antibiotic therapy service.

1) BNF - Xydalba (https://bnf.nice.org.uk/drugs/dalbavancin/medicinal-forms/) 2) 2023/25 NHS Payment Scheme (https://www.england.nhs.uk/publication/2023-25-nhs-payment-scheme/) 3) Agenda for Change NHS Pay Bands 2024/25 (https://nursingnotes.co.uk/agenda-for-change-nhs-pay-bands/)

RES-361: Accuracy of Two Novel Tuberculosis-specific Skin Tests in Diagnosing Tuberculosis Infection: Preliminary Report

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Background
Accurate diagnosis of latent tuberculosis infection is essential for targeting tuberculosis preventive treatment, a key strategy in the global effort to end TB. The Tuberculin Skin Test using purified protein derivative (PPD) is widely used but may yield false positives in Bacillus Calmette–Guérin (BCG)-vaccinated individuals. Interferon Gamma Release Assays (IGRAs) offer improved specificity but are costly and require laboratory infrastructure. To address these limitations, the World Health Organization recently endorsed tuberculosis antigen-based skin tests (TBSTs) that detect ESAT-6 and CFP-10 antigens, including C-TST (Anhui Zhifei Longcom, China) and Cy-Tb (Serum Institute of India), as alternatives. However, data from high-burden, BCG-vaccinated settings remain limited.

Method
We conducted a cross-sectional study comparing reactions to PPD, Cy-Tb, C-TST, and IGRA among three groups: (1) microbiologically confirmed TB cases, (2) individuals at low risk, and (3) individuals at high risk of TB infection. Positive test criteria were induration ≥10 mm for PPD and ≥5 mm for Cy-Tb and C-TST.

Results
As of July 31, 2025, 124 participants were enrolled (10 in Group 1, 100 in Group 2, 14 in Group 3). Using IGRA as the reference, sensitivity for Cy-Tb and C-TST exceeded PPD (63.9%, 69.4%, and 50.0%, respectively), with high specificity (100%, 98.9%, and 94.3%). Concordance between C-TST and Cy-Tb was excellent (Kappa = 0.924). Among positive reactions, indurations ≥15 mm were commonly observed particularly with Cy-Tb and C-TST (87.0% for Cy-Tb, 88.5% for C-TST, 46.4% for PPD).

Conclusions
Preliminary findings suggest that C-TST and Cy-Tb offer IGRA-comparable performance, outperform PPD, and offer clearer, more interpretable results.

Table: Diagnostic Accuracy in diagnosing Tuberculosis

Test Name	Sensitivity (95% CI)	Specificity (95% CI)	Likelihood ratio of a positive test (95% CI)	Likelihood ratio of a negative test (95% CI)
Using IGRA as a gold standard (n=124)				
PPD (10 mm)	50.0% (32.9–67.1)	94.3% (87.2–98.1)	8.80 (3.54–21.90)	0.53 (0.38–0.74)
Cy-Tb (5 mm)	63.9% (46.2–79.2)	100.0% (95.9–100.0)	ND	0.36 (0.23–0.56)
C-TST (5 mm)	69.4% (51.9–83.7)	98.9% (93.8–100.0)	61.11 (8.60–434.20)	0.31 (0.19–0.51)

ND= not determined due to zero denominator.

RES-363: Shortening the Course of Carbapenem for Acute Pyelonephritis in Female Patient Caused by Escherichia coli and Klebsiella pneumoniae Resistant to Ceftriaxone: Short vs Long Duration of Treatment Comparison (SCAPER study)

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Background
Recent guidelines favor shorter antibiotic regimens for upper urinary tract infections (uUTIs), including bacteremic cases. However, evidence supporting this approach in infections caused by resistant organisms remains limited.

Method
We retrospectively reviewed medical records of adult patients with uUTIs caused by ceftriaxone-resistant E. coli or K. pneumoniae from a two-year period. Patients were categorized by intravenous antibiotic duration: short course (6–8 days) vs. long course (13–15 days). A 1:2 propensity score-matched, non-inferiority analysis assessed clinical cure, 90-day recurrence, and adverse events.

Results
A total of 54 patients were analyzed (18 in the short-course group and 36 in the long-course group). Clinical cure rates were 91.7% and 94.4%, respectively (difference: –2.8%; 95% CI: –16.1% to 21.7%). Recurrence within 90 days occurred in 25.0% of the short-course group and 33.3% of the long-course group (difference: –8.3%; 95% CI: –41.1% to 24.4%). No adverse events were observed in either group.

Conclusions
Shorter antibiotic regimens (6–8 days) appear comparable to longer regimens (13–15 days) for treating uUTIs due to ceftriaxone-resistant E. coli or K. pneumoniae. These findings support the safety and effectiveness of shorter courses in selected cases, though larger prospective studies are warranted to confirm non-inferiority across broader populations.

Outcome	Shorter Regimen (N=12)	Longer Regimen (N=18)	Difference [95%CI]	Total (N=30)	p-value
Clinical cure (n (%))	11 (91.7%)	17 (94.4%)	-2.8% [-16.1% to 21.7%]	28 (93.3%)	1.00
90-day Recurrence (n (%))	3 (25.0%)	6 (33.3%)	-8.3% [-41.1% to 24.4%]	9 (30.0%)	0.670
Adverse events (n (%))	0 (0%)	0 (0%)		0 (0%)	-

RES-364: Efficacy and Safety in a Phase 2 Study of Intravenous BV100 Combined with Polymyxin B Versus Best Available Therapy in Adult Subjects with Ventilator-associated Bacterial Pneumonia Suspected or Confirmed to be Due to Carbapenem Resistant Acinetobacter bau

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Background
BioVersys is developing BV100 (rifabutin for infusion) for the treatment of serious infections caused by carbapenem-resistant A. baumannii (CRAB). This report presents a multicenter, open-label, randomized, active-controlled, Phase 2 study to evaluate the efficacy, safety and tolerability, and pharmacokinetics of intravenous BV100 combined with polymyxin B (pmxB) versus Best Available Therapy (BAT) in adult subjects with ventilator-associated bacterial pneumonia (VABP) suspected or confirmed to be due to CRAB (NCT05685615).

