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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10.1136/sextrans-2017-053264.124

Introduction Reducible susceptibility to azithromycin (AzRS) 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 AzRS 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 mtr loci and selected for AzRS (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 AzRS. Phylogenetic patterns support frequent AzRS-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 AzRS. Within gonococcal populations, reduced nucleotide diversity at mtrE (π = 0.0022, p = 0.0034) 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 AzRS 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 AzRS.

P1.17 EFFECTIVENESS OF SYNDROMIC CASE MANAGEMENTS (SCM) IN CONTROL OF SEXUALLY TRANSMITTED INFECTION AND ANTIBiotic RESISTANCE
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10.1136/sextrans-2017-053264.125

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 confirmed 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 divulgues 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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10.1136/sextrans-2017-053264.126

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