previous warts, HIV status to IMIQ 5% (16W), or PDX 0.15% cream (4W, extended to 16W if warts persist). Simultaneous blinded randomisation to Gardasil® or saline control (0–2–6 months). Composite primary outcome of wart clearance at 16W and remaining clear to 48W; analysis by logistic regression with multiple imputation for missing follow-up values. Economic evaluation considered the costs per quality-adjusted life year (QALY) for the National Health Service in England.

Results 503 participants enrolled; mean age 31 years; 66% male (20% of males MSM); 50% previous warts; 2% known HIV+. Adjusted OR (95%CI) for IMIQ relative to PDX 0.81 (0.54, 1.23); vaccine relative to placebo 1.46 (0.97, 2.20). aOR for primary outcome components (same comparators) of wart-free at W16 0.77 (0.52,1.14) and 1.30 (0.89,1.91) and remaining wart-free at 48W (in those wart-free at W16) 0.98 (0.54,1.78) and 1.39 (0.73,2.63) respectively. PDX without qHPV vaccine had the highest probability of being cost-effective across willingness-to-pay thresholds of GBP0–50,000/QALY. Adding qHPV vaccine to PDX exceeded GBP80,000/QALY.

Conclusion Though the effect of vaccine was not statistically significant, the odds of clearance at 16W+48W (primary outcome) were 46% higher with vaccine, consistent with the effects seen in component outcomes, wart-free at 16W, and 48W. IMIQ and PDX had similar efficacy; there was no evidence of a lower recurrence with IMIQ. PDX without qHPV vaccine is likely most cost-effective at the current qHPV price, but addition of qHPV may become cost-effective with reduced pricing.

Disclosure No significant relationships.

O06.5 DO TREATMENT RATES SUFFER IN A LOW-TOUCH SCREENING MODEL? NEW YORK CITY SEXUAL HEALTH CLINICS, 2017–2018

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Background Low-touch (i.e. limited staff interaction) models for asymptomatic STI screening have been widely adopted in sexual health clinics (SHCs) and can improve clinic flow and patients' experience. In New York City SHCs, asymptomatic patients who do not report contact to STI screen for urogenital and extragenital bacterial STI using self-collected specimens without a medical encounter. We evaluated treatment rates for Neisseria gonorrhea (GC) cases detected by this low-touch, self-screening model.

Methods We identified men-who-have-sex-with-men (MSM) who tested GC-positive by urogenital or extragenital nucleic acid amplification testing at any visit type (self-screening or standard clinician) during 01/2017–06/2018. Among GC cases that had not been presumptively treated, we assessed the number and percent of asymptomatic cases that returned for treatment within 30 days, and HIV pre-exposure prophylaxis (PrEP) use. We used Kaplan-Meier methods to examine time-to-treatment by visit type.

Results Of 3,944 GC cases, 2,268 were presumptively treated and 1,676 needed to return for treatment. Among returning patients, median time-to-treatment was 6 days (IQR: 4–8). Cases detected at self-screening visits had shorter time-to-treatment than those detected at standard visits (p=0.008). Among GC cases detected at self-screening visits, 85% (454/534) were treated ≤14 days, and 90% (480/534) ≤30 days, compared to 80% (917/1,142) of standard cases treated ≤14 days, and 87% (991/1,142) ≤30 days after the visit. HIV-negative men with rectal GC had shorter time-to-treatment following self-screening versus standard visits (p=0.007), and fewer remained untreated by 30 days (self-screening: 7% versus standard: 13%; p=0.02). Of 76 HIV-negative men with rectal GC who were lost to follow-up, 22 (29%) were documented to be taking HIV PrEP at time of testing/screening.

Conclusion Among HIV-negative MSM with rectal GC, a group for whom delayed treatment may increase risk for HIV acquisition, a low-touch/self-screening model results in overall treatment rates and times-to-treatment that compare favorably to a standard clinician model.

Disclosure No significant relationships.

O06.6 REDUCTION IN ADHERENCE TO ANTIRETROVIRAL THERAPY DURING POSTPARTUM: FINDINGS FROM A PROSPECTIVE COHORT STUDY

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Background The WHO recommended breastfeeding as the best feeding option for women with HIV in sub-Saharan Africa. Adherence to anteretroviral therapy is important for breastfeeding mothers to prevent vertical transmission of HIV. There is evidence that pregnancy tends to drive adhrence of antiretroviral therapy among women living with HIV, however it is unclear whether they main the level of adherence at pregnancy during the postpartum period.This study assesses the rate of drop-off in adherence in the post-partum period from the prospective cohort study of mother-infant pairs in Eastern Cape, South Africa.

Methods We conducted a follow up study on 485 mothers with HIV at 18 months post delivery to elucidate on their adherence to ART during their postpartum period. We obtained relevant items on demographic, lifestyle and self-reported adherence to ART. Adherence was measured using 7-items questions to probe adherence to ART since birth of their child to the previous night of the survey. Logistic regression (model) analysis was fitted to determine the predictors of good adherence in the cohort.

Results The mean age of the participants was 32.91 years (Standard Deviation 5.74). About 64% of the women reported complete adherence to ART representing a 5% percentage drop-off in adherence compared to the rate recorded during pregnancy. In the adjusted model, alcohol use in the last 12

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 parter transmission of HIV.
Disclosure No significant relationships.

O07 – 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

O07.1 MULTIPLE LINEAGES OF MULTIRESISTANT *SHIGELLA* IN AUSTRALIA

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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.

O07.2 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.