Method
Patients were randomized into three trial arms in a 1:1:1 scheme comparing two doses of BV100 (200mg or 300mg q12h) plus pmxB, and BAT. The study population included patients aged between 18 and 82 years with VABP documented by clinical signs showing new or worsening infiltrate. Initial evidence of CRAB infection was obtained using Rapid Diagnostic on a respiratory sample. Treatment duration ranged from 7-14 days. The micro-CRMITT was the primary efficacy population.

Results
BV100 arms showed a significant survival benefit, with combined 14-day and 28-day all-cause mortality in the micro-CRMITT population of 12.5% and 25% for the BV100 arms, respectively, versus 40% and 60% for BAT. The microbiological response at test of cure (ToC), was 75% in the BV100 arms and 50% in the BAT arm. Clinical cure at ToC was 75% in the combined BV100 arms versus 30% in the BAT arm. BV100 treatment was considered safe and well tolerated, with no drug-related SAEs, AE's leading to drug discontinuation or BV100-related AEs.

Conclusions
BV100 plus polymyxin B was generally safe and well-tolerated and demonstrated a substantial survival benefit compared to BAT.

RES-365: The High-level Disinfectant Formulation STEREX ULTRA: From Bench Lab to Infection Prevention and Control, Product of Thailand

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Background
The prevalence of antibiotic resistance among bacteria has been increasing worldwide. In our previous study, we developed a novel cationic disinfectant formulation, STEREX ULTRA, targeting antibiotic-resistant microbial pathogens. This study aimed to develop novel cationic formulation to prevent and control cross-transmission and cross-contamination of antibiotic-resistant microbes.

Method
The antimicrobial activity of the formulation was tested against various antibiotic-resistant pathogens, including methicillin-resistant S. aureus ATCC 25923, vancomycin-resistant enterococci, Acinetobacter baumannii, Pseudomonas aeruginosa ATCC 27853, ESBL-producing Escherichia coli, Klebsiella pneumoniae, Proteus mirabilis, Salmonella enteritidis, Bacillus subtilis, Stenotrophomonas maltophilia, Clostridium perfringens, Cryptococcus neoformans, Trichophyton rubrum, Clostridioides difficile, multidrug-resistant Mycobacterium tuberculosis (MDR-TB), M. tuberculosis H37Rv, and M. avium (Nontuberculous mycobacteria; NTM). Moreover, we investigated additional cationic disinfectant formulations for possible destruction effects of extracellular bacterial DNA, including resistance plasmids carrying blaNDM-1, blaCTX-M, and mcr-1 genes, respectively.

Results
The effects of our formulations were compared to a high-level disinfectant product imported from the European Union. The novel cationic formulation at the concentration of 1.0% exhibited the antimicrobial activity against antibiotic-resistant pathogens within 1 minute of exposure time and 5 minutes for P. mirabilis. Notably, our formulations can eliminate the presence of bacterial DNAs in the mixing reactions with the exposure time of 5-10 minutes. Furthermore, the developed formulation showed no skin irritation (ISO10993-23), skin sensitization (ISO10993-10), mutagenicity (OECD471), and oral toxicity in mice.

Conclusions
We have produced the novel cationic disinfectant formulations effective in killing antibiotic-resistant pathogens along with their resistance genes that may be released upon killing action.

RES-366: Characteristics of Needlestick Injuries Caused by Pen-Type Injector Needles

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Background
In Japan, needlestick injuries from pen-type injectors occur more frequently compared to the United States. Blood contamination is observed on needles after insulin injection, and blood reflux into pen-type injectors can occur, making reuse of injectors prohibited. Therefore, this study aimed to analyze the circumstances under which needlestick injuries from pen-type injectors occur and propose effective preventive measures.

Method
Using data from EPINet 2024 (65 facilities, 6,799 cases, fiscal years 2021-2023), we compared needlestick injuries caused by pen needles (Group P: 426 cases) with those caused by other hollow-bore needles (Group H: 2,967 cases). For each group, we analyzed age, years of experience, occupation, location of occurrence, circumstances of occurrence, and anatomical site of needlestick injury. Continuous variables were tested using the Mann-Whitney U test. Categorical variables were analyzed using the chi-square test.

Results
Regarding the timing of needle use, the proportions of injuries occurring before, during, and after use were 22.9%, 10.4%, and 66.8% in Group P, compared to 6.6%, 44.0%, and 49.4% in Group H, respectively, with Group P showing significantly higher rates of injuries before and after use. Detailed analysis revealed that cases involving used devices left on tables or other surfaces occurred in 12.7% of Group P cases compared to 3.1% of Group H cases, representing approximately a 4-fold higher rate.

Conclusions
Pen-type injector needlestick injuries frequently resulted from improper disposal practices. This safety concern extends beyond healthcare facilities to home care and self-injection settings. Proper disposal education and safety-engineered devices could reduce these risks.

RES-368: Lipidomic Profiling Reveals Interactions Between Uropathogenic Escherichia coli and Actinotignum Schaalii

