

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 GONORRHOEA* VIA INTRAGENUS RECOMBINATION

Crista Wadsworth, Yonatan Grad. Harvard Th Chan School of Public Health, Boston, MA, USA, USA

10.1136/sextrans-2017-053264.124

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* ($n=1102$, $\pi=0.0054$) compared to *mtrRCD* ($\pi=0.014$) 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 SYNDROMIC CASE MANAGERMENTS (SCM) IN CONTROL OF SEXUALLY TRANSMITTED INFECTION AND ANTIBIOTIC RESISTANCE

¹Subash C Sonkar, ²R Bharti, ¹K Wasnik, ²A Kumar, ¹Mishra Pk, ²P Mittal, ¹D Saluja. ¹Medical Biotechnology Lab, Dr. B. R. Ambedkar Centre For Biomedical Research, University of Delhi, D, Delhi, India; ²Department of Obstetrics and Gynaecology, Vardhman Mahavir Medical College and Safdarjung Hospital, New, New Delhi, India

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 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

¹Elizabeth Marlowe, ²Takashi Kawana, ³Tomohiko Onoe, ⁴Yasuhiko Onoe, ⁵Masayuki Sawamura, ⁶Kenichi Hayakawa, ¹Michael Lewinski, ⁷Rui Ohse, ⁷Ai Takiyama. ¹Roche Molecular Systems, Pleasanton, USA; ²Teikyo University Mizonokuchi Hospital, Kanagawa – Japan; ³The Jikei University Katsushika Medical Centre, Tokyo – Japan; ⁴Miyamoto-Cho Central Clinic, Kanagawa – Japan; ⁵Shinjuku Sakura Clinic, Tokyo – Japan; ⁶Seiwakai Hayakawa Clinic Medical Corporation, Osaka – Japan; ⁷Roche Diagnostics K.K., Tokyo – Japan

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