27th SMLTSA CONGRESS

24 - 26 October 2025

Stellenbosch · South Africa

BOOK OF ABSTRACTS

WELCOME TO SMLTSA

SAVING LIVES, ONE SPECIMEN AT A TIME

Science | Technology | People

The Society of Medical Laboratory Technology of South Africa (SMLTSA) is committed to promoting the ideals of medical laboratory science that align with the needs of our community within a unified healthcare system. SMLTSA hosts a bi-annual national congress to provide a platform to showcase studies and developments within our profession. We encourage all medical laboratory professionals to participate in national and international congresses pertinent to their scope of profession.

Our Vision

To remain the voice of Medical Technology in South Africa, ensuring that the perspectives of Medical Laboratory Professionals are considered in policy-making that impacts pathology testing across Southern Africa.

Leading Innovation

SMLTSA supports scientific research with a world-class journal that empowers laboratory professionals to contribute to the advancement of laboratory medicine. By embracing research, we guarantee that our services remain current and relevant to the local healthcare landscape.

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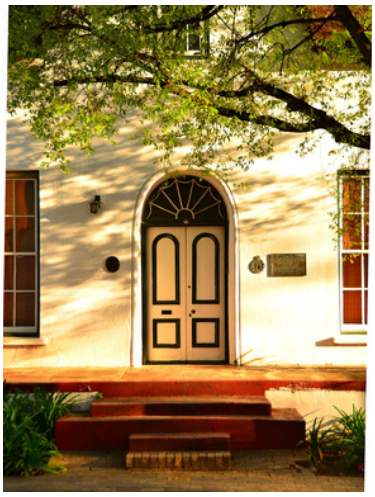

#SMLTSA2025

WELCOME TO STELLENBOSCH!

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On behalf of the Society of Medical Laboratory Technology of South Africa (SMLTSA) and the Local Organising Committee, we are thrilled to welcome you to the **27th National Congress of the Society of Medical Laboratory Technology of South Africa.**

This year's congress theme, "**Beyond Boundaries: Transforming Lab Science Through Technology & Innovation,"** encapsulates the spirit of progress and innovation that drives our profession forward. The 2025 Congress will celebrate the pivotal role of laboratory science in harnessing cutting-edge advancements, such as artificial intelligence, molecular diagnostics, and sustainable practices. It is a call to action for all professionals and industry leaders to collaborate in shaping the future of healthcare across the African continent and beyond.

Let us come together to **celebrate Africa's extraordinary contributions** to laboratory science, foster meaningful connections, and explore the endless possibilities of what lies beyond boundaries.

We look forward to collaborating with you and to create an unforgettable gathering of minds, ideas, and innovation.

Welkom - Wamkelekile - Welkom!

The Local Organising Committee
SMLTSA 2025 Congress

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ABSTRACTS
ORAL PRESENTATIONS

LISTED ALPHABETICALLY BY AUTHOR SURNAME

ADDRESSING GAPS IN LOCAL VIROLOGICAL SURVEILLANCE THROUGH AUTOMATED DATA VISUALIZATION TOOLS

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Background:
South Africa's virology laboratories generate large volumes of diagnostic data daily, yet much of this information remains underutilized for public health planning or operational improvement. Virology-based epidemiological research is particularly sparse at a local level, limiting our ability to monitor viral disease trends, identify outbreaks early, or address service delivery inefficiencies. This project aimed to build an automated and secure data pipeline that transforms routine laboratory results into interactive dashboards for epidemiological insight and performance monitoring.

Methods:
Routine laboratory test result files from the National Health Laboratory Service (NHLS) were anonymized, cleaned, and merged using Python scripts and custom modules. Cleaned datasets were visualized using Streamlit dashboards hosted on a secure Linux-based server. Dashboards display test volumes, weekly positivity trends, age and sex distribution of positives, turnaround time metrics, and hospital-level sample distribution. Access to data and downloadable content is password-restricted to ensure compliance with the Protection of Personal Information Act (POPIA). Development was supported by generative AI tools to accelerate coding and interface design.

Results:
The dashboards enable dynamic exploration of both epidemiological and operational trends across multiple virological test sets. Users can track weekly positivity rates for key infections such as Human Immunodeficiency Virus (HIV), Hepatitis B, and respiratory viruses. Turnaround time visualizations highlight processing delays, particularly for inter-provincial sample referrals. Within the Tygerberg Virology Laboratory, daily test volumes and result completion rates can be monitored to assess workload distribution and laboratory efficiency. These insights provide an adaptable framework for identifying bottlenecks, reallocating resources, and guiding public health response.

Conclusion:
Automated data visualization tools can bridge the gap between routine virology diagnostics and meaningful public health intelligence. By combining open-source technologies with strict data governance, such platforms enable timely identification of operational challenges and epidemiological patterns—empowering laboratories to contribute more actively to public health strategy and local research.

THE FUTURE OF DIAGNOSTICS AND THE ROLE OF INDUSTRY IN BROADENING ACCESS TO CARE

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Poverty-related diseases cause a huge burden on global health, yet there is limited public health and laboratory information surrounding many of these communicable and non-communicable diseases in low to middle income countries (LMICs). Use of high-quality diagnostics at the point-of-care may provide valuable epidemiological data, fundamental to the development and implementation of strategies for diagnosis, treatment, and prevention. Access to reliable, available, and affordable diagnostic testing remains a challenge in LMIC's with disparity in healthcare institutions. There are industry activities which can be prioritised to support improved access to new technologies for patient care and treatment

Clinical diagnostic tests generally require access to clinical laboratories with sophisticated technologies, expensive equipment, and highly skilled personnel, with testing often centralized to larger central laboratories, demanding specialised logistics further increasing costs and turn-around time to results. Some rapid diagnostic tests used outside the laboratory, at the point-of-care level, often do not meet the necessary quality standards to be reliable in the environment where they are most needed.

In resource-limited laboratory settings, healthcare providers are forced to make treatment decisions based solely on clinical presentation, which may yield incomplete diagnoses and thus affect patient's healthcare and safety.

While diagnostic testing accounts for minimal global healthcare spending, they impact approx. 70% of medical decisions and thus in many LMIC's where healthcare systems are in development, the use of quality, safe diagnostics can help direct evidence-based treatment resulting in improved allocation of resources and funding.

To ensure greater equity in access to new technologies, priority support activities for industry could encompass the following:

- ✔ Strengthening of global and regional leadership
- ✔ Surveillance and sharing of data to enable tracking the next outbreak and the tools required to mobilise responses and resources.
- ✔ Investment in localised manufacturing of products which could suit African populations and allow for broader access to vaccines, therapeutics and diagnostics
- ✔ Alignment of regulatory systems continent-wide to ensure safe, efficacious and quality products.

A CROSS-SECTIONAL STUDY OF ALLOIMMUNIZATION AND INFLAMMATORY MARKERS IN MULTI-TRANSFUSED SICKLE CELL PATIENTS

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Background: Sickle cell disease (SCD) is a haemolytic anaemia commonly treated with frequent blood transfusions which is associated with high levels of alloimmunization and alloantibody development. Although controversial, it has been suggested that the increased chronic inflammation observed in SCD could be the cause. This study therefore aimed to explore the relationship between haematological parameters, inflammatory markers, and alloimmunization in multi-transfused SCD patients recruited from the Obafemi University Health Centre in Nigeria.

Methods: A comparative cross-sectional study which enrolled 50 multi-transfused adults with homozygous SCD and 50 similarly transfused age- and sex-matched individuals without SCD was performed. Full blood counts and differentials were processed on an SFRI H18 Light auto-analyser (France) while red cell antigen typing was carried out using saline and anti-human globulin methods. Blood groups (ABO and Rhesus) were determined by direct tile testing and inflammatory markers including C-reactive protein (CRP), tumour necrosis factor (TNF), interleukin-6 (IL-6), and interleukin-1β (IL-1β) were measured using ELISA. Data analysis was performed using SPSS v24.0 and GraphPad Prism v8. A p value of <0.05 was considered significant.

Results: As expected, patients with SCD had reduced red cells and haemoglobin. Platelet counts were elevated however values remained within normal limits. White cell and neutrophil counts were increased suggesting inflammation and additional markers such as CRP and TNF were significantly higher compared to those without SCD. Participants with SCD had developed elevated alloantibodies to Kell, Jka and Fya however no significant association between any inflammatory marker and alloimmunization rates was observed.

Conclusion: In this study those with SCD had high levels of alloimmunization as well as increased markers of inflammation when compared to controls, however, no significant association with alloimmunization could be detected. This suggests that the causes of the high alloimmunization rates are multifactorial and involve other processes which require further investigation.

INTEGRATING GENOMICS INTO MEDICAL LABORATORY SCIENCE EDUCATION: PREPARING GRADUATES FOR A MOLECULAR FUTURE

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Since the dawn of the genomics era and the advent of massively paralleled sequencing technologies, there has been an increasing global shift towards personalized or precision medicine. These advances have been rapidly absorbed into molecular diagnostic methodologies, steadily transforming the landscape of biomedical laboratory science.

In a responsive step, the Department of Biomedical Sciences at Cape Peninsula University of Technology (CPUT) has introduced Genomics as a dedicated subject within the Bachelor of Health Science (BHSc) in Medical Laboratory Science degree programme with the aim to equip students with fundamental and applied genomics knowledge to keep abreast with developments in molecular diagnostics.

This presentation reports on the rationale, conceptualization and implementation of the Genomics subject for the BHSc Medical Laboratory Science degree at CPUT. The curriculum centres around the core concepts in genetics, and various molecular methods of detection of genetic variation.

A blended learning model is used, integrating lectures, case-based learning, wet lab practical sessions, and bioinformatics exercises to support both theoretical understanding and skill development. In this presentation, we highlight how academic training can align with industry evolution to ensure future readiness of graduates. We also highlight key teaching innovations in resource-constrained contexts and how lessons learned during planning and implementation of the subject will be able to aid other institutions considering similar curriculum offers.

OPTICAL GENOME MAPPING: A NEW FRONTIER IN CYTOGENOMICS FOR RARE DISEASE AND CANCER DIAGNOSTICS

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Optical Genome Mapping (OGM) is an emerging, high-resolution technology that is revolutionizing molecular diagnostics, particularly within the realm of cytogenetics. This presentation will explore how OGM overcomes limitations in current cytogenetic testing methods, offering a more comprehensive and higher-resolution view of structural variations (SVs) across the genome.

Traditional cytogenetic techniques, such as karyotyping and fluorescence in situ hybridization (FISH), have long been the cornerstone of genetic analysis. Karyotyping, while providing a global view of the genome, suffers from low resolution, often missing critical SVs. FISH, conversely, is targeted and limited by the number of probes used. Chromosomal microarrays (CMAs) detect copy number variations but fail to identify balanced rearrangements, which are crucial in disease pathogenesis. OGM addresses these limitations by directly visualizing long, intact DNA molecules labelled at specific sequence motifs. This approach enables detection of all classes of SVs; including deletions, duplications, inversions, translocations, and complex rearrangements, in a single assay, without the need for cell culture.

In haematological malignancies, where accurate genomic profiling directly informs prognosis and treatment decisions, OGM has demonstrated superior sensitivity in detecting clinically relevant aberrations. We present cases from our experience where OGM uncovered cryptic translocations in B-cell Acute Lymphoblastic Leukaemia (B-ALL) and complex rearrangements in Diffuse Large B-cell Lymphoma (DLBCL) that were either missed or would not have been detected using standard cytogenetic techniques. These findings directly impacted clinical management and risk stratification.