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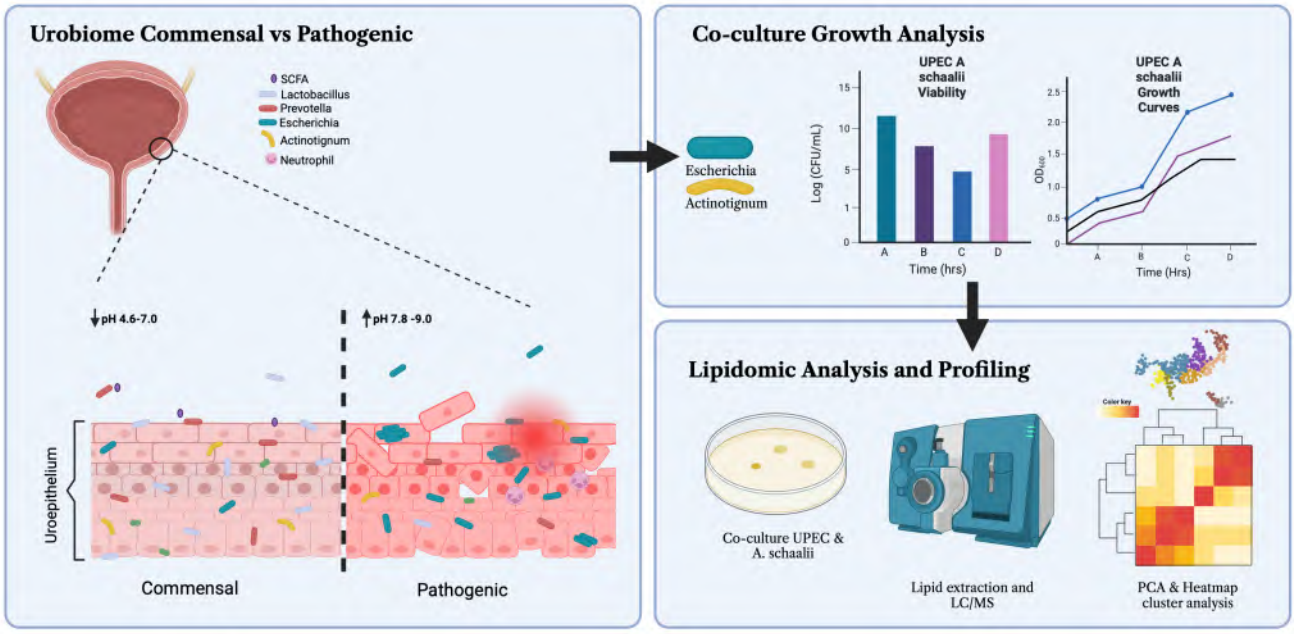
Background
The urobiome—the community of microbes in the urinary tract—plays a crucial role in urinary health and disease. Recent discoveries show its diversity beyond traditional pathogens, revealing interactions that could affect infection risk, pathogen survival, and treatment success. Uropathogenic Escherichia coli (UPEC) remains the main cause of UTIs, but how it behaves in the diverse urobiome is not well understood. This study investigates interactions between UPEC and Actinotignum schaalii, often found together within the urobiome.

Method
UPEC and A. schaalii were cultured in liquid medium, both independently and together, on agar to evaluate their growth ability and interaction behaviors. Our results show that A. schaalii's growth is enhanced in the presence of UPEC. To investigate possible biochemical interactions, an untargeted lipidomic analysis was conducted using high-resolution mass spectrometry and liquid chromatography.

Results
The growth of A. schaalii was enhanced in the presence of UPEC. Co-culture conditions induced significant alterations in the lipidome of both bacterial species. Specifically, our analysis identified 16 distinct lipid features, including species of phosphatidylcholine, phosphatidylethanolamine, and 3-hydroxy decanoic acid. These lipids are critical for maintaining membrane structural integrity and functionality, as well as mediating intercellular interactions. These findings suggest the potential existence of metabolic crosstalk or competitive adaptation mechanisms between the species, which may modulate virulence expression and colonization capacity.

Conclusions
This study offers new insights into interspecies interactions within the urobiome and highlights the value of lipidomics in revealing molecular mechanisms behind microbial coexistence in the urobiome.



RES-369: Direct Antimicrobial Resistance Prediction from Surface-Enhanced Raman Scattering Spectra Using Artificial Intelligence

Hao-Chieh Chiu[3], Wen-Ling Lin[3], Tsai-Wen Wan[2], Yu-Tsung Hunag[4], Yu-Hui Liao[1], Wei-Cheng Chang[1], Nai-Shun Liao[1], Chun-Yi Hsu[1]

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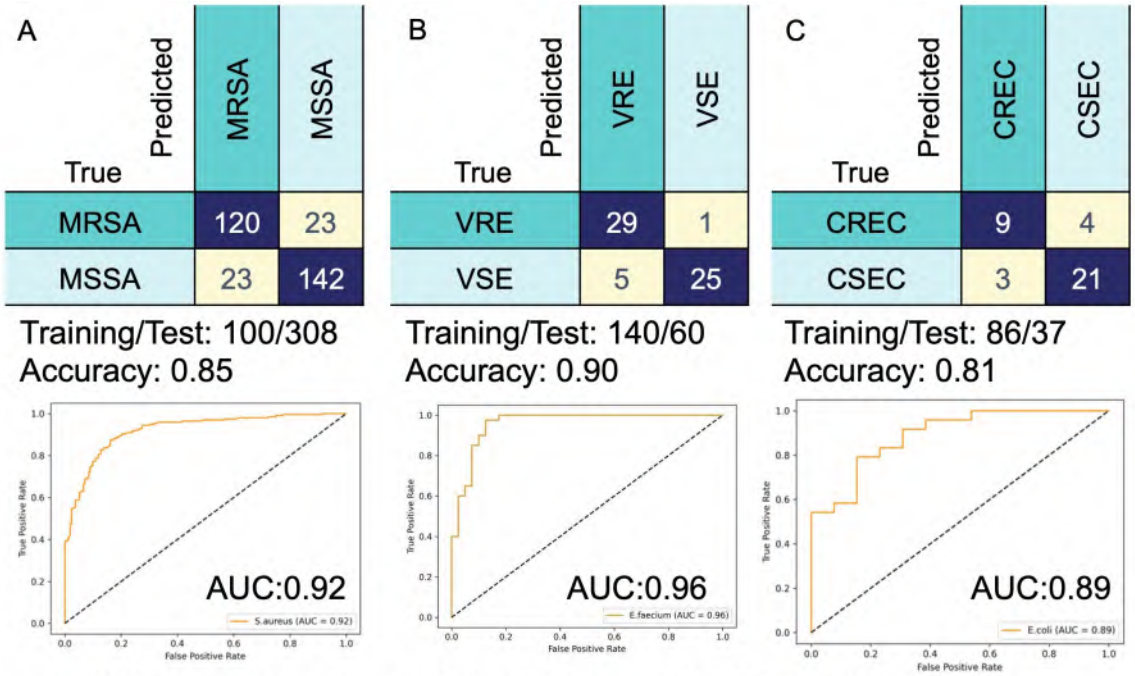
Background
Infectious diseases are the third leading cause of death globally, with bacterial infections accounting for nearly half of the cases. The increasing prevalence of antibiotic-resistant bacteria presents a major public health challenge. While accurate antibiotic selection is essential, conventional culture-based antibiotic susceptibility testing (AST) typically requires up to 72 hours. To address this limitation, we partnered with ITRUST MedTech Inc. to develop a rapid, AI-driven antibiotic resistance prediction system based on Raman spectroscopy.

