

months [AOR:2.36; CI:1.57–3.55], younger age [AOR:3.32, CI:1.45–7.63], cohabiting marital status [AOR:2.71, CI:1.10–6.72], not knowing partners' status [AOR:2.11, CI: 1.28–3.48], unemployed [AOR:1.70; CI:1.09–2.68] were associated with a higher likelihood of non-adherence to ART.

Conclusion Drop-off in the postpartum adherence are linked to lifestyle behaviours in the study setting. Targeted screening of these lifestyle behaviours among reproductive age women for intervention would be crucial to prevention of breastfeeding and partner transmission of HIV.

Disclosure No significant relationships.

007 – BUGS, BEHAVIOUR AND BEYOND: NEW CHALLENGES FOR STI CONTROL AMONG GAY, BISEXUAL AND OTHER MEN WHO HAVE SEX WITH MEN

Monday, July 15, 2019 4:15 PM – 5:45 PM

007.1 MULTIPLE LINEAGES OF MULTIRESTANT *SHIGELLA* IN AUSTRALIA

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10.1136/sextrans-2019-sti.140

Background In developed countries, the burden of shigellosis is either in returning travellers, or in men who have sex with men (MSM). Here, we combine genomic data with comprehensive epidemiological data on sexual exposure and travel to describe the spread of multidrug-resistant *Shigella* lineages in an urban centre in Australia.

Methods We undertook a population-level study of all cultured *Shigella* isolates in the state of Victoria, Australia between 1 January 2016 through to 31 December 2018. Antimicrobial susceptibility testing, whole genome sequencing (WGS) and bioinformatic analysis of 610 *Shigella* isolates was performed on all isolates, and long-read sequencing was performed on representative isolates. Risk factor data on travel and sexual exposure were collected through enhanced surveillance forms or by interview.

Results Rates of antimicrobial resistance were high in both *S. sonnei* and *S. flexneri*, particularly to ciprofloxacin and azithromycin. There were strong associations between antimicrobial resistance, phylogeny and epidemiology; specifically, two major MSM-associated lineages were identified, a *S. sonnei* lineage and a *S. flexneri* 2a lineage. Of concern, the majority of isolates within the *S. sonnei* MSM-associated lineage harboured mutations associated with reduced susceptibility to recommended oral antimicrobials, namely ciprofloxacin, trimethoprim-sulfamethoxazole and azithromycin. Long-read sequencing demonstrated global dissemination of multidrug-resistant plasmids across *Shigella* species and lineage, but

predominantly associated with MSM isolates. A global analysis demonstrated the presence of these plasmids in *Shigella* from both Europe and South-East Asia.

Conclusion Our contemporary data highlight the ongoing public health threat posed by multidrug-resistant *Shigella*, both in Australia and globally, and further highlights the 'collateral damage' caused by azithromycin. Urgent multidisciplinary public health measures are required to interrupt transmission and prevent infection.

Disclosure No significant relationships.

007.2 USE OF WHOLE-GENOME SEQUENCING TO IDENTIFY SEXUAL TRANSMISSION OF *SHIGELLA* IN MEN WHO HAVE SEX WITH MEN IN ENGLAND

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10.1136/sextrans-2019-sti.141

Background In 2015, routine whole-genome sequencing (WGS) of *Shigella* spp. was introduced by Public Health England (PHE) to identify transmission clusters, but limited behavioural information hampers interpretation. We investigated whether WGS can distinguish between clusters of sexual transmission among men who have sex with men (MSM) and other modes of transmission.

Methods WGS data for non-*sonnei* *Shigella* were sorted into clusters based on single nucleotide polymorphism (SNP) typing at various SNP distances (standard is 10-SNPs). Clusters were defined as 'household', 'travel-associated', 'community' or 'adult male' using data submitted with laboratory isolates (age, gender and foreign travel). PHE contacted cases to pilot a new exposure questionnaire, including information on sexual behaviour, from July 2015-March 2017. Questionnaire data were used to validate whether 'adult male' clusters represented likely sexual transmission between men.

Results 201 isolates had questionnaire and linked WGS data, of which 106 clustered with at least one other isolate (10-SNPs). 95.1% (77/81) of self-reported MSM belonged to an 'adult male' cluster and 4.9% (4/81) to a 'community' cluster; most (74.1%; 60/81) reported recent same-sex sexual contact. 70.6% (12/17) of non-MSM belonged to a 'community' cluster, 23.5% (4/17) to an 'adult male' cluster and 5.9% (1/17) to a 'travel-associated' cluster. 73.2% (71/97) of all MSM isolates belonged to the same phylogenetic lineage; for which 10-SNP clustering identified multiple discrete clusters (7 'adult male'; 2 'community') suggesting they should be re-classified as a single 'adult male' cluster. Genetic markers of azithromycin resistance were detected in 84.7% (304/359) of 'adult male' and 20.5% (9/44) of other clusters.

Conclusion Our study suggests that SNP clustering can be used to identify *Shigella* transmission in MSM with high precision to inform infection control. Defining clusters requires a flexible approach in terms of genetic relatedness to avoid misclassification or unnecessary follow-up of clusters that may belong to the same transmission network.

Disclosure No significant relationships.