THEME 2: COMMUNICABLE DISEASES

ABSTRACTS FOR ORAL AND POSTER PRESENTATIONS

ORAL PRESENTATIONS

CD-O-01

Voluntary Medical Male Circumcision and Female Condom Uptake during the COVID-19 Pandemic in Gauteng Province, South Africa

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Abstract: Voluntary Medical Male Circumcision (VMMC) and female condoms are important biomedical and cost-effective interventions against Human immunodeficiency virus (HIV) transmission. Particularly, female condoms prevent unwanted pregnancy and sexually transmitted infections. However, there is a knowledge deficit of COVID-19's impact on these interventions in Gauteng, one of the most hit provinces in South Africa by the COVID-19 pandemic. This study aimed to compare VMMC and female condom uptake in Gauteng province before and during COVID-19. We used a longitudinal study design to compare the District Health Information System data before (2019) and during (2020) COVID-19. Medical schemes supplemented VMMC data. We describe the percentage change in female condom uptake and VMMC in Gauteng province and its five districts. In 2020, during COVID-19, Gauteng province experienced a 43.7% increase in female condom uptake and a decline in VMMC of 33.8% for ≥10 years, 32.4% for 10-14 years, and 35.8% for ≥15 years. Although there was a substantial district variation in both VMMC and female condom uptake during COVID-19, the West Rand district witnessed the highest disruption in both services. Exceptionally, the Tshwane district recorded an increase of 21.8% in ≥10 years in VMMC during COVID-19. Overall, Gauteng province experienced a remarkable improvement in female condom uptake and disruption in VMMC in 2020 during COVID-19. This study suggests that different healthcare services and geographical areas were impacted differently by the COVID-19 pandemic, which warrants equitable service access and delivery support policies for HIV, sexual and reproductive health post-COVID-19 and during future emergencies.

Keywords: Voluntary Medical Male Circumcision and Female Condom Uptake during the COVID-19 Pandemic in Gauteng Province, South Africa

CD-O-02

The use of atazanavir limits cross-resistance to darunavir in the South African Public Sector

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Abstract: Background: The 2023 South African ART Clinical Guidelines recommend the use of dolutegravir. However, some patients might still require treatment with protease inhibitors (PI). Atazanavir/ritonavir (ATV/r) is preferred over lopinavir/ritonavir (LPV/r), except for patients on TB treatment. We reviewed resistance profiles obtained from patients failing PI-based treatment in the public sector in South Africa. METHODS: Patients failing PI-based regimens that had an HIV drug resistance test performed at the HIV Molecular Laboratory in Johannesburg in 2022 were included in this retrospective data analysis. Pol sequences were obtained by Sanger sequencing and submitted to Stanford HIVdb v9.4 to generate resistance profiles. Resistance was defined as low-level resistance or higher. Statistical analysis was performed using GraphPad Prism 9.0, a p-value < 0.05 was considered significant for the two-tailed 2 test. RESULTS: The population consisted of 769 (62.0%) females. Most patients were failing LPV/r (n=951), whereas 293 patients failed ATV/r-based regimens. Accumulation of ≥3 major PI mutations was significantly more in patients failing LPV/r-based treatment (194/951, 20.4%), versus ATV/r-based regimens (12.3%, p=0.0018). Cross-resistance to darunavir (DRV/r) was more common in the LPV/r group (14.5%) compared to the ATV/r group (8.8%, p=0.0126). CONCLUSION: These findings justify the preference of ATV/r over LPV/r as the preferred PI, as accumulation of ≥3 major PI mutations was less common in patients failing ATV/r regimens. These patients presented with less cross-resistance to DRV/r, thereby, preserving the drug for use in third-line regimens in these cases.

Keywords: HIVDR, ART, Darunavir

CD-O-03

The antifungal and antivirulence properties of Nauclea latifolia against Candida albicans

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Abstract: Candida albicans is an opportunistic pathogen that affects mostly immunocompromised individuals and causes candidiasis. Orally, its pathogenicity is influenced

by its ability to adhere to oral epithelial cells, germ tube and biofilm formation, and the production of hydrolytic enzymes. Current treatment is threatened by the abuse of antifungal agents and that results in the emergence of drug resistance, which prompts to search for alternative treatment. Medicinal plants have been used traditionally for treating dental caries and septic mouth including Nauclea latifolia. This study aimed to investigate the effect of the N. latifolia plant extract against C. albicans. Microdilution method was used to determine the minimum inhibitory and fungicidal concentrations. Subsequently, the effect of the plant extract on adherence, germ tube and biofilm formation, were investigated at MIC, ½ and ¼ MIC's. Data was analyzed using One-way Anova. The MIC and MFC was 0.16 and 0.63 mg/ml respectively. The plant extract reduced the adherence of yeast to the epithelial cells by 85 % ($p<0,0001$) at 0.16 mg/ml and 73 % at 0.04 mg/ml. The plant extract also inhibited germ tube formation by 51% ($p<0.05$) at 0.16 mg/ml. After 6 hours, N. latifolia reduced biofilm formation by 50 % at MIC. Nauclea latifolia affected C. albicans adherence the first step of pathogenicity, it inhibited germ tube formation, so affecting the transition of the hyphae from the blastospores form and oral thrush infection which makes it a potential antifungal agent.

Keywords: Candida albicans, Nauclea latifolia, Candidiasis, Virulence

CD-O-04

Genomic characterization of Enterococcus species isolated from wastewater treatment plants in South Africa

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Abstract: Background: Multi-drug resistant especially vancomycin-resistant enterococci are important pathogens of public health concern. Wastewater-based epidemiology offers a cost-effective and non-invasive method to track Enterococcus species in a population using the One-Health approach that can supplement clinical surveillance. We investigated and characterized Enterococcus species from wastewater to determine their antibiotic resistance genes, virulence genes, and sequence types. Methods: Wastewater samples were recovered from 13 treatment plants across 5 provinces in South Africa over six-months. We used selective agar medium to optimize isolation and culture of enterococci from wastewater. We confirmed the identification of enterococci isolates, performed Antimicrobial susceptibility and determined resistance mechanisms using both PCR and whole genome sequencing (WGS). Preliminary results: 802 Enterococcus species were isolated and resistance to several classes of antibiotics were observed, including resistance mechanisms to aminoglycosides (91%), macrolides (55%), glycopeptides (35%) and tetracycline (28%). Of these isolates, only 4.3% possessed vancomycin-resistance

genes (2.4% for vanC1 and 1.9% for vanC2/3 genes). Resistance genes were detected for the following drugs: tetracycline, glycopeptide, aminoglycoside, quinolone and macrolides, which correlated with their antibiotic resistance phenotypes. MLST analysis revealed 24 different STs, including 3 previously described (ST32, ST6 and ST361). Two strains belonged to CC17 and CC2, often associated with hospital outbreaks. Conclusion: Enterococcus hirae was the most dominant species, a recently emerged human pathogen causing urinary tract infections, especially in patients with underlying diseases. Enterococcus species with a diverse range of antibiotic resistance genes exist in wastewater and genomic analyses offers insights into antibiotic-resistant Enterococcus species using the one-health approach.

Keywords: Enterococci, resistance mechanisms, wastewater, whole-genome sequencing

CD-O-05

Mutations in the haem binding regions of SARS-COV-2 spike proteins from Gauteng, South Africa

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Abstract: Haematologic disorders in SARS-CoV-2 infected individuals are particularly concerning for those who received licensed vaccines. The S1 subunit of the spike protein binds both haemoglobin and haem. We aimed to assess the frequency of mutations in known haem binding regions of SARS-CoV-2 spike proteins from South African strains. We analyzed 2,738 SARS-CoV-2 sequences and the Wuhan reference from the Global Initiative on Sharing All Influenza Data (GISAID, https://gisaid.org/) database, using Nextclade (https://clades.nextstrain.org/) and BioEdit for sequence alignment and mutation analysis, respectively. Mutation analysis was done across the following regions: 17NLTTRTQ23, 72GTNGTKR78, 110LDSKT114, 256SGWTA260, 449YNYLYRLFRKSNLKP463, and 494SYGFQPTNGVGYQPYRVVVL513. Omicron (1294/2738, 47%) was the predominant variant of concern (VOC), followed by Delta (748/2783, 27%). Beta, Kappa, and Alpha VOCs were also identified along with recombinants and other lineages. Mutations in region 17-23 include L18F, T19R/I, R21I, and T22I. T19R/I result in the loss of a potential N-linked glycosylation site. Region 72-78 include G75D/V, T76I and R78M. Mutations in region 449-463 include Y449H, N450K/D, L452R, S459Y, and N460K. Region 494-513 includes the following mutations G496S Q498R, N501Y, and Y505H. Mutation frequencies were 15.3% in region 17-23, 9.6% in region 449-463, and 25.5% in region 494-513. Mutations at positions 452 and 501 are associated with immune escape and are signature mutations of VOCs especially Beta and Delta that were associated with severe disease. Further work will aim to manipulate identified regions to reduce haem binding affinity of SARS-CoV-2 spike proteins.

Keywords: Haem binding, SARS-CoV-2 Spike protein, mutations

CD-O-06

The Relationship between Adverse Childhood Experiences and HIV Prevalence among Adolescent Girls and Young Women in Mpumalanga: An HPTN068 Analysis; 2017

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Abstract: Adverse Childhood Experiences (ACEs) include various forms of childhood adversity such as abuse, neglect, and household dysfunction. Adolescent Girls and Young Women (AGYW) in sub-Saharan Africa are at high risk of HIV infection, and ACEs have been linked to increased HIV risk. This study explores the relationship between ACEs and HIV prevalence among AGYW in rural South Africa, focusing on cumulative ACEs and individual categories. Utilizing a cross-sectional design and data from the HPTN 068 trial, the study conducted a descriptive analysis to determine ACEs' prevalence and their association with HIV status. Logistic regression assessed the relationship between cumulative and individual ACEs and HIV prevalence, while mediation analysis explored potential mediators between childhood physical abuse and HIV status. The study found an HIV prevalence of 11.48% among the population. 62% of participants experienced at least one ACE. There was no significant association between cumulative ACEs and HIV prevalence. However, childhood physical abuse (aOR: 1.57) and witnessing physical violence at home (aOR: 1.63) were significantly associated with higher HIV odds. Conversely, witnessing community violence was linked to lower HIV odds (aOR: 0.69). Early sexual debut, emotional abuse, and witnessing verbal violence were not significantly associated with HIV prevalence. Mediation analysis revealed no significant mediators between childhood physical abuse and HIV status. The study concludes that specific ACEs, particularly childhood physical abuse and witnessing physical violence at home, significantly contribute to higher HIV odds among AGYW in rural South Africa, highlighting the need for targeted, trauma-focused interventions.