Method
Clinical isolates of three key drug-resistant bacterial species—methicillin-resistant Staphylococcus aureus (MRSA), vancomycin-resistant Enterococcus (VRE), and carbapenem-resistant Escherichia coli (CREC)—were obtained from the Department of Laboratory Medicine at National Taiwan University Hospital. Species identification and AST were validated using MALDI Biotyper and the VITEK 2 system. Raman spectra were acquired using ITRUST's fully automated high-throughput Raman spectroscope.

Results
A total of 408 S. aureus, 200 E. faecium, and 123 E. coli clinical isolates were collected. Of these, 100 S. aureus, 140 E. faecium, and 86 E. coli strains were used to construct a spectral database and train the AI model, while the remaining isolates were used for validation. Compared with VITEK 2 results, the AI system achieved prediction accuracies and AUCs of 85% (AUC 0.92) for MRSA, 90% (AUC 0.96) for VRE, and 81% (AUC 0.89) for CREC.

Conclusions
This study demonstrates the feasibility of an AI-assisted Raman spectroscopy platform for rapid antimicrobial resistance prediction, with potential to reduce diagnostic delays, support targeted therapy, and improve clinical outcomes.



Antibiotic resistance prediction by the artificial intelligence system.

RES-370: Evaluation of IgM Anti-PGL-1 Levels in Leprosy Diagnosis: Correlation with Bacteriological Index and PCR

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Background
Leprosy, caused by Mycobacterium leprae, is a chronic neglected disease often associated with delayed diagnosis and severe disabilities. Accurate classification into paucibacillary (PB) and multibacillary (MB) forms is essential for effective treatment and transmission control. This study evaluates the diagnostic utility of the IgM anti-PGL-1 serological test in differentiating leprosy types.

Method
A cross-sectional study was conducted on 62 newly diagnosed leprosy patients at Cipto Mangunkusumo and Sitanala Hospitals. Serum IgM anti-PGL-1 levels were measured using ELISA. Bacteriological Index (BI) was determined from slit skin smears, and M. leprae DNA was confirmed via real-time PCR. Statistical analyses included T-tests, Chi-square tests, and ROC curve analysis. The optimal IgM anti-PGL-1 cut-off was determined using the Youden Index.

Results
The optimal IgM anti-PGL-1 cut-off was 170.76 pg/ml (Youden Index: 0.806), with 100% sensitivity and 80.6% specificity. All MB patients (n=32, 100%) had IgM levels above the cut-off, compared to 6 of 30 PB patients (20%). BI ranged from +1 to +5 in MB and was 0 in all PB cases. PCR positivity was 100% in MB and 53.3% in PB cases. There was strong agreement between IgM levels and BI classification (Kappa = 0.838, $p<0.001$). ROC analysis showed high discriminatory power for BI (AUC = 0.984) and IgM anti-PGL-1 (AUC = 0.9098).

Conclusions
Although IgM anti-PGL-1 serology has limitations in diagnosing all forms of leprosy, it serves as a valuable supplementary tool for distinguishing between paucibacillary and multibacillary, aiding in accurate classification and management.

RES-373: Comparison of Two Multiplex Respiratory Virus Panel including SARS-CoV-2: The PowerChek™ Respiratory Virus Panel1/2/3/4 with BioFire® FilmArray Respiratory Panel 2.1 Plus

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Background
Accurate detection of respiratory viruses has become more important since the COVID-19 pandemic, due to changes in seasonal circulation and transmission patterns. We evaluated the performance of PowerChek™ Respiratory Virus Panel 1/2/3/4—Korea's first multiplex PCR covering 15+ viruses including SARS-CoV-2—by comparing it with the BioFire® FilmArray RP 2.1 Plus panel.

Method
Nasopharyngeal swabs were collected from pediatric patients with respiratory symptoms at Kangwon National University Hospital between 2023 and 2024. FilmArray results were used for clinical diagnosis. Residual samples were retested with PowerChek™ after RNA extraction. Diagnostic performance and concordance were analyzed via 2×2 contingency tables.

Results
Among 327 total samples, 223 were positive and 104 negative by FilmArray. Overall concordance between two platforms was 88.07% (288/327), with 39 discordant cases. When excluding HRV/HEV from the analysis, concordance increased to 94.2%.

When using FilmArray as the reference, PowerChek™ showed negative results for 3 cases of adenovirus, 1 case of HCoV-NL63, 1 case of influenza B, 1 case of parainfluenza virus type 3, and 2 cases of influenza A, despite being positive by FilmArray.

Conversely, when PowerChek™ was used as the reference, FilmArray yielded negative results in 22 cases of HRV/HEV, 2 cases of adenovirus, 1 case of HCoV-NL63, and 5 cases of parainfluenza viruses (types 1, 2, 3, and 4), which were positive by PowerChek™.

Among 30 SARS-CoV-2 positive samples, concordance was 96.7%, increasing to 100% when PowerChek™ inconclusive results were considered positive.

Conclusions
The PowerChek™ panel demonstrated comparable diagnostic performance to the FilmArray. Optimization of Ct for HRV/HEV, may further enhance diagnostic concordance.

RES-377: Rapid Differentiation of Colistin-Resistant and -Sensitive Klebsiella pneumoniae by MALDI-TOF MS Protein Profiling

Umaporn Yordpratum

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Background
Colistin-resistant Klebsiella pneumoniae (CRKP) refers to strains that are resistant to colistin, a last-resort antibiotic used for treating severe, multidrug-resistant infections, particularly those caused by carbapenem-resistant K. pneumoniae. The emergence of CRKP poses a critical public health threat due to severely limited therapeutic options and high patient mortality rates. Early and accurate detection of colistin resistance is crucial for effective antimicrobial stewardship and managing potentially life-threatening infections. MALDI-TOF MS (Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrometry) can be a valuable tool for rapid identification of colistin-resistant Klebsiella pneumoniae (CRKP). This technology allows for quick detection of resistance patterns, potentially guiding timely and appropriate antibiotic treatment.

Method
In this study, we investigated the protein patterns of K. pneumoniae by analyzing 30 colistin-sensitive and 30 colistin-resistant isolates using MALDI-TOF MS. A decision tree algorithm was used to identify the most significant peaks for differentiation.

Results
Of the 1095 raw peaks detected, twelve were identified as significant (m/z 4772.98, 5144.17, 2689.48, 3580.16, 4060.76, 4439.26, 4343.17, 4708.23, 2507.79, 2517.38, 7648.29, and 8665.42). These twelve peaks were further analyzed using Principal Component Analysis (PCA), and the peaks at m/z 4772.98 and 4343.17 were identified as potential biomarkers for discriminating between colistin-resistant and colistin-sensitive K. pneumoniae.

