



2024 GERM Poster Session Presenters and Abstracts



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Katherine Olivia Yanes is an MD/PhD candidate at the University of California, Irvine, focusing on the impact of *Toxoplasma gondii* infection on the host immune response in Alzheimer's disease. She earned her BA in Biochemistry from Wellesley College and completed her undergraduate thesis research on host-parasite interactions during Cryptosporidium infection at Tufts University. Following her undergraduate education, she engaged in research as an Intramural Research Trainee at the National Institutes of Health in the Laboratory of Parasitic Diseases, Molecular Parasitology Section. There, she studied the role of *T. gondii* secreted proteins in modulating host virulence. Yanes is broadly interested in infectious diseases, especially parasitic diseases of the nervous system, and how infectious agents control host immune response. Beyond her research, Yanes is deeply committed to science outreach and training. Past and present work include mentoring undergraduate research students, organizing diversity and equity initiatives as Chair of the Equity Committee for the UCI Medical Scientist Training Program (MSTP), and serving on the MSTP Admissions Committee. Yanes aims to pursue a career in neuroinfectious disease research as a physician scientist.

Abstract

Toxoplasma gondii Drives Immune Cell Recruitment to Amyloid Plaques in Alzheimer's Mice Through a Partially TREM2-Dependent Mechanism

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Background: *Toxoplasma gondii* is an intracellular foodborne parasite infecting approximately 30% of the global population. *T. gondii* infects the host's brain, where it induces a neuroimmune response. In Alzheimer's model mice, *T. gondii* infection is known to result in amyloid plaque reduction, but it is unclear whether peripheral cells are recruited to plaques during infection and by what mechanism. Hypothesis: *T. gondii* infection recruits peripheral immune cells to amyloid plaques in the brain, contributing to plaque reduction.

Methods: 3-month-old 5xFAD (AD model) mice were injected with 200 *T. gondii* tachyzoites or PBS (control). After 2-6 weeks, brains were harvested and analyzed by flow cytometry and microscopy to characterize infiltrating immune cells. The extent of peripheral immune cell localization to plaques was assessed using 5xFAD bone marrow chimeric mice. Infection of 5xFAD TREM2 KO mice was used to determine the role of TREM2 in these processes.

Results: *T. gondii* infection reduced amyloid plaque volume in 5xFAD mice, whereas colocalization of amyloid with myeloid cells and CD68 (phagocytic marker) increased after infection. Bone marrow chimera experiments demonstrated that infection recruited peripheral immune cells into the brain and near plaques. TREM2 was required for the increased myeloid cells surrounding plaques but not for immune cell recruitment to the brain during *T. gondii* infection of 5xFAD mice.

Conclusions: *T. gondii* infection reduced amyloid plaques, partly due to the recruitment of peripherally derived immune cells and activated microglia near plaques. Future studies will focus on the effect of *T. gondii* infection in human AD patients.



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Maximillian Wu is currently a fourth-year medical student at SUNY Upstate Medical University. He received his BS in global and public health sciences with a Minor in health policy at Cornell University. Wu was a 2022 GERM Program award recipient, working with Dr. Elizabeth Asiago-Reddy on determining the viability of MRSA nares PCR/culture as a screening tool post initiation of systemic anti-MRSA antibiotic therapy. For this research he was also awarded SUNY Upstate's College of Medicine summer research fellowship. He is interested in a career in Internal Medicine and is currently in the process of applying to residency.

Abstract

Viability of Methicillin-Resistant *Staphylococcus aureus* (MRSA) Nares Testing as a Screening Tool Post Initial Days of Systemic Anti-Staphylococcal Antimicrobial Therapy

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Background: Methicillin-resistant *Staphylococcus aureus* (MRSA) nasal colonization is closely associated with invasive MRSA disease. Negative results from MRSA culture or DNA screen of the nares have been shown to strongly predict the lack of MRSA isolation at other cultured body sites.⁴ However, the typical duration of positive DNA tests for MRSA in the nares of patients receiving systemic anti-MRSA antimicrobials is unknown.

Methods: Eligible patients were adult inpatients with an initial positive MRSA nares DNA test or culture <36 hours after their initial dose of a systemic anti-MRSA antibiotic and who had continually received ≥ 1 anti-MRSA systemic antibiotic for a duration of 48-96 hours in standard doses. Follow-up swabs were collected from consented patients at a goal timepoint of 72 hours (accepted range 48-96 hours) post anti-MRSA antibiotic initiation.

Results: 113 patients were included. The median time between initial and follow-up MRSA nares samples was 66.1 hours. On repeat testing, 100 (88.50%) of the 113 samples had a positive MRSA nares result. There was no significant association between positive follow-up test and time on anti-MRSA antibiotics, time between baseline and follow-up MRSA nares testing, type of antibiotic received, nor any patient characteristics in single or multivariate logistic regression.

Conclusions: Our results demonstrate that MRSA DNA nares positivity persists in close to 90% of patients after 48-96 hours of continuous systemic administration of anti-MRSA antibiotics. These results suggest that MRSA nares swabs can still be used as a screening tool even after the patient has received multiple days of systemic anti-MRSA therapy.



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Samuel Wilk is a third-year medical student at Tufts University School of Medicine. He received his BS in biology and community health from Tufts University. Wilk's research interest is in the field of antimicrobial resistance with a focus on policies and programs in jails and prisons. He has a specific interest in implementing improved systems of equitable access to penicillin allergy de-labeling in jails and prisons

Abstract

Penicillin allergy prevalence and impact on antimicrobial prescribing in Hennepin County jail

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Background: Inappropriate antibiotic prescriptions drive the threat of increasing antibiotic resistance. Patients labeled with a penicillin allergy often receive more broad-spectrum antibiotics. Our study aims to identify predictors of penicillin allergy and differences in rates of antibiotic prescription.

Hypothesis: We hypothesized that female sex, older age, and white race would be associated with higher likelihood of penicillin allergy. We also hypothesized penicillin allergy would be associated with increased prescription *Clostridioides difficile* associated antibiotics.

Methods: We conducted a retrospective cohort study of the Hennepin County Jail that included incarcerated patients who received antibiotics from 2020 to 2022. We performed univariable and multivariable logistic regression analyses to evaluate (1) the demographic factors associated with penicillin allergy and (2) the association between penicillin allergy and the prescription of antibiotics with the highest risk of *Clostridioides difficile* infection (CDI). Both analyses were adjusted for age, race, ethnicity, and country of origin.

Results: After race-based exclusion criteria, the final study cohort consisted of 1,832 individuals, with a penicillin allergy prevalence of 9.2%. In multivariable regression analysis, individuals with penicillin allergies were more likely to be female, White non-Hispanic, or American Indian/Alaska Native. After adjusting for multiple factors, individuals with penicillin allergy had significant increased odds of receiving antibiotics posing the highest risk for CDI.

