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.

P037 HIV TRANSMISSION AND PREVIOUS PREP AWARENESS AND USE IN MEN WHO HAVE SEX WITH MEN (MSM)

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Background HIV Pre-Exposure Prophylaxis (PrEP) has been available to men who have sex with men (MSM) via clinical trials or self-funding (online) in the UK since 2017. Despite its effectiveness and availability, we are still observing HIV transmission in MSM. This study aimed to assess prior awareness, prior usage and reasons for non-uptake of PrEP in MSM newly diagnosed with HIV.

Methods All MSM who were diagnosed with HIV at this sexual health clinic between January 2017 and September 2020 were identified and their clinical records examined for information on previous clinic attendances; PrEP discussion with a clinician and PrEP use prior to HIV diagnosis.

Results 59 MSM were diagnosed with HIV during the study period, with a median age of 42 [IQR=31.0–50.4]. 24 (41%) had attended the sexual health clinic between the time PrEP became available and HIV diagnosis. 24 (41%) had a concurrent bacterial STI at HIV diagnosis and 23 (39%) reported recreational drug use prior to HIV diagnosis, with 4 (7%) reporting intravenous drug use. 16 (27%) had prior awareness

of PrEP. Of these, 1 MSM had used PrEP inconsistently due to concern about stigma and low self-perceived HIV risk, 5 were unable to access PrEP due to insufficient clinical trial spaces or barriers to self-funding, 2 cited no specific reason for non-uptake and 8 were found to be HIV positive at date of first PrEP discussion.

Conclusion The majority of MSM diagnosed with HIV had poor prior PrEP awareness. Access to PrEP was poor despite evidence of risk taking behaviour such as bacterial STIs and drug use. Barriers to uptake included lack of places in clinical trials, difficulty self-funding, low perceived risk and stigma. PrEP is now freely accessible in the UK, but continued efforts are needed to increase awareness and accessibility to further reduce HIV transmission.

P038 PREVALENCE OF SYPHILIS IN PEOPLE LIVING WITH HIV/AIDS IN THE AMERICAS: A SYSTEMATIC REVIEW AND META-ANALYSIS OF PREVALENCE STUDIES

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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's 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).