Beyond oncology, multiple international studies have demonstrated the utility of OGM in diagnosing rare genetic diseases, particularly in cases where conventional testing, sequencing and CMA yield inconclusive results.

This presentation will explore how OGM is redefining the landscape of molecular diagnostics, bringing us closer to comprehensive, genome-wide precision diagnostics for both cancer and rare genetic disorders.

THE IN VITRO ANTIMICROBIAL EFFECT OF SOUTH AFRICAN GERANIUM (PELARGONIUM SIDOIDES) HOMEOPATHIC PLANT-BASED REMEDIES ON VARIOUS MULTIDRUG-RESISTANT ESKAPE PATHOGENS

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The widespread use of antibiotics in clinical practice and non-compliance by patients, has resulted in drug resistance. It is estimated that over 700 000 people die from antimicrobial resistant (AMR) infections every year, and that by 2050 AMR will surpass cancer as a cause of death. The World Health Organization (WHO) recognises AMR as a serious threat to global health and has singled out the emergence of high risk ESKAPE spp. pathogens (Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, Enterobacter cloacae and Escherichia coli), as a potential cause of highly invasive infections in susceptible patients. The increasing incidence of AMR raises an urgent need to identify and isolate new bioactive compounds from medicinal plants. The South African geranium plant called Pelargonium sidoides does exhibit some forms of antimicrobial properties. However, current studies lack the utilisation of modern analytical procedures when investigating medicinal plants' antimicrobial properties, in relation to their possible mechanisms of action and bioactive components.

This quantitative in vitro study investigated various homeopathic preparations of Pelargonium sidoides remedies as a treatment option for infections caused by the above identified major WHO AMR ESKAPE spp. The antimicrobial minimal inhibitory concentration (MIC) of these extracts were determined using standardised in vitro antimicrobial susceptibility Kirby Bauer disk diffusion and broth microdilution methods, with comparatives to conventional antibiotics, as well as investigated its safety and toxicity profile utilising mammalian cell culture.

Since no studies to date have explored the utilisation of accredited Pelargonium sidoides homeopathic preparations against WHO AMR ESKAPE spp., the outcomes from this study led to original and novel research, whereby the possible future use of these medicinal plant-derived remedies to treat AMR infections could possibly become a reality.

THE IN VITRO ANTIFUNGAL EFFECT OF NATIVE SOUTH AFRICAN CALENDULA OFFICINALIS AND PELARGONIUM SIDOIDES MEDICINAL PLANT EXTRACTS ON VARIOUS MULTIDRUG-RESISTANT STRAINS OF CANDIDA SPECIES

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Background: It is estimated that more than one billion people suffer worldwide from fungus-related infections which places a massive burden on healthcare professionals in choosing these anti-fungal agents. *Candida species* (*Candida spp.*) can cause highly invasive infections in susceptible patients. Currently it has become increasingly difficult to treat some *Candida spp.*-related infections, as they have developed antifungal resistance (AFR). According to the severity ranked by the World Health Organization (WHO), *C. albicans*, *C. glabrata*, *C. tropicalis*, and *C. parapsilosis*, are categorised as high-risk and *C. krusei* as medium-risk strains for multidrug resistance.

Objectives: To evaluate the following phytochemical plant extracts in singular form as a possible complementary treatment against AFR fungi: *Calendula officinalis*, belonging to Asteraceae family, commonly known as pot marigold, extracts have shown excellent anti-inflammatory properties and antifungal activity against *C. albicans*, making it an effective and safe alternative treatment to treat fungal infections. *Pelargonium sidoides* root extract has shown *in vitro* activity against *C. albicans* infections, by increasing the oxidative burst of human phagocytes. However, both these extracts have not been investigated in research as a possible AFR treatment in homeopathic and herbal preparations and so warrant further investigation.

Methodology and results: This quantitative *in vitro* study using CLSI guidelines, investigated the above-mentioned medicinal plant-derived extracts as possible complementary treatment for AFR fungi. The minimal inhibitory concentration (MIC) was determined using accredited *in vitro* antifungal susceptibility and the Kirby Bauer disk diffusion and broth microdilution methods, with comparatives to conventional antibiotics, as well as investigated their safety and toxicity profiles using MTT mammalian cell culture.

Outcome: The outcomes of this study led to original and novel research, with significant findings and so future research on these medicinal plant extracts is warranted to validate their plausibility to treat AFR infections *in vivo*.

THE CLINICAL UTILITY OF NEXT GENERATION SEQUENCING (NGS) IN THE DIAGNOSIS OF INHERITED HAEMOLYTIC ANAEMIA.

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Introduction

The inherited haemolytic anaemias are caused by abnormalities of the red cell membrane, haemoglobin or red cell enzymes. Whilst in most cases, a diagnosis can be made using conventional diagnostic methods, there are instances when genetic analysis becomes necessary for definitive diagnoses. A study was therefore conducted to investigate the clinical utility of next generation sequencing (NGS) for the diagnosis of inherited haemolytic anaemia in South Africa.

Methods

Patient samples for this study were selected from routine specimens submitted to the laboratory for haemoglobinopathy screening. A total of 53 samples were collected over a period of 24 months (Jan 2021 – Dec 2022). Targeted NGS was performed using an Agilent SureSelect$^{XT\ HS}$ protocol, with a custom designed panel, with a size of 152.16 kbp (Design ID: 3366281) according to the manufacturer's protocol. The resulting libraries were sequenced on an Illumina NextSeq 2000 using a P1 flow cell, generating 6.25 million reads per sample. Bioinformatics analysis was completed via the Illumina DRAGEN somatic pipeline. Coverage of the genes included genes encoding globin chains, selected red cell membrane proteins and red cell enzymes.

Results

The following abnormalities were obtained:

- Fifteen red cell membrane disorders viz.: a) Ten hereditary spherocytosis of which two were previously diagnosed on red cell membrane protein analysis, b) Two pyropoikilocytosis, c) Two elliptocytosis, d) One hereditary xerocytosis. Of the red cell membrane disorders, 13 were suspected on blood smear microscopy.
- Fourteen Hb variants viz.: a) Ten sickle cell disease (homozygous and compound heterozygous states), b) Three Hb variants that were not detected or identified by conventional methods (one alpha chain and two beta chain variants), c) one HbA2 variant
- Ten red cell enzyme defects viz.: a) Six glucose-6-phosphate dehydrogenase, of which four were incidental findings, b) Two glucose phosphate isomerase, of which one was previously diagnosed through quantitative enzymatic assay; c) One pyruvate kinase, d) One pyrimidine 5'nucleotidase

The diagnosis remains obscure in 4 subjects since no pathogenic abnormalities were detected.

Conclusion:

NGS is a useful tool that can be employed as an adjunct to conventional diagnostic methods for the diagnosis of inherited haemolytic anaemias, and has the advantage of sequencing a large number of genes in a single run.

A SOUTH AFRICAN PERSPECTIVE OF THE PREVALENCE AND ASSOCIATION OF COMMON MYELOPROLIFERATIVE MUTATIONS WITH AGE AND GENDER

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Introduction: Advancements in molecular diagnostics have revolutionised the identification and understanding of myeloproliferative neoplasms (MPNs), yet Africa remains underrepresented in global cancer statistics due to insufficient population-based data. Harnessing big data and technology-driven analytics, this study aims to bridge that gap by evaluating the frequency and association of common MPN mutations with patient demographics in South Africa.

Methods: This retrospective cross-sectional study evaluated MPN cytogenetic results (JAK-2 V617F, JAK-2 exon 12, CALR, MPL, and BCR/ABL1) and patient demographic (age and gender) to determine associations and MPN mutation frequencies. Data was extracted from the National Health Laboratory Service Central Data Warehouse for patients aged 18-years and older from 01/01/2018 to 31/05/2023. Statistical associations were analysed using Fisher's Exact Test and Pearson Chi-Square Test ($p<0.05$ significant), with effect size calculated using Phi or Cramer's V respectively.

Results: Out of 11,384 patient records analysed, 8,934 were included for statistical analysis, while 2,450 were excluded due to incomplete information or patients being under 18-years. Among the included records, 58% were male (n = 5,175) and 42% were female (n = 3,759), revealing a skewed testing ratio. The mean patient age was 50 ± 17 years. Mutation frequencies were BCR/ABL1 (18.2%, n = 1,627/3,329) with an equal sex incidence, JAK-2 V617F (8.5%, n = 756/5,090) with a female predominance and increased frequency with age, and low frequencies for CALR (0.5%, n = 48/333) and MPL (0.04%, n = 4/222). JAK-2 exon 12 was not detected (n = 0/108).

Conclusion: This study highlights the transformative potential of large-scale laboratory data analytics in uncovering population-specific genetic trends in MPNs. BCR/ABL1 mutations were most prevalent, especially in younger individuals, while JAK-2 V617F showed a significant association with aging and female predominance. CALR, MPL and JAK-2 exon 12 are rare occurrences in South Africa.

TITLE: ELEVATED LEVELS OF TNF-A ASSOCIATED WITH ENDOTHELIAL DYSFUNCTION

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Keywords: Cardiovascular disease, Diabetes mellitus, Endothelial dysfunction, Cytokines, Carotid intima-media thickness.

Introduction: Cardiovascular disease (CVD) is the most common complication and leading cause of death in individuals with type 2 diabetes mellitus. Endothelial dysfunction (ED) and inflammation are considered early events of CVD. Early detection of these processes could enable timely intervention, reducing long-term complications. Current methods for ED have many disadvantages and fail to detect its early onset. This study aimed to investigate a panel of endothelial-associated inflammatory cytokines and chemokines as early biomarkers of ED.

Methods: This quantitative study involved 38 participants of mixed ancestry in an urban South African population. Serum samples were analysed for the expression of interleukin 8 (IL-8), interferon-gamma (IFN-γ), Tumour necrosis factor-alpha (TNF-α), and the macrophage inflammatory protein-1 beta (MIP-1β) using the Bio-Plex ProTM Human Cytokine Assay kit, processed on a Lasec Bio-Rad Bio-Plex 200 multiplex instrument. Ultrasound was used to measure CIMT, which served as a surrogate marker of vascular health to classify participants into groups with and without ED. Appropriate statistical tests were used to compare the levels of measured cytokines, where a p-value of <0.05 was considered statistically significant.

Results: There was a significant difference in the median expression of TNF-α in those participants with ED compared with the normal group ($P=0.016$). Spearman correlation revealed that TNF-α had a moderate positive association with IFN-γ ($r=0.337$; $p=0.039$) and MIP-1β ($r=0.488$; $p=0.002$). A strong positive correlation was noted between Total Cholesterol (TC) and Low-Density Lipoprotein (LDL) ($r=0.805$; $p = <0.001$); suggesting an increased risk of thrombotic events, a common complication of ED.

Conclusion: The main finding of this study was the significantly increased TNF-α expression in those with ED. This suggests that the measurement of endothelial-associated cytokine and chemokine expression may be a useful alternative to more cumbersome methods. Future studies are needed to validate these findings and expand the panel of cytokines.

THE DIAGNOSTIC USE OF CELL BLOCK TECHNIQUE VERSUS THE CONVENTIONAL SMEAR IN SEROUS FLUID FOR CYTOLOGICAL ASSESSMENT IN GA-RANKUWA, SOUTH AFRICA

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BACKGROUND AND OBJECTIVES:
The accurate identification of cells as either malignant or reactive mesothelial cells is a diagnostic problem in conventional cytological smears. Distinguishing benign from malignant cellular changes may require meticulous screening, scrutiny of cellular features and an understanding of the range of reactive changes. Cell block preparation increases the sensitivity of detecting malignancies and could reduce false-positive interpretations. The aim of the study was to determine the diagnostic accuracy of cell block technique by comparing with conventional cytological smears for cytopathological diagnosis of serous effusion.