Conclusions: This study highlights the predictive factors associated with penicillin allergy and the consequences of these allergies. No studies to date have shown the increased prevalence of penicillin allergy in Native American/Alaskan Native populations. This drives new focus for antimicrobial resistance and allergy desensitization.



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Joshua Vogel is a MD candidate at Yale School of Medicine (YSM). He received his BS in cell & molecular biology from Missouri State University (MSU). He was selected for the Postbaccalaureate Intramural Research Training Award program at the National Institute of Allergy and Infectious Diseases (NIAID) at the National Institutes of Health. Vogel's research interests include evaluation of the clinical impact of diagnostic tests, with a particular interest in the impact of microbial diagnostics on antimicrobial stewardship. He has previously performed basic science research using virology, bacteriology, and molecular biology techniques, studying HIV-1, *Mycobacterium tuberculosis*, and HSV-2 under the respective mentorship of Dr. Amy Hulme (MSU), Dr. Jeffrey Cirillo (Texas A&M Health Sciences Center), and Dr. Jeffrey Cohen (NIAID). Vogel serves as codirector of the Latent Tuberculosis Initiative at HAVEN Free Clinic, YSM's student-run free clinic for uninsured patients in New Haven, CT. Vogel plans to pursue internal medicine residency and aspires to make an impact through patient care, teaching, and research.

Abstract

Impact of a Blood Culture PCR Assay in Transplant Recipients

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Background: Blood culture-based multiplex polymerase chain reaction (PCR) assays reduce time to species identification, antimicrobial susceptibility testing (AST), and appropriate therapy in patients with bloodstream infection (BSI). No study has specifically evaluated these outcomes in recipients of solid-organ (SOT) or bone marrow transplants (BMT).

Hypothesis: BioFire Blood Culture Identification (BCID2) multiplex PCR assay will identify >80% of species and >90% of tested AST patterns earlier than conventional testing among transplant recipients with BSI. BCID2 will lead to clinically significant earlier adjustment of antimicrobial therapies in the general population.

Methods: We performed a retrospective chart review of adult transplant recipients at our center with a monomicrobial BSI tested with BCID2 within 5 years of SOT/BMT in a 14-month period. Timepoints of BCID2 results and conventional testing were collected. The first antibiotic change after Gram stain was classified as escalation or de-escalation.

Results: Of 52 BSI episodes, BCID2 identified 47/52 species (90%); all unidentified species were off-target. BCID2 correctly predicted 41/43 (95%) of on-target AST phenotypes (Table 1). Species and AST results were significantly earlier by BCID2 than conventional testing (Table 2). Of 45 antimicrobial changes made based on blood culture results, BCID2 informed 25 and led to most (13/16) escalations while most AST-based (13/15) adjustments were de-escalations. Escalations occurred earlier than de-escalations.

Conclusions: BCID2 provided species and resistance information earlier than conventional testing, leading to appropriate modifications in antimicrobial therapy. Evaluation of clinical outcomes associated with early institution of appropriate therapy for BSI in transplant recipients is warranted.



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Palak Shah is a second-year medical student at Boston University Chobanian and Avedisian School of Medicine. She received her BA in Molecular and Cellular Biology at Harvard University and subsequently worked as a Clinical Research Coordinator at Massachusetts General Hospital (MGH) to develop and evaluate point-of-care diagnostic tests for sexually transmitted infections. She also supported the development of a clinical registry on mpox at MGH and extended this work as a medical student to examine mpox vaccination as a pathway for linkage to HIV prevention and care, for which she received a GERM fellowship. Palak is interested in infectious diseases and global health. She aims to become a physician-investigator to continue building tools that strengthen diagnostic capacity, improve estimates of infectious disease burden, and guide policy-making to reduce health disparities.

Abstract

Linkage to HIV Prevention among Individuals Seeking Mpox Vaccination

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Background: Mpox vaccination may provide an opportunity for linkage to HIV prevention. We examined linkage to PrEP and HIV testing after mpox vaccination in an STI clinic.

Hypotheses: Individuals attending vaccine-only visits will differ demographically from those vaccinated during non mpox clinic visits. Mpox vaccination will facilitate linkage to HIV prevention.

Methods: We used medical record data to categorize individuals vaccinated for mpox July 2022-April 2024 and not known to be on PrEP into cohorts by first vaccination visit type: vaccine-only visit (Cohort 1) or non mpox visit (Cohort 2). We compared demographics between cohorts and determined linkage to PrEP and HIV testing within 90 days.

Results: In the study period, 3290 people received a first vaccine dose (median age 34y, Black 6.0%, Hispanic 13.1%). Among 2755 people not on PrEP, those in Cohort 2 (non-mpox visits, N=240) were younger than those in Cohort 1 (vaccine-only visits, N=2515; median 30y vs 34y; $p<0.0001$) and were more likely to identify as Hispanic (25.7% vs 12.2%; $p<0.0001$). In Cohort 2, 151 (63%) were prescribed PrEP and 208 (87%) received HIV testing concurrently with vaccination. Overall, 44 (1.6%) were prescribed PrEP within 90 days after vaccination: 30 (1.2%) and 14 (5.8%) in Cohorts 1 and 2, respectively, and 178 (6.5%) received HIV testing: 99 (3.9%) and 79 (32.9%).

Conclusions: Individuals vaccinated during non-mpox-related visits were more likely to be younger and Hispanic. While some people received PrEP or HIV testing after vaccination, many did not; this may represent a missed opportunity for HIV prevention.



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Hannah Schult is a second-year medical student at the University of Nevada, Reno School of Medicine. She received her BS in Microbiology and immunology from the University of Nevada, Reno, while also minoring in public health. Schult began medical school in July 2023 and is currently interested in pursuing infectious diseases. Schult recently received the 2024 G.E.R.M. Program Grant and conducted research focused on *Candida auris* with the help of her mentor, Dr. Samuel Lee. Her research concentrated on the in vitro activity of doxycycline, heparin, and ethanol against *C. auris* and *C. albicans* biofilms. This topic was of interest to Schult due to the increasingly high number of *C. auris* infections in her home state of Nevada. Outside of class, Schult is the Immunization Manager for her school's Student Outreach Clinic, which provides care to the underserved in their community. She is also involved in K-12 STEM outreach through her role on the Medical Education Outreach Committee, and she works with pre-med students and those going through the medical school application process through her role on the Student Outreach and Recruitment Committee. She participated in the Hazelden Betty Ford Medical Education Program, designed to introduce medical students to addiction medicine. Finally, Schult serves as a student leader for her school's Infectious Disease and Tropical Medicine Student Interest Group.