Conclusions
This study provides significant protein biomarkers that allow for the differentiation of colistin-resistant and colistin-sensitive K. pneumoniae. This information could aid in the future development of rapid identification methods for CRKP

RES-378: Evaluation of In Vitro Efficacy of Aztreonam-Nacubactam and Cefepime-Nacubactam Against Clinical Isolates of Stenotrophomonas maltophilia

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Background
Stenotrophomonas maltophilia harbors L1 metallo-β-lactamase and L2 serine β-lactamase, conferring resistance to most β-lactams. Diazabicyclooctanes (DBOs) such as nacubactam (NAC) have intrinsic antibacterial activity via penicillin-binding protein 2 (PBP2) binding, potentially enhancing β-lactam efficacy even against metallo-β-lactamase (MBL)-producing organisms. The in vitro activity of aztreonam (ATM)-NAC and cefepime (FEP)-NAC against S. maltophilia has not been previously evaluated.

Method
We tested 53 blood culture isolates of S. maltophilia (2012–2024, Keio University Hospital, Tokyo) by broth microdilution per CLSI M100 (35th ed.). NAC was combined with ATM or FEP at a 1:1 ratio. MIC50/MIC90 values were determined, and differences with/without NAC were analyzed using the Wilcoxon signed-rank test after log transformation. Whole-genome sequencing confirmed sequence types, clonality, and β-lactamase genes.

Results
Most isolates (94.3%) harbored both blaL1 and blaL2. MIC50/MIC90 values (μg/mL) were >128/>128 for ATM, 32/64 for FEP, >128/>128 for NAC alone; with NAC, ATM MICs fell to 8/16 and FEP to 4/16. Both combinations significantly reduced MICs versus monotherapy ($p<0.001$). Median fold-reduction was greater for ATM (32-fold) than FEP (8-fold) ($p<0.001$). Using a provisional susceptibility breakpoint of 8 μg/mL for Enterobacterales, 81.1% of isolates were susceptible to FEP-NAC.

Conclusions
ATM-NAC and FEP-NAC showed substantial in vitro activity against S. maltophilia blood isolates. Given the desire to preserve RESERVE agents like ATM, FEP-NAC—using a WATCH category drug—may represent a promising alternative, warranting further pharmacokinetic, pharmacodynamic, and in vivo evaluation.

RES-379: Analysis of Patients with Clostridioides difficile Infection in a Hospital

Yi-Ching Huang

Jen-Ai Hospital, Taichung

Background
Clostridioides difficile infection (CDI), a common healthcare-associated infection, associated with antimicrobial use, can cause mortality and morbidity in older hospitalized patients. The clinical manifestations range from asymptomatic carriage to fulminant disease. In Taiwan, the incidence of CDI was 1.1-7.3 per 10,000 patient-days and the overall in-hospital mortality was 20-26.2 %. The recurrence rate of CDI in medical centers was 7.2-10.9% in Taiwan.

Method
The data was from the records of medical charts and microbiology laboratory at Jen-Ai Hospital, Taichung, a 600-bed regional teaching hospital in central Taiwan. This study enrolled patients with the presence of diarrhea and at least one toxin gene testing from 1 January 2023 to 31 December 2024. The following information was collected: age, gender, chronic diseases, antimicrobial treatment, length of hospital stay, the use of proton pump inhibitors, and outcomes.

Results
Totally 200 patients were enrolled, and 22 patients had positive result of toxin gene testing. The average age was 72 years old (80% were over 65). The most common comorbidities included diabetes mellitus, end-stage renal disease, cancer. More than half of the patients received vancomycin, and the others received metronidazole or no treatment.

Conclusions
In this retrospective study, patients with CDI were mostly elderly, with chronic diseases, prior use of antibiotics or recent hospitalization. Most patients had nonsevere CDI and good response to treatment. The recurrence rate was 13%.

RES-380: Antimicrobial Potential of Polyphenol-Containing Medicinal Plants: A Study on the Antibiotic-Resistant Staphylococcus aureus from Cattle and Poultry Farms

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Background
Livestock-associated antibiotic-resistant Staphylococcus aureus poses significant implications for animal and public health. We assessed the prevalence and resistance patterns of S. aureus in cow and poultry farm samples and examined the efficacy of medicinal plant extracts on their growth.

Method
We selected poultry and cow farms based on their hygiene and housing status through a survey. Subsequently, we collected 250 samples from the farm environment, poultry oral mucosa, cow nasal passages, and human swabs, enriched them in nutrient broth, isolated S. aureus on Mannitol Salt Agar, and confirmed it with a coagulase test. The cefoxitin disk diffusion test was used to assess antibiotic resistance patterns. The methanolic extract of plants was then evaluated for its effect on S. aureus growth by measuring inhibition-zone diameters.

Results
Of 250 samples, 166 were confirmed as S. aureus through coagulase testing (PR:0.664, 95%CI:0.71,0.72). Poultry showed high prevalence of S. aureus (PR:0.76, 95%CI:0.64, 0.88). However, the farm workers recovered 36% (PR:0.36, 95%CI:0.23, 0.49). The prevalence was significantly different between rural and urban farms ($p<0.001$) at 5 % significance level. About 19.87% were resistant to cefoxitin (<19-mm inhibition zone) (PR:0.2, 95%CI:0.17, 0.22) according to CLSI. The polyphenol content of Centella asiatica, Scoparia dulcis, Heliotropium indicum, Moringa oleifera, and Musa acuminata were 281.5, 278.1, 269.3, 305.4 and 215.49 µg/ml GAE, respectively. The Centella asiatica and Moringa oleifera showed the most potent inhibitory effects (14±1.2-mm and 16±1.6-mm zones) against the resistant S. aureus ($p>0.001$).

Conclusions
Although the plant extract showed potential activity, further molecular-based studies are warranted to confirm its applications.