METHODS:

Randomly sampled serous fluids were divided for analysis by both conventional cytological methods and the cell block technique. Conventional smears were stained with May-Grünwald-Giemsa and Papanicolaou stains, while cell blocks underwent histological processing. The slides were examined and data from 50 samples were analysed using Epi Info version 7.1.5 to calculate sensitivity, specificity, positive predictive value, and negative predictive value, with results cross-tabulated for comparative analysis. The International System for Reporting Serous Fluid Cytopathology was employed to document both conventional smear and cell block results.

RESULTS:
The study analyzed 50 serous effusion samples, with 62% from males and 38% from females, with a median age of 54 years. Of these cases, 68% were from the pleural cavity, while 32% were from the peritoneal cavity. The agreement for both methods to identify benign was 76.0% with moderate kappa statistics of 0.487% and sensitivity of 89.7%. While the positive and negative predictive values were 74.2% and 80.0%, respectively.

CONCLUSION:
The study concludes that cell block technique when used as an adjuvant to routine smear examination increases diagnostic yield because of availability of more material for evaluation and better preservation of the cytoarchitectural pattern.

THE EFFECT OF THE COVID-19 PANDEMIC ON CERVICAL CANCER SCREENING ACROSS GAUTENG DISTRICTS

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Introduction

Cervical cancer ranks as the fourth most common cancer globally and is the second leading cause of cancer-related deaths in South Africa. Routine screening for precursor lesions, followed by timely referral and treatment, is essential to prevent progression to cervical cancer. In 2017, South Africa implemented the Cervical Cancer Control Policy, which strengthened national screening guidelines. However, in March 2020, the onset of the COVID-19 pandemic and subsequent lockdowns, though effective in limiting virus transmission, severely disrupted routine healthcare services—including cervical cancer screening programs.

Methodology

This retrospective study assessed the impact of the COVID-19 pandemic on cervical cancer screening services across the five districts of Gauteng Province. Facility-level pap smear data was extracted from the National Health Laboratory Service (NHLS) Central Data Warehouse (CDW) for the period January 2017 to December 2022. Data were stratified into three periods: pre-COVID (2017–2019), COVID phase (2020–2021), and post-COVID phase (2022). Screening coverage, precancerous lesions and cervical cancer prevalence is presented graphically by district.

Results

Pap smear screening volumes in Gauteng increased from 2017 to 2019 aligning with the 2017 Department of Health cervical cancer policy. However, during the COVID phase, screening volumes declined sharply and continued to decrease in 2022. Rates of abnormal smears requiring biopsy referral peaked in 2020 in two of the five districts. However, cytological diagnoses of cervical cancer declined during both the COVID and post-COVID periods.

Conclusion

The COVID-19 pandemic significantly disrupted cervical cancer screening services in Gauteng, with declines persisting into the post-pandemic period. Strengthening screening recovery efforts, risk-based screening and ensuring timely referral for abnormal findings are essential to improve outcomes and reduce cervical cancer-related morbidity and mortality.

APPLICATION OF SIGMA METRICS IN INTERNAL QUALITY CONTROL OPTIMISATION FOR A NEWLY IMPLEMENTED SIEMENS ATELLICA AUTOMATION LINE IN THE NATIONAL HEALTH LABORATORY SERVICE (NHLS), CHARLOTTE MAXEKE JOHANNESBURG ACADEMIC HOSPITAL (CMJHA) CHEMICAL PATHOLOGY DEPARTMENT

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Introduction: Sigma Metrics, derived from Six Sigma methodology, provides an objective framework to evaluate analytical performance and guide internal quality control (IQC) strategies. Applying Sigma principles allows laboratories to optimize IQC frequency, reduce operational costs, and maintain patient safety through improved diagnostic accuracy.

Objective: To evaluate assay performance on the newly implemented Siemens Atellica automation system using Sigma Metrics, and to apply the results to risk-based internal quality control (IQC) optimization at the CMJAH Chemical Pathology Laboratory between November 2024 and April 2025.

Method: IQC data from the 1 November 2024 to 30 April 2025 was analysed following implementation of the Siemens Atellica platform, using third-party Biorad Multiqual IQC materials. A total of 23 levels of Biorad Multiqual IQC were utilized for general chemistry tests. Total Allowable Error (TEa) targets were based on minimum European Federation of Clinical Chemistry and Laboratory Medicine (EFLM) analytical performance specifications. Sigma values were calculated using the formula: Sigma = (TEa - Bias) / CV, where CV was determined from internal QC and bias from EQA/PT results. Analytes were classified based on Sigma thresholds to guide QC decision-making.

Results: The Sigma Metrics classification for the evaluated analytes indicated varying levels of performance across the parameters assessed. Excellent performance (Sigma >10) was observed for Alkaline Phosphatase (up to 14.5), AST, Iron, and LDH, reflecting highly reliable analytical quality. Very good performance (Sigma 6–10) was achieved by ALT, Magnesium, and Creatinine, while acceptable performance (Sigma 4–6) was noted for Calcium, Total Cholesterol, Uric Acid, and Phosphorus. In contrast, suboptimal performance (Sigma <3) was observed for CO_2, LDL Cholesterol, Total Protein, and Chloride. It is important to note that the initial suboptimal performance observed for CO_2 was attributed to pre-analytical IQC handling challenges, which have since been resolved.

Conclusion: The Six Sigma analysis enabled risk-based optimisation of the laboratory's IQC protocol. Based on assay performance, QC frequency may be safely reduced for high-performing assays, while IMT electrolytes (Sodium, Potassium, Chloride) are scheduled for increased QC frequency (three times daily) due to their clinical importance and observed variability. Continued Sigma monitoring is recommended to ensure ongoing performance and alignment with ISO 15189:2022 standards.

ESSENTIAL IMMUNOHISTOCHEMISTRY PANEL FOR CNS TUMOURS: BRIDGING MORPHOLOGY AND MOLECULAR DIAGNOSTICS

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Background: Accurate classification of central nervous system (CNS) tumours is critical for therapeutic decision-making and prognostication. The 2021 WHO Classification incorporates molecular alterations into essential diagnostic criteria, but access to advanced molecular techniques remains limited in many regions. Immunohistochemistry (IHC) provides a cost-effective surrogate for certain molecular alterations, bridging morphology and genetics.

Methods: We reviewed the diagnostic utility of IHC markers available at JDW Pathology, guided by the 2021 WHO framework and recent literature. An essential IHC panel was constructed to categorise tumour cell lineage, proliferation, and entity-defining molecular alterations. Validation emphasised antibody clone reliability, internal controls, and interpretive thresholds.

Results: The essential panel included GFAP and OLIG2 to prove glial lineage, and IDH1 R132H, ATRX and p53 for gliomas. INI1 and BRG1 identified rhabdoid tumours, while H3K27me3 and H3K27M confirmed histone-altered gliomas. Ki-67 provided insight into proliferative activity. Additional markers such as BRAF V600E, LIN28A, and BCOR expanded diagnostic precision in selected scenarios. Characteristic IHC combinations reliably distinguished IDH-mutant astrocytoma (ATRX loss, p53+) from oligodendroglioma (ATRX retained, p53–). Loss of H3K27me3 staining prompted further testing to identify diffuse midline glioma. In young patients, negative IDH1 IHC warranted sequencing to detect non-R132H variants, while in older adults, IDH1 IHC-negative cases were generally accepted to be IDH wild-type.

Conclusion: The essential IHC panel offers a reproducible, resource-efficient approach to CNS tumour classification, approximating molecular profiles where sequencing is unavailable. Utilising IDH1 R132H, ATRX, p53, and H3K27me3 as a panel approach in adult diffuse gliomas, enables accurate diagnosis and prognostic assessment, thereby enabling optimal therapeutic decision-making. Incorporation of novel markers further refines classification, underscoring the role of IHC as a cornerstone of precision neuro-oncology.

VALIDATION AND ACCREDITATION OF 16S RRNA NEXT GENERATION SEQUENCING AS A DIAGNOSTIC TEST IN A MOLECULAR PATHOLOGY LABORATORY

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Introduction: Next-generation sequencing (NGS) is a powerful tool for pathogen identification, used predominantly in research settings in South Africa, but could be useful in a routine diagnostic microbiology laboratory and integral to effective management of patient care. The aim of this study was the validation, optimization of 16S rRNA NGS and to obtain accreditation for the protocol to be introduced as a diagnostic test in a molecular pathology laboratory. Two sequencing platforms, i.e. MiSeq (Illumina) and Ion Chef™ and S5 XL sequencer (Thermofisher Scientific) were evaluated using American Type Culture Collection (ATCC) and External Quality Assurance (EQA) bacterial cultures.

Methods: DNA was extracted on the Promega Maxwell® automated analyzer using the Maxwell® RSC Cell DNA Purification kit. The QIAseq® 16S/ITS Panel and Ion 16S™ metagenomics kits were used for the MiSeq; and Ion Chef and S5 XL sequencers respectively. Library preparation was followed by quality control using the Qubit (quantitation) and Tape Station (quality) before sequencing. Bioinformatics analysis software, namely, Basespace (Ilumina) and Ion Torrent (Thermofisher) were used for statistical data and bacterial identification. Comparison and sensitivity were performed for the two sequencing platforms by using Bray-Curtis plots.

Results: Both sequencing platforms detected the same species in similar abundance as indicated by a Bray-curtis plot for both the ATCC and EQA bacterial cultures. Diagnostic specificity was 100% and results obtained from both sequencing platforms exhibited 100% correlation to the expected result confirmed by EQA grading. Both assays were accurate, reliable, fit for purpose and validated for use in Lancet Molecular Pathology laboratory.

Conclusion: The Ion Chef™and S5 XL platform exhibited more automation over the MiSeq and was, thus chosen for use on clinical samples. Future studies will involve application of the Ion Chef™and S5 XL sequencing platform for analysis of bacterial diversity in cases of placental inflammation.

Keywords: 16S rRNA Next Generation Sequencing; Validation; Accreditation.

LOW SPERM CONCENTRATIONS AND ITS EFFECT ON FERTILIZATION RATES AND EMBRYOGENESIS IN COUPLES UNDERGOING INTRA CYTOPLASMIC SPERM INJECTION

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Background: Assisted Reproductive Technology (ART) has become a way forward for couples struggling with natural conception. Male infertility is a major indication for ART and, with the use of the Embryoscope, embryos can be better monitored in vitro, improving the selection criteria for embryo transfer. Male infertility has become a growing problem factor globally. In South Africa, little research has been performed on its impact on ART and embryo selection and therefore the aim of this study was to utilize the embryoscope to investigate the effects of decreased sperm concentrations ($<10 \times 10^6$ spermatozoa/ml) on ovum fertilization and embryonic development up until the blastocyst stage.

Methodology: Sixty patients were split into 3 sperm concentration groups, Group A $<10 \times 10^6$ spermatozoa/ml, Group B $10 - 50 \times 10^6$ spermatozoa/ml and Group C $>50 \times 10^6$ spermatozoa/ml. 586 ova which underwent ICSI were monitored using the Embryoscope time-lapse monitoring system. The annotation data was analysed for each of the following stages: 2cell (t2), 4 cell (t4), 8 cell (t8), Morula (tMp) and Early Blastocyst (t8) and statistically compared using SPSS.