Abstract

An in vitro analysis of doxycycline, heparin, and ethanol activity against *Candida auris* and *Candida albicans* biofilms

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Background: *Candida auris* is an emerging fungal pathogen characterized by hospital-associated outbreaks and antifungal drug resistance. *C. auris* forms biofilms, although the pathogenesis is not well understood. Previously, we demonstrated that high-dose doxycycline, heparin, or ethanol have in vitro activity against *C. albicans* biofilms.

Hypothesis: Doxycycline, heparin, or ethanol will have in vitro activity against *C. auris* biofilms, which may differ from that of *C. albicans*.

Methods: Mature *C. auris* and *C. albicans* biofilms were incubated with doxycycline, heparin, or ethanol at varying concentrations, up to a maximum of 2048 g/mL of doxycycline, 10 KU/mL of heparin, or 70% EtOH for 24 hours. Biofilm metabolic activity was assessed using XTT-reduction in a static microplate model.

Results: *C. albicans* biofilm metabolic activity required ethanol concentrations of 9.21% or higher to demonstrate >95% reduction, while *C. auris* biofilm metabolic activity required concentrations of 46.66% or higher to demonstrate a >95% reduction, or 13.82% or higher to demonstrate a >90% reduction. *C. albicans* biofilm metabolic activity was reduced by 96.01% at a doxycycline concentration of 2048 g/mL, whereas *C. auris* biofilm metabolic activity was reduced by 87.27%. *C. albicans* biofilm metabolic activity was reduced by 48.40% at a heparin concentration of 10 KU/mL, while *C. auris* biofilm metabolic activity was reduced by 69.21%.

Conclusions: Higher concentrations of ethanol and doxycycline, but lower heparin concentrations, are required for inhibitory activity against mature *C. auris* biofilms compared to *C. albicans*. These findings have implications for future antifungal lock and decolonization strategies against *C. auris*.



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Andrea Scallon is a second-year medical student at Washington State University's Elson S. Floyd College of Medicine. She received her BA in international studies from the University of Washington and, upon graduating, spent one year studying Mandarin in Taiwan on the Huayu Enrichment Scholarship. As a student organizer, senator, and researcher, Andrea's professional interests lie within the clinical and political sphere, and she hopes to continue engaging in infectious disease and global health research to advance the health care system to a more equitable goal. Her research interests include HIV drug resistance, global health, immigrant/refugee health, healthcare policy, and structural and social barriers to accessing care.

Abstract

Social determinants of health associated with HIV drug resistance among children living with HIV in western Kenya

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Background: HIV drug resistance is a significant barrier to the success of antiretroviral therapy (ART), especially for children living with HIV (CLHIV). We leveraged the Opt4Kids study, a randomized control trial for HIV treatment monitoring among CLHIV aged 1-14 years in Kenya, to assess individual- or household-level social determinants of health (SDoH) and the development of drug resistance mutations (DRMs).

Hypothesis: Individual- or household-level SDoH, including but not limited to household income, food insecurity, transportation access, and caregiver depression or intimate partner violence, will be significantly associated with the presence of a major HIV DRM.

Methods: We assessed the risk of having at least one major DRM among CLHIV exposed to several SDoH factors. Exposures were captured repeatedly, longitudinally for 12 months, with some participants followed for five years. We conducted a multivariate modified Poisson regression model to analyze the SDoH factors associated with the presence of a DRM, adjusting for age, ART adherence, caregiver type/age/ART status, and ART duration and regimen.

Results: Of 704 children enrolled, the median age was 9 years and the median time on ART was 5 years. 93 (87.7%) had major and 13 (12.3%) had minor DRMs. Among participants with major DRMs, 87 (93.5%) had NNRTI resistance, 70 (75.3%) had NRTI resistance, and 10 (10.8%) had PI resistance. Multivariate model results are in-progress.

Conclusion: Our data suggests certain individual- or household-level SDoH factors influence development of major DRMs, and additional research is needed to elucidate the pathways through which this might occur and be modified for treatment success.



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Dr. Sanford is a resident physician (PGY-2) and StARR scholar at the Tulane-Ochsner Pediatric Residency Program. She earned her BSPH, MPH&TM, and MD from Tulane University. She is currently a second-year pediatrics resident with plans to apply to pediatric infectious disease fellowship. Dr. Sanford's research interests are primarily in the pathophysiology of postinfectious sequelae, particularly musculoskeletal sequelae. She has experience with diagnostic studies, field studies, and statistical analysis (R). She has been published in multiple articles in the fields of infectious diseases and global health. She was selected as a StARR scholar (R38) to further develop her research skills. She was designated as the American Academy of Pediatrics (AAP) representative for her residency program and has been recognized with several honors, including the Alpha Omega Alpha (AOA) designation, DeBakey Scholar award, and Hawthorne and Whitehead scholarships for medical school.

Abstract

Characterizing Musculoskeletal Sequelae in Ebola Virus Survivors Over Seven Years Since Hospital Discharge in Eastern Sierra Leone

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Background: Longitudinal analyses of musculoskeletal (MSK) sequelae in post-Ebola syndrome (PES) are lacking and needed to understand which Ebola virus disease (EVD) survivors are likely to develop MSK sequelae.

Hypothesis: We expected MSK sequelae in EVD survivors to follow the same post-viral arthralgia pattern demonstrated after infection with Chikungunya virus (CHIKV) and COVID-19, with higher rates in females and older age groups. We also anticipated MSK sequelae to decrease steadily over time.

Methods: We followed 379 survivors and 1040 household contacts from March 2016 to March 2022 in Eastern Sierra Leone. We describe the cumulative incidence of MSK sequelae in EVD survivors over seven years and predictive factors using generalized linear mixed models.

Results: Reported joint pain (38.4%) and joint tenderness to palpation on exam (17%) were the most common MSK sequelae found in survivors at enrollment. Most survivors with MSK sequelae at enrollment and throughout the study were 15-40 years of age. Females were not more likely to demonstrate MSK sequelae. Generally, MSK signs decreased over time. Reported MSK symptoms also decreased in most years. Self-reported depression predicted MSK symptoms at first visit and throughout the study.

