thorat symptoms and simultaneous pharyngeal chlamydia and urethral and rectal gonorrhoea. We excluded repeat testers within 3 months of treatment including test of cure samples from the analysis.

Results A total of 6613 MSM attended for pharyngeal testing and 383/6613 (5.8%) had a confirmed positive pharyngeal gonorrhoea NAAT. Pharyngeal gonorrhoea culture samples were taken in 270/383 (70%) and 73/270 (27%) were culture positive with available antimicrobial sensitivities. Only 7/73 (10%) had a fully sensitive organism. 28 (7%, 95% CI=5.11–10.36) reported throat symptoms at presentation. Overall, the presence of pharyngeal symptoms was not associated with positive gonorrhoea cultures (OR=1.9, CI=0.78–4.62, p=0.2), pharyngeal chlamydia (OR=1.6, CI=0.19–13.32, p=0.7), HIV status (OR=1.1, CI=0.47–2.57, p=0.8), or age [p=0.3].

Conclusions Pharyngeal gonorrhoea is usually asymptomatic and culture sensitivity is poor. Increasing effort is required to increase pharyngeal gonorrhoea culture testing and sensitivity, including ensuring clinical staff are using optimal sampling techniques and reliable transport of gonorrhoea culture samples to testing laboratories to maintain gonorrhoea AMR surveillance.

P035 THE SENSITIVITY AND ASSOCIATED FEATURES OF CULTURE POSITIVE RECTAL GONORRHOEA IN MEN WHO HAVE SEX WITH MEN

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Background Rectal Neisseria gonorrhoea is an important sexually transmitted infection in men who have sex with men (MSM). The past decade has seen and increasing rates of rectal gonorrhoea and antimicrobial resistant (AMR) gonorrhoea associated with recreational drug use, geo-social mobile phone dating apps and HIV risk reduction strategies including undetectable = untransmissible (U=U) and HIV pre-exposure prophylaxis (PrEP). Our aims were to review the microbiological findings and clinical characteristics of MSM with rectal gonorrhoea.

Methods A cross sectional study between January 2018-December 2019 to characterise the clinical and laboratory features of MSM with rectal gonorrhoea from our large clinic population of MSM attending the sexual health clinic in Brighton, UK.

Results There were 12,186 MSM attendances during the study period, of which 379/12186 (3.1%, CI=2.8–3.4) had a positive rectal gonorrhoea NAAT. The median age was 34 (IQR=27–34), 103/379 (27%) were HIV positive and 72/379 (19%) also had rectal Chlamydia. HIV positive MSM with rectal gonorrhoea were significantly older than HIV negative MSM (p=0.001). 73/379 (19%, 95%CI= 15.6 to 23.5) presented with ano-rectal symptoms. Gonorrhoea culture was performed in 291/379 (77%) overall and was positive in 190/291(65%); MSM with symptomatic gonorrhoea were more likely to be culture positive than asymptomatic MSM (OR= 8.04, CI 3.34–19.35, p<0.0001). There were no differences in age or HIV status between MSM with symptomatic versus asymptomatic mono or dual (Chlamydia) infections.

Conclusion Most MSM with rectal gonorrhoea are asymptomatic and asymptomatic MSM are significantly less likely to have gonorrhoea cultures taken and have a positive culture than symptomatic MSM. Measures are needed to ensure that all MSM (including asymptomatic) with rectal gonorrhoea have cultures taken prior to treatment to maintain adequate surveillance of AMR to prevent the urgent threat of multidrug resistance to gonorrhoea in MSM.
HIV TRANSMISSION AND PREVIOUS PREP AWARENESS

PREVALENCE OF SYPHILIS IN PEOPLE LIVING WITH HIV/AIDS IN THE AMERICAS: A SYSTEMATIC REVIEW AND META-ANALYSIS OF PREVALENCE STUDIES

Background
Syphilis remains a public health threat, particularly in People Living with HIV/AIDS (PLWHA), due to its potential complications. The prevalence of syphilis in PLWHA in the Americas is not well characterised. Therefore, the aim of this systematic review and meta-analysis was to estimate the prevalence of syphilis in this population and to investigate sources of variation in these prevalences (PROSPERO CRD42020189246).