Results: Group A had a significantly lower percentage of ova reaching fertilization compared to those in Group B and C (66% vs. 79% vs. 77% $p<0.01$). The rate at which groups A, B and C progressed through each of the five stages of embryogenesis was similar, however, all five stages were found to have significant differences in the rate each group reached a growth stage (P values: tPN $p<0.001$, t2 $p<0.01$, t4 $p<0.01$, t8 $p<0.001$, tMP $p<0.01$ and tB $p<0.01$). Further investigation noted a significant dwindling downward trend and growth halting ($p<0.01$).

Conclusion: The findings of this study show that participants with low sperm concentrations had significantly lower fertilization. Low sperm concentrations did not impact the rate of embryogenesis but rather the dwindling number of ova reaching blastocyst stage.

ENHANCING STUDENT PREPAREDNESS AND LEARNING IN LABORATORY PRACTICAL CLASSES THROUGH ONLINE PRE-LABORATORY RESOURCES

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Background:
Laboratory practical classes form a critical component of the BHSc Medical Laboratory Science course, often accounting for up to 50% of contact hours. However, students face challenges such as information overload and limited preparation time, which can hinder achievement of intended learning outcomes. Cognitive Load Theory (CLT) highlights the importance of reducing extraneous load and supporting germane processing during complex learning activities. In response, online pre-laboratory resources were introduced in a Microbiology subject to improve student engagement, preparedness, and learning effectiveness.

Aim
This study aimed to evaluate the effectiveness of online pre-laboratory resources specifically, pre-recorded instructional videos and tutorials on students' motivation and preparedness in laboratory practical classes.

Methods
A mixed-methods approach was used. Quantitative data were collected through a structured electronic questionnaire administered via the Blackboard Learning Management System to 59 enrolled students. The questionnaire included 21 items across five constructs (motivation, preparedness, learning effectiveness, demographics, and suggestions), using a five-point Likert scale and open-ended questions. Cronbach's alpha was used to assess internal reliability. Qualitative data were analysed thematically using Braun & Clarke's framework to capture student perceptions.

Results
The online pre-laboratory resources demonstrated strong internal consistency (α = 0.80–0.90) across all constructs. Most students agreed that the resources enhanced their motivation (79.7%), helped them prepare effectively for lab classes (88.1%), and improved their conceptual understanding (86.4%). Thematic analysis revealed key themes: visual learning support, early exposure benefits, practical session preview, and clearer practical insight. Students appreciated the ability to engage with content at their own pace, which fostered confidence and improved readiness for hands-on activities. Minimal suggestions for improvement were noted, indicating general satisfaction with the intervention.

Conclusion
Online pre-laboratory resources serve as effective pedagogical tools that reduce cognitive load and enhance student engagement, preparedness, and learning in laboratory-based courses. Incorporating these resources into curriculum design aligns with evidence-based strategies for improving practical skills acquisition and academic outcomes in medical laboratory science education.

DEVELOPMENT OF QUALIFICATIONS FOR PHLEBOTOMY TECHNIQUES

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Background:

The Phlebotomy qualification began in 2006 using the SAQA unit standard 59345 to train the outcomes, which expired on June 30th, 2023. The Minister of Higher Education, Science and Innovation, Honourable Blade Nzimande, announced that all Pre-2009 Qualifications under the SAQA Act must be re-registered with QCTO as an occupational qualification according to the Occupation Qualification Sub Framework. The OQSF provides directions, principles, limits, guidelines, and facilitates the development and registration of quality assured occupational qualifications from NQF Level 1 to 8. The PBMT requested that the SMLTSA undertake and lead the development process, which is headed by the Phlebotomy Scientific Advisory Committee, SMLTSA EXCO representatives, and the Professional Board for Medical Technology. After 23 months and overcoming many obstacles, final approval from QCTO was received, allowing the development process to begin.

Purpose or Aim of the Presentation:

The aim of the presentation is to highlight the structured and audited process that requires to be followed during the qualification development process. The development involves three phases. Phase 1 involves the application process which includes QCTO acknowledging and evaluating the application and providing feedback. Phase 2 requires the Quality Partner to develop and evaluate the qualification and Phase 3, the final phase, requires the QCTO to evaluate and recommend the qualification for SAQA registration.

Expected Outcome of the Process:

Upon completion of all of the above phases of development, the qualification will be registered and recognized for training. Career pathway and articulation options will be included.

INVESTIGATING THE INTERPLAY OF TYPE 2 DIABETES MELLITUS AND CARDIAC BIOMARKERS IN CARDIOVASCULAR RISK: A CASE-CONTROLLED STUDY IN KWAZULU-NATAL

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Background: This study investigates the relationship between glycaemic control, indicated by HbA1c levels, and cardiovascular risk biomarkers (high-sensitivity Troponin-T, Troponin-I, and NT-ProBNP) in patients with Type 2 Diabetes Mellitus (T2DM).
T2DM is associated with an increased risk of cardiovascular complications, including heart failure and myocardial infarction, and poor glycaemic control exacerbates these risks.

Methods: A retrospective case-controlled study was conducted using data from January to December 2023, involving 230 patients with type 2 diabetes mellitus (T2DM) at a tertiary hospital in KwaZulu-Natal-. The study analysed correlations between HbA1c levels and the cardiac biomarkers across different age groups.

Results: Results showed a significant positive correlation between elevated HbA1c levels and high-sensitivity troponin-T (ϱ = 0.250, p < 0.001), suggesting an increased risk of myocardial injury. Additionally, older participants exhibited higher NT-ProBNP levels (ϱ = 0.116, p = 0.040), indicating a higher risk of heart failure.

Conclusion: These findings highlight the importance of managing glycaemic control to mitigate cardiovascular risk in T2DM patients, particularly in older individuals. The study underscores the need for regular monitoring of HbA1c and cardiac biomarkers for early detection and intervention. Further research is needed to explore the combined effects of glycaemic control, comorbidities, and treatments on these biomarkers.

Keywords: Type 2 Diabetes Mellitus (T2DM); glycaemic control; HbA1c; cardiac biomarkers; high-sensitivity troponin-T; NT-ProBNP; myocardial injury

THE MOST FREQUENT MICRODELETION SYNDROMES IDENTIFIED BY MULTIPLEX LIGATION-DEPENDENT PROBE AMPLIFICATION (MLPA) AT GROOTE SCHUUR HOSPITAL OVER SIX YEARS.

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Introduction

Microdeletion syndromes are genetic conditions caused by the loss (deletion) of small chromosomal segments (<5Mb), including conditions like DiGeorge syndrome (22q11.2 deletion), Prader-Willi/Angelman syndromes (15q11-q13 deletion), Williams-Beuren syndrome (7q11.23 deletion) and Smith-Magenis syndrome (17p11.2 deletion). Multiplex Ligation-dependent Probe Amplification (MLPA) is a sensitive molecular cytogenetic technique used to detect microdeletions which are often missed by conventional karyotyping which detects larger chromosomal changes.

At the Human Genetics Laboratory (HGL), Groote Schuur Hospital (GSH), MLPA analysis for microdeletion is frequently requested, as they represent 5%–10% of genetic disorders when no other chromosomal abnormalities are found. This study investigated the frequency and types of microdeletion syndromes (MDS) detected by MLPA in our population and compared the results with international findings.

Methods

A retrospective study was conducted to determine the detection rate of patients positive for a microdeletion syndrome. Testing was performed at the National Health Laboratory Service (NHLS) Human Genetics Laboratory (HGL) at Groote Schuur Hospital (GSH) between 2019 and 2024. MLPA is a multiplex Polymerase Chain Reaction (PCR) method used to detect abnormal copy numbers of up to 50 different genomic DNA sequences. DNA extracted from peripheral blood was tested for known deletions, duplications, and specific copy number variants (CNVs) using the Microdeletion Syndromes-1 kit (P245-B1, MRC Holland) to simultaneously target multiple chromosomal regions associated with 23 recurrent microdeletion/duplication syndromes. MLPA products were then resolved by capillary electrophoresis using a 3500 Genetic Analyser (Thermo Fisher Scientific) and sequence data analysed using the GeneMapper v5.0 (ThermoFisher Scientific) and Coffalyser.NET software (www.mlpa.com).

Results

From 2019 to 2024, 690 patient samples were evaluated. Of these 690 patients, 157 tested positive for a microdeletion syndrome, with a positivity rate of 22.75%. The four most frequently detected syndromes were 22q11.2/Di George (22q11.2DS), Williams-Beuren, Prader Willi/Angelman, and Cri du Chat. The positivity rate for these four syndromes was 13%, 3.5%,2% and 1.3 %, respectively.

Conclusion

The frequency of microdeletion detection within our patient population is consistent with international findings, with the four most frequently found microdeletion syndromes being reflected in the South African population.

STRENGTHENING QUALITY FROM SAMPLE TO RESULT: PRE-ANALYTICS, PHLEBOTOMY & POCT UNDER ISO 15189:2022

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Background: Pre-analytical processes contribute to approximately 70% of laboratory testing errors, often arising from specimen collection, identification, or handling issues. Phlebotomy (sample collection) and point-of-care testing (POCT) are critical stages within this phase that directly influence diagnostic accuracy and patient safety. The revised ISO 15189:2022 standard, aligned with ISO 22870:2023 for POCT, strengthens the emphasis on risk-based quality management, competence, and traceability across all phases of testing.

Objective: To illustrate how integration of pre-analytical quality control, standardized phlebotomy practices, and structured POCT oversight under ISO 15189:2022 improves reliability, compliance, and patient outcomes.

Methods: Key clauses of ISO 15189:2022 (7.2.2, 7.4, and 8.5) were reviewed to identify requirements relevant to pre-analytics, specimen collection, and POCT. Implementation approaches, including staff training, authorization, competency assessment, and risk mitigation, were analyzed within typical laboratory and clinical workflows.

Results: Applying ISO 15189:2022 principles lead to measurable quality improvements, including reduced hemolysis and labeling errors, improved sample acceptance rates, consistent POCT performance, and enhanced documentation. Integration of laboratory oversight and operator competency ensures harmonized standards from sample collection to result reporting.

Conclusion: Strengthening the interconnection between pre-analytics, phlebotomy, and POCT under ISO 15189:2022 fosters a unified quality culture. Embedding risk-based management and continuous competence evaluation enhances accuracy, compliance, and patient safety, supporting diagnostic excellence in all testing environments.