Keywords:1. Adverse Childhood Experiences (ACEs) 2. HIV prevalence 3. Adolescent Girls and Young Women (AGYW) 4. Rural South Africa

CD-O-07

Post (PEP) to Pre-Exposure Prophylaxis (PrEP) Transition Among Clients Accessing HIV Prevention Services in South Africa

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Abstract: Background: HIV post-exposure prophylaxis (PEP) and pre-exposure prophylaxis (PrEP) are both effective components of HIV prevention. PEP has been underutilised in primary care settings and understanding of PEP to PrEP transition patterns for those requiring ongoing HIV prevention is limited. We describe patterns of PEP to PrEP transition among clients accessing routine services in South Africa. Methods: We analysed routinely collected clinical data, within a PrEP implementation study, from 107 clients aged 15-40 who received PEP between June and November 2023. We describe their demographics, self-reported reasons for requiring PEP, proportion of those who came back for a follow-up visit post-PEP, the number of days between PEP provision and follow-up, and whether PrEP was initiated at follow-up. Results: Of the 7,060 clients who accessed services during the study period, 107 were provided PEP after being screened for eligibility (1.5%): 62.6% were female (n=67); majority were aged 18-24 (n=81; 75.7%). Most noted unprotected sex (n=83; 77.6%) as a reason for requesting PEP, followed by condom breakage (n=18; 16.8%). Twenty-nine (27.1%) individuals returned for a post-PEP follow-up visit, 65.5% returning within six weeks. Despite the delayed and low post-PEP follow-up visit rate, most who returned post-PEP, transitioned to PrEP (n=21; 72.4%). Conclusions: Although overall PEP uptake and post-PEP follow-up were low, we found a high rate of PEP-to-PrEP transitioning, highlighting PEP-to-PrEP acceptability among clients. More is needed to improve PEP awareness and access. Reducing post-PEP loss to follow-up offerd an opportunity to introduce and improve PEP-to-PrEP transition for eligible clients.

Keywords: PEP, PrEP, South Africa, HIV prevention

CD-O-08

Characterizing the biological function of Ami1, a Mycobacterium tuberculosis amidase protein

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Abstract: Tuberculosis (TB), a disease caused by the bacterium Mycobacterium tuberculosis (Mtb), remains a significant global threat to human health as it claims approximately 1.5 million lives annually. The development of drug resistance by Mtb is a major contributor to the persistence of TB in society, despite the existence of treatment. Therefore, there is a need to find new drug targets for the development of novel anti-TB drugs. One such target is the

peptidoglycan (PG) structure of the bacterial cell wall as it is involved in vital cellular processes including cell growth and division. N-acetylmuramyl-L-alanine amidases (amidases) are PG hydrolases that remodel the PG during cell growth and division. The aim of this study was to determine the biological role of Ami1 in the laboratory H37Rv strain of Mtb. This was achieved by assessing the phenotypes of H37RvS (wild-type), H37Δami1S (mutant strain lacking the ami1 gene) and H37Δami1S::ami1 (genetically complemented strain). There were no differences in cell growth and division between the Mtb strains under normal growth conditions. However, the H37Δami1S mutant displayed poor growth kinetics under conditions of carbon starvation. The strain also displayed increased cell-wall permeability, and increased susceptibility to isoniazid (INH), a first-line TB drug. Furthermore, ami1 expression increased upon INH exposure in H37RvS and H37Δami1S::ami1. Collectively, the results suggest that Ami1 is vital for the survival of Mtb under stressful conditions and thus, highlight the potential for the development of an anti-Ami1 drugs as a supplement to the current drug regimen for TB treatment.

Keywords: Drug resistance, Ami1, M. tuberculosis, Isoniazid

CD-O-09

Antimicrobial resistance in adult women with culture-confirmed community-acquired uncomplicated urinary tract infections at a primary healthcare facility in Gauteng Province, April 2022-June 2023

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Abstract: Introduction We conducted surveillance in an urban township community to describe the epidemiology of community-acquired urinary tract infections (CA-UTIs) and determine the prevalence of antimicrobial resistance (AMR). Method We conducted a cross-sectional study at a clinic in Alexandra township during 1 April 2022-30 June 2023. We collected midstream urine from enrolled non-pregnant female patients aged ≥18 years with UTI signs and symptoms. Cultured uropathogens were identified using MALDI-TOF-MS (Bruker-Daltonik, USA). Antimicrobial susceptibility testing was performed using the MicroScan WalkAway system (Beckmann-Coulter, USA) or disk diffusion. Multiplex real-time PCR was performed on isolates resistant to third-generation cephalosporins to detect extended-spectrum beta-lactamases and AmpC-β-lactamases. Results Of 4675 screened women, 406 (9%) fulfilled the enrolment criteria, 31% (125/406) had culture-confirmed UTI. The median age was 30 years (interquartile range: 27-37) and 14% (17/125) were HIV-seropositive. Lower abdominal pain was the most frequent symptom (88%, 110/125). Most case-patients were treated with regimens including

metronidazole (62%), azithromycin (62%) and ceftriaxone (60%). Among 130 uropathogens, Escherichia coli (58%) and Group B Streptococcus (15%) predominated. Gram-negative (n=91) susceptibility to tested antibiotics was ≥80%, except to trimethoprim-sulfamethoxazole (47%, 95% CI 36-57) and tetracycline (59%, 95% CI 48-69). Only bla-CTX-M (n=3) and bla-TEM (n=2) were detected in 11 tested isolates. Susceptibility to gentamicin among Gram-positives (n=39) was 63% (95% CI 36-84). Conclusion We found typical community uropathogens and a low AMR prevalence, supporting current treatment guidelines including gentamicin as first-line agent for uncomplicated CA-UTIs. However, reduced susceptibility to gentamicin in Gram-positive bacteria underscores the need for ongoing community-based surveillance.

Keywords: Antimicrobial resistance, Community-acquired urinary tract infection

CD-O-10

"Every run is hard": Endurance athletes' experiences of return to sports participation after COVID-19

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Abstract: Background: Protracted return to sport commonly results from long-COVID and may result in emotional distress for athletes. The aim of this study was to explore symptom management and quality of life as South African endurance athletes return to pre-illness level of participation in sport. METHOD: A cross-sectional survey-based mixed-methods study was conducted among long-distance athletes. Quantitative data included sport and disease characteristics, fatigue scores, and management of persistent symptoms was expressed as percentages and frequencies. Qualitative data were collected through open-ended questions exploring the challenges faced when returning to sport post-COVID-19 convalescence and the impact on quality of life. RESULTS: A total of 295 survey responses were included. The mean age was 45.3 (10.2) years and 54.7% were male. High physical and mental fatigue scores were found. Three themes emerged: Challenges in returning to cardiopulmonary fitness, societal restrictions, and the impact on biopsychosocial wellness. Cardiopulmonary consequences, severity of the illness, exertional symptoms, long-standing fatigue, emotional distress, and individual resilience influenced return to sport. CONCLUSION: The biopsychosocial well-being of endurance athletes, especially in the masters-age group should not be overlooked. CLINICAL IMPLICATIONS: A multidisciplinary approach to managing long-term sequelae in a diverse population of athletes is vital, as the importance of resuming exercise exceeds the recreational value. These results suggest that coping strategies and training programs should be specific to disease severity, sex, fatigue, and endurance exercise. Understanding the perceived return to

sport challenges can achieve better outcomes for future health challenges resulting in a long-term exercise hiatus.

Keywords: COVID-19, return to sport, cardiopulmonary, quality of life

CD-O-11

Investigation of mono- and polymicrobial antibiofilm activities of Defensin-like antimicrobial peptide-2 against Candida auris and Pseudomonas aeruginosa

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Abstract: Multispecies infections and polymicrobial biofilms are increasing in prevalence and clinical significance around the globe and are becoming more challenging to treat due to increased expression of resistance genes. The focus pathogens, Candida auris MRL 6057 and Pseudomonas aeruginosa ATCC 27853, have three clinically significant characteristics in common, they, i) cause nosocomial infections and outbreaks; ii) are multi-drug resistant and iii) can form biofilms. Additionally, defensin molecules have been identified as potent and broad-spectrum potential antimicrobials, in serious need of further evaluation. The aim of this study was, therefore, to investigate the mono- and polymicrobial antibiofilm activities of DLAP-2 against C. auris and P. aeruginosa. The antimicrobial and antibiofilm effect of this defensin-like antimicrobial peptide was determined at immature and mature stages of development. Both treated and untreated biofilms were also grown, and visualised, using fluorescence microscopy. Additionally, the impact of DLAP-2 on membrane integrity of planktonic cells was evaluated using fluorescence microscopy. For the cytotoxicity assessment of DLAP-2, a haemolytic assay was performed. The results of this study suggest that DLAP-2 shows promising antimicrobial (with MIC and MBC/MFC values ranging from 62,5-250 µg/ml) and antibiofilm activity against polymicrobial biofilms (inhibition levels ranged from 20%-98%). Additionally, the mode of antimicrobial activity for DLAP-2 was confirmed as cell membrane permeabilization. The haemolytic assay also showed that, at lower concentrations (125 µg/ml and 250 µg/ml), DLAP-2 shows low levels of toxicity (< 10%). These results show that DLAP-2, if developed further, could be an effective therapeutic agent against complex and multispecies infections.