Table 1: Average inhibition zone (mm) of the medicinal plant extracts on the antibiotic-resistant *S. aureus*

Name of isolate	Origin	Average diameter of inhibition zone (mm)				
		Centella asiatica	*Scoparia dulcis*	*Heliotropium indicum*	*Moringa oleifera*	*Azadirachta indica*
S. aureus	Animal	14±1.2[a]	10.6±0.9[b]	12.5±1.4[a]	16±1.6[a]	12.5±1.6[a]
	Environment	13.5±2.3[a]	11.3±1.8[b]	12.3±2.1[a]	15.5±1.6[a]	12.3±2.4[a]
	Worker	13.3±1.2[a]	10.6±0.8[b]	10.6±1.4[b]	15.5±1.2[a]	10.6±0.6[b]

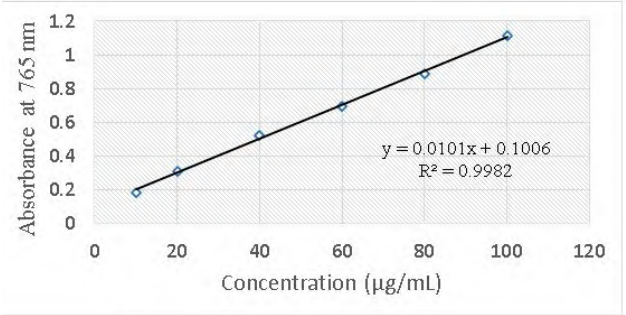

Figure 1: Standard curve of GA

Table 2: Polyphenol content of selected medicinal plants

Name of plant	Scientific name	Total phenolic content (µg/ml GAE)
Thankuni	*Centella asiatica*	281.52 ± 1.10[a]
Misri dana	*Scoparia dulcis*	278.16 ± 1.25[a]
Hatisur	*Heliotropium indicum*	269.25 ± 1.40[a]
Sajna	*Moringa oleifera*	305.40 ± 1.80[b]
Neem	*Azadirachta indica*	276.57± 1.25[a]

RES-386: Influenza in the Philippines: Age-Related Trends in Hospitalization, Treatment, and Mortality

Janice Caoili, Hylee Kwin Rubio, Gina De Guzman Betito

Makati Medical Center

Background
Limited influenza data exist in the Philippines; recent access to rapid antigen and multiplex PCR tests for influenza has improved diagnostic confirmation in hospitals.

Method
This retrospective review analyzes influenza cases at a tertiary care center in the Philippines from January 1, 2023, to August 5, 2025.

Results
Of 13,745 individuals tested, 2,949 (21.5%) were positive for influenza. Adults comprised a significantly larger portion of cases than children (1,774 vs. 1,175; $p < 0.001$). There was no overall sex-based predominance (51% female vs. 49% male), but adult cases were more likely to be female compared to pediatric cases (56% vs. 44%; $p < 0.0001$).

Hospitalization occurred in 559 (19%) cases, with adults admitted more frequently than children (375/1,774 vs. 184/1,175; $p < 0.001$). Oseltamivir was administered to 87% of admitted patients, with higher usage in adults (91% vs. 78%; $p < 0.00001$). Antibiotics were given to 52% of hospitalized cases, with no significant difference between children and adults ($p = 0.08$).

Pneumonia was detected via chest radiography in 11% of admitted cases, with no significant difference between age groups overall ($p = 0.48$). However, children aged 0–6 years were more likely to have pneumonia than older children ($p < 0.001$). Adults over 90 had the highest pneumonia rate (29%) and mortality rate (11.8%; $p < 0.001$). Overall mortality was low at 1%, occurring exclusively in adults.

Conclusions
This review highlights key demographic patterns, treatment practices, and outcomes among hospitalized influenza cases, with age emerging as a critical factor in severity and mortality.

Table 1: Demographics, Treatment and Mortality Among Hospitalized Flu Cases at Makati Medical Center, Philippines from January 1, 2023 to August 5, 2025

Age Range in Years	Flu Cases	% of Total flu cases	Female	% Female	Given Oseltamivir	% Given Oseltamivir	Given Antibiotics	% Given Antibiotics	Pneumonia on Chest Xray	% With Pneumonia on Chest Xray	Expired	% Expired
0-6	106	19%	39	37%	81	76%	67	63%	20	19%	0	0%
7-12	46	8%	22	48%	36	78%	25	54%	2	4%	0	0%
13-18	30	5%	14	47%	24	80%	13	43%	0	0%	0	0%
Pedia	182	33%	75	41%	141	77%	105	58%	22	12%		0%%
19-30	69	12%	43	62%	62	90%	22	32%	5	7%	1	1%
31-60	131	24%	69	53%	121	92%	51	39%	11	8%	0	0%
61-90	158	28%	80	51%	144	91%	99	63%	17	11%	4	3%
>90	17	3%	9	53%	15	88%	15	88%	5	29%	2	12%
Adult	375	67%	201	54%	342	91%	187	50%	38	10%	7	2%
All Cases	557	100%	276	49.6%	483	87%	292	52%	60	11%	7	1%

RES-388: Identification of Key Genetic Targets for Tuberculosis Diagnosis: Advancing Molecular Detection within a One Health Approach

Siti Kurniawati

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Background
Introduction: Tuberculosis (TB) is one of the infections caused by the Mycobacterium tuberculosis complex (MTBC) and remains a major zoonotic (animal-to-human) disease. Current diagnostic methods often lack the speed, specificity, and cross-species applicability required for early detection. This study aimed to identify and characterize genetic targets for the development of molecular diagnostics. As follows, four essential genes, leuS (leucyl-tRNA synthetase), ku (DNA repair protein), gyrB (DNA gyrase subunit B), and rpoB (RNA polymerase β-subunit), were selected based on their critical biological functions, high conservation across MTBC species, and diagnostic relevance.

Method
Primer pairs were designed using Clone Manager software using NCBI reference sequences NC_000962.3 and aligned using bioinformatics tools to identify conserved regions. Primer pairs were confirmed using conventional PCR using DNA from M. tuberculosis H37Rv and DNA samples.

Results
All four gene targets have shown the specific amplicons, and no band was observed in Non-Tuberculous Mycobacteria (NTM). Sequencing also confirmed 100% identity with the reference genome of M. tuberculosis H37Rv. The leuS, ku, gyrB, and rpoB genes showed strong indication of clarity, indicating their potential as reliable genetic markers for TB diagnosis.

Conclusions
This study successfully identified and verified leuS, ku, gyrB, and rpoB as potential molecular targets for tuberculosis diagnosis. Their high specificity could be developed for rapid diagnostics, such as nucleic acid lateral flow assays. These findings advance the development of cross-sectoral TB diagnostic tools in alignment with One Health strategies. A broader evaluation involving multiple geographic regions is recommended.