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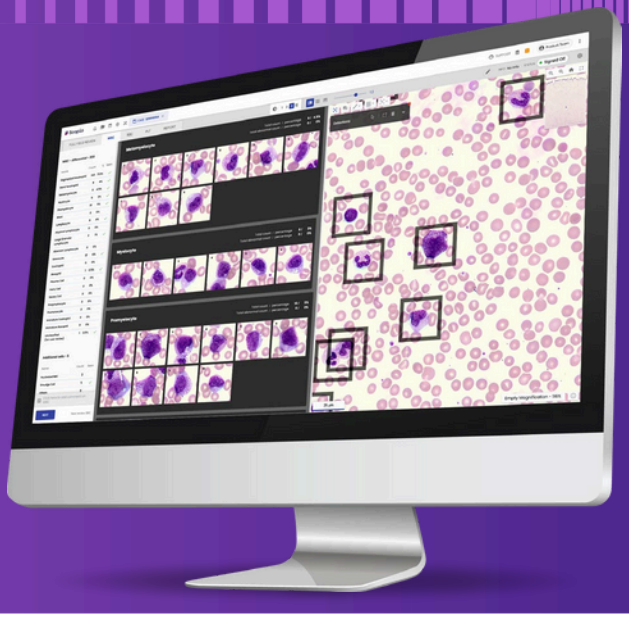

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ABSTRACTS

POSTER PRESENTATIONS

LISTED ALPHABETICALLY BY AUTHOR SURNAME

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Poster display number	**Author Name**	**Category/discipline**	**Topic**
1	Eva Rienhardt	Clinical Chemistry	Optimising serum immunofixation electrophoresis for monoclonal protein identification using beta-mecaptoethanol: a quality improvement initiative
2	Jessica Valentine	Clinical Chemistry	Prevalence of Vitamin D deficiency and its correlation to clinical features in the elderly population of Sharpeville, South Africa
3	Imtatia Ngcakaza	Clinical Chemistry	Neuroprotective Effects of Cocoa Against cART and T2DM-Induced Changes in the Male Sprague Dawley Rat Hippocampus: Insights From Biochemical and Histological Analyses
4	Don Matshazi	Molecular	The utility of serum miR-126-3p and miR-146a-5p expression as early indicators of dysglycaemia in an urban South African community.
5	Likenkeng Thobejane	Molecular Pathology	PREVALENCE OF rs1041163 and rs5498 AS CARDIAC RISK MARKERS IN A BLACK ELDERLY POPULATION IN SHARPEVILLE SOUTH AFRICA.
6	Shanel Raghubeer	Other - incl mental health	Perceived body image and weight management in a South African population
7	Venessa Patharoo	Virology	Evaluation and validation of an Eliza for the detection of IGM antibodies to Sindbis virus in human sera
8	Duduzile Valashiya	Virology	Seroprevalence of HBsAg among STI service attendees from 2021 to 2024: findings from the South African National Sentinel Surveillance
9	Valencia Petje	Virology	Bridging Eras: Influenza Virus Isolation in the Age of Molecular and Genomic Methods
10	Rivashni Jagaroo	Virology	Evaluation of the accuracy of Dual HIV/Syphilis and Syphilis Rapid Tests for the RT-41-1-2020 Tender for use as Point of Care Devices at Antenatal Facilities
11	Zinhle Brukwe	Virology	Monitoring the quality of HIV Rapid Test Device kits through HIV Rapid Kit Evaluations and Post Market Surveillance of Rapid kit batches - The South African Experience
12	Thandekile Vinolia Ryumeko	Virology	The prevalence of abnormal CD4+ count and Viral Load in People Living with HIV post SARS-CoV-2 infection. An evaluation of routine results from a private laboratory.
13	Cara Mia Dunaiski	Molecular & Virology	Molecular Surveillance of Influenza A and B in Namibia: Seasonal Patterns and Clinical Correlates (2021–2023)
14	Cara Mia Dunaiski	Microbiology	Macrolide and Fluoroquinolone Resistance-Associated Mutations in Mycoplasma genitalium in women with vaginal discharge syndrome in Namibia

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16	Yolanda Gantana	Multidiscipline - Microbiology, medicinal plants	Green Synthesis, Characterization, and Antimicrobial Activity of Agathosma betulina-mediated Silver Nanoparticles
17	Hlengiwe Ngomane	Microbiology	Profiling Uncommon Nontyphoidal Salmonella enterica Serovars causing Human Disease in South Africa, 2019-2021
18	Daphne Taylor	Haematology & Cytogenetics	The Significance of 3'IGH and 5'IGH Region Deletions in Multiple Myeloma
19	Cellice Lendoor	Cytogenetics	A Case Report: Optical Genome Mapping in the Diagnosis of Multiple Myeloma
20	Tshifhiwa Tshavhungwe	Quality Management Systems	Enhancing Laboratory Quality Management Systems Through Technology: Supporting Compliance with ISO standards Requirements
21	Snandile Majikijela	Phlebotomy Training	Innovative Staff Training in Clinical Laboratories: A Review of Simulation, Virtual Reality, Gamification, and Mentorship for Quality Assurance.

MONITORING THE QUALITY OF HIV RAPID TEST DEVICE KITS THROUGH HIV RAPID KIT EVALUATIONS AND POST MARKET SURVEILLANCE OF RAPID KIT BATCHES

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Introduction: To ensure that ALL HIV infected individuals know their status, widespread Rapid Testing in SA is conducted through health facilities, mobile clinics, and home-based services, with 18,5 million tests performed in 2022-2023 financial year. NICD developed a robust process for HIV rapid kit verification for the national government tender (2020-2023) and post market surveillance (PMS) of rapid kit batches that were approved through the tender process.

Method: For verification and PMS procedures, the NICD collaborated with WHO/CDC and attended training at Paul Ehrlich Institute. NICD reviewed product dossiers for WHO Prequalification (PQ), ISO certification, market duration, reproducibility data, and evidence of three manufactured batches for verification. A screen panel with challenging sero-conversion, mixed titre, HIV-2 and recent infection panels, followed by sensitivity/specificity analysis with approximately 500 specimens (known negative and known positive for HIV) was evaluated. Dilutions were tested to determine analytical sensitivity of the rapid kit to set a baseline, low titre, recent infection, HIV-1 and HIV-2 panels as part of PMS. Evaluation reports are provided for the verification and PMS testing processes to relevant stakeholders.

Results: Sixteen kits (12 professional HIV Rapid kits and 4 HIV Rapid self-test kits) were received from the RT41-2020 government tender. The documents submitted with these kits were reviewed (dossier review). Three professional HIV Rapid kits and one HIV Rapid self-test kit were rejected during dossier review. Rejections were due to bidders not having WHO PQ or ISO13485 certification. The test kits that passed the dossier review went through to the evaluation stage that involved sensitivity and specificity testing. Five professional test kits (ABON HIV 1/2/O Tri-line, Diagnostic kit for HIV (1+2) antibody, First Response HIV 1-2.O, One Step Anti HIV (1&2) and Toyo Anti-HIV 1/2) and two self-test kits (INSTI HIV Self-test and Oraquick HIV 1/2 Self-test) met evaluation criteria. Four HIV professional and one HIV self-test kit failed to meet evaluation criteria. Failures were due to sensitivity/specificity below 99%. The batches of kits that passed the evaluation were then subjected to PMS testing from 2020 until 2024. PMS was carried out on 682 new batches from the approved rapid kits between July 2020 - December 2024.

Conclusion: Rigorous evaluation criteria are paramount for ensuring the high performance and consistency of HIV Rapid kit batches. The testing conducted at the NICD for the national government tender confirmed that the kits evaluated (5 professional HIV kits and 2 HIV Self-test kits) met the stringent performance standards and criteria which is in line with WHO and CDC procedures to ensure that HIV Rapid test devices perform with high degree of accuracy. All new PMS batches were successfully verified by the NICD and reports issued prior to being distributed to end-users.

MOLECULAR SURVEILLANCE OF INFLUENZA A AND B IN NAMIBIA: SEASONAL PATTERNS AND CLINICAL CORRELATES (2021–2023)

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Background: Influenza viruses cause widespread respiratory illness. Due to limited surveillance, influenza dynamics in Namibia remain poorly understood. This study aimed to conduct molecular surveillance of influenza A and B viruses from 2021–2023, characterize circulating strains, and explore symptom correlations to inform public health responses and improve case management.

Methods: From October 2021 to December 2023, nasopharyngeal or oropharyngeal swabs were collected from patients with influenza-like illness (ILI) in a clinic-based setting. Viral detection, subtyping, and genotyping were conducted using real-time reverse-transcription polymerase chain reaction (RT-PCR). Seasonal trends of influenza and SARS-CoV-2, as well as symptom co-occurrence patterns were examined using statistical and visualization tools in R, Epi Info, and SPSS.

Results: A total of 1186 nasopharyngeal and oropharyngeal samples from ILI patients were collected. Influenza was detected in 24% (280/1186) of samples, with influenza A accounting for 20% (235/1186) and influenza B for 4% (45/1186). Among influenza A cases, A(H1N1)pdm09 was detected in 26% (62/235) and A(H3N2) in 67% (157/235). Influenza B (Victoria) accounted for nearly all influenza B cases (96%), while no influenza B(Yamagata) cases were detected. SARS-CoV-2 was detected in 19% (227/1186) of samples. Significant associations were observed between influenza infection and cough (OR 2.2, 95% CI 1.2–3.9, p = 0.0076) and myalgia (OR 2.3, 95% CI 1.5–3.6, p = 0.00044). The strongest correlation was between loss of smell and loss of taste ($r = 0.71$, $p < 0.001$).

Conclusions: Influenza activity followed distinct seasonal patterns, with influenza A more common than B. Cough and myalgia were stronger predictors of infection, while sore throat and loss of smell were less so. These findings highlight the importance of ongoing influenza surveillance and preparedness to manage seasonal outbreaks, while symptom correlations can enhance case management and monitoring.

MACROLIDE AND FLUOROQUINOLONE RESISTANCE-ASSOCIATED MUTATIONS IN MYCOPLASMA GENITALIUM IN WOMEN WITH VAGINAL DISCHARGE SYNDROME IN NAMIBIA

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Background: Mycoplasma genitalium is a common cause of sexually transmitted infections. The aetiological diagnosis and antibiotic susceptibility testing of M. genitalium infections is lacking and syndromic management is mainly used in low-to-middle-income countries. Given the emergence of antimicrobial resistance in M. genitalium infection, this study aimed to determine the presence of macrolide and fluoroquinolone resistance-in M. genitalium-positive specimens from women with vaginal discharge syndrome in Namibian women.

Method: Fourteen M. genitalium positive specimens from women with vaginal discharge syndrome obtained in a cross-sectional study and a prospective cohort from Windhoek, Namibia, were tested for Mycoplasma genitalium using a modified real-time PCR assay. M. genitalium DNA was investigated for macrolide drug resistance associated mutations in the 23S rRNA via real-time PCR coupled with melting curve analysis, followed by Sanger sequencing. Additionally, quinolone resistance associated mutation was detected by sequencing quinolone-resistance determining regions of the parC and gyrA genes.

Results: Eight specimens (57%) exhibited a melting peak dissimilar to that of the wild type strains, suggestive of the presence of resistance-related mutations. Three (38%) of these harboured a mutation at position A2071/2G of the 23S rRNA gene, associated with macrolide resistance. Sequencing of the quinolone resistance-determining regions revealed a Met95→Ile amino acid substitution and an 83Ser→Ile amino acid substitution in the parC gene associated with moxifloxacin resistance.

Conclusion: Macrolide- and quinolone-resistance, although of low prevalence, in M. genitalium is described for the first time in Namibia. Since azithromycin is presently used in the syndromic management of VDS in Namibia, the treatment of macrolide resistant M. genitalium could become problematic.

GREEN SYNTHESIS, CHARACTERIZATION, AND ANTIMICROBIAL ACTIVITY OF *AGATHOSMA BETULINA*-MEDIATED SILVER NANOPARTICLES

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Background: Diabetes mellitus often leads to chronic skin infections and delayed wound healing, particularly in underserved regions. Current treatments can be costly and ineffective due to rising resistance. Medicinal plants such as *Agathosma betulina* offer a promising alternative due to their low toxicity and traditional therapeutic use. This study investigates the green synthesis of silver nanoparticles (AgNPs) using *A. betulina* and evaluates their antimicrobial activity for potential diabetic wound care.

Aim: To synthesize silver nanoparticles using *Agathosma betulina* extracts and assess their antimicrobial activity.