Keywords: Biofilms, multispecies infections, antimicrobial and antibiofilm therapeutic agent development

CD-O-12

The antimicrobial and toxicity analysis of essential oils used for vaginal infections

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Abstract: Current treatment options for vaginal infections are increasingly limited due to bacterial and fungal resistance. Furthermore, these treatments often have adverse effects on the vaginal microbiome. With existing therapies losing effectiveness, there is a drastic need for alternative approaches. Essential oils, known for their antimicrobial properties, have not been extensively studied for treating vaginal infections alone or in combination despite their recommended use by the layman. This study evaluates the antimicrobial activity by determining the minimum inhibitory concentration, (MIC) and toxicity (brine shrimp lethality assay) of 46 essential oils, both individually and in combination, against pathogens causing vaginal infections. These included Enterococcus faecalis, Gardnerella vaginalis, Peptostreptococcus anaerobius, Candida albicans, Candida tropicalis, Candida krusei, and Candida gasseri. Additionally, the effects of these essential oils on the vaginal probiotic bacteria (Lactobacilli) were assessed, followed by an interactive assessment using the fractional inhibitory concentration index (ΣFIC) to determine synergistic profiles. The in vitro susceptibility tests revealed that the essential oils Melissa officinalis exhibited one of the lowest MIC values at 0.16 mg/ml against bacterial pathogens, while Coriandrum sativum demonstrated the lowest MIC value at 0.13 mg/ml for fungal pathogens. Notably, Melissa officinalis interfered least with the Lactobacilli. The combination of Citrus bergamia with Styrax benzoin demonstrated antimicrobial synergy (ΣFIC ≤ 0.5). Toxicity assays indicated variability, with some oils displaying higher toxicity levels than others. These findings suggest that selected essential oils hold promise as alternative treatments for vaginal infections while having minimal effects on the vaginal biome.

Keywords: Vaginal infections; Essential oils; Bacterial vaginosis; Vulvovaginal candidiasis

CD-O-13

Optimization and validation of a nanofluidic qPCR method for serotyping Klebsiella pneumoniae

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Abstract: Background: Klebsiella pneumoniae is a leading cause of neonatal sepsis in Sub-Saharan Africa. Robust Surveillance systems and methods that allow for fast and reliable serotype detection are needed to guide research priorities and direct interventions aimed at reducing the

burden of K. pneumoniae disease. Method: A high throughput nanofluidic qPCR reaction set was developed to detect and serotype 13 O-loci (O1/O2v1, O1/O2v2, O1/O2v3, O3/O3a, O3b, O4, O5, O8, O12, OL101, OL102, OL103, OL104), 5 O-types (O1, O2a, O2ac,O2afg, O2aeh), and 15 K-loci (KL2, KL3, KL10, KL15, KL22, KL25, KL28, KL30, KL37, KL39, KL62, KL102, KL110, KL149, KL171) of K. pneumoniae. Clinical blood cultures collected from South African children ≤90 days of age, previously serotyped by Whole genome sequencing were used for comparison. Results: All assays within the nanofluidic qPCR reaction set effectively amplified all 37 targets within the prescribed efficiency range (92-107%). The variance from the linear equation of the regression curve was low (R2>0.99) while the analytical sensitivity was high (limit of detection: 10-100 gene equivalents). A blind analysis of 77 bacterial cultures showed perfect agreement between the methods for the detecting all O-loci and 99% agreement for detecting the O-types, with the methods being discrepant for a single sample (qPCR: O1, WGS: O2afg). Further, there was a 97% agreement between the methods for detection of the K-loci qPCR serotyping two samples as KL102 and KL28, whereas WGS typed them as KL149 and KL146, respectively. Conclusion: continuous monitoring, including relevant serotyping, will be important both before and after introducing new vaccines to assess their effectiveness. The nanofluidic qPCR method is a promising method to detect and serotype K. pneumoniae; however, additional K-loci targets will be needed to increase the number of serotypes that can be identified.

Keywords: Nanofluidic qPCR, Serotyping, Klebsiella pneumoniae, Neonatal Sepsis

CD-O-14

Dysfunctional glucose and fatty acid uptake in monocytes of people living with HIV

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Abstract: Cellular metabolism is a major determining factor in immunological function with implications for antiviral immunity. Metabolic dysfunction in people living with HIV (PLWH) leads to non-AIDS-related conditions. However, the metabolic function of innate immune cells in PLWH, particularly HIV controllers, is poorly reported in South African settings. We investigated the metabolic profiles of innate immune cells in PLWH. Human peripheral blood mononuclear cells (PBMCs) from HIV-elite controllers (n=11), HIV-progressors (n=10), PLWH on antiretroviral therapy (ART) (n=20) and HIV-uninfected persons (n=17) were assessed for metabolic uptake and mitochondrial health. Glut1 antibody for glucose transporter expression, fluorescently tagged metabolites 2-NBDG (2-[N-(7-nitrobenz-2-oxa-1,3-diazol-4-yl)amino]-2-deoxy-D-glucose) and BODIPY FL C16 (4,4-Difluoro-5,7-Dimethyl-4-Bora-3a,4a-Diaza-s-Indacene-3 Hexadecanoic-Acid)

for glucose and fatty acid uptake, and Mito Trackers Green and Deep Red for mitochondrial mass (MM) and membrane potential were measured by multicolour flow cytometry. Glut1 expression on monocytes of HIV-progressors was elevated compared to HIV-uninfected (p=0.03) and PLWH-ART (p=0.01). Reduced glucose uptake in monocytes was observed in HIV-elite controllers compared to HIV-uninfected individuals (p=0.04) and PLWH-ART (p=0.004). Fatty acid uptake was reduced in monocytes of HIV-progressors compared to PLWH-ART (p=0.0002) and HIV-uninfected individuals (p=0.02). Additionally, no significant differences in MM were observed between groups. There was, however, a trend towards increased MM in HIV-infected groups compared to HIV-uninfected individuals. In conclusion, innate immune cells in PLWH exhibit metabolic dysfunction demonstrated by the inability to uptake essential metabolites. These metabolic irregularities were also observed in HIV-elite controllers, despite spontaneous viral control, and may contribute to non-AIDS-related conditions.

Keywords: Immunometabolism, HIV controllers, Antigen-presenting cells, Glucose uptake

CD-O-15

Signal peptide mutations prevalent among RSV A AND B strains from Africa

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Abstract: Background: The RSV fusion protein is the major target for most vaccine development due to its conserved sequence. Aim: The aim of this study was to determine the amino acid diversity among African RSV strains F glycoproteins' signal peptides. Methods: The RSV F sequences were retrieved from GenBank and GISAID. Nextclade was used align F protein sequences and to construct phylogenetic trees. Sequences were compared to the RSV/A A2 long strain and RSV/B B1 reference strains using BioEdit and AliView. Results: Among 1035 African RSV F sequences from 2007-2022 the most prevalent subtype was RSV/B (89,86%, 930/1035). The dominant genotypes among RSV/A strains were GA2.3.5 (47.61%; 50/105) and GA2.3.3 (34.29%; 36/105). Both belongs to clade A23. While GB5.0.5a (66.88%; 622/930) and GB5.0.2 (28.93%; 269/930) were most prevalent for RSV/B and belongs to clade B6. Mutations in RSV/A F signal peptides were identified at four amino acid positions (I5T, A8T, T12A/I and L15F) at frequencies of <3%. T12AI and T8I/A mutations were found in genotype GA2.3.5 (clade A23) South African sequences from 2018 and 2020. The I5T and L15F mutations were among Egyptian strains from 2018-2019. L4P, H6Y, F12L and L15F mutations were observed in RSV/B strains. Discussion: Dominant African RSV/A genotypes were GA2.3.5 (A23) and GA2.3.3 (A23) and among RSV/B

strains GB5.0.5a (B6) and GB5.0.2 (B6). Signal peptide mutations identified in RSV/A include I5T, A8T, T12A/I and L15F and for RSV/B L4P, H6Y, F12L and L15F.

Keywords: RSV F protein, Signal peptide, Mutations, Sequences

CD-O-16

The impact of the ethical implications intertwined with Household Contact Investigation in households with newly diagnosed persons with TB: a qualitative study

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Abstract: Despite the widespread use of Household contact investigation (HCI), there is limited understanding regarding the influence and value placed on contact investigation by participants and how HCI impacts psychosocial factors (stigma, confidentiality, and disclosure) among persons with TB, their families, and communities. A qualitative study was conducted to understand the impacts of HCI on people living with TB and their household members in Limpopo province (Vhembe, and Capricorn) and in Soshanguve, Gauteng, South Africa. In-depth interviews and focus group discussions were conducted to explore the individual, interpersonal, and community-level perceptions of the impact of HCI to understand the ethical considerations in this commonly used approach. Thematic analysis was used to identify key themes. Twenty-four individual interviews and six focus group discussions (n=39 participants) were conducted. At the individual level, participants viewed HCI as an effective approach for identifying people with undiagnosed TB, educating households about TB symptoms and reducing health-related service barriers. At the interpersonal level, HCI assisted people in disclosing their TB status to family members for safety and facilitated family and social support. The introduction of HIV testing during HCI was reported as making household members uncomfortable, this influenced whether people tested for TB. HCI was felt to negatively impact community-level TB and HIV-related stigma because of healthcare worker visibility during investigation. If HCI is to be used as an approach to identify people with newly developed TB, greater efforts should be made to ensure concerns about ethical implementations such as community stigma and HIV testing are addressed.