Conclusions: EVD survivors 15-40 years demonstrate the highest rates of MSK sequelae. MSK symptoms fluctuated over time, which may be due to waxing and waning of MSK sequelae. MSK signs on physical exam decreased more steadily. Future studies are needed to determine whether immune response to EVD changes with age or the incidence of MSK sequelae over time



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Originally from Houston, Texas, Kyle Robinson attended the University of Alabama for his undergraduate studies where he completed his BS in biology and BA in Spanish languages and literature. He earned his medical degree from the Mayo Clinic Alix School of Medicine. Dr. Robinson was awarded the G.E.R.M grant in 2020 and has received grants for various other global health and infectious disease initiatives. He serves as the executive director of Mada Clinics Inc., which provides free medical care for communities across Northern Madagascar, where he helped establish a certified health care center and several schools. His professional interests include public health research, especially in Madagascar, and tropical medicine. He is currently completing family medicine residency at Family Health Centers of San Diego, where he is working toward certification as an HIV specialist. At this institution, he cares for a largely underserved population including many migrants and refugees.

Abstract

Unearthing a Growing HIV Epidemic Amongst Madagascar's General Population

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Background: Despite decades of progress against HIV/AIDS in sub-Saharan Africa, HIV infections and deaths due to AIDS are exponentially rising in Madagascar.

Hypothesis: Due to scarce general-population screening data, and a limited focus on key populations, official models may underestimate the true population prevalence of HIV in Madagascar.

Methods: In collaboration with the Malagasy Ministry of Health, we implemented the largest general population HIV screening study to date in Northern Madagascar. This was accomplished by providing point-of-care HIV screening and subsequent confirmatory testing for over 1000 participants from 73 towns, villages, and cities.

Results: We observed an overall HIV prevalence of 2.94%. Notably, we observed a 13.1% HIV rate among urban populations and showed that proximity to a major route of travel was significantly associated with HIV risk. We observed a link between HIV risk and various occupations, especially those associated with increased mobility.

Conclusions: This direct-testing study demonstrated a greatly higher HIV prevalence (2.9%) than prior official modeling-based figures (0.4%). Results were shared with NGO's in Southern, Western, and Central Madagascar. Their subsequent investigations demonstrated more concerning results than what was found here. The UNAIDS director for Madagascar took special interest in our research, shared the results amongst UN colleagues, and they are hosting an HIV colloquium in October to support further investigation. Funds for HIV programs in Madagascar have subsequently increased, but more is needed. Our findings underscore the need for investment into comprehensive HIV screening and control initiatives in Madagascar.



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Jessica Perez is a medical student researcher with the Klausner Research Group in the Department of Population and Public Health Sciences at the University of Southern California (USC). She received her BA in biology with a concentration in cell/molecular biology and genetics from Boston University, where she did research in sickle cell disease. Perez is in her fourth year of the MD program at the Keck School of Medicine of USC and will complete her MD in 2025. Perez is primarily interested in reproductive health and infectious diseases and aspires to work with underserved communities as a future physician. Jessica has been involved in research in the areas of genital herpes, syphilis in pregnancy and congenital syphilis. She is a recipient of a GERM award from the IDSA Foundation and HIV Medicine Association for her research in syphilis.

Abstract

Evaluating Treponemal and Nontreponemal Serologic Tests for Syphilis Detection in Pregnancy: Insights from a Review and Meta-Analysis

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Background: The increase in congenital syphilis in the U.S. emphasizes the necessity for effective prenatal screening and treatment. This review and meta-analysis aimed to assess the diagnostic accuracy of approved treponemal and nontreponemal serologic tests for maternal syphilis screening.

Hypothesis: Treponemal and nontreponemal serologic tests have high sensitivity and specificity for detecting syphilis in pregnant women.

Methods: We searched PubMed, Embase, and Cochrane Library up to February 2022 for diagnostic accuracy studies of serologic tests for syphilis in pregnant women. Study quality was assessed using QUADAS-2. A meta-analysis using bivariate random effects models was conducted to generate pooled sensitivity and specificity estimates for treponemal and nontreponemal tests, and forest plots were used to evaluate heterogeneity.

Results: From over 5000 abstracts and 78 full texts, 10 studies included pregnant women, evaluating 11 treponemal assays (N=4143) and 2 nontreponemal assays (N=9383). Sensitivity analysis of six studies yielded pooled estimates of 0.81 (95% CI = 0.56 to 1.05) for treponemal tests and 0.90 (95% CI = 0.87 to 0.93) for nontreponemal tests. Specificity analysis of eight studies gave pooled estimates of 0.99 (95% CI = 0.98 to 1.00) for treponemal tests and 1.00 (95% CI = 1.00 to 1.00) for nontreponemal tests. Subgroup analyses showed low heterogeneity between test types.

Conclusions: Despite the limited number of studies, the high specificity of both treponemal and nontreponemal tests should reassure clinicians about positive results. However, moderate sensitivity highlights the need for repeat screening per current guidelines. More studies on pregnant women using newer assays and rapid point-of-care tests are necessary.



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Abstract

Screening for Depression in Malaysian Prisons

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Background: People deprived of liberty (PDL) experience nearly twice the prevalence of mental health disorders compared to the general population. There is a paucity of data on screening for mental disorders in prisons.

Hypothesis: This study aims to identify (a) the prevalence of depressive symptoms and (b) factors associated with depression among PDL. We hypothesized that co-morbidities such as Hepatitis C, HIV, and TB would be associated with depression.

Methods: As part of a parent study examining screening for tuberculosis on entry to Malaysia's largest prison, Kajang men's prison in Kuala Lumpur, we administered a questionnaire gathering sociodemographic data, TB symptoms, CES-D 10, RODS, and medical history. Depressive symptoms were defined as CES-D > 10. The data was analyzed using regression analysis.

Results: Among 548 participants, 29.7% completed secondary school, 68% were Malay, 9.5% Chinese, and 20% were Indian; 65 (11.9%) had depressive symptoms. Hepatitis C (OR 1.93, 95%CI 1.04 – 3.56) and prior psychiatric care (OR 6.45 95% CI 2.54 – 16.17) was associated with depression. Being married (OR 0.42, 95% CI 0.19 – 0.83) or completing secondary school (OR 0.42, 95% CI 0.20-0.84) were protective against depression. Notably, TB and HIV did not have a significant bearing on depressive symptoms. Longitudinal data showed that the proportion with depression increased upon repeat screening.

Conclusions: More than 1 in 10 among patients entering prison had depressive symptoms. Screening and treating mental health disorders among PDL may be valuable to improving outcomes from concurrent infectious diseases such as TB and HIV.



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Abstract

Investigating and Summarizing Information Resources Related to the Clinical Presentation and Diagnosis of Cutaneous Manifestations of Infectious Diseases in Patients with Skin of Color

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Background: Patients with skin of color (SOC) present diseases differently in many circumstances, yet there is a lack of information regarding the presentation and diagnosis of cutaneous manifestations in such patients experiencing infectious diseases. Therefore, we conducted a scoping review to investigate and summarize information pertaining to the clinical presentation and diagnosis of cutaneous manifestations of infectious diseases in patients with SOC. This scoping review identified literature gaps regarding cutaneous manifestations of infectious diseases in patients with SOC.

