

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*, *Megasphaera* 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