Keywords: Tuberculosis, Qualitative research, Household contact investigation, Ethics

CD-O-17

The relationship between the combined effects of life-course trauma and HIV on cognitive impairment in rural South African adults

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Abstract: Lifecourse traumatic events (TE) refers to both childhood and adult trauma. Research suggests that lifecourse TE are independently associated with HIV and neurocognitive impairment, NCI. Little is known of the combined effect of life-course TE and HIV on NCI in adulthood. We used data from the Health and Aging in Africa: A Longitudinal Study of an INDEPTH Community in South Africa (HAALSI) to fill this gap. TE and HIV positive status were examined in relation to NCI measured by the Oxford Cognitive Screener (OCS-plus). We constructed unadjusted and adjusted logistic regression models to examine the combined effect of life course TE and HIV on NCI in older adults. We specified models to consider HIV and composite TE separately with an interaction term between HIV and TE. Of the 5,059 HAALSI cohort participants, the most prevalent TE was "ever experiencing severe financial hardship." The prevalence of NCI was 7% (n=352). The multiple logistic regression model with the interaction term of HIV and TE, suggested that those with HIV and composite TE had an increased odds of NCI 1.78 (95% CI: 1.04-3.04). The model further suggests that the odds of having NCI decreased by 64% (AOR=0.36; 95%CI: 0.25-0.52) and 59% (AOR=0.41; 95%CI: 0.24-0.75) among those who had some primary school (1-7 years) and some secondary school (8+ years), respectively compared to no education. Results suggest that lifecourse TE and HIV infection influence NCI. The effect of TE data collected at baseline and incident NCI at later waves.

Keywords: Adverse Childhood Experiences (ACEs), HIV prevalence, Adolescent Girls and Young Women (AGYW), Rural South Africa

CD-O-18

Building bridges: Exploring the integration of traditional and conventional medicine for infectious diseases.

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Abstract: The World Health Organisation in its' Traditional Medicine Strategy (2014 - 2023) highlighted integrative medicine as central to achieving extended patient healthcare. However, interactions between traditional and conventional medicine poses concern. A two-phase study was designed. Phase 1 aimed at investigating the prevalence of dual use of traditional and conventional medicines, amongst patients at a large public hospital in both Johannesburg (JHB) and KwaZulu-Natal (KZN). Phase 2 aimed to determine the in vitro interactive profiles of

conventional antimicrobials in combination with the most popular traditional medicinal plants for infectious diseases, purchased from two major muthi markets. Phase 1: A descriptive, cross-sectional, self-administered survey was conducted. Ethical clearance was obtained for the study. Phase 2: Interactive antimicrobial profiles between botanically validated plant material and conventional antimicrobials were determined using minimum inhibitory concentration assays and the interactions classified by calculating the sum of the fractional inhibitory concentration. A total of 1,632 antibiotic-plant combinations were tested against ESKAPE pathogens. Furthermore, 272 antifungal-plant combinations were tested against two yeasts. Phase 1: A far higher prevalence of traditional medicine use was found amongst participants in KZN (94%), as opposed to JHB (77%), with dual traditional-conventional medicine use exhibited in 32% (KZN) and 11% (JHB) of patients. Furthermore, medicinal plants were revealed commonly for their use in treating infections. Phase 2: Antibiotic-plant combinations exhibited synergistic (5.6%), antagonistic (49.6%), additive (7.5%) and non-interactive (37.3%) profiles. Antifungal-plant combinations demonstrated synergistic (0.7%), antagonistic (60.8%), additive (3.5%) and non-interactive (35.0%) profiles. The high prevalence of traditional health practices in South Africa, potential dual health system uses, and vast antagonism noted warrants attention to ensure safe, holistic patient treatment. Synergistic interactions offer foundational knowledge, potentially allowing for positive future clinical translations.

Keywords: Integrative medicine, prevalence, medicinal plants, antimicrobial interactions

POSTER PRESENTATIONS

CD-P-01

In vitro olorofim susceptibility testing against South African dimorphic fungal isolates

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Abstract: Dimorphic fungal infections pose significant risks to individuals with weakened immune systems. Emergomyces, Talaromyces, and Sporothrix schenckii are pathogens that change from hyphae to yeast upon entering the human host. Despite their complexity, these infections present various clinical symptoms, including oral, pharyngeal, and cutaneous manifestations. Existing treatments, such as amphotericin B and azole-class drugs, often have limited efficacy and may exacerbate conditions due to side effects. The emergence of new antifungal agents like olorofim offers promising alternatives. Olorofim inhibits fungal dihydroorotate dehydrogenase, disrupting pyrimidine biosynthesis and impeding fungal cell cycle progression. Previous studies

have shown olorofim's effectiveness against certain fungal species, indicating its potential as a therapeutic option. This research aims to evaluate olorofim's in vitro activity against South African dimorphic fungal isolates, including Emergomyces africanus, Emergomyces pasteurianus, Sporothrix schenckii, and Talaromyces marneffei. The study involves subculturing isolates, confirming their identification, and performing olorofim susceptibility testing using the broth microdilution method. Minimum inhibitory concentration (MIC) values of olorofim will be compared with those of other antifungal agents to assess its potency. The study anticipates olorofim demonstrating superior efficacy with lower MIC values compared to existing antifungal agents. Data analysis involves descriptive statistics and MIC comparisons. Ethical clearance has been obtained, and the project is funded by NICD-Centre for Healthcare Infections, Antimicrobial Resistance, and Mycoses (CHARM). This study aims to address the urgent need for better alternative medications against dimorphic fungal infections, particularly in immunocompromised populations.

Keywords: Olorofim, Dimorphic fungi, Antifungal-therapy

CD-P-02

Design of soluble envelope trimers from highly neutralization-resistant HIV-1 strains for the isolation of broadly neutralizing antibodies

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Abstract: Emerging resistance to existing broadly neutralizing antibodies (bNAbs) in circulating HIV-1 variants may compromise the efficacy of bNAbs used as prophylactics or those elicited by a future vaccine. Therefore, new bNAbs that are effective against these difficult-to-neutralize strains are needed. This project aims to use soluble envelope (Env) trimers derived from difficult-to-neutralise virus strains to isolate novel bNAbs from donors living with HIV, who developed broadly neutralising plasma antibody responses. Initially, 183 viruses were screened against 6 bNAbs in a pseudovirus-based neutralisation assay. The five most resistant viruses were selected for further screening using an expanded panel of 18 bNAbs. Three isolates displayed a highly neutralisation resistant phenotype and were not neutralised by 12/18 bNAbs tested. Plasma from

CAPRISA donors, with >30% neutralisation breadth, were screened for neutralisation activity against each isolate. The FRESH1388 isolate was potently neutralised by plasma from CAP287 (ID50>60000). A soluble Env SOSIP trimer, based on the FRESH1388 isolate, was designed, expressed and purified by nickel-affinity and size-exclusion chromatography. Characterisation by negative-staining electron microscopy confirmed the trimer was in the closed conformation. Antibody binding revealed the antigenicity of the trimer was similar to the envelope on the pseudovirus. B cells will be sorted from the peripheral blood mononuclear cells of CAP287, using the FRESH1388 trimer, followed by the isolation of antibodies from these cells. Trimers derived from difficult-to-neutralise strains can provide highly selective sorting baits, enabling the isolation of novel bNAbs from participants with cross-reactive neutralising plasma.

Keywords: HIV-1, bNAbs, neutralisation resistant

CD-P-03

Epidemiological distribution of Staphylococcus epidermidis in Gauteng Province, 2010-2014

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Abstract: Staphylococcus epidermidis is a commensal bacterium of human skin and mucus membranes, yet it has emerged as an important opportunistic pathogen, particularly in healthcare settings. The objective of this study was to characterise staph epi. Isolated from human samples submitted to the diagnostic laboratories in Gauteng province. 5455 Staphylococcus epidermidis isolates were obtained from diagnostic laboratories in Gauteng between 2010 and 2014. Crude- and factor-specific proportions for categorical variables and the corresponding 95% confidence intervals. A temporal graph was used to depict annual variation in the proportion of these isolates. Out of 5455 isolates, 51.9% were males and 46.8% were females. The highest proportion of isolates (24.7%) were obtained from children 0-4 years old, while the adolescents contributed the least proportion of isolates(1.7%). The highest proportion of isolates came from the City of Johannesburg district(46.1%), and the least came from Ekurhuleni district(4.4%). The majority were skin specimens (46.4%), with the least from respiratory specimens (6.7%). Seasons did not vary significantly. The proportion of isolates increased from 22.7% to 25.8% in 2010 and 2011, then declined from 15.9% to 13.2% from 2011 to 2013. There were no significant differences in the distribution across sexes and seasons with p=0.622 and p=0.211, respectively, but a significant association was found between age and specimen type in the chi-squared test(p=0.076). The burden of Staphylococcus epidermidis infection in the Gauteng province was underscored. Further research is required to investigate

the factors that contribute to the observed variations in the proportion of Staphylococcus epidermidis between the districts.

Keywords: Staphylococcus, Epidermidis, Proportion, Isolates, Specimens

CD-P-04

Pneumococci serotype distribution among hospitalized adults with community acquired pneumonia in South Africa in the COVID-19 era

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ALIVE;

Abstract: Recommendations for pneumococcal vaccination require periodic updating considering the ever-changing pneumococci epidemiology and licensure of new vaccines. Pneumococci epidemiology in the COVID-19 era remains unclear in South Africa. This study investigated pneumococci serotype distribution among hospitalized adults with presumed Community-Acquired Pneumonia (CAP) in the COVID-19 era in South Africa. We conducted secondary analysis of oronasopharyngeal and blood serotypes from lytA PCR positive samples from 317 adults admitted between March 2020 and October 2021 and followed up for two years. Prevalence and incidence rates (IR) were calculated, and incidence drivers explored by Poisson regression. Pneumococcal CAP prevalence was 23% (95% CI: 20.1 -25.3). Serotypes 1, 3, 4, 5, 8, 9A/V, 12A/B/F/44/46, 19F, 22A/F, 33A/F/37 had leading prevalence and IR in oronasopharynx while serotypes 1, 3, 4, 8, 6A/B, 11A/D, 19A had leading prevalence in blood. The oronasopharyngeal prevalence for the 13-valent pneumococcal conjugate vaccine (PCV13) serotypes was 13.6% (95% CI: 11.9-15.3). Oronasopharyngeal carriage prevalence for all serotypes was significantly higher in males (70%), 35-49 years old participants (75%) and smokers (73%) while prevalence for the 23-valent pneumococcal polysaccharide vaccine serotypes was significantly higher in HIV positive participants on ART (66%). The IR varied with period of testing with the lowest all-serotype incidence rate in March 2020-October 2020 when compared to March 2021-June 2021 (IRR= 0.30, 95% CI: 0.07-1.20). Pneumococci remained important in CAP

epidemiology in the COVID-19 era in South Africa albeit a big drop in 2020. Majority of the serotypes circulating in the COVID-19 era are included in PCV20.

