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

1D Getman*, 1M O’Donnell, 2S Cohen, 1A Jiang, 1Hologic Inc, San Diego, USA; 2Occidental 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/C).

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%) had unique complement of Mgen 23s-MT and/or wild-type sequences at each anatomic site. For male subjects with both urethral 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 anatomic 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.

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

1V Donà*, 1S Schneider, 1R Tinguely, 2M Hilty, 1T Bodmer, 1A Endimiani*. 1Institute for Infectious Diseases, Faculty of Medicine, University of Bern, Bern, Switzerland; 2Department of Infectious Diseases, Bern University Hospital and University of Bern, Bern, Switzerland; 3Laboratoriums Zentrum D 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