Hypothesis: We hypothesized there would be a lack of literature regarding infectious disease skin manifestations in skin of color.

Methods: In our scoping review, the databases PubMed and ScienceDirect were used to acquire only research and review articles; moreover, only resources provided in English were considered in the literature search. Articles were reviewed to see if they addressed cutaneous manifestations of infectious diseases in patients with SOC as a key topic.

Results: The initial search yielded a total of 2894 articles. After all exclusion criteria were applied, a total of 21 articles were included.

Conclusions: This scoping review identified literature gaps regarding cutaneous manifestations of the infectious in patients with SOC. The lack of literature regarding cutaneous manifestations of infectious diseases in patients with SOC may contribute to care barriers in patients with SOC in our healthcare system. Health care disparities in infectious diseases and dermatology are clearly present and affect the care of such patients



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Abstract

BMI and Vaccine-Induced Immune Response in Children Living with HIV

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Background: With the widespread use of highly active antiretroviral therapy (HAART), people living with HIV have experienced longer life spans, but also higher rates of obesity due to HAART-related side effects and the increasingly obesogenic environment. Negative effects of obesity have been observed in some studies of vaccine-induced immune responses. Obesity and HIV, both known to cause immune dysregulation, could be additive in limiting the response to vaccination by children living with HIV (CLWH).

Hypothesis: Children with high body mass index z-scores (BMI_z), defined as >85th percentile for their sex and age, will be less likely to achieve and maintain a robust immune response to pneumococcal, hepatitis B, and hepatitis A vaccines.

Methods: This study used data from three completed clinical trials for safety and immunogenicity of pneumococcal, hepatitis B, and hepatitis A vaccines in CLWH (age 2.4 to 20.4 years). Adjusted linear regression for interval-censored data and logistic regression models were used to assess associations of BMI_z with antibody response eight and at least 32 weeks after vaccine series.

Results: BMI_z and antibody response were not statistically significantly associated for four of five studied serotypes in the pneumococcal vaccine (n=214) or the hepatitis A vaccine (n=94). BMI_z was associated with hepatitis B (n=154) antibody levels achieved eight weeks after vaccination (p=0.026); however, differences in antibody levels were not clinically significant.

Conclusions: The vaccine schedules for pneumococcal, hepatitis B, and hepatitis A are likely adequate and protective for the growing population of children living with both HIV and obesity



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Abstract

Risk Factors and Associated Mortality and Morbidity in Carbapenem Resistant *Acinetobacter baumannii* Infections in Hospitalized Patients: A Single-center, Retrospective Cohort Study

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Background: Multidrug-resistant organisms have emerged as an urgent threat to public health. Carbapenem-resistant *Acinetobacter baumannii* (CRAB) is a bacteria associated with hospital acquired infections designated as an urgent threat by the United States Centers for Disease Control. In 2017, an estimated 8,500 cases of CRAB infections occurred in U.S. hospitals with 700 estimated deaths. We aimed to characterize the risk factors and clinical outcomes associated with CRAB infections.

Hypothesis: CRAB infections are associated with high rates of intensive care unit (ICU) admission, indwelling devices and/or individual factors such as underlying comorbidities.

Methods: Patients ≥ 18 years of age hospitalized at The University of Kansas Health System between Jan 1, 2019, and Dec 31, 2023, with CRAB infections. Patients included had an *A. baumannii* isolated from a non-urinary source with a meropenem minimum inhibitory concentration (MIC) ≥ 8 . Patients treated with antibiotics for <72 hours were excluded.

Results: Among our cohort of 83 unique CRAB isolates, all-cause mortality at 30-days and 90-days was 9.63% and 21.68%, respectively. 71% had a recent long-term acute care facility (LTAC) stay. The most common primary infection source was osteomyelitis (46.99%). Patients were found to have numerous comorbidities, the most frequent being hemiplegia (59%) and diabetes (45%).

Conclusions: High morbidity and mortality associated with CRAB infections were observed in our cohort, along with a high frequency of recent LTAC stays. Further research is warranted to better delineate risk factors and discover ways to limit spread of this highly morbid infection among LTAC residents in the midwestern U.S.



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Eesha Irfanullah, B.BmE, BS. M.D Candidate. Eesha is a final year medical student at the University of Minnesota Medical School. She has a bachelor of biomedical engineering and a BS in Technical Writing from the University of Minnesota. She is currently applying for residency in internal medicine. Her research interests include global health, HIV, and opportunistic infections. Under the mentorship of Dr. Mahsa Abassi, and Dr. David Boulware, she has spent 3 months in Kampala working on clinical trials for HIV-associated cryptococcal meningitis. Her current work centers around the use of point-of-care ultrasound for management of sepsis and hyponatremia in patients with advanced HIV, for which she was awarded a 2023 G.E.R.M. grant from IDSA. She has been awarded additional research grants to support her ongoing work, including an NIH T-35 summer fellowship, and the Benjamin Kean Travel Fellowship in Tropical Medicine from the American Society of Tropical Medicine and Hygiene

Abstract

Implementation and Evaluation of a Point-Of-Care Ultrasound Course for Volume Status Assessment in Kampala, Uganda

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Background: Individuals admitted to the hospital with advanced HIV often present with sepsis physiology. Rapid initiation of appropriate antibiotics and volume expansion are known to improve outcomes. In resource-limited settings, excess fluid administration may lead to respiratory failure and adequate respiratory support may not be available. Conversely, over-resuscitation may lead to inadequate fluid administration and poor outcomes. Point-of-care ultrasound (POCUS) is a noninvasive tool that can aid in assessing volume status and support clinical decision-making. This study evaluated a hybrid training course designed to teach participants how to leverage POCUS for volume assessment and sepsis management in Uganda.

Hypothesis: Our course will enhance participants' confidence and proficiency in using POCUS for sepsis management.

Methods: An online course was developed and hosted through Canvas. The course provided a comprehensive review of ultrasound and then focused on the assessment of the heart, lungs, and inferior vena cava. The course included 3 hours of interactive online learning and 6 hours of in-person training. Participants were recruited from the Infectious Disease Institute of Makerere University in Kampala, Uganda. Pre- and post-course knowledge was assessed through online quizzes. Participants individually performed POCUS exams on five patients. De-identified images were reviewed by study personnel. Pre- and post-course surveys were completed by all participants.