Keywords: Pneumococci, serotype, distribution, COVID-19

CD-P-05

Evaluation of qualitative CMV-PCR using urine samples collected for the routine screening of congenital cytomegalovirus.

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Abstract: Congenital cytomegalovirus (cCMV) is a global public health concern and is one of the leading causes of sensorineural hearing loss. The burden of cCMV infection in developing countries is greater, with prevalence rates of 80-100% and over twice that reported in developed countries. The current standard of care is to screen all cCMV clinically symptomatic newborns within three weeks of life. While the qualitative detection of CMV from urine using PCR is the gold standard; however, this test has not been verified in some South African public health diagnostic laboratories. Therefore, this study aims to evaluate the performance of an existing qualitative cCMV DNA rt-PCR test using urine samples collected from newborns within three weeks of birth for the routine screening of cCMV infection at Charlotte Maxeke Johannesburg Academic Hospital. The accuracy was assessed using 46 samples, and precision (intra-assay) was determined using three replicates of urine samples with three different concentrations across three days. The level of detection (LoD) was verified by spiking cCMV controls in clinically negative urine samples. A total of 30 samples of varying concentrations were tested. The accuracy was represented by Cohen's Kappa of 0.909 (95% CI, 0.785-1.000), 94.44% sensitivity, 96.43% specificity, 44.99% PPV and 99.82% NPV. The overall coefficient of variation (CV) of the replicates tested was 7.37%. The verified LoD was a cycle threshold of =37.5. The findings illustrate the effectiveness of rt-PCR using urine samples, demonstrating a precise and accurate method to screen for, detect and diagnose cCMV infections in newborns.

Keywords: Congenital CMV, Real-time qualitative PCR, Newborn, Urine screening

CD-P-06

Design of smart eutectics for oral delivery of bio-sensitive active pharmaceutical ingredients for the treatment of diarrhoeal diseases

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Abstract: The present research proposes the formulation of a eutectic microparticulate system for the delivery of an antimicrobial peptide for the treatment and prevention of infectious diseases, specifically diarrhoeal diseases. Infectious diarrhoea is a leading cause of infant mortality. Antimicrobial peptides have demonstrated direct killing of bacterial cells, and some can play a role in the innate immune system. Although antimicrobial peptides have been characterised as early as 1980, this form of drug therapy has yet to see extensive commercial use. This is partly due to peptide drugs being notoriously difficult to deliver via any route other than the parenteral route. The proposed system is designed to overcome the challenges associated with the oral delivery of pharmaceutical peptides in adults and paediatrics, such as poor stability and bioavailability. A eutectic core containing the peptide and components, such as pH modifiers and enzyme inhibitors, as well as polymers for intestinal muco-adhesion, were developed; and coated employing an enteric polymer blend for the site-specific delivery to the small intestine. Various physicochemical and physico-mechanical methods of analysis were undertaken to determine the optimal formulation. A eutectic mixture was successfully developed that melts at 36°C. The eutectic was subsequently incorporated into the enteric microspheres. In vitro studies were performed using Dissolution Apparatus USP II and analysed using UV Spectroscopy demonstrated that pH responsive microspheres protected a model peptide (BSA) from the harsh gastric environment (pH 1.2) and slowly released the peptide in the small intestine (pH 6.7). The eutectic microparticulate

Keywords: Infectious-Disease, Anti-Microbial Resistance, Anti-microbial Peptide, Eutectic

CD-P-07

Application of Viral like particles (VLP) to mimic SARS-CoV-2 Omicron BA. 4/5 infection

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Abstract: The SARS-CoV-2 pandemic began in 2019 and has since devastated the world. In response to global demand, the first mRNA-based vaccines were developed - these vaccines

encoded for the major SARS-CoV-2 spike (S) protein. This protein is one of four major proteins present within the SARS-CoV-2 viral particle. The others include the membrane (M), envelope (E) and nucleocapsid (N) proteins which play a role in SARS-CoV-2 infective capacity and antibody interactions. Current research and infection models are based on lentiviral vectors pseudotyped with the spike protein, only. Hence, the M, E and N proteins are not included within these models. Therefore, a more accurate infection model is required for better vaccine screening and potential therapeutic development. This model should include spike as well as non-spike proteins to better mimic an in vivo infection. This model should also accommodate for the emergence of new mRNA vaccine-resistant subvariants, namely the Omicron BA. 4/5 subvariant. This study aims to produce and characterise viral-like particles (VLPs) using structural protein encoding sequences from the Omicron BA. 4/5 SARS-CoV-2 subvariants in an attempt to improve infection model efficiency for the development of disease intervention strategies.

Keywords: SARS-CoV-2; Virus-like particles; Omicron BA 4/5 and Infection model

CD-P-08

CITA gene as a potential diagnostic marker for detection of TB-HIV infection

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Abstract: Tuberculosis (TB) and Human Immunodeficiency Virus (HIV) co-infection poses a significant public health challenge globally. Efforts to combat these diseases are hindered by limited diagnostic tools and treatment options. This study aims to investigate the potential of the class II major histocompatibility complex transactivator (CITA) gene as a diagnostic marker for detecting TB-HIV co-infections. The study objectives include extracting RNA from formalin-fixed paraffin-embedded (FFPE) tissue samples, converting RNA to complementary DNA (CDNA), amplifying the CITA gene via conventional polymerase chain reaction (PCR), and comparing CITA gene expression levels between TB-HIV co-infected individuals and healthy controls using real-time PCR. Understanding the role of CITA gene expression in TB-HIV co-infection may provide valuable insights into disease pathogenesis and aid in the development of targeted diagnostic and therapeutic strategies.

Keywords: TB, HIV, CITA, Real-time PCR

CD-P-09

Performance evaluation of the LumiraDx point-of-care analyzer for reliable HbA1c measurement in diabetes diagnosis and monitoring

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Abstract: According to the IDF Diabetes Atlas (2021), undiagnosed diabetes affects 45.4% of South Africans, emphasizing the need for accessible and simplified testing. Point-of-care testing offers a diagnostic solution with remote usability, eliminating centralized laboratory dependency and sample transportation. The LumiraDx point-of-care analyzer was evaluated for measuring glycated hemoglobin (HbA1c) levels, following the Clinical and Laboratory Standards Institute (CLSI) guidelines and assessing precision, accuracy, linearity, and lot-to-lot variation. The evaluation used quality controls and clinical specimens within the assay's measuring range (4.0% to 14.0%) and considered manufacturer claims and external standards for acceptability. The precision analysis over 5 days and inter-instrument analysis for a single day demonstrated overall consistent and accurate measurements, with within-run coefficient of variation (CV) ranging from 0.5% to 0.9% and between-run CV ranging from 0.6% to 1.0% while inter-instrument CV ranged from 0.9% to 9.4%. The linearity analysis showed that the analyzer produced reliable results across the HbA1c measuring range, with a slope of 0.99 and an intercept of 0.48. The LumiraDx analyzer exhibited a strong correlation (r=0.98) and minimal bias (0.06) compared to a gold-standard reference method. Additionally, the lot-to-lot variation analysis showed consistency and agreement between different test strip lots, with a concordance correlation coefficient exceeding 0.95 for each lot. These findings support the reliability, accuracy, and consistency of the LumiraDx analyzer for measuring HbA1c. The performance of the LumiraDx analyzer for the measurement of HbA1c in the laboratory was thus satisfactory. Clinical validation to evaluate performance in a real-world setting (public hospital) is on-going.

Keywords: Diabetes, Point-of-care testing, HbA1c, Evaluation

CD-P-10

Production, characterisation, and immunogenicity testing of novel SARS-CoV-2 BA.2.86-based mRNA vaccines

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Abstract: The first SARS-CoV-2 vaccines approved for emergency use were based on conventional mRNA design. Self-amplifying RNA (saRNA) vaccines are highly immunogenic and able to confer protection at lower doses compared to conventional mRNA vaccines. This may be beneficial in LMICs as they would be cheaper. The SARS-CoV-2 spike genome has continued to mutate resulting in highly immune evasive variants, such as BA.2.86 which possesses over 30 additional mutations in its spike glycoprotein, compared to its ancestral Omicron BA.2 variant. Due to its antigenic divergence, we aim to assess whether an mRNA vaccine based on this variant will elicit strain-specific or cross-reactive antibody responses towards highly conserved sites of the spike, by comparing two SARS-CoV-2 BA.2.86-based mRNA vaccines based on conventional and self-amplifying mRNA technologies. The codon-optimised DNA sequence encoding the BA.2.86 spike was cloned into an mRNA expression vector using Type IIS restriction enzymes. Positive clones were screened before bulk-preparation. Plasmids were linearised prior to in vitro transcription (IVT) and post-transcriptional capping. Purified mRNA will be formulated in an ionizable lipid nanoparticle and injected intramuscularly into mice to establish immunogenicity. We will express and purify the soluble BA.2.86 spike trimer which will be used together with other antigens in a multiplex luminex assay to assess binding responses. Lastly, a pseudovirus-based neutralization assay will be conducted to assess neutralizing responses elicited after vaccination. If the BA.2.86-based saRNA vaccine is observed to elicit broader responses than first-generation conventional mRNA SARS-CoV-2 vaccines, it may serve as a potential next-generation vaccine candidate going forward.

