ToC, the median baseline Ct was 26.9 (IQR: 12.5) vs. 29.3 (IQR: 14.8) among those TV PCR-negative at ToC (p=0.52). Among 7 women who remained TV PCR-positive, the median baseline Ct was 26.4 (IQR: 6.7) vs. 26.2 (IQR: 6.7) at ToC (p>0.05).

Conclusion The prevalence of TV in our sample of South African HIV-infected pregnant women was similar to prior studies. At baseline, culture detected only half of the cases that were positive by TV PCR. The culture-negative cases had significantly higher Ct values, indicating a lower burden of TV nucleic acid. Baseline Ct values did not predict response to TV treatment. Among women testing persistently TV PCR-positive, Ct values did not change between baseline and ToC.

P1.16 ACQUISITION OF AZITHROMYCIN RESISTANCE IN *NEISSERIA GONORRHOEAE* VIA INTRAGENUS RECOMBINATION

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Introduction Reduced susceptibility to azithromycin (Azi^{RS}) is increasing in frequency in *Neisseria gonorrhoeae*. We have shown that non-gonococcal alleles at the *mtr* operon, encoding the MtrCDE efflux pump and the transcription repressor, are associated with Azi^{RS} and sought to define further their role in resistance.

Methods We transformed a susceptible strain (MIC <0.125 μg/mL) using gDNA from gonococcal donors carrying mosaic *mtr* loci and selected for Azi^{RS} (MIC ≥2 μg/mL) transformants. We sequenced the transformants' genomes to define the transformed DNA, compared growth rates of parent and transformant strains, described the phylogenetic distribution of *mtrR*, *mtrC*, *mtrD*, and *mtrE* alleles across Neisserial species, and defined the sequence diversity and π at these loci.

Results Transformation studies confirm mosaic *mtr* alleles cause Azi^{RS}. Phylogenetic patterns support frequent Azi^{RS}-associated recombination of *mtrR*, *mtrC*, and *mtrD* between *N. gonorrhoeae* and other Neisseria. Conversely, *16S* and *mtrE* displayed almost exclusive species-based clade topology and no recombination events associated with Azi^{RS}. Within gonococcal populations, reduced nucleotide diversity at *mtrE* (n=1102, π=0.0054) compared to *mtrRCD* (π=0.014) suggests either equal rates of interspecific recombination across the *mtr* operon with increased levels of purifying selection acting to purge the introduction of novel alleles at *mtrE*, or a 'hotspot' of interspecific recombination at *mtrRCD*. Recombination of mosaic *mtr* alleles into novel gonococcal genomic backgrounds does not deleteriously affect growth rate *in vitro*, raising questions regarding the associated fitness cost.

Conclusion This work supports that Neisseria serve as a reservoir of gonococcal Azi^{RS} through interchange of *mtr* alleles. The genomic epidemiological evidence of multiple acquisitions of these alleles underscores the importance of screening for *mtr* mosaics to prevent outbreaks of Azi^{RS}.

P1.17 EFFECTIVENESS OF SYNDORMIC CASE MANAGEMENTS (SCM) IN CONTROL OF SEXUALLY TRANSMITTED INFECTION AND ANTIBIOTIC RESISTANCE

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Introduction Utility of syndromic case management (SCM) in symptomatic women facing huge misdiagnosis/overtreatment problems due to lack of accurate and confirmed diagnosis. As a consequence antibiotic resistance has accelerated along with an increase in risk of infection to their partner.

Methods symptomatic women (18–56 years old) were recruited in the study and examined by clinician based on subjective judgment and treated vaginal discharge with various clinical symptoms causing microorganisms by NACO-NACP III Algorithms for STI/RTI and comparative analysis using PCR-based diagnostic assay.

Results We found that; 646/3200 (20.18%) female patients reported vaginal discharge and recommended treatment for either CT, NG, TV and Candida and/or co-infection using pre-packed STI/RTI kits under NACP III. Based on PCR, 48/646 (7.43%) subjects tested positive for infection with NG/TV/CT. Amongst 46 patents, 28 (60.86%) were correct and conformed diagnosis by PCR and SCM both. While 18/46 (39.14%) were incomplete treated and overtreatment due to poor diagnosis. Out of 600/646 (92.87) treated patients were uninfected of these three pathogens. Based on PCR and SCM, prevalence of TV, NG and CT were shows huge variations. As a result, SCM is inaccurate as infection caused by any of these pathogens showed similar symptoms: vaginitis, cervicitis, genital ulcers, AVD and LAP. The recent increases of misdiagnosis, overtreatment and antibiotic resistance are cause for public health concern. Here our results clearly demonstrate that prevalence of CT and NG is still significant among female patients.

Conclusion The study underpins the need to implement diagnostic assays for identification of causative pathogen before implementing antibiotic treatment to patients with vaginal discharge. It also divulges the need to review the use of SCM for controlling sexually transmitted diseases.

P1.18 EVALUATION OF THE COBAS® HSV 1 AND 2 TEST IN A JAPANESE POPULATION

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Introduction Herpes is a common cause of sexually transmitted disease, which is often asymptomatic. Identification of genital herpes can impact the clinical management of patients who are HIV positive, immunosuppressed, pregnant, and individuals with HSV seronegative partners. The objective of this

study was to evaluate the performance of the **cobas**® HSV 1 and 2 test in a Japanese population.

Methods A total of 165 specimens of anogential lesions and endocervcal swabs from 122 patients were tested from clinical sites in Tokyo, Kanagawa and Osaka (36% Female, 64% Male). Specimens were tested by **cobas**® HSV 1 and 2 test (cHSV) and compared to shell vial culture (SV) as well as Prime Check HSV Antigen Detection Kit (PCA) and direct immunofluorescence (DFA). Diagnostic agreement was evaluated and discrepant analysis was performed by Sanger sequencing.

