Within this concordant pair, both women reported engaging in oral sex and sharing wet towels during sexual activity. One woman in this pair reported recent sex with a male partner while the other woman denied history of other sexual partners during the past 3 months and had not had sex with a male partner in 5 years. Additionally, a follow-up visit of one of the members of this concordant union demonstrated a RAPD pattern discordant with previous findings indicating that the individual's initial treatment was successful and that she had acquired a new TV infection.

Conclusions Given the phenotypic similarity of banding patterns within one AAWSW sexual partnership, female to female transmission of TV may have occurred. The frequency of TV transmission between WSW is unknown at this time; however, the use of RAPD appears to be informative for differentiating isolates of TV. A prospective study examining the epidemiology and incidence of TV infection among WSW is necessary.

P3-S7.06 VAGINAL DISCHARGE IN WOMEN LIVING WITH HIV ATTENDING AN AIDS CLINIC IN MANAUS, BRAZIL

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Background A vaginal discharge and/or vulvar itching and irritation usually characterise Vaginitis, and a vaginal odour might be present. The three diseases most frequently associated with vaginal discharge are BV (replacement of the normal vaginal flora by an overgrowth of anaerobic microorganisms, (*Gardnerella vaginalis*), trichomoniasis, and candidiasis.

Objectives To estimate the prevalence of vaginal discharge in HIV women attending the Institute of Tropical Medicine in Manaus, Amazonas, Brazil.

Methods A cross-sectional study performed among women attending the AIDS clinic from March to December 2010. They were invited to take pat in the study and answered an interview including demographic, behavioural and clinical data. They underwent in a gynaecological examination and it was collect vaginal samples for diagnosing *Trichomonas vaginalis, Gardnerella vaginalis* and *Candida spp*.

Results A total of 338 women were included in the study. Median age was 32 (IQR (IQR): 27; 38) years and median of schooling nine (IQR: 4; 11) years. Prevalence rate of vaginal discharge was 45.8% (95% CI 40.5% to 51.1%). Prevalence of *Trichomonas vaginalis* was 1.2% (95% CI 0.5% to 2.4%), *Gardnerella vaginalis* 35.8% (95% CI 30.7% to 40.9%) and Candidiasis 21.3% (95% CI 16.9% to 25.7%). Median of first sexual intercourse was 16 (IQR: 14; 17) years and 53.6% were married or reported a stable partner. Risk factors reported were: injecting drug use (1.2%), no-injecting drugs (15.2%), previous STI (32.4%), commercial sex workers (16.4%), more than one partner in the last year (12.4%) and in life (94.7%). Regarding clinical symptoms, 50,9% reported chronic pelvic pain, 53.3% vaginal discharge, 47.6% vaginal itching, 22.8% dysuria and 9.5% genital bleeding. CD4 counts were more than 500 cells/mm^3 in 29.4% and viral load were <1.00 copies/ml in 53.8%. A total of 53.9% of women reporting vaginal discharge had a positive test for at least one disease. In the final model of logistic regression the only variable remained was having viral load <1000 copies/ml decreased the risk of vaginal discharge.

Conclusions Regardless the low cost and large availability of GRAM stain and cytological tests in health services for women with AIDS, there are difficulties which remain to identify interventions that refer to social, cultural and environmental influences on vaginal infections in this group.

P3-S7.07 DETECTION OF *TRICHOMONAS VAGINALIS* IN HIV POSITIVE WOMEN IN PRETORIA, SOUTH AFRICA

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Background The aim of this study was to detect *Trichomonas vaginalis* infection in HIV positive women receiving anti-retroviral therapy in Pretoria, South Africa.

Methods Self-collected vaginal swab specimens from 95 consecutive patients attending the anti-retroviral clinic (Tshwane District Hospital) were analysed. *Trichomonas vaginalis* was diagnosed by wet mount microscopy, culture using InPouch and a commercial PCR assay targeting the DNA repeat units. Trichomoniasis was diagnosed if any test was positive.