Methods: Aqueous *A. betulina* extracts were combined with silver nitrate and incubated at 80°C to synthesize AgNPs, indicated by a reddish-brown colour. The nanoparticles were purified by centrifugation. Characterization was performed using UV-Visible spectroscopy (220–850 nm), Dynamic Light Scattering (DLS) for size and zeta potential, and Fourier Transform Infrared Spectroscopy (FTIR) for functional group analysis. Antimicrobial activity was assessed using the Kirby-Bauer method against six pathogens, including *Staphylococcus aureus (S. aureus)*, Methicillin-resistant *Staphylococcus aureus (*MRSA*)*, *Escherichia coli (E. coli)*, *Klebsiella pneumoniae (K. pneumoniae)*, *Pseudomonas aeruginosa (P. aeruginosa),* and *Candida albicans (C. albicans).*

Results: UV-Visible spectrophotometer confirmed nanoparticle formation; DLS showed uniform size and stable zeta potential. FTIR identified functional groups linked to reduction and stabilization. Synthesized AgNPs demonstrated antimicrobial activity against all bacterial strains tested, with inhibition zones ranging from 10-14 mm. No activity was observed for the plant extract alone or against *C. albicans*.

Conclusion: AgNPs synthesized from *Agathosma betulina* showed promising antimicrobial properties, especially against resistant bacteria. These results support further investigation into their use for diabetic wound treatment. Green synthesis offers an eco-friendly and cost-effective approach to generating novel antimicrobial agents.

Keywords: *Agathosma betulina*, antimicrobial activity, diabetes mellitus, green synthesis, silver nanoparticles.

RISK FACTORS ASSOCIATED WITH SEXUALLY TRANSMITTED INFECTIONS IN WOMEN WITH BACTERIAL VAGINOSIS

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Background: Bacterial vaginosis (BV) is a common cause of vaginal discharge. Women with BV have a higher prevalence of STIs, facilitating the acquisition of these infections due to the disruption of the normal vaginal flora. We determined the risk factors associated with bacterial STIs, including *Trichomonas vaginalis* in the presence of BV.

Methods: Females presenting to STI surveillance sites, in Johannesburg, Durban and Cape Town, with vaginal discharge were recruited after consent from 2021 to 2024. A study questionnaire administered by the surveillance nurse, was followed by examination and collection of samples. Nugent's scoring was used to determine BV status of Gram-stained vaginal smears. *Neisseria gonorrhoeae* (NG), *Chlamydia trachomatis* (CT), *Trichomonas vaginalis* (TV), and *Mycoplasma genitalium* (MG) detection by an in-house multiplex PCR of endocervical swabs. HIV serology was performed on the blood samples. Descriptive analysis and logistic regression were used to describe STI burden and associated factors.

Results: Of 865 women enrolled, 502 (58%) had BV. The median age was 28 years (IQR 25–34), 171 (34.6%) were living with HIV and 223 (44.6%) had one or more STIs: 22.4% (CT), 17.6% (NG), 14.8% (TV) and 6.6% (MG). Age at enrolment (adjusted odds ratio [aOR] 0.94 [95% Confidence Interval 0.92–0.97]), age at first sex (aOR 0.90 [95% CI 0.83–0.97]), living with HIV but not taking ART (aOR 1.49 [95% CI 1.13–1.97]) and enrolment at the Johannesburg facility (aOR 0.59 [95% CI 0.45–0.78]) were factors associated with having any STI in the presence of BV, with similar findings for TV.

Conclusion: Our results show that sexual behaviour plays a role in the acquisition of BV and delaying age at sexual debut is protective against STIs and BV. Integration of STI and HIV services will ensure that women with BV and STIs are tested for HIV and initiated on ART.

EVALUATION OF THE ACCURACY OF DUAL HIV/SYPHILIS AND SYPHILIS RAPID TESTS FOR THE RT-41-1-2020 TENDER FOR USE AS POINT OF CARE DEVICES AT ANTENATAL FACILITIES

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Introduction: Integration of dual testing for syphilis and HIV in prenatal care services offers significant advantages, including simultaneous screening during routine appointments, reducing adverse outcomes for both mother and child. This approach also helps normalize testing, increasing comfort levels and uptake rates while saving costs and streamlining healthcare systems. Early detection prevents complications and long-term expenses, supporting public health initiatives to reduce transmission rates and enhance overall population health.

Method: Four kits, namely First Response Syphilis Anti-TP card, First Response HIV1+2/Syphilis combo card test, Standard Q HIV/Syphilis combo (supplied by ETHITECH and TECPRO), were evaluated using the NICD evaluation procedure for rapid test devices and analysed using the EP Evaluator software. A well characterised set of specimens with known results were tested on each kit. A pre-screen of the documents for each kit was first reviewed, followed by a screen evaluation using challenging specimens. If a pass of >80% and above was achieved on the screen test, the kits were then evaluated for sensitivity, specificity accuracy, and reproducibility.

Results: The results showed exceptional performance in HIV sensitivity and specificity, with both the First Response HIV 1+2/Syphilis Combo Card and Tecpro Standard Q HIV/Syphilis Combo tests achieving 100%. Similarly, for Syphilis, both tests demonstrated robust sensitivity (98.7%) and specificity (100%). The Ethitech Standard Q HIV/Syphilis Combo test had slightly lower specificity (98%) due to one false negative result. Despite this, all kits met the evaluation criteria.

Conclusion: The NICD laboratory's evaluation (RT-41-1-2020) concluded that these four rapid test kits are suitable for dual testing of HIV and syphilis in South African settings. They meet National Department of Health criteria, comply with National Treasury requirements, and fulfil NICD evaluation standards. This assessment underscores their reliability and suitability for widespread use, potentially improving prenatal care and public health outcomes in South Africa.

A CASE REPORT: OPTICAL GENOME MAPPING IN THE DIAGNOSIS OF MULTIPLE MYELOMA

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Background: Optical genome mapping (OGM) offers genome-wide coverage with 10,000x higher-resolution than standard cytogenetic methods, detecting structural variants (SVs) often missed by other techniques. This case report details a patient with Multiple Myeloma (MM). Fluorescence in situ hybridization (FISH) was performed, followed by OGM, to aid in diagnosis. OGM identified genomic aberrations pertinent to the patient's prognosis and risk stratification, which were not observed during FISH analysis.

Methods: OGM was performed using a bone marrow aspirate from the 48-year-old male patient. This process involved ultra-high molecular weight (UHMW) DNA isolation which was fluorescently labelled across the entire genome at specific genomic sites. This labelled DNA was loaded onto a specialized chip containing thousands of nanochannels, and placed on the Saphyr instrument. A sharp-imaging camera inside the instrument captured high-resolution images of the DNA, which were then converted into molecule files. These molecule files were transferred to analysis software, aligned against the GRCh38 human reference genome, and analyzed using Bionano Access and VIA software. The previous FISH results were obtained from a referring clinician.

Results: FISH results showed a gain of 1q21. However, no rearrangements of 14q32 or deletions at 17p13 and 1p32 were identified. In contrast, OGM revealed a gain at 1q21, a t(4;14) translocation resulting in an NSD2::IGH fusion, and a gain at 7q21 overlapping the HGF gene. These OGM findings indicated high-risk MM with poor prognosis – which was not evident solely through FISH.

Conclusion: This case report highlights the elevated diagnostic resolution of OGM, illustrating its potential to reveal prognostically structural variants missed by standard cytogenetic methods. This is part and parcel due to the high-resolution, accuracy and genome-wide coverage of OGM, making it an important tool that effortlessly detects SVs and contributes decidedly to treatment and prognosis, while improving risk stratifications.

INNOVATIVE STAFF TRAINING IN CLINICAL LABORATORIES: A REVIEW OF SIMULATION, VIRTUAL REALITY, GAMIFICATION, AND MENTORSHIP FOR QUALITY ASSURANCE.

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Background: Laboratories are complex environments where highly skilled professionals work together to analyze samples, interpret results, and provide critical information to healthcare providers. The accuracy and reliability of laboratory results are crucial in making informed decisions about patient care, and any errors or inaccuracies can have serious consequences. The importance of effective staff training in laboratories cannot be overstated, as it plays a critical role in ensuring quality assurance and maintaining rigorous standards of diagnostic accuracy and patient safety. Traditional training methods have limitations, and innovative approaches have emerged to address these challenges.

Aim: This presentation aims to examine the effectiveness of innovative approaches to staff training in laboratories, including simulation-based training, virtual reality, gamification, personalized learning paths, and mentorship programs, highlighting its benefits, and challenges.

Methodology: A review of studies, including those by Predescu (Burciu) et al. (2023) on virtual reality's potential to transform teaching and learning, Wittek et al. (2024) on simulation-based training and AI-powered personalized learning, Patsaki et al. (2022) on the effectiveness of simulation-based training, Lampropoulos et al. (2024) on gamification and virtual reality, Pesare et al. (2016) and Szeto et al. (2021) on gamification in medical education, and Feyissa et al. (2019) on mentorship programs, was conducted to assess their impact on staff competence, diagnostic accuracy, and quality assurance outcomes.

Outcome: The review highlights the benefits of innovative training methods. Feyissa et al. (2019) found that mentoring programs enhance staff competence (pooled effect size: 1.34, 95% CI: 0.65-2.03). Gamification (Palmas et al., 2019) and immersive virtual reality training (Lerner et al., 2020) also showed promising results, with improved performance and increased confidence among participants.

Conclusion: Innovative approaches to staff training have the potential to improve quality assurance and staff development in laboratories, aligning with ISO15189:2022 standards that emphasize effective training and competency checks. By incorporating these methods into training programs, laboratories can enhance staff competence, improve diagnostic accuracy, and maintain rigorous quality standards.

THE UTILITY OF SERUM MIR-126-3P AND MIR-146A-5P EXPRESSION AS EARLY INDICATORS OF DYSGLYCAEMIA IN AN URBAN SOUTH AFRICAN COMMUNITY.

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Introduction: The high burden of type 2 diabetes (T2D) worldwide is partly due to the failure of currently adopted diagnostic methods to diagnose individuals early in the disease process before complications or target organ damage. As such, there is a need to explore alternative biomarkers that may facilitate effective screening or early diagnosis. MicroRNAs (miRNAs) regulate glucose metabolism, and their dysregulated expression has been associated with the development of T2D. Therefore, miRNAs have been intensely researched as potential biomarkers for early T2D diagnosis.

Aim: As such, this study aimed to investigate serum miR-126-3p and miR-146a-5p expression levels in various glycaemic states as potential biomarkers for the early diagnosis of T2D in an urban South African mixed ancestry population.

Method: A total of 122 participants aged 20-79 years were recruited in the study and were grouped according to their blood glucose levels as normoglycaemia, prediabetes and T2DM. MiRNA expression was assessed across the groups using reverse transcription qPCR, with data normalised using miR-16-5p.

Results: The expression of miR-126-3p was significantly higher in prediabetes patients ($p=0.013$), whilst miR-146a-5p expression was significantly higher in T2D patients ($p=0.024$) relative to normoglycaemic individuals. Moreover, Spearman correlations revealed a significant positive correlation between miR-126-3p and miR-146a-5p expression with body mass index ($r=0.260$, $p=0.007$; $r=0.208$, $p=0.036$), glycated haemoglobin ($r=0.422$, $p<0.001$; $r=0.400$, $p<0.001$) and fasting plasma glucose ($r=0.259$, $p=0.006$; $r=0.257$, $p=0.008$), respectively.

Conclusion: Findings from this study revealed dysregulated miRNA expression in T2D relative to normoglycaemia, and hence the potential for miR-126-3p and miR-146a-5p to be used for risk stratification and/or effective screening. Furthermore, these findings suggest miRNAs may have an important role in metabolic/glycaemic regulation. However, these observations require validation in other populations and exploration in animal/cell models to identify biological pathways that are directly regulated by these miRNAs.

