P1.36 COMPARISON OF NUGENT CRITERIA, AMSEL'S CRITERIA AND MODIFIED AMSEL'S CRITERIA FOR DIAGNOSING BACTERIAL VAGINOSIS WITH SPECIAL EMPHASIS ON CONCORDANCE OF SELF AND PHYSICIAN-COLLECTED SAMPLES

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Introduction Bacterial vaginosis (BV) is the most common cause of vaginal discharge worldwide including India. Syndromic diagnosis and management is used across the country for STIs/RTIs. Aims of the study were 1) to evaluate the prevalence of BV based on Nugent's, Amsel's and modified Amsel's criteria 2) to analyse concordance between self- and physician collected swabs for the three different criteria.
Methods Study included 550 females attending STI/RTI clinics with abnormal vaginal discharge during the study period of January 2015 to May 2016. Self-collection of swabs was done by patients after instructions followed by physician collection under speculum examination. The samples were analysed by Nugent's, Amsel's and modified Amsel's criteria for diagnosing BV.
Results Based on Nugent scoring, 79 (14.3%), 95 (17.3%), 376 (68.4%) patients were found to be BV positive (+), intermediate and BV negative (-) respectively. However, using Amsel's criteria only 67 (12.2%) patients were observed to be BV+ and 483 (87.8%) were BV-. As modified Amsel's criteria diagnoses BV+ even when only two out of four Amsel's criteria are fulfilled, it could detect 96 BV+ cases (17.5%). All the above results were obtained using the physician-collected samples. Sensitivity for diagnosing BV by self-collected samples using Nugent score, Amsel's criteria and modified Amsel's criteria was 91.1%, 98.5% and 97.9%, while specificity was 100%, 99.6% and 99.6%, positive predictive value 100%, 97.1% and 97.9% and negative predictive value was 98.5%, 99.8% and 99.6% respectively. High concordance of self-collected samples was established by the Cohen's Kappa value of 0.890, 0.975, and 0.993 for Nugent scoring, Amsel's criteria and Modified Amsel's criteria respectively.
Conclusion Apart from Nugent's scorimg, Amsel's and modified Amsel's criteria were equally consistent methods of diagnosis. Establishing reliability of self-collected samples for diagnosing BV shall pave way for validation of syndromic diagnosis even at peripheral health centres.

P1.37 PREVALENCE AND MOLECULAR ANALYSIS OF *MYCOPLASMA GENITALIUM* STRAINS ISOLATED FROM PREGNANT WOMEN AT AN ACADEMIC HOSPITAL IN PRETORIA, SOUTH AFRICA

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Introduction: *M. genitalium* is not usually among organisms for routine testing in sexually transmitted infection screening. Treatment follows syndromic guidelines. As *M. genitalium* cannot be readily cultured, detection of antimicrobial resistance and typing of strains relies on DNA sequence data. It was shown that although there is high intra-strain stability, high levels of sequence variability between clinical isolates are seen which may be associated with antimicrobial resistance.
Methods Endocervical swabs were collected from 100 pregnant women attending a tertiary hospital in Pretoria, South Africa. The specimens were screened for *M. genitalium* using a commercial real time PCR assay. Genotypic resistance markers for macrolide and fluoroquinolones were determined by sequence analysis of the V-region of the 23S rRNA, *gyrA*, and *parC* genes. The strains were typed using mgpB single-nucleotide polymorphism typing (SNP) and MG309 variable number tandem (VNTR) analysis.
Results: *M. genitalium* was detected in 7 (7.0%) of specimens of which one positive sample could not be detected with further methods. No resistance associated mutations were seen in the gyrA and parC genes. In 2 isolates the macrolide associated mutation A2059G was seen. SNP typing revealed Sequence Types 1, 2 and 4. Four different types were seen using MG309 VNTR analysis. Typing assigned *M. genitalium* to 2 major clusters. Genotypic macrolide resistance was found within one of the clusters.
Conclusion: *Mycoplasma genitalium* is a frequent undiagnosed STD in this population. As azythromycin was included in the national syndromic treatment guidelines in 2015, it is alarming to already find resistance associated genes.

P1.38 BACTERIAL POPULATIONS DETECTED WITHIN FIRST VOID URINE SAMPLES OF SYMPTOMATIC MALE PATIENTS WITH URETHRITIS

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Introduction Applying bacterial 16S rRNA profiling we investigated whether species in first void urine (FVU) differed between men presenting with urethritis symptoms with and without urethral inflammation.
Methods 443 patients prospectively attending a London sexual health clinic were classified, based on clinical presentation and Gram stain as: symptomatic urethritis (URE); symptomatic non-urethritis (SYM); and asymptomatic (ASP). Residual FVU's were tested for [K1] *Chlamydia trachomatis* (CT), *Neisseria gonorrhoeae* (NG), *Trichomonas vaginalis* (TV) and *Mycoplasma genitalium* (MG) and subjected to bacterial 16S rRNA profiling (variable region v1-2) Differences in bacterial oligotypes across samples were described using partial least square discriminant analysis tested using permutational multivariate analysis of variance (PERMANOVA). The hypothesis tested was: URE have distinct urinary bacterial 16S rRNA profiles compared to SYM and ASP.
Results 286/443 samples met quality control criteria. Among URE [n=79], SYM [n=83], and ASP [n=124], CT, MG, NG and TV prevalence's were: 12.7% (95 CI 6.6–22.5), 13.9% (95CI 7.5–24), 8.9% (95CI 3.9–7.5), 1.3% (95CI 0.1–7.8); 2.4% (95CI 0.4–9.2), 2.4% (95CI 0.4–9.2), 1.2% (95CI 0.1–7.5); 2.4% (95CI 0.6–7.4), 5.7% (95CI 2.5–11.8), NG not detected, 0.8% (95CI 0–5.1) respectively. *Lactobacillus iners* was the most abundant oligotype observed in all groups. *Streptococcus agalactiae* and *S. anginosus* were highly dominant in ASP along with *S. mitis*, which was relatively increased in both ASP and SYM. A decreased relative abundance of these oligotypes was observed in URE cases. A