RES-389: Trends in CLABSI Rates and Microbiological Patterns in an Adult Critical Care Unit of a Tertiary Teaching Hospital in an Upper-Middle-Income Country

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Background
Patients in critical care units are at high risk of acquiring central line-associated bloodstream infections (CLABSIs), which significantly contribute to prolonged hospital stays, complicated treatment course, increased healthcare costs, and heightened morbidity and mortality. This study aimed to assess the trend and predominant pathogen contributing to CLABSI incidence in adult critical care units over three years.

Method
We conducted a prospective surveillance study from January 2022 to December 2024 in the general, neurological, and cardiac ICUs, including all patients with central venous catheters. CLABSI was defined using CDC/NHSN criteria, and incidence rates were calculated per 1,000 catheter line days. Microbiological data were analyzed from confirmed CLABSI cases.

Results
A downward trend in CLABSI rates was observed, where Neurological ICU rates decreased by 56.7% (from 10.4 to 4.5), Cardiac ICU by 67.3% (from 7.96 to 2.6), and General ICU by 46.3% (from 7.41 to 3.98) per 1,000 line days between 2022 and 2024. The total number of CLABSI cases is 131 with an associated mortality rate of 39.7%. The predominant causative microorganisms isolated from CLABSI episodes were Gram-negative bacteria (54.9%), followed by Gram-positive bacteria (22.9%) and Candida species (22.1%).

Conclusions
The findings underscore the importance of robust surveillance, embedded infection control and prevention initiatives to prevent CLABSI in critical care settings. The predominance of Gram-negative organisms highlights the need for ongoing surveillance and robust antimicrobial stewardship programs to address rising antimicrobial resistance. Continued vigilance is essential to reduce the burden of CLABSI and improve patient outcomes in critical care settings.

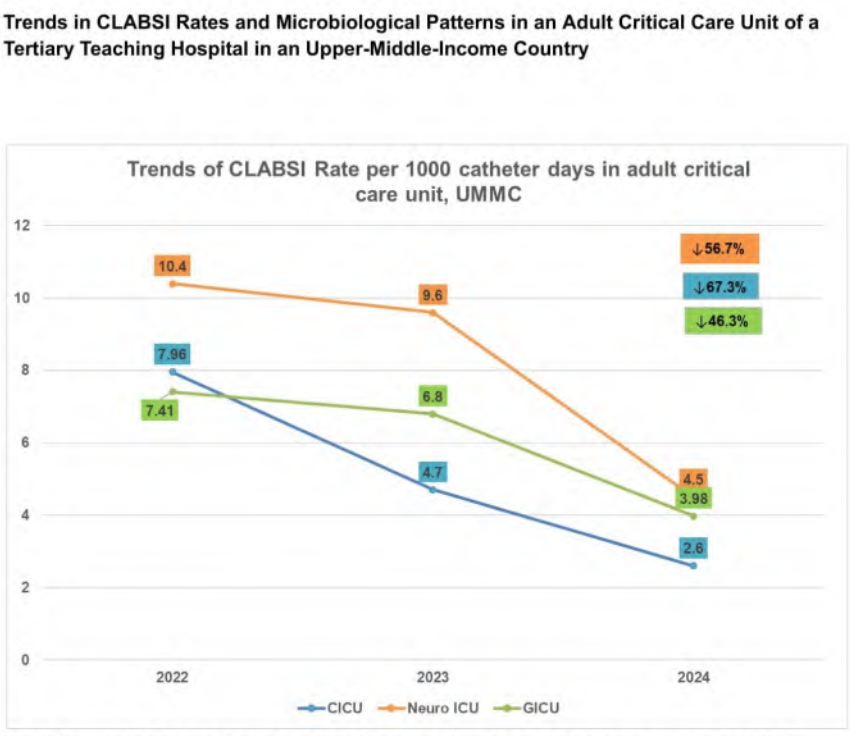

FIg 1: Trends in CLABSI Rates per 1000 Catheter days in an adult critical care unit, UMMC.

RES-390: High Incidence of Antibiotic Resistance and Biofilm Formation Among the Bacteria Isolated from Wound Infections at a Tertiary Care Hospital of Nepal

Dristi Halwai, Pratima Shah, Rinku Sah

B.P Koirala Institute of Health Sciences

Background
The wound infections can be monomicrobial or polymicrobial depending on the nature of injury and wound. The acquisition of drug resistance by the pathogenic bacteria has posed a serious challenge for the optimal wound management leading to delayed wound healing. Therefore, this study was conducted to determine the antimicrobial resistance among bacterial pathogens and biofilm formation.

Method
This is a descriptive cross-sectional study conducted at Department of Microbiology for six months. A total of 1064 pus samples from wound infections cases were obtained in the Microbiology Laboratory. Culture and bacterial isolates were identified as described by American Society for Microbiology. Antimicrobial susceptibility testing and biofilm formation was done following Clinical and laboratory standards institute guidelines.

Results
A total of 1064 pus samples were included in the study among which bacterial growth was observed in 664 samples with culture positivity of 61%. Staphylocooccus aureus (45.48%) was the most common organism followed by Escherichia coli (27.10%), Klebsiella pneumoniae (13.25%) and Acinetobacter baumanii (6.32%). Multidrug resistant (MDR) isolates accounted for 48% and 25% were found to be extensively drug resistant (XDR). Among WHO critical and high priority pathogens such as carbapenem resistant Acinetobacter accounted for 39% and methicillin resistant Staphylococcus aures accounted for 41%, respectively. A total of 35% of bacteria isolated from wound infections were biofilm formers.

Conclusions
High-level antimicrobial resistance was observed in wound infections with alarming incidence of MDR and XDR organisms. Regular surveillance should be carried out to guide the empirical management of wound infections.

RES-391: Prevalence, Antimicrobial Resistance, and Virulence Profiling of Hypermucoviscous Klebsiella pneumoniae in a Cardiac Tertiary Care Hospital in Kathmandu, Nepal

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Tribhuvan University

Background
Hypermucoviscous Klebsiella pneumoniae (hmvKp) is an emerging pathotype associated with severe infections and enhanced virulence, posing growing threat due to multidrug resistance. This study aimed to determine the prevalence, antimicrobial resistance patterns, and virulence gene distribution of hmvKp in a cardiac tertiary care hospital in Kathmandu, Nepal.

