P05.13 PREVALENCE AND ANATOMICAL DISTRIBUTION OF *MYCOPLASMA GENITALIUM* MACROLIDE RESISTANCE MARKERS FROM SUBJECTS ENROLLED IN A MULTI-CENTRE US CLINICAL STUDY

[1]D Getman*, [1]M O'Donnell, [2]S Cohen, [1]A Jiang. [1]*Hologic Inc, San Diego, USA*; [2]*Occidental College, Los Angeles, USA*

10.1136/sextrans-2015-052270.299

Introduction This study evaluated the prevalence and anatomical distribution of *Mycoplasma genitalium* (Mgen) 23s rRNA mutations (23s-MTs) conferring macrolide resistance among male and female subjects enrolled in a prospective multi-site US clinical study.

Methods Specimens obtained from symptomatic and asymptomatic men and women enrolled from 7 diverse US clinical sites, including obstetrics and gynaecology, family planning, public health, and sexually transmitted disease clinics, were tested using a research TMA assay for Mgen (Hologic, Inc.) on the DTS System or TIGRIS DTS System. Samples positive for Mgen by TMA were evaluated by nested PCR or RT-PCR and Sanger sequencing of Mgen 23S rRNA to identify the presence of macrolide resistance mutations at position 2058 (A2058G, A2058C, A2058T) or position 2059 (A2059G).

Results Of 50 male subjects with Mgen 23s rRNA sequence results, 21 (42%) contained 23s-MTs. Slightly more 23s-MTs were found in urethral swabs vs male urine samples (44.8% vs 36.7%, respectively). For female subjects, 65 of 128 (50.8%) harboured 23s-MTs, with higher prevalence found in vaginal swab samples (50.2%) compared to urine (46%), Thinprep liquid Pap (41.7%), and endocervical swabs (37.8%). Sequencing of samples collected from anatomically distinct female urogenital sites (vagina, cervix, urine) revealed 18 of 35 (51.4%) subjects had a unique complement of Mgen 23s-MT and/or wild-type sequences at each anatomic site. For male subjects with both urine and urethral swab samples, 3 of 9 (33.3%) subjects had unique Mgen 23s-MT/WT sequences in each sample type.

Conclusion Mgen strains harbouring 23s rRNA-mediated macrolide resistance phenotypes were highly prevalent in this US cohort of male and female subjects. Detection of different macrolide-resistant Mgen strains in samples collected from different anatomical locations suggests that previous estimates for resistance rates that relied on a single anatomical site sample collection may have underestimated the extent of Mgen macrolide resistance in the population.

Disclosure of interest statement D Getman, M O'Donnell, and A Jiang are scientists employed by Hologic. S Cohen is a student at Occidental College and a summer intern at Hologic.

P05.14 MINIMUM INHIBITORY CONCENTRATIONS OF METRONIDAZOLE AND TINIDAZOLE AGAINST *TRICHOMONAS VAGINALIS*

AN Mtshali*, BC Joubert, P Moodley, AW Sturm. *University of KwaZulu-Natal, South Africa*

10.1136/sextrans-2015-052270.300

Introduction Syndromic management is used to control sexually transmitted diseases in South Africa. *Trichomonas vaginalis* causes trichomoniasis which results in vaginal discharge in symptomatic patients. This is treated with metronidazole which is included in the syndromic management antimicrobial regime. In order for this regime to be effective, the organisms causing each syndrome and their antimicrobial susceptibility profile need to be evaluated periodically to ensure that the most appropriate antimicrobial agents are included.

Methods Women 18 years and older presenting with vaginal discharge were recruited from two different clinics of KwaZulu-Natal province in South Africa. Vaginal specimens were collected using a Dacron swab and cultured in modified Diamonds medium. The minimum inhibitory concentrations (MICs) of *T. vaginalis* to metronidazole and tinidazole were determined in 94 positive clinical isolates using a micro-broth dilution method. Briefly trichomonads were added to Diamonds media containing two-fold dilutions (16 to 0.25 mg/L) of metronidazole or tinidazole and incubated anaerobically for 72 h. The lowest concentration at which no motile trichomonads were visualised under an inverted phase contrast microscope was considered the MIC. Propionibacterium acnes and Bacteroides fragilis were used as the resistant and sensitive controls respectively. MIC ≤ 1 mg/L was considered sensitive, MIC ≥4 mg/L was considered resistant; MIC between 1 mg/L and 4 mg/L was considered intermediate. The MIC of any isolate in the resistant range was repeated to confirm results.

Results Of the 94 isolates, 17 had an MIC ≥4 mg/L indicating *in vitro* resistance to metronidazole while 2 isolates had an MIC ≥4 mg/L for tinidazole. Thirty-five and 33 isolates had an MIC of 2 mg/L (intermediate) for metronidazole and tinidazole respectively.

Conclusion High MIC of *T. vaginalis* to metronidazole is a public health concern however more research is needed to correlate *in vitro* resistance with clinical failure.

Disclosure of interest statement The authors have no conflict of interest to declare. No pharmaceutical grants were received in the development of this study.

P05.15 *UREAPLASMA* SPP. ISOLATED FROM GENITAL SAMPLES IN SWITZERLAND: SUSCEPTIBILITY PATTERNS, RESISTANCE GENES, AND SEQUENCE TYPE DISTRIBUTION

[1]V Donà*, [1]SC Schneider, [1]R Tinguely, [1,2]M Hilty, [3]T Bodmer, [1]A Endimiani*. [1]*Institute for Infectious Diseases, Faculty of Medicine, University of Bern, Bern, Switzerland*; [2]*Department of Infectious Diseases, Bern University Hospital and University of Bern, Bern, Switzerland*; [3]*Labormedizinisches Zentrum Dr Risch, Bern-Liebefeld, Switzerland*

10.1136/sextrans-2015-052270.301

Background Antibiotic resistance in *U. urealyticum* (UUA), *U. parvum* (UPA) and *M. hominis* (MH) poses an increasing issue. However, data regarding antibiotic susceptibility is limited to several countries, whereas information about clonality is available only from China.

Methods We analysed 140 genital samples collected in two laboratories from unique patients in Bern during 2014. Identification and antimicrobial susceptibility tests were obtained using the mycoplasma IST 2 kit (bioMérieux) and sequencing of 16S rDNA. Clonality was analysed with multilocus sequence typing (MLST) and expanded MLST (eMLST), whereas quinolone and macrolide resistance were studied by sequencing *gyrA*/*B*, *parC*/*E*, as well as genes encoding 23S rRNA and L4/22 ribosomal proteins.

Results One-hundred-three samples (74%) were confirmed being positive for UUA/UPA, whereas 21 (15%) were positive for both UUA/UPA and MH. Non-susceptibility was highest to ciprofloxacin (19.4%) and ofloxacin (9.7%), whereas low rates were observed for clarithromycin (4.8%), erythromycin (1.9%), azithromycin and tetracycline (both <1%). Various Sequence Types