Results Five (5.3%) of the 95 specimens were positive by wet mount microscopy, 21 (22.1%) were culture positive and 28 (29.5%) were detected by PCR. All culture and wet mount positive specimens were PCR positive. The sensitivity and specificity of wet mount microscopy compared to culture were 23.8% and 98.7% respectively. PCR detected seven additional positive specimens than culture. The specificity of PCR compared to culture was 100%, with a sensitivity of 90.5%. The prevalence of *T vaginalis* was found to be 29.5% in this study.

Conclusions Previous studies in South Africa focused on the prevalence of trichomoniasis in pregnant women and women without HIV status and from lower socio-economic groups. This is the first report in HIV positive women receiving ARV treatment. There was a high prevalence (29.5%) of *T vaginalis* in this group. This is similar to that reported from Nigeria (24.4%) and Ivory Coast (27.0%), whilst the rate reported in Congolese (18.6%) HIV positive women was lower. Using microscopy alone for the diagnosis of trichomoniasis as is the current practice in most laboratories in South Africa is inadequate and leads to missed infections.

P3-S7.08 CLINICAL EVALUATION OF THE APTIMA® *TRICHOMONAS VAGINALIS* ASSAY ON THE TIGRIS® DTS® SYSTEM IN ASYMPTOMATIC AND SYMPTOMATIC FEMALE SUBJECTS

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Background This study evaluated the clinical performance of the APTIMA® *Trichomonas vaginalis* (ATV, Gen-Probe Incorporated) Assay, a nucleic acid amplification test for the diagnosis of *Trichomonas vaginalis* (TV) infection, in asymptomatic and symptomatic women.

Methods This prospective, multicenter clinical trial enrolled 1025 women attending US OB-GYN, adolescent, family planning, or sexually transmitted disease clinics. Four specimen types were collected from each subject: physician-collected vaginal swab, endocervical swab, ThinPrep specimen, and first-catch urine. Of three vaginal swabs collected from each subject, one was used for wet mount microscopic examination, one for culture, and one for molecular testing for TV. The order of collection for each vaginal swab sample was rotated to minimise sampling bias. Each specimen was tested by ATV assay using the automated TIGRIS DTS system. ATV assay performance in each sample type was determined by comparing ATV assay test result to the patient infected status (positive in saline wet mount and/or culture) for each sample.

Results Of 933 subjects included in the analysis, 59.9% were symptomatic. Compared to patient infected status, ATV assay clinical sensitivities and specificities were 100% and 99.0%, respectively, from vaginal swabs; 100% and 99.4%, respectively, from endocervical swab; 100% and 99.6%, respectively, from ThinPrep specimens; and 95.2% and 98.9%, respectively, from patient-collected urine samples. ATV assay performance was similar in asymptomatic and symptomatic patients, by age group (14–17 years and 18 years or older), and was consistent between testing sites. The ATV assay also demonstrated superior performance compared to wet mount microscopic examination and TV culture, regardless of the specimen type utilised.
Conclusions This study provides clinical validation of the ATV assay for the intended uses of detecting TV rRNA in asymptomatic women, and/or to aid in the diagnosis of trichomoniasis in symptomatic women, in a US population. The use of highly accurate, fully-automated molecular tests such as the ATV assay for testing easily obtained vaginal swab and urine samples should facilitate large-scale screening for TV in the US.

P3-S7.09 MUTATIONS ON GYRA OR PARC GENES OF *MYCOPLASMA GENITALIUM* AND EFFICACIES OF TREATMENT WITH FLUOROQUINOLONES AGAINST *M GENITALIUM*-RELATED URETHRITIS

