activation and inflammation in the genital tracts of adolescents from South Africa.

Methods Cervical cytobrush mononuclear cells were isolated from 148 adolescents (16–22 years) from Cape Town, and expression of T-cell activation and proliferation markers (CD38, HLA-DR, Ki67, CCR5) was measured by FACs. Adolescents were screened for BV (Nugent) and STIs (*C. trachomatis*, N. gonnorhoea, *T. vaginalis*, M. genitalium, HSV-2) by PCR. For comparison, 11 HIV-negative adult women were included. Concentrations of 48 cytokines, chemokines and growth factors were measured in matching menstrual cups by Luminex.

Results Adolescents (median 18 years; IQR 17-20) had significantly higher frequencies of activated CD4+ T-cells (CD38+, HLADR⁺, CD38⁺HLADR⁺: each p < 0.0001) from cervical cytobrushes than adults although CCR5 expression was higher in adults. STIs and BV prevalence was very high, with 71% of adolescents having ≥1 STI and/or BV, and 42% being C. trachomatis positive. Adolescents with an STI, despite these being asymptomatic, had higher frequencies of activated and proliferatcompared to those with no STI/BV $(CD4^{+}CD38^{+}HLADR^{+}: p = 0.047; CD4^{+}Ki67^{+}: p = 0.020).$ Women positive for chlamydia had significantly higher frequencies of CD4+CD38+ T-cells (p = 0.006). Women with both STIs and BV had the most pronounced increase in CD4⁺ T-cell activation (CD38⁺: p = 0.002; CD38⁺HLADR⁺: p = 0.001; Ki67+: p = 0.002). Higher cervical T-cell activation marker expression was directly associated with increased genital cytokine profiles.

Conclusion Heightened levels of genital immune activation and inflammation found in South African adolescent females, partly due to the presence of asymptomatic STIs and BV could increase their risk for HIV infection.

P15.05

PERFORMANCE EVALUATION OF THE APTIMA HIV-1 QUANT DX ASSAY FOR DETECTION OF HIV-1 IN PLASMA AND DRIED BLOOD SPOTS (DBS)

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Introduction The Aptima HIV-1 Quant Dx presented on the Hologic PANTHERTM system provides continuous and random access processing of molecular samples for groups M HIV-1 RNA viral load testing. Significant efficiencies are realised through 3.5 h to first result with over 275 samples processed within 8 h. This study assessed the performance of the system in routine plasma samples and whole blood presented as dried blood spot (DBS).

Methods A total of 181 plasma samples were tested over the analytical range and compared to a benchmark real time PCR system. The study focused on the lower analytical range <5,000 copies/mL HIV-1 RNA (55%). HIV-1 viral load equivalence in non-B subtypes of regional geographical significance was assessed where subtype was available (72%). A further 20 DBS (single 10 mm punch, whole blood) with HIV-1 RNA 500–5,000 cpy/mL and were eluted using a variety of methods, tested and compared with plasma RNA.

Results Overall, Aptima HIV-1 Quant Dx correlated with the routine analytical platform (r2 = 0.9605). Samples ranged undetectable (16, 8.8%), below the benchmark test lower limit of detection (<20 cpy/ml) (16, 8.8%), low range (20-5,000) (84,

46.4%), medium (5,000–50,000) (36, 19.9%) and high range (>50,000 cpy/ml) (29, 16%). Samples in the lower analytical range <1,000 cpy/ml showed little variance when compaired with the Roche (CAP/CTM) assay using Bland-Altman correlation analysis. Reproducibility was assessed in the high, medium and low range within 1–2SD of mean. DBS samples with HIV-1 RNA results >1,000 were well correlated with plasma.

Conclusion The Aptima HIV-1 Quant Dx automated random access platform correlated with a commonly used HIV RNA test in plasma and offered significant workflow advantages. Promising results obtained using DBS samples could potentially overcome logistics encountered with conventional plasma. Further correlations and limit of detection studies are needed to validated DBS.

Disclosure of interest statement No conflict of interest to declare.

P15.06

MOLECULAR VALIDATION OF PUTATIVE ANTIMICROBIAL PEPTIDES FOR IMPROVED HUMAN IMMUNODEFICIENCY VIRUS DIAGNOSTICS VIA HIV PROTEIN P24

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Introduction The Human Immunodeficiency Virus-1 (HIV-1) is responsible for causing Acquired Immunodeficiency Syndrome (AIDS), and to date remains a pandemic. More than 40 million people are infected globally, with 60% of the infected people residing in Sub-Saharan Africa. Earlier detection translates into earlier treatment, which ensures improved quality of life. However, difficulties remain in the field of HIV diagnostics. The p24 antigen detection tests are preferred due to its ability to decrease the window period. The current p24 diagnostic assay displays great insensitivity, due to the p24 antibody produced by the body, binding to the C-terminal of the p24 antigen. This interaction obstructs detection, the basis of the current p24 test. Using in silico approaches, novel antimicrobial peptides (AMP) were identified which bind to the N-terminal, instead of the C-terminal domain (antibody binding pocket) of the p24 antigen (provisional patent). This is important because if the p24 antibody binds to the C-terminal, the unoccupied N-terminal domain would provide a binding pocket for the AMP. Successful conjugation of nanoparticles to the positively validated AMP, can lead to the development of a diagnostic lateral flow device.

Methods In silico site-directed mutagenesis and docking studies to identify additional AMPs that bind the N-terminal domain of protein p24 with increased binding affinity.

Preliminary study: Lateral flow design with identified AMPs to test HIV positive sera.

P24 recombinant protein expression.

P24 protein-AMP binding studies.

Results In silico studies identified 9 AMPs which could be used to bind p24 antigen for HIV diagnostics.

Preliminary study: Lateral flow successfully detected HIV in HIV positive sera.

Successful p24 recombinant protein expression.

Successful validation of binding AMPs against the p24 protein.

Conclusion Binding interaction between AMPs and p24 protein is validated. Subsequently a sensitive lateral flow device could be developed that successfully detects HIV in positive HIV sera.