Results: Ten participants completed the evaluations, showing significant knowledge improvement, with median scores increasing from 60% (IQR 43%-68%) to 93% (IQR 90%-95%) between the pre and post course quizzes. All participants scored $\geq 90\%$ on their final assessments. The course was well-received, with 90% of participants reporting high or very high understanding of sepsis management with POCUS post-course.

Conclusions: The hybrid POCUS course significantly improved knowledge and confidence among participants, indicating its potential to enhance sepsis management in resource-limited settings. This training is the first phase of a larger project aimed at integrating POCUS protocols to improve sepsis outcomes in patients with advanced HIV.



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Abstract

IL-6 as a Potential Prognostic and Therapeutic Marker in Preterm Birth

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Background: Preterm birth (PTB) is a critical global health issue, and microbial-induced intrauterine inflammation contributes to at least 40% of cases. Common, curable sexually transmitted infections (STIs) like *Chlamydia trachomatis*, *Neisseria gonorrhoeae*, and *Trichomonas vaginalis* are linked to increased risk of PTB. In low-resource settings, however, where both STIs and PTB are prevalent, many STI cases go untreated in pregnancy due to their often-asymptomatic nature and high diagnostic screening costs. My project aims to address gaps by identifying inflammatory biomarkers associated with key STIs and adverse pregnancy outcomes. Subsequently, a pilot study in South Africa will assay for these biomarkers using vaginal swabs from asymptomatic pregnant women.

Methods: To date, I've searched the literature on PubMed through August 2024 for studies on antenatal biomarkers of PTB and infection, key STIs, or inflammation. My search included systematic reviews, clinical studies, and in vitro studies.

Results: Interleukin-6 (IL-6) emerged as a frequently reported cytokine associated with PTB, also often elevated in pregnant women with genital infection or living with HIV infection. Additionally, animal studies have demonstrated reduced PTB rates when IL-6 receptors were blocked. Overall, studies exploring common STIs were limited. However, the association of IL-6 with PTB induced by infection in pregnancy, including with *Ureaplasma* and *Mycoplasma* species, was consistent.

Conclusions: IL-6, a readily measurable cytokine, has been consistently linked to infection-induced PTB. Further research on its prognostic or therapeutic role could enhance antenatal care, especially in low-resource settings with high STI burden, by enabling targeted interventions to improve pregnancy outcomes.



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Abstract

TA preliminary analysis of providers' perspectives on severe malaria care

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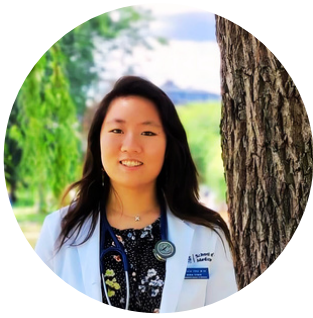
Background: Severe malaria disease is challenging to treat and prevent in rural endemic settings, often a result of delayed access to care. Perspectives among providers including doctors, nurses, and community health workers are rarely considered in severe malaria case management research. Most studies that do encompass providers' perspectives often focus on compliance to treatment guidelines without consideration of the local context or legacies of colonialism.

Hypothesis: We aimed to determine the facilitators and barriers to severe malaria training, resource allocation, referrals, and care coordination among providers and traditional medicine practitioners applying a decolonial lens. The study setting is at Sussundenga-Sede Rural Health Center (RHC) in Sussundenga, Mozambique, a rural village in Manica Province bordering Zimbabwe with moderate-high malaria transmission. We hypothesize that providers and traditional medicine practitioners rely on community-based solutions for severe malaria case management.

Methods: A trained data collector fluent in Mozambican Portuguese and English conducted semi-structured interviews with 13 health providers involved in severe malaria case management at the RHC. Doctors, nurses, administrators, health directors, lab technicians, community health workers, and ambulatory workers will be interviewed. Two traditional medicine practitioners in Sussundenga village involved in a referral program with the RHC will be included. The interview guide was piloted in August 2023. Transcription, translation, and thematic analysis will be conducted in NVivo. Transcripts in Mozambican Portuguese and will undergo linguistic and cultural translation before coding with a code book developed from the interview guide topics. Thematic analysis will be used to analyze the data

Results: Data collection is ongoing and will finish in August 2024. To date, interviews have been conducted among 3 nurses, 1 community health worker, 1 hospital administrator, and 1 director.

Conclusions: The findings of this preliminary analysis will identify provider-level determinants of severe malaria case management, as well as community-based approaches to overcoming common challenges.



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Abstract

A Host Genetic Determinant of Severe Babesiosis Caused by *Babesia microti*

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Background: Asplenia and immune suppression are known risk factors for severe babesiosis caused by *Babesia microti*. Host genetic determinants, however, remain unidentified. Using a mouse model that is amenable to forward genetics, we identified the *nxpe* locus as containing determinants of *B. microti* parasitemia.

Hypothesis: The *nxpe* locus contributes to severe babesiosis in humans.

Methods: We enrolled babesiosis patients in a multicenter, unmatched case-control study. For the 210 patients who had a spleen and were not immunosuppressed, we classified anemia as mild (hemoglobin 10.0-12.9 g/dL in males; 10.0-11.9 in females), moderate (8.0-9.9), or severe (<8.0). We classified thrombocytopenia as mild (100-149 x1000 platelets/ μ L), moderate (50-99), or severe (<50). We classified levels of lactate dehydrogenase (LDH), a marker of cell lysis, as low (281-840 U/L) or high (>840). We extracted genomic DNA from patient blood and used Taqman probes to distinguish the major allele from the minor allele at 24 single nucleotide polymorphisms (SNPs) across the *nxpe* locus.

Results: There is an association between the recessive allele at one SNP and severe anemia ($p=0.045$) or severe thrombocytopenia ($p=0.038$). For carriers of the homozygous recessive genotype, the relative risk of being severely anemic is 2.82 whereas the relative risk of being severely thrombocytopenic is 1.68. There is no association with LDH.

Conclusions: Given the association with anemia but not cell lysis and given that *B. microti* does not invade platelets, we conclude that the *nxpe* locus may promote clearance of erythrocytes and platelets, thereby contributing to severe babesiosis.



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Anne Claire Burghard (Claire) is a third-year medical student at the Renaissance School of Medicine at Stony Brook University with a strong interest in pediatrics, obstetrics and gynecology, and infectious diseases. She received her BA in biology from Barnard College of Columbia University. Burghard's research interests include clinical and translational research in pediatric and perinatal infectious diseases, particularly in the mechanisms of Group B *Streptococcus* GI colonization and the impact of novel GBS strains on vaccine development. She aims to pursue a career as a physician-scientist and combine her clinical knowledge with research to improve maternal/fetal outcomes. Burghard is also passionate about medical education and mentorship, serving as the President of the Pediatrics Interest Group and co-director of the Peer Mentor Initiative at Stony Brook. She is also a member of the Pediatric Infectious Diseases Society (PIDS) and the Phi Beta Kappa Honors Society.