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Background *Mycoplasma genitalium* is one of the pathogens of male urethritis. Macrolides as azithromycin can be the first line-treatment, but macrolides-resistant *M genitalium* strains were isolated. We tried to use some fluoroquinolones against *M genitalium*-related urethritis. In these studies, some patients could not treated by fluoroquinolone. In any bacteria, genetic mutations on gyrase genes were related to fluoroquinolone-resistance. In this study, quinolone-resistant determining regions (QRDR) on gyrase genes of *M genitalium* were analysed and the relationship between the efficacies of fluoroquinolone against *M genitalium*-related urethritis and genetic mutations on QRDR of *M genitalium* was examined.
Methods The QRDR on gyrA and parC genes of *M genitalium* were sequenced and analysed. DNA samples were purified from *M genitalium*-positive first-voided urine specimens before and after the treatment with fluoroquinolones as gatifloxacin or sitafloxacin. The QRDR of gyrA and parC genes of *M genitalium* were analysed by using primers according to Shimada's report (Int J Antimicrob Agent, 2010).
Results Twenty-two genomes of *M genitalium* before the treatment with fluoroquinolones and four genomes from patients with treatment-failure were analysed. Before the treatment, *M genitalium* genomes have no mutation on gyrA, but had four mutations on parC gene with amino-changes (Ala-69 to Thr, Pro-72 to Ser, Asp-87 to His and Ser-83 to Ile). After the treatment, *M genitalium* was found in four patients and all remained *M genitalium* were found mutations on gyrA or parC with amino-changes. *M genitalium* with mutation on parC (Pro-72 to Ser and Ser-83 to Ile) before treatment was remained. *M genitalium* with mutation on parC (Pro-72 to Se and Ser-83 to Ile) before treatment was remained and was found additional gyrA mutation (Asp-99 to Asn). In two patients, *M genitalium* without mutations before treatment remained after treatment. However, these genomes were found with newer mutations on gyrA (Asp-99 to Asn) or on parC (Ser-83 to Ile).
Conclusion From the urine specimens of patients with treatment-failure of fluoroquinolones, some mutations with amino-change were found on QRDR of gyrA or parC genes of *M genitalium*. It was suggested that these mutations are related with treatment-failure with fluoroquinolones.

P3-S7.10 COMPOSITION OF VAGINAL MICROBIOTA IN BACTERIAL VAGINOSIS PATIENTS AND HEALTHY WOMEN: BASIS FOR GENETIC DIAGNOSIS OF BACTERIAL VAGINOSIS?

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Background Bacterial vaginosis (BV) is the most common vaginal infection/disorder. BV is characterised by imbalance in the normal vaginal microbiota with a shift towards higher bacterial diversity and increased pH. The aim of the present study was to describe the differences in vaginal microbiota composition in women suffering from BV compared to healthy women, using massive parallel 454 pyrosequencing.
Methods 163 vaginal samples were collected from women diagnosed with characteristic BV (n=73), women with intermediate BV (n=11), and from healthy women on their regular check-ups (n=79). DNA from the samples was isolated and the bacterial compositions as well as the relative abundance of these bacteria were analysed using 454 pyrosequencing, with GS Titanium amplicons kit (Roche Inc.), of the hypervariable region V4 on the 16S rRNA gene. Finally, 17 different species-specific PCRs were used to verify the species of bacteria found in the 454 pyrosequencing.
Results Extensive imbalance of the vaginal microbiota of women with BV compared to healthy controls was revealed. The dominating taxons of the 73 BV cases were Gardnerella, Atopobium, Prevotella, Lactobacillus, Megasphera and Sneathia, while most of the 79 healthy controls had a microbiota totally dominated by Lactobacillus with the BV associated taxons hardly detectable. Furthermore, the 11 patients with intermediate BV predominantly had a mix of the BV associated taxon Gardnerella as well as Lactobacillus. A few of the healthy controls seemed to have a microbiota changing towards the intermediate microflora. Gardnerella may be the first bacteria to establish in the transition from healthy vaginal flora towards a BV associated flora.
Conclusions A clear difference in the composition of the vaginal microbiota between individuals suffering from BV and healthy controls was identified. The present findings are important steps towards the determination of valid potential bacterial markers for BV, are shedding light upon why some women develop BV, as well as show how the microbiota is involved in the development of BV. Knowledge of the composition of the vaginal microbiota is crucial in the development of a BV diagnostic tool and for elucidating appropriate treatment for use in clinical practice.

P3-S7.11 FACTORS ASSOCIATED WITH PERSISTENT BACTERIAL VAGINOSIS AMONG YOUNG REPRODUCTIVE AGE WOMEN IN MYSORE, INDIA

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Background Bacterial vaginosis (BV) is a common infection and has been associated with adverse health outcomes including preterm birth, pelvic inflammatory disease and acquisition of HIV and other sexually transmitted diseases. There are limited data on persistent