NEUROPROTECTIVE EFFECTS OF COCOA AGAINST CART AND T2DM-INDUCED CHANGES IN THE MALE SPRAGUE DAWLEY RAT HIPPOCAMPUS: INSIGHTS FROM BIOCHEMICAL AND HISTOLOGICAL ANALYSES

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Background: Antiretroviral therapy (cART) is associated with an increased risk of type 2 diabetes mellitus (T2DM), which can lead to cognitive decline due to oxidative stress. This study evaluates cocoa's protective effects against hippocampal changes caused by cART and T2DM, given its antioxidant and anti-inflammatory properties.

Methods: Seventy-two male Sprague Dawley rats (200g-300g) were assigned to six treatment groups over 45 days. The control group received gelatin cubes and distilled water. The T2DM group was fed a 10% fructose diet with gelatin cubes and treated with 40 mg/kg of streptozotocin. The cART group received gelatin cubes containing 9.625 mg/g of Atripla® and normal saline. The T2DM + cART group received both treatments. The Cocoa group was given 2000 mg/kg of natural cocoa in gelatin cubes with normal saline. Lastly, the T2DM + cART + Cocoa group received the three treatments. Blood glucose was measured before T2DM induction and after 45 days, along with body weight. Terminal brain tissue samples were analyzed for oxidative stress markers, proinflammatory cytokines, and histological assessments of the hippocampus. Data analysis was performed using one-way ANOVA with post-hoc tests.

Results: Type 2 diabetes mellitus (T2DM) and combined antiretroviral therapy (cART) led to significant weight loss and increased blood glucose levels compared to the control group. However, cocoa supplementation mitigated these effects in the T2DM + cART + Cocoa group. The T2DM + cART group exhibited increased oxidative stress, as evidenced by higher MDA and CAT levels and lower SOD levels; however, cocoa helped mitigate these markers. NF-$\varkappa$B levels were elevated in the cART group, while BDNF levels decreased in the T2DM + cART group, with cocoa restoring BDNF levels. Additionally, hippocampal volume and neurogenic activity decreased, and pyknotic cells increased. Cocoa counteracted these negative effects, suggesting it may help prevent the brain's harmful impacts of cART-associated T2DM.

PROFILING UNCOMMON NONTYPHOIDAL *SALMONELLA ENTERICA* SEROVARS CAUSING HUMAN DISEASE IN SOUTH AFRICA, 2019-2021

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Introduction
Nontyphoidal *Salmonella* (NTS) causes gastroenteritis and invasive disease worldwide. In South Africa, *Salmonella* Typhimurium and *Salmonella* Enteritidis cause about 60% of infections, but emerging uncommon serovars warrant the need for surveillance.

Methods
We retrospectively analysed *Salmonella* isolates archived at National Institute for Communicable through the national surveillance 2019-2021. Serovars were characterised by phenotypic (2019) or whole-genome sequencing (WGS) based serotyping (2020-2021), and categorised by frequency, with uncommon serovars defined as those causing 4–10 cases. Antimicrobial susceptibility testing was performed on 172 isolates, and WGS data were analysed for 91 isolates.

Results
Among the 186 isolates representing thirty uncommon serovars, *Salmonella* Oranienburg and *Salmonella* Stanleyville each accounted for 5.4% (10/186). Most infections were noninvasive 87% (161/186), with 13% (25/186) invasive. Cases were more frequent in the private sector 59% (110/186) than the public sector 41% (76/186). Adults aged 15-64 years carried the highest burden 49% (91/186), followed by children <5 years 34.4% (64/186). Extended-spectrum β-lactamases (ESBLs) were detected in three 2019 isolates (*S.* Bredeney, *S.* Eastbourne, *S.* Corvallis), all nonsusceptible to ciprofloxacin. Overall, 2.9% (5/172) isolates were ciprofloxacin-nonsusceptible. Of the sequenced isolates, two *S.* Idikan (2020) and one *S.* Concord (2021) were multidrug resistant (MDR), showing antimicrobial resistance (AMR) determinants to ≥3 antimicrobial classes.

Conclusion
Uncommon NTS serovars contribute to human disease in South Africa, with sporadic emergence of MDR and ESBL-producing strains. Continued genomic surveillance is essential to detect emerging threats and guide public health responses.

EVALUATION AND VALIDATION OF AN ELISA FOR THE DETECTION OF IGM ANTIBODIES TO SINDBIS VIRUS IN HUMAN SERA

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Introduction: Sindbis virus (SINV) belongs to the genus *Alphavirus* in the *Togaviridae* family. Symptoms include arthralgia, rash, mild fever, headache and malaise. Clinical diagnosis of SINV infection needs laboratory confirmation which is based primarily on serological assays that can detect immunoglobulin G (IgG) and immunoglobulin M (IgM) antibodies to SINV. The Arbovirus Reference Laboratory (ARL) at the Centre for Emerging, Zoonotic and Parasitic Diseases (CEZPD), National Institute of Communicable Diseases of the National Health Laboratory Service (NICD-NHLS) is the national reference laboratory for confirmation of human cases of arboviruses including Sindbis virus infection in South Africa. A SINV IgM ELISA is used as part of the algorithm for SINV diagnosis at the lab and is an "in-house" historically developed assay that was not fully validated. Here, we aimed to evaluate, standardise and validate the "in-house" anti-Sindbis virus IgM capture ELISA by establishing the cut-off values and test performance characteristics.

Method: A panel for the validation of the SINV IgM ELISA was established and then run on the SINV IgM ELISA. The optimal diagnostic cut-off values were determined by two-graph receiver-operating characteristic (TG-ROC) analysis. "Limits of detection" (LOD) were validated alongside the assay's uniformity, accuracy, and inter-assay performance.

Results: We selected a threshold at 95% confidence level under assumption of 50% disease prevalence and equal costs of false-negative and false-positive test results. At a ROC-derived cut-off value of 2.3PP, the sensitivity of the IgM ELISA was 97.50%, with a specificity of 93.60%. The assay shows good repeatability (intra- and inter-assay of CV < 10%) during routine use. At this cut-off a positive predictive value of 93.84% and a negative predictive value of 97.40% was calculated.

Conclusion: These results indicate that the Sindbis IgM ELISA is highly accurate and therefore may be confidently utilised for the early detection of Sindbis infection in humans.

BRIDGING THE ERAS: INFLUENZA VIRUS ISOLATION IN THE AGE OF MOLECULAR AND GENOMIC METHODS

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Introduction: Influenza remains a significant global public health threat, causing pandemics and seasonal epidemics. We aimed to demonstrate the role of influenza virus isolation in the age of advanced molecular and genetic characterisation methods.

Methods: In January–December 2024, patients meeting case definitions at South African sentinel sites were enrolled in respiratory illness surveillance. Nasopharyngeal specimens were tested for influenza using real-time reverse transcription polymerase chain reaction (RT-PCR). Positive specimens (cycle threshold < 30) were randomly selected for culture using Madin-Darby Canine Kidney (MDCK) cells. Cultures were monitored for cytopathic effects and positives confirmed using immunofluorescence assay (IFA). Representative isolates and clinical specimens were submitted to World Health Organization Collaborating Centres (WHO-CCs) for neuraminidase inhibitor susceptibility testing and antigenic characterisation using ferret antisera in haemagglutination inhibition (HAI) assays to identify antigenic drift from the 2024 Southern Hemisphere vaccine strains. Low reactors were defined by a ≥ 8-fold reduction in titre compared to the vaccine strains.

Results: Among 7 690 enrolled individuals, 997 (13%) tested influenza positive by RT-PCR with predominantly A(H1N1) pdm09 (59%, 587/997) and B/Victoria (34%, 334/997) detected. Among these, culture was attempted for 20% (202/997) and 73% (147/202) were successful: 70% (77/110) A(H1N1) pdm09, 60% (9/15) A(H3N2) and 79% (61/77) B/Victoria.
Among representative isolates sent to WHO-CCs, 4% (1/26) A(H1N1) pdm09 viruses showed highly reduced inhibition to oseltamivir and peramivir. Normal inhibition was observed in 96% (25/26) A(H1N1) pdm09, 100% (2/2) A(H3N2) and 100% (10/10) B/Victoria viruses. All isolates submitted to WHO-CCs were vaccine-like: 32/32 A(H1N1) pdm09, 2/2 A(H3N2) and 21/21 B/Victoria, with no low reactors identified.

Conclusion: As a result of virus isolation, antiviral susceptibility and antigenic characterisation data was generated for guiding antiviral treatment and pandemic preparedness. South African data was shared with WHO to guide decisions for the 2025 Southern Hemisphere vaccine strains, reinforcing virus isolation as a vital component of influenza surveillance.

PERCEIVED BODY IMAGE AND WEIGHT MANAGEMENT IN A SOUTH AFRICAN POPULATION

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Background: Misperception of body image is common and may prevent individuals from undertaking healthy corrective measures. This study aimed to investigate how misperception of body image and weight among adults may hinder engagement in weight loss efforts or health interventions.

Methods: This study involved 1889 adults aged 20 years and older. Participants were required to estimate their weight prior to weight, height, and waist and hip circumference measurements. The Stunkard Figure Rating Scale (FRS) was used for participants to select silhouettes that they believed closely resembled their body types. Biochemical parameters related to metabolic syndrome (MetS) were measured for all participants.

Results: The median age was 49 years for males (n=455) and 52 years for females (n=1434). Obesity (51.2 vs. 15.9%) and MetS (49.9 vs. 25.5%) were more prevalent in women than men. Most overweight/obese participants underestimated their body size and over 75% reported no intention to lose weight. Only 13% reported efforts to lose weight. Approximately 65% of normal weight individuals accurately estimated their weight, while 20.8% of obese men estimated their weight correctly compared to 49.2% of obese women. The FRS results showed poor body size recognition, particularly in obese men. Logistic regression analyses adjusted for age, sex, and MetS parameters showed that waist circumference significantly predicted weight management efforts (OR: 5.7, 95% CI: 3.8-8.4, $p<0.0001$).

Conclusions: Men and women in this cohort underestimate their weight and misperceive their body shape, which hinders participation in healthy initiatives or weight loss efforts. Incorporating visual body shape guides in obesity management settings can help bridge this perception gap and promote healthier behaviours.

OPTIMISING SERUM IMMUNOFIXATION ELECTROPHORESIS FOR MONOCLONAL PROTEIN IDENTIFICATION USING Β-MERCAPTOETHANOL: A QUALITY IMPROVEMENT INITIATIVE.

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Background: Investigation of monoclonal gammopathies (associated with malignant conditions such as multiple myeloma) involves the analysis of a patient's serum using agarose gel electrophoresis and immunofixation (serum IFE). This technique separates proteins based on their molecular weight and charge, producing distinct fractions. Monoclonal proteins appear as specific restricted bands, usually in the gamma fraction, and can be of any immunoglobulin (Ig) class (IgG, IgA, IgM, IgD, or IgE) or light chain type (kappa or lambda). Increases in the gamma globulin fraction with diffuse staining suggest polyclonal gammopathies linked to non-malignant conditions. Immunoglobulins can exist in various oligomeric forms and may form heterodimers, which may appear as overlapping restricted bands or diffuse bands, leading to potential misinterpretation of results. Beta-mercaptoethanol (BME) can reduce disulfide bonds within oligomeric structures and potentially improve the accuracy of result interpretation. However, literature on its use in serum IFE is limited and lacks consistent details on experimental conditions, including BME concentration, incubation time, and temperature. The present study aims to optimize the laboratory protocol for the use of BME to improve the resolution and quality of serum IFE results at a tertiary hospital in South Africa.