Results The overall percent agreement (OPA), sensitivity and specificity of cHSV compared to SV for HSV-1 was 98.8% (95% CI 95.7–99.9), 100% (95% CI 97.8%–100%), and 98.5% (95% CI 95.3–99.8), and for HSV-2 was 87.9% (95% CI 81.9–92.5), 98.6% (95% CI 95.4%–99.8%), and 79.6% (95% CI 72.6%–85.4%), respectively. For HSV-1 there were 2 cHSV+/SV-. For HSV-2 there were 20 discordant results, 19 cHSV+/SV- and 1 cHSV-/SV+. Sanger Sequencing for HSV-1 confirmed 1 of 2 positive for HSV-1 and for HSV-2 confirmed 20/20 as HSV-2 positive. Both PCA and DFA missed more than twice as many confirmed positive HSV specimens as SV. The OPA, sensitivity and specificity of cHSV compared to DFA for HSV-1 was 84.8% (95% CI 78.4–89.9), 85.7% (95% CI 79.4%–90.7%), and 84.7% (95% CI 78.3%–89.8%), and for HSV-2 was 59.8% (95% CI 51.9%–67.4%), 100% (95% CI 97.8%–100%), and 53.2% (95% CI 45.3%–61.0%), respectively. PCA does not type positive HSV. The OPA, sensitivity and specificity of cHSV compared to PCA was 74.5% (95% CI 67.1%–81.0%), 98.8% (95% CI 95.6%–99.8%), and 51.8% (95% CI 43.9%–59.6%).

Conclusion This study demonstrated improved diagnostic performance of the **cobas** HSV 1 and 2 test compared to routine methods in a Japanese population.

P1.19 HIGH-THROUGHPUT IDENTIFICATION OF SEXUALLY TRANSMITTED INFECTIONS AND BACTERIAL VAGINOSIS ASSOCIATED PATHOGENS ON OPENARRAY™ NANOFLUIDICS QPCR PLATFORM IN SOUTH AFRICA

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Introduction Cheap and efficient pathogen detection solutions are required to replace syndromic STI management in low and middle income countries. One solution may be point-of-care technologies at clinic level, another could be centralised high-throughput technologies. ThermoFisher recently launched the TaqMan Vaginal Microbiota Assays, in combination with OpenArray Nanofluidics qPCR platform, which is capable of testing 192 samples for 34 individual STI and bacterial vaginosis (BV) pathogens in a 2 hour qPCR run. The goal of this study was to evaluate OpenArray against an established multiplex PCR assay, and further optimise its workflow.

Methods Evaluation of the TaqMan Vaginal Microbiota assays on OpenArray platform was performed for 50 vaginal micobiota vaginal swab samples that had been characterised for *N. gonorrheae* (NG), *C. trachomatis* (CT), and *T. vaginalis* (TV) on an established CDC-approved multiplex PCR assay. Blind samples were provided for testing on the OpenArray platform. Nugent scores were obtained in parallel to molecular testing and results were compared for 11 specific bacterial strains indicative of BV.

Results High specificity (97.4%–100%) was observed at initial testing of STI samples, however the sensitivity was not as expected (NG 81.8%, CT 38.5%, TV 50.0%) due to concentrations of STI pathogens below the limit of detection on OpenArray, which was confirmed by 384-well plate testing (C_{RT} range 33–38). Pre-amplification of STI samples improved the sensitivity significantly (NG 100%, CT 92%, TV 82%). Nugent scores for 46/50 samples were compared with the qPCR results for the BV-associated targets on OpenArray. BV-associated pathogens like *G. vaginalis*, *A. vaginae*, BVAB2, *Megasphaera 1*, *Megasphara 2*, *M.hominis*, and *M. mulieris* were predominate in the samples with Nugent Scores 7–10, while commensal lactobacillus were predominate in Nugent Scores 0–3.

Conclusions After optimisation, the OpenArray Nanofluidics qPCR platform may provide a high-throughput solution for STI pathogen detection and for characterising the vaginal microbiota.

P1.20 ANALYSIS OF BACTERIAL DIVERSITY IN HIV/HPV COINFECTED PATIENTS WITH CERVICAL INTRAEPITHELIAL LESIONS THROUGH NEXT-GENERATION SEQUENCING

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Introduction Several studies have shown an increase in bacterial diversity in HPV-positive cervical cancer patients and the association of specific bacteria with cervical intraepithelial lesions. However, little is known about the cervical microbiome of HIV/HPV coinfected patients. HIV patients have a high prevalence of high-risk HPV and a greater chance of developing persistent HPV infection. The aim of this study is to evaluate the bacterial profiles of the cervical region of HIV/HPV coinfected patients, looking for a putative association of such profiles with cervical intraepithelial lesions.

Methods We analysed 89 HIV^+ cervical smear samples of women collected from 2010 to 2013. Samples have been categorised according to collection timepoint, $CD4^+$ T-cell counts and cervical intraepithelial lesions (CIN). The bacterial 16S rRNA gene was PCR-amplified and processed for next-generation sequencing in an Illumina HiSeq 2500 platform. After sequencing, reads were processed and compared against the 16S database. All bioinformatics analyses were carried out using QIIME.

Results The most abundant bacterial species found was *Lactobacillus iners*. We found a negative association of the *Moryella* genus with CIN, independent of the collection timepoint. On the other hand, we observed increased abundance of *Gardnerella vaginalis*, *Shuttleworthia*, *Veillonellaceae* and *Aerococcus* in CIN, but adjusted p-values were non-significant after false discovery rate and/or Bonferroni corrections.

Conclusion This is first study reporting the *Moryella* genus in HIV/HPV coinfected women and its potential absence in CIN.