Keywords: Conventional mRNA, Self-amplifying RNA, BA.2.86, Immunogenicity

CD-P-11

Cryptococcus surveillance for flucytosine susceptibility testing in South Africa

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Abstract: Cryptococcal meningitis (CM) is mainly caused by two species-complexes within the Cryptococcus genus: Cryptococcus neoformans and Cryptococcus gattii. Flucytosine combined with amphotericin B and fluconazole is essential for HIV-associated CM induction treatment. Flucytosine resistance could theoretically occur in recurrent episodes despite initial combination treatment. We aimed to perform flucytosine susceptibility of recurrent isolates. Cryptococcus isolates from patients with recurrent CM (defined as laboratory confirmation >30 days after first confirmed laboratory diagnosis) were submitted to a reference laboratory from 01/09/2022 to 03/01/2024. Isolates were identified to species-complex level using matrix-assisted laser desorption/ ionisation time of flight mass spectrometry and flucytosine susceptibility was

performed by broth microdilution using Clinical and Laboratory Standards Institute (CLSI) guidelines. The CLSI epidemiological cut-off values (ECVs) for flucytosine are ≤8 μg/ml for C. neoformans and ≤4 μg/ml for C. gattii. Ninety-eight percent (127/130) of recurrent isolates were C. neoformans and 2% were C. gattii (3/130). Out of 81 isolates that were tested for flucytosine susceptibility, 64 (79%) had a minimum inhibitory concentration (MIC) value of ≤8 μg/ml (MIC50: 4 μg/ml, MIC90: 16 μg/ml, range: 0.125 - 64 μg/ml); however, there were 17 C. neoformans isolates (21%) that had a MIC ≥16 μg/ml. More than a fifth of isolates from recurrent disease episodes had flucytosine MICs in the non-wild type range. Analysis of mutations in resistance genes needs to be performed to determine whether these isolates are truly non-wild-type. Incident isolates for these cases also need to be tested to determine if MICs changed substantially from baseline.

Keywords: Cryptococcus, Flucytosine, Susceptibility testing

CD-P-12

Exploring HIV Risk Factors, Risk Perception, and Risk-Taking among Adolescent Girls and Young Women in Rural South Africa

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Abstract: Adolescent girls and young women (AGYW) face a disproportionately high risk of HIV acquisition, with biological susceptibility, sexual risk behaviours, and structural factors contributing to this vulnerability. Despite these risks, AGYW often perceive themselves as being at low risk of HIV acquisition, which can hinder engagement with HIV prevention services. This study seeks to explore the complex landscape of HIV risk among AGYW in the high HIV-burden setting of uMkhanyakude district, rural KwaZulu-Natal, South Africa. Specifically, this study aims to explore the correlations between behaviour-based risk, self-perceived risk, and risk-taking propensity among AGYW. This cross-sectional study will recruit a representative sample of n=250 AGYW aged 18-30 years from the Africa Health Research Institute (AHRI) demographic surveillance area. Risk-taking propensity will be assessed using the Balloon Analogue Risk Task (BART), alongside two self-reported measures (Perceived Risk of HIV Scale and VOICE Risk Score) to assess self-perceived risk of HIV and HIV risk factors. Findings from this study will explore the relationship between AGYWs HIV risk factors based on behaviour-based risk, subjective self-

perceived risk, and appetite for risk taking, which may influence risky sexual behaviours. Furthermore, the feasibility of the BART as a tool to measure risk-taking propensity in this population is a novel approach to understanding AGYWs likelihood of risk-taking behaviour. This study will inform the development of tailored HIV prevention strategies for AGYW in the district, addressing the unique challenges they face in the context of rural South Africa's high HIV burden.

Keywords: AGWY; Risk Perception; BART

CD-P-13

Title: An evaluation of laboratory-based techniques for the detection of Mycobacterium tuberculosis complex

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Abstract: The World Health Organisation lists Tuberculosis as the world's second leading cause of death in 2022 from a single infectious agent. Diagnostic innovations are a key component in managing the global burden of disease, including molecular-based pre-processing. The aim of this project is to evaluate and compare extraction and extraction-free pre-processing techniques for the detection of Mycobacterium tuberculosis complex (MTBC) for potential use in high-throughput downstream testing. Two automated extraction kits, TB-DNA (TianLong, China) and Hamilton NucleoMag Pathogen (Machery-Nagel, Germany) were used. Thermal lysis, vortex bead-beating, and Stabilyse (MolBio Diagnostics, India) were used as extraction-free methods. Each method was performed three times, consisting of ten-fold serial dilutions (neat, 1:10, 1:100, 1:1000, 1:10000, 1:100000) of ATCC 25177 MTBC reference strain (Davies Diagnostics, South Africa), in triplicate, giving a total of 54 specimens per method. A quantitative PCR (qPCR) was performed to analyse the efficiency of MTBC detection by comparing the cycle threshold value for MTBC insertion elements, IS6110 and IS1081. The methods were also evaluated based on ease-of-use. The detection rate of the methods for each dilution are as follows: TB-DNA (7/9, 7/9, 7/9, 7/9, 7/9, 9/9), Hamilton NucleoMag (9/9, 8/9, 8/9, 9/9, 9/9, 9/9), thermal lysis (9/9, 9/9, 8/9, 9/9, 9/9, 7/9), vortex bead-beating (9/9, 9/9, 9/9, 9/9, 9/9, 8/9) and Stabilyse (9/9, 9/9, 9/9, 9/9, 9/9, 9/9). The ease-of-use of extraction-free methods is better as they are simple and fast. Extraction-free methods also show efficient MTBC detection and potential as a pre-processing method for high-throughput testing.

Keywords: Mycobacterium tuberulosis, diagnostics, molecular-based techniques, high-throughput screening

CD-P-14

Cryptococcal Antigenaemia Screening and Treatment - Observations from the field in South Africa (CASTOFF-SA)

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Abstract: Cryptococcal meningitis accounts for 19% of HIV-associated deaths globally. Cryptococcal antigenaemia (CA) is a silent health condition that precedes meningitis in asymptomatic patients and is defined by presence of cryptococcal antigen (CrAg) in the blood that has not yet spread to the cerebrospinal fluid. Whilst current guidelines suggest single antifungal medication for CA, the EFFECT trial is assessing the efficacy of dual therapy for meningitis prevention. This sub-study uses questionnaires and focus group discussions (FGDs) with primary care staff at 12 South African EFFECT sites and data from EFFECT patient tracing logs to elucidate healthcare professionals' perspectives and identify barriers to care for patients with cryptococcal disease. While 58% of questionnaire responses (n=52) correctly identified Cryptococcus as a fungus and 87% recognised advanced HIV disease as a risk factor, only 25% were aware of asymptomatic disease, and 24% correctly defined CA, the majority of whom were doctors. Common FGD themes included infrequent encounters with asymptomatic CrAg-positive patients, heterogeneous methods to identify CrAg-positive results (leading to delay and missed cases), and difficulties contacting patients due to expired phone numbers, informal addresses and high migration rate. EFFECT staff logged a median of 2 contact attempts per participant (n=219), requiring 30 minutes of time. 64% of patients were successfully traced and attended

clinic within 7 days of a positive CrAg result. This project identifies multiple challenges at several stages of primary care management of early cryptococcal disease in South Africa. Future efforts should prioritise practical, sustainable solutions and evaluate their effectiveness.

Keywords: HIV, Cryptococcus, primary care

CD-P-15

Molecular characterisation of Escherichia coli collected from an urban river in Johannesburg, South Africa - A one Health Approach

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Abstract: The Jukskei River is polluted by sewage inflows from nearby buildings without sewage systems, stormwater runoffs, and informal settlements along the riverbank. This study aimed to detect and characterize Escherichia coli from the Jukskei River. Traditional culture methods were used to enumerate and isolate E. coli from water samples collected from five locations along the Jukskei River. Oxford nanopore was used to determine serotypes, sequence types, and genes associated with virulence and antibiotic resistance. The relationship between E. coli from the Jukskei River, human, and animal origin was investigated using genomes from Enterobase. Water samples were contaminated with varying levels of E. coli at the five collection sites, with mean counts ranging from 4.94 to 6.52 log10CFU/mL. Most isolates were non-diarrhegenic strains, with 44% being enterotoxigenic and one being an atypical enteropathogenic strain. Most of the isolates were ST1946 and were further classified into seven serotypes, with 59% being O16:H48. There were eight FimTypes identified among the E. coli isolates, including fimH27 (55%), fimH34 (11%), and fimH305 (11%). All the E. coli harbored various virulence genes and no resistance genes were detected. Escherichia coli isolates from the Jukskie were unrelated to any of the isolates included in the phylogenetic tree from humans and animals. In conclusion, the Jukskei River has the potential to serve as a vehicle for transmitting waterborne diseases, particularly in the already vulnerable Alexander informal settlement located along the river banks.

Keywords: Escherichia coli, River, Whole genome sequencing

CD-P-16

Seroprevalence of anti-rubella virus and anti-hepatitis A virus immunoglobulin G antibodies among Health Science students at the University of the Witwatersrand

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Deaprtment of Vaccinology

abstract: Background: Rubella and hepatitis A virus (HAV) are endemic in South Africa. Rubella is important because of the risk of Congenital Rubella syndrome in infants. The seroprevalence of rubella in South Africa is unknown and the vaccine has only been integrated in the national immunization program in early 2024. This study aimed to determine the seroprevalence of rubella in this population prior to vaccine roll out. HAV is important because South Africa is at the cusp of transitioning from an area of high to intermediate endemicity. FHS students are in the middle of this transition because of their age and their future role as health workers. Understanding the seroprevalence of HAV among this population may influence policy for the introduction of the HAV vaccine in South Africa. Hence, this study aimed to assess the seroprevalence of rubella and hepatitis A IgG among students of the faculty of health sciences of the university of the Witwatersrand. Method: Blood samples were collected and tested for anti-rubella and anti-HAV IgG. Results: The seroprevalence of rubella and hepatitis A among students of the FHS was 93.3% and 53.7% respectively Sex, degree of study and vaccination history were significantly associated with rubella seropositivity while race, level of study (clinical vs preclinical) and vaccine history (recall) were significantly associated with HAV seropositivity. Conclusion: Rubella seroprevalence was high in this population. Seroprevalence of HAV was low in this population indicating an increasing immunity gap in the population as South Africa has transitioned to intermediate endemicity.