Methods: Following serum IFE for specimens that were received at our laboratory for routine analysis (from January to December 2024), those that displayed poor resolution were used. Various BME concentrations (0.25%, 0.5%, 1%, 2%, and 5% v/v), incubation periods (5-, 15-, 20-, 30-, and 120-minutes), and incubation temperatures (room temperature, 37 °C, 100 °C were investigated. Results under various experimental conditions were visually assessed.

Results: BME improved the resolution of serum IFE results in a dose-dependent manner and the best resolution was observed with 2% (v/v) BME. Superior serum IFE resolution was observed when incubating serum with BME at 37 °C compared to room temperature. A 30-minute incubation of serum with BME resulted in the best serum IFE resolution.

Conclusion: The optimal experimental protocol identified in this study was observed when serum was incubated with 2% (v/v) BME for 30 minutes at 37 °C.

THE PREVALENCE OF ABNORMAL CD4+ COUNT AND VIRAL LOAD IN PEOPLE LIVING WITH HIV POST SARS-COV-2 INFECTION. AN EVALUATION OF ROUTINE RESULTS FROM A PRIVATE LABORATORY.

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Introduction: In 2020, South Africa was confronted with a dual health disaster, fighting the HIV epidemic alongside the COVID-19 outbreak, disrupting the healthcare system. Nearly 7.8 million people live with HIV(PLHIV) in the country, and 31% are not receiving antiretroviral therapy (ARV). The pandemic worsened their vulnerabilities as healthcare resources were reallocated to address the disaster.

Research on the interaction between COVID-19 and HIV has yielded conflicting outcomes, highlighting the need for in-depth studies. The study aimed to determine the prevalence of abnormal CD4+ count and Viral Load (VL) in PLHIV before and after COVID-19 infection, as well as before and after the pandemic.

Methodology: This retrospective study involved 64 PLHIV who tested positive for SARS-CoV-2, utilising data from a private laboratory in Gauteng. Demographic data, including age, gender, Tuberculosis, CD4+, and VL results, were collected. IBM SPSS v29.0 was used for statistical analysis. The Kolmogorov-Smirnov test was used to assess normality. Student's t-test was performed for normally distributed data, while the Wilcoxon signed-rank test was applied for non-normally distributed data.

Results: The average CD4+ count dropped from 696.55 before COVID-19 and 668.61 after infection, with a degree of variation of 0.788. The CD4+ count rose from 635.38 before the pandemic and increased to 678.83 afterwards, with a degree of variation of 0.706. The average VL decreased from 14742.95 to 6959.16 post-infection, and 78724.88 to 4721.83 after the pandemic. Most participants showed well-controlled HIV, with a CD4+ count above 500 cells/mm^3 and a VL below 50 copies/ml.

Conclusion: PLHIV with well-managed HIV did not experience negative impacts from COVID-19 or the pandemic. Further studies are needed to confirm these findings, especially in low- and middle-income settings.

THE SIGNIFICANCE OF 3'IGH AND 5'IGH REGION DELETIONS IN MULTIPLE MYELOMA

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Introduction: This study aimed to determine if deletions of the immunoglobulin heavy chain (IGH) gene region are associated with IGH rearrangements. This investigation is crucial for guiding reporting of Multiple Myeloma (MM) fluorescence in situ hybridisation (FISH) results and optimising testing strategies.

Methods: A retrospective study was conducted on patients undergoing FISH testing for MM between 2019 and 2024. Patients with either a 3' or 5' IGH deletion were identified, and the signal patterns of the reflex panels were analysed. Twenty-one of 570 cases (3.7%) had a deletion, and reflex testing done for t(4;14)(p16;q32), t(14;16)(q32;q23), and t(11;14)(q13.3;q32). Data analysis involved reviewing FISH test results to correlate IGH deletions with the signal patterns of the reflex probes.

Results: The review of data revealed that 50% cases with a 3' IGH deletion exhibited a t(4;14) translocation, whilst the remaining cases did not indicate an IGH rearrangement. In cases positive for a 5' IGH deletion, two cases demonstrated a t(11;14) translocation, and the remaining cases (67%) did not indicate an IGH rearrangement. These findings suggest an association between IGH deletions and specific translocations, but not a correlation between a deletion of the IGH gene-region and the presence of an IGH rearrangement.

Conclusion: According to our data, deletion of either the 3' or 5' IGH region does not always represent an IGH rearrangement. It is therefore important not to report these signal patterns (1F1R or 1F1G) as positive for IGH rearrangement; instead, reflex testing should be performed before a rearrangement can be confirmed.

PREVALENCE OF RS1041163 AND RS5498 AS CARDIAC RISK MARKERS IN A BLACK ELDERLY POPULATION IN SHARPEVILLE SOUTH AFRICA.

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Introduction: Single nucleotide polymorphisms (SNPs) have been previously associated with diseases including cardiovascular disease (CVD). The study aimed to determine the prevalence of rs1041163 and rs5498 SNPs and determine their association with Vitamin D in the elderly population.

Methods: The study was carried out using purposefully selected samples. MassARRAY System was used for Genotyping to detect the polymorphisms rs1041163 and rs5498. The Vitamin D test was conducted using a Microplate reader RT – 2100C and an Enzyme – linked immunoassay (ELISA) assay. International Business Machines Corporation (IBM)® Statistical Package for the Social Sciences ® (SPSS) version 29 was used for statistical analysis.

Results: The heterozygous and homozygous genotypes of the 2 SNPs were detected. For rs1041163 the T allele was the most common with 80% prevalence, followed by TC 19% and C allele 2.73%. Notably, the T allele demonstrated moderate association with Vitamin D levels using Eta measurement test. For rs5498 genotype A, G and AG were detected and G was found to have a weak association with Vitamin D levels. Both genotype associations showed no significance with the p value > 0.05 on the Anova.

Conclusion: This study indicated a poor correlation between rs1041163 and rs5498 SNPs and Vitamin D status in a low economical black elderly population. It is proposed that future studies investigate more SNPs in larger sample populations.

ENHANCING LABORATORY QUALITY MANAGEMENT SYSTEMS THROUGH TECHNOLOGY: SUPPORTING COMPLIANCE WITH ISO STANDARDS REQUIREMENTS

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Introduction:

Laboratories are expected to produce reliable results while complying with stringent international standards, including ISO 15189:2022, ISO/IEC 17025:2017, ISO/IEC 17043:2023, ISO 13485:2016, and ISO 45001:2018. However, traditional paper-based Quality Management Systems (QMS) often struggle to meet these evolving requirements efficiently. This study explores how digital technologies such as cloud computing, artificial intelligence, big data analytics, and the Internet of Things (IoT) can strengthen laboratory QMS and support compliance with ISO standards.

Methods:

A qualitative literature review and thematic analysis were conducted using data from ISO standards, peer-reviewed journals, case studies, and accreditation reports published between 2015 and 2024. Themes extracted include digital documentation, quality control automation, equipment maintenance, workforce training, and audit readiness.

Results:

Key findings reveal that digital tools improve documentation and traceability through cloud-based QMS and Laboratory Information Management Systems (LIMS), supporting clauses across the different ISO standards such as ISO 15189, ISO/IEC 17025, and ISO 13485. Automation of quality control and proficiency testing using AI and IoT enhances accuracy and response times. Equipment maintenance is optimized via Computerized Maintenance Management Systems (CMMS), while e-learning platforms and digital tracking tools support training compliance and workplace safety (ISO 45001). Centralized dashboards and audit trails increase readiness for internal and external audits.

Conclusion:

Integrating technology into laboratory QMS enhances quality outcomes by fostering a more responsive, data-driven, and proactive quality culture. They also build a stronger culture of accountability, competence, and continuous improvement. Strategic implementation aligned with accreditation standards and staff engagement is critical, and digital tools assist with streamlining compliance processes. Future research should explore scalable digital solutions for resource-limited settings and assess cost-benefit impacts.

SEROPREVALENCE OF HBSAG AMONG STI SERVICE ATTENDEES FROM 2021 TO 2024: FINDINGS FROM THE SOUTH AFRICAN NATIONAL SENTINEL SURVEILLANCE

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Introduction: In South Africa, over 1.9 million people are chronically infected with the Hepatitis B virus. Infections remain a global public health concern despite the introduction of the vaccine in the Expanded Program on Immunization (EPI) in 1995 as part of the routine childhood immunisation programme. We determined trends in the prevalence of Hepatitis B Surface Antigen (HBsAg) – a marker of active hepatitis B infection – amongst males and females seeking care in the primary clinics in South Africa (2021–2024).

Methods: Consenting male and female adults seeking care at the STI surveillance sites in Gauteng, KwaZulu-Natal and Western Cape and presenting with male urethral syndrome (MUS), vaginal discharge syndrome (VDS) and genital ulcer syndrome (GUS) were recruited. Questionnaires were administered by the study nurse onsite, blood and genital samples were collected. HBsAg was detected using the ARCHITECT i1000SR immunoassay analyzer (Abbott Laboratories, Chicago, Illinois, USA). Descriptive statistics were used to describe HBsAg positivity overall and by year, facility, age, HIV status, STI syndrome and having an STI detected in genital samples.

Results: From 3 265 attendees enrolled, 3 193 were tested (median age 30 years [interquartile range 26–37 years], 71% male, 26.9% living with HIV and 79% had STI detected in genital samples) with 126 (3.95%) positive for HBsAg. The seroprevalence rate of HBsAg increased from 2.8% in 2021 to 4.6% in 2025 (χ^2 p-value = 0.136). HBsAg prevalence was higher among those enrolled at the KZN sentinel site (5.6% vs. 2.6% at GP), living with HIV (7.9% vs. 2.8%), presenting with GUS (6.5%) and MUS (4.2%) vs. VDS (1.6%) and those with an STI detected (4.3% vs. 2.4% among those without).

Conclusion: Hepatitis B infection was common among symptomatic STI service attendees. STI services are a good platform to screen for active Hepatitis B infection and initiate treatment.

PREVALENCE OF VITAMIN D DEFICIENCY AND ITS CORRELATION TO CLINICAL FEATURES IN THE ELDERLY POPULATION OF SHARPEVILLE, SOUTH AFRICA

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INTRODUCTION
Vitamin D plays an essential role in Cardiovascular health, bone health and autoimmune diseases. Recently, vitamin D deficiency has been considered a global health problem affecting approximately 50% of the worldwide population. It is associated with poor disease outcomes in diabetes mellitus, cardiovascular diseases, autoimmune diseases among others. This study is going to determine the prevalence of vitamin D deficiency and identify symptoms associated with insufficient Vitamin D in the elderly population.

METHODS
This study was ethically approved and carried out using purposefully selected sample. Serum vitamin D analysis was conducted using an enzyme-linked immunosorbent assay (ELISA). The results were analysed using the International Business Machines Corporation (IBM)® Statistical Package for the Social Sciences ® (SPSS) version 29 for presentation of descriptive and inferential statistics.

RESULTS
The mean age of the participants was 75, of which 76,7% were women. The mean ± SD for 25(OH) VITAMIN D was 26.86. The majority of the participants 76,7% had insufficient vitamin D levels, 23,3% had sufficient levels and none of the participants had deficient levels. A higher percentage of males (35,3) had adequate vitamin D levels compared to females. The chi-square correlation showed a borderline association (ϱ=0,057) for joint pain, which indicated no significance but a possible trend. Analysis also showed one significant association (ϱ = 0,009) between vitamin D and skin disease.

CONCLUSION
A large percentage of the elderly participants indicated a compromised vitamin D status. Significant association was detected between vitamin D and the presence of skin disease, as well as a trend towards the prevalence of skeletal/joint complaints in the vitamin D insufficient group. Future research should explore these associations in larger samples.

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