Abstract

Group B *Streptococcus* ST1010 is a hypervirulent capsule switch strain with multinational spread

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Background: Group B *Streptococcus* (GBS) is an important cause of invasive disease in both neonates and adults. We recently identified local expansion of a serotype IV GBS sequence type (ST)1010 lineage among pregnant people in the Dominican Republic (DR). ST1010 is closely related to ST452, which originated from a large recombination event between clonal complex (CC)23 (ST24) and CC17 (ST291) strains.

Hypothesis: We hypothesize that ST1010 also arose from a large recombination event and represents a capsule switch strain of GBS with increased virulence.

Methods: We analyzed whole-genome sequences from 17 ST1010 pregnancy carriage isolates from the DR, 5 invasive ST1010 isolates from CDC Active Bacterial Core Surveillance (ABCs), 11 clinical isolates from New York City (NYC), and 25 non-ST1010 strains. We constructed a genome-distance tree using mashtree and used SNP density plots to identify potential recombination areas.

Results: ST1010 strains did not segregate by geographic origin. 32 of 33 ST1010 isolates clustered into a single clade, closely related to ST17 and ST452 isolates. Unlike ST452, ST1010 strains contain genes encoding HvgA and Srr2, important virulence determinants of hypervirulent CC17 GBS. SNP analysis suggests that the ST1010 genome is composed of two parts with high similarity to regions of CC23 and CC17 and includes a serotype IV capsule locus.

Conclusions: ST1010 likely arose from a large recombination event between CC23 and CC17 and likely represents a hypervirulent capsule switch strain of GBS with multinational spread. These results have implications for ongoing GBS surveillance and understanding emergence of novel GBS lineages.



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Abstract

Three Drugs, Two Pills, One Algorithm: HIV PrEP, PEP, Treatment Initiation Consolidated Guidelines for Resource-Limited and NonSpecialty Settings

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Background: Accessing HIV prevention and treatment remains difficult throughout the United States (US). Increasing the number of clinicians offering pre-exposure prophylaxis (PrEP), post-exposure prophylaxis (PEP), and Test & Treat (T&T) (where individuals testing positive for HIV are rapidly engaged in HIV treatment) is imperative. The project's goal was to create a consolidated algorithm for HIV treatment and prevention that simplifies care for providers with few resources or limited experience.

Methods: The algorithm was designed using HIV care guidelines and includes PrEP, PEP, and T&T. The combination of tenofovir disoproxil fumarate and emtricitabine provides low-cost, generic PrEP regardless of gender, pregnancy, or intravenous drug use while also providing the backbone needed for PEP and T&T. Dolutegravir, the third medicine, was chosen for PEP and T&T because of its approval in pregnancy. The algorithm was tested with U.S. medical students who completed an eight-question test then repeated those questions with the algorithm. Questions included scenarios about HIV testing, PrEP, PEP, and T&T. Students were recruited by email. Pearson's chi-squared compared pre vs post test scores.

Results: 97 students from 13 medical schools completed pre and posttest questions. Correctness increased from 3 of 8 (pretest) to 7 of 8 (posttest) ($p < 0.001$). All individual questions saw a statistically significant improvement in correctness when assisted by the algorithm.

Conclusion: This algorithm significantly improved medical students' ability to accurately answer HIV care questions and has the potential to expand access to HIV care. Further studies are needed to understand the algorithm's effect with practicing clinicians



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Abstract

HIV PrEP prescribing rates in high-risk urban youth quality assessment

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Background: Greater than 20% of HIV cases are found in youth populations, with racial minorities disproportionately affected. Prescriber hesitance hinders PrEP prescription in young and emerging adults aged 19-29 (YEAs). At the NJMS infectious disease practice (IDP) and pediatric clinic (PC), higher PrEP uptake was observed compared to national averages. However, prescription rates lag in the internal medicine clinic (IMC).

Hypothesis: Implementing an EPIC smart-phrase reminder tool (PrEP2023) will increase total PrEP and IMC prescriptions. However, interventions with an optimized tool (PrEP2024) and "physician champions" are necessary for a significant, longitudinal, department-wide increase in prescription rates.

Methods: Retrospective chart review of patients aged 19-29 prescribed PrEP from Jan 1, 2022, to Dec 31, 2023 was performed. Demographic analysis in 2023 excluded 2 individuals due to unavailable data.

Results: PrEP prescriptions increased from 25 in 2022 to 28 in 2023. 22 patients identified as Black or Latinx (88.0% in 2022, 78.7% in 2023) ($p=0.36$). In the IMC, prescriptions increased from 0 in 2022 to 2 in 2023 (7.14%). In the IDP, prescriptions decreased from 23 in 2022 (92.0%) to 18 in 2023 (64.3%) ($p<0.05$), while PC saw an increase from 2 (8.00%) in 2022 to 8 (28.6%) in 2023 ($p=0.056$).

Conclusions: PrEP prescription rates increased, though without statistical significance, in clinics serving majority POC YEAs from 2022 to 2023, specifically in the IMC utilizing PrEP2023, and non-IDP clinics, reflecting smart-tool and resident education efficacy. Further interventions are imperative.



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Abstract

Adoption of a Real-Time Culture Alert System (TD) by an Outpatient Parenteral Antimicrobial Therapy (OPAT) Program

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Background: Outpatient Parenteral Antimicrobial Therapy (OPAT) programs facilitate the administration of intravenous antimicrobial treatments outside of the hospital and reduce hospital length of stay. After hospital discharge, OPAT patients continue their medications at home. Weeks later, the antimicrobials are reviewed by infectious disease (ID) during a follow-up appointment. Lack of continual monitoring after discharge can cause delays in appropriate adjustment of antimicrobials. In March 2021, Tufts Medical Center (TMC) implemented a real time culture reporting system, TheraDoc (TD), to alert the OPAT team of updated microbiology results after discharge. The goals of this project are to 1) retrospectively analyze changes in antimicrobial regimens and the timeliness of each change and 2) to determine why some patients with a TD alert did not require antibiotic changes.

Methods: This study analyzes data from April 1, 2021 to March 31, 2022. During this period, OPAT saw 465 patients, and 118 of these patients had a TD alert after hospital discharge. Demographic data, patient diagnosis, and antimicrobial regimens were recorded for each patient.

