Background The occurrence of azithromycin resistance in M. genitalium infection is unknown in Africa, where diagnostic resources are limited and STIs are managed syndromically. This study aims to gain insight in the molecular epidemiology including antimicrobial resistance of M. genitalium infection in South Africa.

Methods We collected 87 M. genitalium-positive samples obtained from participants in three study cohorts: HIV-infected pregnant women residing in townships in Pretoria (n=44), men and women accessing primary healthcare services in rural Mopani District (n=32), and men accessing sexual health services in Johannesburg (n=11). Molecular typing was performed using single nucleotide polymorphism (SNP) analysis of the MG191 gene to determine sequence type (ST) combined with variable-number of tandem-repeat (VNTR) assessment of the MG309 gene. Molecular detection of macrolide resistance-associated mutations in the 23S rRNA gene was done and, if detected, subsequent sequencing of the parC and gyrA genes for quinolone resistance.

Results SNP analysis was successful in 22 specimens and showed 17 different STs (9 known and 8 new STs). VNTR assessment was successful for 36 specimens and showed variation in the number of repeat, ranging from 8 to 19; four strains had the same number of repeats (11). There was no geographic clustering of specific STs or number of repeats observed. Azithromycin resistance was detected in only 1/87 specimens (1.1%); a mutation in the parC gene associated with quinolone resistance was also detected in this case. This specific strain was a unique novel ST, but with similar tandem repeats, compared to the drug-susceptible stains.

Conclusion This study shows a well-established, genetically diverse epidemic of M. genitalium infection in South Africa. The prevalence of azithromycin resistance was low, which is probably the result of the relatively recent introduction of azithromycin in the syndromic management guidelines. Nevertheless, introduction of diagnostics and surveillance of resistance is urgently warranted.

Disclosure No significant relationships.

P618  MACROLYCE AND QUINOLONE RESISTANCE IN MYCOPLASMA GENITALIUM: DATA FROM A UK SEXUAL HEALTH CLINIC

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Background Rates of macrolide resistance (MR) in Mycoplasma genitalium (Mgen) globally remain alarmingly high (30-100%) and quinolone resistance (QR) is now an increasing concern. In the UK, testing for Mgen is in its infancy and data for MR and QR are therefore lacking. The recent publication of guidelines by British Association for Sexual Health and HIV (BASHH) delivers hope that testing and experience in managing Mgen infection will increase. We aimed to measure infection rates and to determine the prevalence of MR and QR in men with urethritis and women with pelvic inflammatory disease (PID) attending a UK sexual health clinic.

Disclosure No significant relationships.

P619  MOLECULAR TYPING OF MYCOPLASMA GENITALIUM SHOWS A DIVERSE EPIDEMIC WITH LIMITED AZITHROMYCIN RESISTANCE IN SOUTH AFRICA

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Background The occurrence of azithromycin resistance in M. genitalium infection is unknown in Africa, where diagnostic resources are limited and STIs are managed syndromically. This study aims to gain insight in the molecular epidemiology including antimicrobial resistance of M. genitalium infection in South Africa.

Methods We collected 87 M. genitalium-positive samples obtained from participants in three study cohorts: HIV-infected pregnant women residing in townships in Pretoria (n=44), men and women accessing primary healthcare services in rural Mopani District (n=32), and men accessing sexual health services in Johannesburg (n=11). Molecular typing was performed using single nucleotide polymorphism (SNP) analysis of the MG191 gene to determine sequence type (ST) combined with variable-number of tandem-repeat (VNTR) assessment of the MG309 gene. Molecular detection of macrolide resistance-associated mutations in the 23S rRNA gene was done and, if detected, subsequent sequencing of the parC and gyrA genes for quinolone resistance.

Results SNP analysis was successful in 22 specimens and showed 17 different STs (9 known and 8 new STs). VNTR assessment was successful for 36 specimens and showed variation in the number of repeat, ranging from 8 to 19; four strains had the same number of repeats (11). There was no geographic clustering of specific STs or number of repeats observed. Azithromycin resistance was detected in only 1/87 specimens (1.1%); a mutation in the parC gene associated with quinolone resistance was also detected in this case. This specific strain was a unique novel ST, but with similar tandem repeats, compared to the drug-susceptible stains.

Conclusion This study shows a well-established, genetically diverse epidemic of M. genitalium infection in South Africa. The prevalence of azithromycin resistance was low, which is probably the result of the relatively recent introduction of azithromycin in the syndromic management guidelines. Nevertheless, introduction of diagnostics and surveillance of resistance is urgently warranted.

Disclosure No significant relationships.