Keywords: Rubella, Hepatitis A, Immunoglobulin G, Seroprevalence

CD-P-17

Development of immunoreagents and assays for immunological surveillance of respiratory syncytial virus

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Abstract: Respiratory Syncytial Virus (RSV) is a leading cause of infant and child mortality, particularly in low- and middle-income countries (LMICs). The imminent roll-out of maternal RSV prefusion-F-protein (pre-F) vaccines locally highlights the need for immunological surveillance. We describe the development of immunoreagents and assays to monitor the impact of RSV Fusion protein (F) mutations. We expressed and purified seven anti-pre-F mAbs (2.4K, ADI-15560, Clesrovimab, CR9501, MPE8, Nirsevimab, and Palivizumab), validating their purity and function using SDS-PAGE and ELISA. We produced RSV F vesicular stomatitis virus (VSV) pseudoparticles (VSV-F) and optimized their infection across 37 conditions, varying cell type and density, incubation times, cell-seeding, freezing, and thawing conditions. Additionally, pseudovirus constructs with F cytoplasmic tail (CT) modifications were evaluated for infectivity compared to unmodified pseudoviruses. Lastly, we identified pre-F antigenic site mutations in currently circulating South African RSV sequences. In-house anti-pre-F mAbs bound successfully to RSV F protein, with CR9501, Nirsevimab and 2.4K mAbs showing high preference for the quaternary conformation. CT modifications resulted in 4- to 8-fold increase in RSV pseudovirus infection, with infection optimal in Vero cells, at 5x106 cells/plate after 24 hours. We identified N63S, S276N, and S211N mutations in F sites targeted by approved anti-RSV mAb prophylactics, Palivizumab and Nirsevimab. Overall, we produced functional anti-RSV mAbs and VSV-F pseudoparticles, the latter which offers advantages over lentiviral pseudoviruses in regions with high ARV usage. We identified mutations with potential implications on RSV interventions and population immunity, which will be confirmed for impact in future studies.

Keywords: RSV, Immunoreagents, Assays, Immunosurveillance

CD-P-18

Limited toxicity and initial evidence of influenza A/B viruses' neuraminidase inhibition by plants used by South Africans to treat respiratory symptoms

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Abstract: Respiratory diseases fall in the top 10 leading causes of death worldwide and approximately 550 million individuals worldwide experience respiratory infections including with influenza A and B viruses. Synthetic drugs have adverse effects like toxicity and influenza vaccines are required to be updated yearly and limited doses are annually available in South Africa.

Medicinal plant product use for primary health care in Africa is as high as 80% of populations, compared to licensed antiviral therapies. Herbal and purified natural medicine products offer valuable resources for novel drug development. Parts of 39 plants species were dried and milled. A dichloromethane solution were used for organic extraction. Organic plant extracts' toxicity was determined in a brine shrimp lethality assay. Extracts were screened to assess the ability to inhibit influenza viruses' neuraminidases using the NA-XTD assay (Thermofisher). A total of 41 organic plant extracts were toxic of which 4 (9.8%) displayed toxicity over 24 hrs, and 8 (19.5%) over 48 hrs at 2mg/ml. The influenza assay resulted in 16 (39.0%) plant extracts with an average inhibition percentage greater than 95% against influenza SF30/18 Byam strain, at 2mg/ml. Furthermore, 17 (41.5%) plant extracts have an average inhibition percentage greater than 95% against influenza 1092/18 A H1N1 strain at 2mg/ml. There are predominantly 15 plant species that have exhibited activity against the Influenza H1N1 and Byam strains. Plant extracts displayed inhibitory properties against influenza A and B. Next steps will be to estimate the 50% inhibitory concentrations for the plants that showed inhibitory activity,

Keywords: Plant extracts, Toxicity, Influenza, Inhibition

CD-P-19

The functional capacity of antigen presenting cells is altered in South African HIV-1 elite controllers

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Abstract: HIV controllers can spontaneously control HIV-1 infection without antiretroviral treatment but remain at risk of developing non-AIDS-related conditions. Studies on elite controllers (ECs) have demonstrated that the adaptive immune system is key in mediating viraemic control. However, the innate immune response remains understudied. We assessed the quality of the innate immune response by measuring the phenotype and function of antigen-presenting cells (APCs) in people living with HIV (PLWH) in South Africa. A total of 76 black South

Africans comprising HIV-elite controllers (n=17), HIV-progressors (n=20), PLWH on antiretroviral therapy (n=20) and HIV-uninfected individuals (n=19) were included in this study. Multicolour flow cytometry using cryopreserved peripheral blood mononuclear cells was performed to analyse monocyte subpopulations, monocyte activation and the capacity of APCs to produce TNF-α, INF-α, and IL-1β, following stimulation with Toll-like receptor TLR-4 (LPS), TLR-7/8 (CL097), and TLR-9 (CpG) ligands for 18 hours. Additionally, plasma biomarkers, soluble CD14 (sCD14) and D-dimer were measured using enzyme-linked immunosorbent assay. Our findings show a reduced frequency of classical monocyte subsets in ECs (p=0.02), and HIV-progressors (p=0.04) compared to HIV-uninfected individuals. Additionally, TNF-α production in mDCS, pDCs and monocytes was lower in ECs compared to HIV-uninfected individuals post-stimulation with TLR-4, TLR-7/8 (all $p<0.05$) and sCD14 levels were elevated in ECs compared to HIV-uninfected individuals (p=0.01). D-dimer levels were elevated in HIV-progressors compared to PLWH-ART (p=0.01) and ECs (p=0.04). In conclusion, the innate immune profile of ECs was characterised by high levels of activation, reduced frequency of classical monocytes and biomarkers associated with unfavourable disease outcomes.

Keywords: Elite controllers. TLR-ligands. Antigen-presenting cells.

CD-P-20

Epidemiology and antimicrobial susceptibility profile of Escherichia coli blood culture isolates in South Africa, April to September 2023

Naseema Bulbulia

Abstract: Invasive infections caused by Escherichia coli can result in serious consequences, including death. We aimed to describe the epidemiology of E. coli bloodstream infections (BSI) and antimicrobial susceptibility testing (AST) patterns. We conducted surveillance at 17 public-sector hospitals in 4 provinces between April and September 2023. We enrolled patients with E. coli cultured from normally-sterile sites and confirmed identification using MALDI-TOF-MS (Bruker-Daltonik, USA). NHLS diagnostic laboratories' AST results for confirmed isolates were obtained from the NICD Surveillance Data Warehouse. We report clinical and epidemiological characteristics, and AST patterns of cases of BSI (i.e. E. coli cultured from blood). Of the 1694 cases reported, 51% (n=865) were BSI and 54% (438/811) of these were community-acquired (defined as an infection diagnosed ≤48 hours of admission). The median age was 45 years (interquartile range (IQR): 22-63) and 52% (443/860) were females. Most patients had ≥1 underlying condition (63%, 474/749) and diabetes mellitus was the most common (21%, 149/722); 27% (176/645) were HIV-seropositive with a median CD4 cell count of 145 cells/µl (IQR: 41-365). At specimen collection, 89% (671/758) had an intravenous line in-situ and 32%

(236/509) had an indwelling urinary catheter. The 30-day in-hospital mortality was 36% (284/785). Susceptibility to ciprofloxacin was 65% (524/811), 94% (532/568) to nitrofurantoin, 67% (544/813) to 3rd-generation cephalosporins, 76% (621/817) to aminoglycosides and 92% (752/815) to carbapenems. Among patients with E. coli BSI, infections mainly originated from the community and in-hospital mortality was high. Nonetheless, antimicrobial susceptibility was relatively stable.

Keywords: Epidemiology, Antimicrobial susceptibility , Ecol

CD-P-21

To bee or not to bee: The anti-Helicobacter pylori activity of South African bee products

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Abstract: Helicobacter pylori is implicated in numerous ailments, including gastric ulcers. Current treatments for H. pylori infections often results in a rapid gain in resistance and gut microbiome dysbiosis. Bee products have been used for centuries for medicinal purposes, including treating inflammation and gastric ulcers. While several studies globally have investigated the anti-H. pylori properties of honey, investigation into a comprehensive range of southern African honey was yet to be explored. Propolis, a resin-like substance produced by bees, has shown anti-H. pylori activity globally. South African propolis, however, was yet to be explored. This study aimed to investigate South African honey and propolis for its antimicrobial activity against H. pylori. Honey (76 samples) and propolis (51 samples) were sourced directly from apiarists in South Africa. The broth microdilution and agar dilution assays were carried out to determine the minimum inhibitory concentrations (MIC) of ethanolic propolis extracts and honey respectively. A total of 27 propolis extracts had noteworthy antimicrobial activity against at least one H. pylori strain (MIC ≤ 0.51 mg/mL). All propolis extracts investigated were considered non-toxic when evaluated using the brine shrimp lethality assay. A third of the investigated honey samples demonstrated noteworthy anti-H. pylori activity (MIC ≤ 8.33% v/v). Selected combinations of honey with probiotics showed a greater increase in anti-H. pylori activity. The results of this study show the in vitro potential of utilizing honey and propolis as treatment options for H. pylori infections, as well as the benefit of including probiotic species as a potentiator of activity.