Methods
PubMed, Embase, Lilacs and Web of Science were searched for studies reporting the prevalence point of Likely Exposure to Treponema Pallidum (LETP) by treponemal tests or Likely Current Syphilis Infection (LCSI) by the combination of treponemal and non-treponemal tests, in a broadly representative sample of PLWHA in the Americas. Published studies with less than 200 PLWHA, languages other than Spanish or English, and conference abstracts were excluded. A standardised data extraction form was used. A random-effects meta-analysis was performed to obtain the pooled prevalence of LETP and LCSI with their corresponding 95% prediction intervals (95%PI). Heterogeneity was investigated by a priori defined subpopulations diagnostic algorithm and geographical region. Heterogeneity was assessed via the Cochran Q test and I2 statistic, while Egger’s test was used to assess for publication bias.

Results
25,848 records were identified, of which 49 unique studies with 67 prevalence points were included. The pooled prevalence in the Americas was 16.4% (95%PI 2.3–49.3) for LETP, and 7.2% (95%PI 0.01–25.15) for LCSI, with high heterogeneity (I2 >75%, p-value <0.001). The prevalence of LETP was higher in men who have sex with men (MSM), while the prevalence of LCSI was higher in Latin America. There was no evidence of publication bias (Egger p-value >0.5).

with resistance to zoliflodacin, all located in the gyrB gene: D429N, K450N, and K450T. To determine the prevalence of those mutations within N. gonorrhoeae whole genome sequences, we searched PathogenWatch, an online global database for genomic surveillance.

Methods
We downloaded all available N. gonorrhoeae genomes from PathogenWatch (https://pathogen.watch/) on November 17th, 2020. The gyrB and gyrA gene sequences were obtained from the EzBioCloud database. We used the N. gonorrhoeae FA 1090 genome as our reference, and the wild-type gyrA sequence was included in our search as a control. BLAST (2.2.26+) was used to query each of the two genes to the reference genomes with a 60% identity/length threshold value. Biopython BLAST IO package was used to parse the result, and subsequent DNA translation to protein was conducted. The counts of the mutations of interest were measured using in-house python code, which generates the counts of different amino acids with given position value. Some fragmented genes were manually validated after the protein alignment using MUSCLE (3.8.31).

Results
In total, 12,943 N. gonorrhoeae genomes were searched. No sequences contained the D429N, K450N, or K450T mutations in gyrB. One sequence was identified with a D429V mutation, a mutation previously unreported but similar to D429N. In total, 5395 sequences harbored the gyrA S91F mutation, while 5392 (99.9%) of those sequences were correctly identified by PathogenWatch. The three gyrA sequences with discrepancies were confirmed manually.

Conclusion
Of the 12,943 publicly available N. gonorrhoeae genomes on the PathogenWatch database, none were found to harbor mutations in gyrB known to be associated with zoliflodacin resistance. When zoliflodacin becomes clinically available, resistance due to known mutations in gyrB is likely to be rare.

Background
HIV Pre-Exposure Prophylaxis (PrEP) has been shown to reduce HIV transmission. PrEP is now freely accessible in the UK, but continued efforts are needed to increase awareness and accessibility to further reduce HIV transmission.

Methods
We downloaded all available N. gonorrhoeae genomes from PathogenWatch (https://pathogen.watch/) on November 17th, 2020. The gyrB and gyrA gene sequences were obtained from the EzBioCloud database. We used the N. gonorrhoeae FA 1090 genome as our reference, and the wild-type gyrA sequence was included in our search as a control. BLAST (2.2.26+) was used to query each of the two genes to the reference genomes with a 60% identity/length threshold value. Biopython BLAST IO package was used to parse the result, and subsequent DNA translation to protein was conducted. The counts of the mutations of interest were measured using in-house python code, which generates the counts of different amino acids with given position value. Some fragmented genes were manually validated after the protein alignment using MUSCLE (3.8.31).

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