Method
A total of 1576 clinical samples were processed using standard microbiological protocols. K. pneumoniae isolates were identified and screened for hypermucoviscosity using the string test. Antimicrobial susceptibility testing was conducted via the Kirby-Bauer disk diffusion method. Virulence genes were analyzed by PCR in 35 multidrug-resistant (MDR) K. pneumoniae isolates.

Results
Of 1576 samples, 351 (22.27%) were culture-positive, with K. pneumoniae being the most frequently isolated organism (22.51%). Sixteen (20.25%) of the 79 K. pneumoniae isolates exhibited a hypermucoviscous henotype. Most isolates originated from respiratory samples and ICU patients, with higher infection rates among neonates and elderly individuals. High resistance was observed to cephalosporins, carbapenems, and fluoroquinolones, while colistin remained highly effective (98.73%). MDR was present in 81.01% of K. pneumoniae isolates, including 87.5% of hmvKp and 79.37% of non-hmvKp strains ($p = 0.367$). Virulence gene analysis showed irp2, entB, and terW were most prevalent, with rmpA significantly associated with hmvKp strains ($p < 0.001$).

Conclusions
Hypermucoviscous K. pneumoniae is present in cardiac care settings in Kathmandu, Nepal, exhibiting high multidrug resistance and notable virulence gene profiles. The strong association of rmpA with hmvKp strains highlights the need for robust molecular surveillance and targeted antimicrobial stewardship to prevent public health threats.

RES-A01: A Review of Common Sources of Error in Bacteriology External Quality Assessment Programs

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Introduction
The Royal College of Pathologists of Australasia Quality Assurance Programs (RCPAQAP) delivers External Quality Assessment (EQA) services to laboratories worldwide, supporting the reliability of diagnostic methods and promoting excellence in laboratory practice. While laboratory concordance rates remain high overall, this study explores the root causes of discordant results in 2024 and reviews how laboratories responded to these findings.

Presentation
Our analysis identified three primary sources of discordance: failure in culturing the pathogen, incorrect organism identification, and transcription errors during sample processing and reporting. Notably, in the 2024 Bacteriology: Urine program, an overall 5% discordance rate was recorded due to unsuccessful organism identification at the species level (44%), incorrect pathogen identifications (20%), unsuccessful culture (20%), and reporting transcription errors (16%). In response to these outcomes, only two laboratories requested repeat samples, and one requested a reassessment.

Similarly, participants in the Bacteriology: Skin/Eye/Ear program reported up to 35 discordant results (a total 5% discordant rate), with 97% of them stemming from the misidentification of the pathogen. Non-routine opportunistic pathogens such as Mycobacterium species posed the most significant challenge in this context. For routine pathogens such as MRSA, some participants were unsuccessful in reporting the identification of the pathogen to a species-level required for concordance.

Conclusion
These findings underscore the critical role of EQA in detecting systemic issues in laboratory diagnostics and guiding targeted improvements. By highlighting common pitfalls and follow-up practices, this analysis provides actionable insights to help laboratories enhance diagnostic accuracy and overall quality.

RES-A02: Clinical and Microbiological Profile of Myroides Species Isolated from Urinary Tract Infections: A Retrospective Study from North India

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Background
Myroides species are gram negative bacilli, prevalent in the environment and cause a variety of illnesses, including urinary tract infections (UTI), sepsis, meningitis, cholecystitis, pneumonia, and soft tissue infections, particularly among immunocompromised people. These are usually multi-drug resistant. This study sought to establish the clinical profile, underlying comorbidities, and antibiotic susceptibility of Myroides isolates derived from nosocomial UTI cases.

Method
We retrospectively analysed cases admitted at a tertiary care centre and diagnosed with Urinary tract infection due to Myroides species. Case records of patients with urine culture positive for Myroides were analyzed for demographic data, clinical characteristics, management and clinical outcomes.

Results
Between January 2019 and July 2025, 53 positive Myroides species cultures were identified from urine culture. The maximum number of cases (50.9%) were from the Urology and General medicine. The average age (mean) of patients was 44 years. All patients had catheters inserted. All of the isolates were multidrug resistant. Minocycline sensitivity was done in 8 patients and all were sensitive (100%). Co-trimoxazole was sensitive in 8 patients (15%) out of 53 isolates.

Conclusions
Myroides species are rare pathogens that can cause urinary tract infections in immunocompromised and catheterised patients. Minocycline followed by co-trimoxazole has been shown to be effective in treating such infections.

RES-A03: Elizabethkingia meningoseptica Outbreak Investigation and Management at a Regional Hospital in Southern Taiwan

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Background
Elizabethkingia spp. is found in hospital environments. Certain venerable patients are at high risks of acquiring E. meningoseptica infection, which significantly increased mortality due to the characteristics of multidrug resistance.

Method
During 2023 Aug. to Sep., there were 172 samples collected from sputum, blood, bronchial lavage, twenty-six yielded E. meningoseptica, tracing back from Jan to July, only sixteen positive in 377 sample (<0.001), which depicted an outbreak in adult ICU. Among three cases of hospital-associated infection, there were two catheter-related bacteremia, the remaining one was pneumonia complicated with bacteremia. Total twenty-one spots were surveyed and specimens collected. Infection control nurse also observed the hand hygiene compliance of ICU stuffs.

Results
Connect tubing of ventilator and humidified wastewater collector were positive for E. meningoseptica. Incorrect method to clear the wastewater in tubing, lack of collector in each ventilator, wearing gloves to working station were observed. Also feeding equipment and nebulizing tools are placed too close to water tanks which make them prone to contamination. Infection control measures were instituted:
1. Environment disinfect twice a day.
2. Relocated feedingand nebulizing equipment.
3. Implant and emphasized the compliance of VAP, CABSI bundle and hand hygiene.
4. Using adequate length of tubing and collector; clearance the humidified wastewater correctly.
5. Antimicrobial stewardship program promotion.

Conclusions
We reported an E. meningoseptica outbreak in a reginal hospital adult intensive care unit and how we efficiently tackle by multidisciplinary infection control measurement.

Aggressive efforts to identify possible source, enhanced staff hand hygiene and prompt antimicrobial stewardship are recommended.