Keywords: Helicobacter pylori, Honey, Propolis, Antimicrobial activity

CD-P-22

DIVERSITY AND IMPACT OF MUTATIONS AMONG SOUTH AFRICAN SARS-COV-2 SPIKE PROTEINS' SIGNAL PEPTIDES, 2020-2022

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Abstract: The S13I mutation in the signal peptide of SARS-CoV-2 was reported to improve secretion of the spike (S) protein. This study aims to assess the diversity of South African SARS-CoV-2 S proteins' signal peptides from 2020 to 2022. In this study, 2618 genomic sequences of SARS-CoV-2 strains circulating in South Africa between 2020 and 2022 were downloaded from GISAID and analyzed using BioEdit and Aliview. Nextclade was also used to find the differences between other sequences and the SARS-CoV-2 reference sequence and to design phylogenetic trees. Among South African sequences, Omicron accounted for 48.62% (1273/2618), Delta for 29.18% (764/2618), and Beta for 11.88% (311/2618). Most of the Omicron VOCs in South Africa were lineage BA.4.1 (29.69%, 378/1273). South Africa had limited circulation of the Alpha VOC (0.95%, 25/2618). Only 9.9% (239/2417) of derived S proteins had complete or partial SP sequences. Positional amino acid variations were observed at positions 3 (V>G), 5 (L>F), and 9 (P>L) at rates of 7.36% (178/2417), 0.29% (7/2417), and 2.23% (54/2417), respectively. The V3G mutation was mainly observed in Omicron VOC BA.4 (89.9%, 160/178) sublineages. The P9L mutation was predominantly observed in the C.1.2 lineages (98.1%, 53/54). Globally, the V3G, L5F, and P9L dominated among North American strains at 39.04% (32150/82340), 58.7% (49369/84153; 2020-2021), and 40.5% (2321/5733; 2022), respectively. Further work will assess the impact of these mutations on SARS-CoV-2 spike proteins' expression.

Keywords: SARS-COV-2, Mutations, Spike protein, Signal peptide

CD-P-23

Production of M. tuberculosis (TB) mRNA-based vaccine candidates

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Abstract: TB incidence in South Africa remains stubbornly high with World Health Organisation estimates at 468 infected individuals per 100,000 of the population in 2022. Most immunocompetent individuals eliminate or restrict TB infection. To identify potential suitable antigens for use in vaccines, TCR sequencing was done in antigen specific CD4+ T cell milieu of 166 individuals with M. tuberculosis that either progressed to tuberculosis (n=48) or controlled infection (n=118). Analysis of T cells in the cohort of M. tuberculosis infected individuals enabled identification of peptides (CFP-10, PE13, PPE18 and WbbL1) targeted by TCR-ß sequences associated with the control of infection. Consequently, codon optimised, and uridine-depleted coding sequences derived from peptide sequences were used for in vitro transcription (IVT) with co-transcriptional capping and subsequent lipid formulation containing the SM102 ionisable lipid (Moderna). Vaccine candidate characterisation in culture confirmed antigen expression as well as intra-cellular, membrane and extracellular localisation of peptides. The data produced permits further work, namely, immunogenicity, and challenge studies to proceed.

Keywords: TB, vaccine, mRNA

CD-P-24

Characterisation of Candida species that colonise the skin of neonates admitted to a regional hospital in Gauteng Province, South Africa

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Abstract: Microorganisms that colonise the gastrointestinal tract, mucous membranes, skin, monitoring devices, and indwelling lines of admitted neonates are implicated in healthcare-associated invasive infections. We aimed to determine the prevalence and characterisation of Candida species colonising the skin of neonates admitted to a regional South African hospital. Between October 2021 and April 2022, skin samples of admitted neonates were collected from the umbilicus, axilla and groin area using flocked swabs, throughout their hospital stay. Candida species isolated were identified. Antifungal susceptibility testing and whole genome sequencing

was performed for Candida auris and C. parapsilosis isolates. A total of 265 skin swabs were collected from 93 neonates. Candida colonisation was detected in 92 skin swabs from 42/93 (45%) neonates. In this neonatal unit with intermittently-reported clusters of candidaemia, C. parapsilosis was the most common Candida species (70%, 64/92) followed by C. auris (20%, 18/92), C. albicans (10%, 9/92), and C. krusei (1%, 1/92). The odds of colonisation by Candida spp was higher among neonates admitted for >72 hours (34/42) compared to neonates admitted for <72 hours (1/13) (OR = 0.02, 95% CI, 0.00-0.18; p<0.001). Most C. parapsilosis (70%, 45/64) and C. auris (94%, 17/18) isolates were fluconazole-resistant (MIC ≥ 8 μg/mL and ≥32 μg/mL respectively), and 28% (5/18) of C. auris isolates were considered amphotericin B-resistant (MIC of ≥2 μg/mL). Understanding the prevalence, distribution and susceptibility of Candida colonizing isolates in a unit can help guide infection prevention measures, and empiric treatment options for neonates with suspected invasive Candida infection.

Keywords: Candida, Neonates, Colonisation, Antifungal susceptibility

CD-P-25

Evaluation of the antimicrobial bioactivity of trihydroxy benzoic acid derivatives.

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Abstract: This study aims to evaluate the bioactivity of hydroxybenzoic acid (HBA) derivatives. Primarily, HBAs are used in pharmaceuticals, cosmetics, and food because of their bioactivity. Some HBA bioactivity features include antioxidant, antibacterial, anti-inflammatory, anticancer, and neuroprotective properties. HBAs are ideal candidates for medicinal applications because of their bioavailability, low toxicity, and antioxidant properties. Additionally, their ability to circulate in the body and manifest antimicrobial activity underscores their potential to combat microbial infections. An inherent need for more affordable and potent drugs alongside the rise in microbial resistance to conventional drugs, has necessitated the design and development of novel compounds to combat diseases. Objectives aligned with the aim toward addressing the aforementioned challenges include; the design of novel derivatives, determination of bioactivity through in silico techniques, synthesis, characterization of the derivatives (using Fourier Transform Infrared spectroscopy (FTIR), Nuclear Magnetic Resonance spectroscopy (NMR), and Mass Spectrometry (MS)), and determination of antimicrobial potential against four bacterial and four fungal species through microbial assays (Minimum Inhibitory Concentration, Minimum Bactericidal Concentration, and Minimum Fungicidal Concentration: Staphylococcus aureus,

Streptococcus pyogenes, Escherichia coli, Pseudomonas aeruginosa, Candida albicans, Candida glabrata, Candida parapsilosis, and Candida tropicalis). Computational screening conducted showed that derivatives fulfilled requirements for orally active drugs and displayed desirable potential bioactivities. Confirmation of synthesis of derivatives was through MS and FTIR. Full characterization will ensue as well as determination of the microbial activity and cytotoxicity (on normal HEK cells) resulting in the identification of antimicrobial derivates.

Keywords: Hydroxybenzoic acid, in-silico, antimicrobial activity

CD-P-26

Adeno-associated viral vector delivery of anti-HBV TALENs

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Abstract: Hepatitis B Virus (HBV) infection is a global health problem that is responsible for significant morbidity and mortality from chronic liver disease. The number of people co-infected with Human Immunodeficiency Virus (HIV) and HBV is around 5% to 30%, placing great strain on our debilitated healthcare system. This emphasis the need to find a suitable therapy for HBV despite the availability of several approved drugs. Gene editing technologies such as those using transcription activator-like effector nucleases (TALENs) designed to target the four open reading frames of the HBV genome have demonstrated good efficacy in vitro and in vivo. Progression of these anti-HBV TALENs to clinical application has been delayed due to the lack of a suitable delivery vehicle. Adeno-associated viruses (AAVs) have demonstrated great potential as delivery vehicles with many being translated into Food and Drug Administration (FDA) approved therapies. This study aimed to generate and characterize rAAV2 and rAAV8 viral vectors that express anti-HBV TALENs. Thus far, delivery of AAV packaged Firefly Luciferase has resulted in Luciferase expression observed in Huh 7 cells and HBV transgenic mice for 12 weeks. AAV packaged anti-HBV TALENs were able to demonstrate gene silencing in cell culture models as well as in mice infected with AAV8 carrying the HBV genome. No vector induced toxicity was detected in vitro and in vivo. These promising results indicate that AAVs can be used as a delivery tool for anti-HBV therapies. This is the first study to identify AAVs as a delivery vehicle for

Keywords: AAVs, Anti-HBV Talens, HBV, Gene silencing

CD-P-27

Assessing HIV prevention effective use in routine service settings: a methodology using self-report at last sex

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Abstract: Background: Daily pill taking during exposure periods is required for oral PrEP to effectively prevent HIV acquisition. However, oral PrEP use may be cyclical, used during risk periods. Other methods may effectively prevent HIV acquisition. We propose a simple method of assessing HIV prevention effective use, that could be used in routine services. Methods: We analysed self-reported data on PrEP and condom use at last sex, from a cohort of participants enrolled in a PrEP implementation science study, attending follow-up visits between August - November 2023. We determined whether their last sex act was protected by PrEP, condoms, or both. Condom protection definition: having used a condom at last vaginal and/or anal sex; Oral PrEP protection definition: having taken PrEP for seven days prior, on the day of, and 7 days after sex (or if sex was ≤7 days ago, every day since last sex). Results: Data for 272 follow-up visits, among 241 oral PrEP users were analysed, after excluding observations among participants missing key data variables. Of 272 sex acts reported, 21.0% (n=57) were protected by condoms and PrEP, 53.3% (n=145) by PrEP only, 9.6% (n=26) by condoms only and 16.2% (n=44) were not protected. Conclusions: Self-reported PrEP and condom use at last sex may be a useful indicator of effective prevention use in routine service settings. Participant recall of date of last sex, condom and PrEP use was high, although incomplete. Adaptation to this method to calculate effective dapivirine ring and cabotegravir use, by sex type, is planned.

Keywords: PrEP, effective use, HIV prevention