Disclosure No significant relationships.

P622  THE USE OF SEEGENE’S ALLPLEX™MG & AZIR ASSAY FOR THE DETECTION OF MYCOPLASMA GENITALIA AND MACROLIDE RESISTANCE IN WALE.

Andrew Barratt, Laura Gifford, Sophie Jones, Owen Spiller, Catherine Moore. Cardiff University, Medical Microbiology, Cardiff, UK; Public Health Wales, Medical Microbiology, Cardiff, UK; Cardiff University School of Medicine, Medical Microbiology, Cardiff, UK

Background Mycoplasma genitalium (Mgen) is a sexually transmitted bacteria, associated with cervicitis and pelvic inflammatory disease in women and non-gonococcal urethritis in men. These bacteria lack cell walls and many prokaryotic metabolic pathways, mediating inherent resistance to most antimicrobials. Furthermore, Mgen has garnered concern as the prevalence of both fluoroquinolone and macrolide resistance has increased significantly in recent years, further restricting possible therapeutic avenues.

Methods In January 2019, Public Health Wales deployed the Seegene Allplex™MG & Azir assay to determine the presence of MG and its susceptibility to macrolides from genitourinary samples. This kit is novel in its ability to not only detect MG, but also define which specific 23S rRNA gene macrolide-resistance mediating mutations (MRM) are present without requirement for sequencing.

Results Mgen prevalence with suspected NG/CT patients was 5/87 (5.7%) with 4 (80%) containing MRM (2x A2058G and 2x A2059G), while prevalence within the Mgen-suspected group was 11/83 (13.3%) with 5 (45.5%) containing MRM (4x A2059G and 1x A2058G mutations). Further up-to-date cumulative data to be presented at IUSTI.

Conclusion Mgen prevalence was 5.7% in the non-targeted cohort, while targeted patients gave 13.3% prevalence for a South Wales GUM clinic. Macrolide resistance prevalence was 56% on average. These results justify the implementation of routine Mgen and macrolide resistance testing in South Wales, abiding by European and BASHH guidelines.

Disclosure No significant relationships.

P624  CULTURE FOR URETHRAL GONORRHOEA FROM ASYMPTOMATIC MEN POSITIVE FOR NEISSERIA GONORRHOEAE BY URINE APTIMA COMBO 2 TESTING

Melanie Bissessor*. Melbourne Sexual Health Centre, Sexual Health, Carlton, Australia

Background In a previous study of men attending Melbourne Sexual Health Centre who did not report urethral symptoms were screened between 1 July 2017 and 30 September 2018, men were recalled and a urethral swab performed for N. gonorrhoeae by nucleic acid amplification testing (NAAT) of urine.

Methods Between 1 July 2017 and 30 September 2018, men reporting sex with men attending Melbourne Sexual Health Centre who did not report urethral symptoms were screened for N. gonorrhoeae by AC2 testing of urine. NAAT positive men were recalled and a urethral swab performed for gonococcal culture using modified Thayer Martin media with determination of minimum inhibitory concentrations (MICs) for penicillin, azithromycin, ceftriaxone and ciprofloxacin by agar dilution.

Results There were 612 cases (538 individuals) positive for N. gonorrhoeae detected by urine APTIMA Combo 2 testing.

Conclusion Our results provide new insights into the post-transcriptional regulation of genes by sRNAs in Neisseria gonorrhoeae.

Disclosure No significant relationships.

P623  POST-TRANSCRIPTONAL REGULATION OF GENES BY NON-CODING RNA IN NEISSERIA GONORRHOEAE, AN OBLIGATE HUMAN PATHOGEN

Poorni Tanwer*, Daman Saluja. University of Delhi, Dr. B.C. Ambedkar Center for Biomedical Research, Delhi, India; Indian Institute of Technology, Delhi, India

Background Small non-coding RNAs (sRNAs) play an important role in bacterial gene expression and regulation. The knowledge of sRNA in Neisseria gonorrhoeae is scarce despite of its clinical significance. We utilized the available RNA-seq data under aerobic and anaerobic condition to identify non-coding RNA. We further identified sRNAs which are differentially expressed under anaerobic condition and their mRNA targets.

Methods The normalized reads (RPKM) under aerobic and anaerobic conditions were compared and a three-fold or greater difference in the expression level of sRNAs was scored as differentially expressed sRNA. sRNA targets were found using online available tools (CopraRNA, targetRNA). We further predicted the sRNA-mRNA interactions using intaRNA software.

Results A total of 26 sRNAs were identified. Out of which, ten sRNAs were differentially expressed under anaerobic condition, physiologically important stage during infection. We further identified mRNA targets of these sRNAs based on deep sequencing of N. gonorrhoeae transcriptome under aerobic and anaerobic conditions. These results indicated that several sRNAs target genes that are involved in energy metabolism processes, stress response and various other networks.

Conclusion Our results provide new insights into the post-transcriptional regulation of genes by sRNAs in Neisseria gonorrhoeae.

Disclosure No significant relationships.