Results: Of the 118 patients with a TD alert, five patients had both an alert and a subsequent antibiotic change

(4.2%). The data revealed that antibiotic changes were driven by delayed growth of organisms that were not picked up on preliminary culture results. For the patient with alerts and no medication changes, it was determined that original regimens were broad enough to cover any organisms that may have grown after discharge. The average time between the date of the TD alert and the date of follow-up appointment was 14.8 days. Before TD, patients waited weeks before antibiotic review by a physician. After TD, an alert prompted a review of antimicrobial regimen by an ID specialist in 52 minutes, on average.

Conclusions: The TD program reduced time to antimicrobial adjustment in the OPAT program at TMC. TD is a valuable safety monitoring system that ensure that patients are being appropriately followed post-discharge and may have prevented worsening infection in the five patients with antibiotic changes



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Abstract

Identifying *Plasmodium falciparum* Antigens that Elicit Antibody Responses Correlating with Partial Parasitological and Clinical Immunity in a Repetitive Controlled Human Malaria Infection Study

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Background: Malaria's burden underscores the need for effective vaccines. Identification of blood-stage proteins that elicit protective immunity would inform blood-stage vaccine development. In a repetitive Controlled Human Malaria Infection (CHMI) study, malaria-naïve volunteers were infected with *P. falciparum* by mosquito bite over two years. After three or four challenges, all participants exhibited fewer symptoms, and five showed that time to parasite detection by blood smear increased significantly (delayed patency), indicating partial immunity. We studied antibody responses to multiple *P. falciparum* antigens to identify those associated with a delay in patency.

Hypothesis: Following repeated CHMI exposure in malaria-naïve individuals, antibody levels against bloodstage antigens will be increased in individuals with delayed blood-stage patency compared to those without it.

Methods: Sera from 12 participants were probed on a peptide microarray containing overlapping 16-amino acid peptides representing 353 *P. falciparum* proteins. Log-transformed, smoothed IgG signal intensities along each protein were used to define an immunodominant epitope (amino acid with maximum signal intensity) and identify proteins with higher responses post-infection compared to baseline. Fold-changes in antibody response were compared among the delayed patency and nondelayed group to identify proteins associated with partial clinical immunity

Results: Forty-five proteins had higher antibody responses post-infection compared to baseline. Generally, antibody responses showed a stepwise increase in signal intensity over the four CHMI. For six proteins, the fold-change response was > two-fold higher in the delayed- vs. non-delayed-patency group.

Conclusions: In a repetitive CHMI study, antibody responses to six proteins were associated with partial parasitological and clinical immunity.



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Abstract

Increasing Birth Dose Hepatitis B Vaccination in Nigeria: Qualitative Analysis of Data from a Crowdsourcing Open Call

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Background: Nigeria has substantial mortality and morbidity associated with hepatitis B infection. The WHO and the Nigerian government recommend birth-dose hepatitis B vaccination to prevent infection and cancer, yet only one-third of Nigerian newborns receive a timely hepatitis B birth dose (HepB-BD) vaccination. This study aimed to identify promising strategies to increase HepB-BD vaccination based on textual data from a crowdsourcing open call in Nigeria.

Methods: An open call was made for teams of individuals across Nigeria to submit ideas of less than 500 words describing the best approach to increase HepB-BD vaccination. Independent judges evaluated all submissions based on predefined criteria. We analyzed textual data from the top 30 submissions by iteratively coding the data and conducted thematic analysis using a socioecological model (Figure 1) to identify priority facilitators of HepB-BD in Nigeria.

Results: The open call received 351 submissions with most participants (206/35, 58.7%) identifying as women. From the top 30 submissions, our analysis identified six priority facilitators (Table 1) for increasing HepB-BD: 1) Involve and support religious and health care leaders to educate pregnant women on HepB-BD's importance (24/30, 80%), 2) Develop stronger national policies to support vaccinations, track vaccination status, and scheduling (20/30, 67%), 3) Promote attitude and behavioral changes by countering HepB-BD vaccination misconceptions (18/30, 60%), 4) Utilize existing rural infrastructure including community town halls and radio programs to disseminate information and improve rural vaccination rates (10/30, 33%), 5) Consider community diversity by translating educational material into local languages like Pidgin (9/30, 30%), and 6) Motivational strategies like financial (e.g., conditional cash transfer) and social incentives (e.g., recognition programs) to encourage mothers to vaccinate their children (9/30, 30%).

Conclusion: Our crowdsourcing open call identified facilitators and strategies to increase HepB-BD vaccination in Nigerian newborns that leverage the strengths of effective vaccine uptake programs. The data from this study will inform subsequent pilot projects and a randomized controlled trial.



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Joelle El Hamouche is a second year medical student at the Albert Einstein College of Medicine in the Bronx, NY. She received her BS in Chemistry with a concentration in Biological Chemistry from Stony Brook University in 2022. As an undergraduate student, El Hamouche conducted genomic analysis of antibiotic-resistant *Klebsiella pneumoniae* and *Pseudomonas aeruginosa* isolates at New York Medical College. She also conducted research in the lab of Dr. Eszter Boros as part of work to develop siderophore-antibiotic conjugates. Most recently, she analyzed sera for Powassan and Dengue virus reactivity under the mentorship of Dr. Emily Miller

Abstract

Screening for Therapeutic Monoclonal Antibodies Against Powassan Virus

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Background: Powassan virus (POWV) is an emerging tick-borne flavivirus that can cause encephalitis, and meningitis. Approximately 10 to 15% of neuroinvasive POWV infections are fatal, and there are currently no approved vaccines or therapies available. Rates of asymptomatic or mild infection are poorly understood and as the geographic range of ticks is expanding, there is concern for increasing POWV prevalence.

Hypothesis: In this study, we screen sera of cadets attending the US Military Academy (USMA) in West Point, NY, who are at high risk of contracting tick-borne illnesses. Through this study we seek to determine the prevalence of POWV seropositivity in a high-risk population and to identify neutralizing antibodies that could be developed as therapeutic antibodies.

Methods: Sera samples (n=1,051) from the Cadet class of 2017 were screened using an ELISA assay for domain III (EDIII) of the POWV envelope glycoprotein. Putative positives were further assessed for binding and neutralization of POWV reporter virus particles (RVPs) expressing the full-length E protein. Cross-reactivity to Dengue virus, a closely related flavivirus, was also tested.

Results: Of sera samples tested, 14/1,051 (1.3%) were identified as positives. Testing of paired sera samples pre-USMA enrollment suggested that most cadets seroconverted while attending USMA. Further studies of positive sera demonstrated POWV RVP binding as well as neutralization. Cross-reactivity to Dengue EDIII was not observed.

Conclusions: These results confirm that USMA Cadets are at risk of POWV exposure and that screening this population may prove valuable for POWV antibody discovery