

**P1.26** EVALUATION OF TWO DIAGNOSTIC SYSTEMS FOR THE DETECTION OF *CHLAMYDIA TRACHOMATIS* (CT) AND *NEISSERIA GONORRHOEAE* (NG) USING MALE URETHRAL SWABS

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**Introduction** Urine is the specimen of choice for CT and NG molecular testing from males and many of the next generation testing platforms are not FDA approved for use with urethral swabs. Urethral swabs remain valuable in research settings that may require that the specimen is collected in a manner preserving organism viability. The goal of this study was to assess the Abbott *m2000* Realtime (*m2000*), and Roche COBAS 4800 (*c4800*) systems for the identification of CT and NG in urethral swabs collected in chlamydia transport medium (CTM).

**Methods** Archived male urethral swabs collected in CTM from STD clinic attendees were tested. These specimens were originally tested for CT and NG on a platform FDA-approved for urethral swabs collected in CTM (Roche COBAS Amplicor, (*cAMP*)). Two-hundred  $\mu$ l of CTM was added into each manufacturer's collection device. This was subsequently tested on the *m2000* and *c4800* systems according to the manufacturer's instructions. CT and NG results obtained from each platform were compared to the original *cAMP* results to determine sensitivity and specificity. Agreement between platforms was measured by calculating the kappa coefficient.

**Results** One hundred urethral swab specimens were available for testing (28 CT and 25 NG positives). When compared to results obtained with the *cAMP*, the sensitivity and specificity of the *m2000* for the detection of CT was 100% and 98.6%, respectively; the sensitivity and specificity on the *c4800* was 96.4% and 98.6%. For NG, the sensitivity and specificity of the *m2000* assay was 100% and 98.7%; the *c4800* assay was 100% sensitive and specific. Agreement was excellent for both platforms when compared to *cAMP* with kappa scores of  $>0.95$  for CT and  $>0.97$  for NG.

**Conclusion** The *m2000* and *c4800* platforms have similar performance characteristics to *cAMP* for the detection of CT and NG using urethral swabs in CTM. This study will provide investigators with additional options when designing protocols that require the preservation and ability to recover viable organisms from men.

**P1.27** HPV IS ASSOCIATED WITH AN ALTERED METABOLOMIC PROFILE IN THE VAGINAL TRACT

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**Introduction** Recent studies have reported associations between bacterial vaginosis (BV) and cervicovaginal HPV. To obtain further insight into this relationship, we examined the vaginal

microbiota and metabolome of women who were HPV+ and HPV-.

**Methods** Thirty-nine women self-collected mid-vaginal swabs that were profiled for bacterial composition by 16S rRNA gene amplicon sequencing, metabolites by both GC/MS and LC/MS-based metabolomics and 37 types of HPV DNA with the Roche HPV Linear Array genotyping test. Data were analysed by multiple linear regression controlling for confounding factors, as well as principal components analysis, partial least squares discriminatory analysis and linear discriminant analyses. All reported results have an adjusted p-value (q-value)  $<0.05$ .

**Results** Vaginal microbiota were clustered into community state types CST-I (*L. crispatus*-dominated), CST-III (*L. iners*-dominated) and CST-IV (low-*Lactobacillus*/BV-associated taxa). Overall, HPV+ women had higher polyamine and phospholipid concentrations than HPV- women in a model which controlled for CST and smoking status. Significant differences in metabolomic profiles of HPV+ and HPV- women were also evident in each stratum of CST. Among women who were CST-III, HPV+ women had higher concentrations of biogenic amines and glycogen-related metabolites compared to HPV- women. Within CST-IV, HPV+ women had lower concentrations of glutathione, glycogen, and phospholipid-related metabolites than HPV- women. Women with high-risk HPV strains had lower concentrations of amino acids, lipids and peptides compared to women who were hrHPV-.

**Conclusion** Detection of HPV was associated with altered vaginal concentrations of biogenic amines, glutathione and lipid-related metabolites. Reduced glutathione and oxidised glutathione have known associations with HPV and may be representative of increased oxidative stress and total glutathione depletion. Elucidating a causal relationship between microbial metabolites associated with increased oxidative stress and HPV infection warrants further investigation.

**P1.28** PRODUCTION OF A POLYCLONAL ANTIBODY AGAINST THE VAGINOLYSIN OF *GARDNERELLA VAGINALIS*

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**Introduction** Bacterial vaginosis (BV) is a polymicrobial syndrome characterised by the decrease in Lactobacilli and an increase of anaerobic bacteria, mainly *G. vaginalis* a Gram-positive coccobacillus that is isolated in up to 98% of BV cases. This bacteria produces different virulence factors like sialidase, succinate, biofilm formation, phospholipase C, and vaginolysin (VLY). The VLY is a protein of 56 kDa that belongs to the family of cholesterol-dependent cytolysins, the function of this protein is the cellular lysis of erythrocytes and epithelial cells through the binding to the CD59 receptor and cholesterol present in cell membranes. The production of a polyclonal antibody against VLY will allow the study of this cytolysin in the pathogenesis of *Gardnerella vaginalis* in the vaginal tract.

**Methods** We use as antigen the ATCC 14018 of *G. vaginalis* which was obtained from a extract of total proteins by electrophoresis. The band corresponding to the molecular weight of the VLY (56 kDa) was cut, macerated and resuspended in PBS. Two New Zealand rabbits were immunised for 6 weeks,