007.3 MOLECULAR INVESTIGATION OF *TREPONEMA PALLIDUM* STRAINS ASSOCIATED WITH OCULAR SYPHILIS IN THE UNITED STATES

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10.1136/sextrans-2021-sti.88

Background Ocular syphilis cases continue to be identified in the United States since two clusters were reported in late 2014 into early 2015. Ocular syphilis (OS) is an inflammatory eye condition that can occur at any stage of syphilis with vision loss and blindness reported in some patients. We performed genotyping and whole genome sequencing (WGS) on *Treponema pallidum* strains from OS cases as part of molecular surveillance activities.

Methods A total of 79 specimens from 57 patients with suspected or confirmed OS were received from 14 states between February 2016 and November 2020. Specimens included CSF, whole blood, serum, plasma, vitreous fluid, and a throat swab. *T. pallidum* DNA was detected with a real-time PCR assay targeting the *tpoA* gene. Genotyping was done using the four-component typing scheme (*tpoE*, *G*, & *J*; *arp*, *tp0548*, and *tp0279*). *T. pallidum* genomic DNA was enriched by selective whole genome amplification (SWGA) using Multiple Displacement Amplification (MDA) with custom oligonucleotides followed by WGS on an Illumina MiSeq v2 500 cycle platform.

Results Twenty-three patients (40.4%) were MSM and HIV positive, respectively; 41 (71.9%) identified as White race, 4 (7%) Hispanic, and 3 (5.3%) Black. Twenty-three specimens from 18 (31.6%) patients tested positive for *T. pallidum* DNA. Thirteen of 23 (56.5%) specimens were CSF, while the remaining 10 included whole blood, serum, vitreous fluid, and a throat swab. Specimens from 3 patients were fully typed, revealing strain types 14b9g, 14d10g, and 14e9f. Six patients had partial genotypes. WGS was successful on 1 CSF and 2 vitreous fluid specimens from 2 cases resulting in 87% – 98% genome coverage with at least 5 reads/site. Phylogenetic analysis showed that the 2 strains belonged to the Street 14 clade.

Conclusions Our findings show that multiple strain types are responsible for ocular syphilis in the United States.

007.4 INTERSECTION OF SYPHILIS AND HIV NETWORKS TO IDENTIFY OPPORTUNITIES TO ENHANCE HIV PREVENTION IN NORTH CAROLINA, UNITED STATES

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10.1136/sextrans-2021-sti.89

Background High syphilis and HIV co-infection rates are disproportionately affecting men who have sex with men (MSM) and transgender women (TGW) of racial/ethnic minority groups in the United States (US). The integration of

HIV genetic clustering with contact tracing efforts can provide important insight into epidemic trends in this population.

Methods We evaluated contact networks of Black and Latinx MSM/TGW diagnosed with early syphilis and/or HIV infection between 2018–2020 in two high-morbidity metropolitan areas in North Carolina, US. HIV genetic clusters were constructed from *pol* sequences collected through statewide surveillance. A combined ‘HIV-risk’ network, including persons with any links (genetic or contact) to HIV-positive persons, was evaluated by component size, demographic factors, and HIV viral suppression.

Results Between May 2018 –February 2020, we identified 1,289 index persons who were Black or Latinx MSM/TGW, of which 33.2% had early syphilis, 30.4% had newly diagnosed HIV, and 36.4% had both infections. Most index persons were Black (88.1%) and young (median age 30 years). Fifty-five percent of index persons referred 1,153 sexual partners. In the contact network, the HIV prevalence was 45.7%. Overall, 62% of persons with HIV had a reported HIV sequence (*n*=697), of which 64.5% were identified in an HIV genetic cluster. The combined HIV-risk network (1,590 contact network and 1,500 cluster members) included 287 distinct components; however, 1,586 (51.3%) were in one component connecting 85 clusters and multiple regions. Among HIV-negative early syphilis cases, 20.8% were identified in the HIV-risk network. Overall, 52.9% of the HIV-risk network had no evidence of HIV suppression.

Conclusions We identified a high HIV prevalence within the contact network of minority MSM/TGW with syphilis and/or HIV, with close ties to HIV clusters indicating potential ongoing transmission. Integration of HIV cluster and viral loads illuminates areas and networks where public health interventions could be intensified.

007.5 FREQUENCY AND PREDICTORS OF REPEAT INFECTIOUS SYPHILIS INFECTIONS IN MEN WHO HAVE SEX WITH MEN IN THE NETHERLANDS

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10.1136/sextrans-2021-sti.90

Background Syphilis rates are increasing globally among men who have sex with men (MSM). Repeat infections within core groups could contribute to ongoing transmission of syphilis. The aim of this study was to measure the frequency and to explore predictors of repeat infectious syphilis infection among MSM attending Sexual Health Centres (SHCs) in the Netherlands.

Methods We analysed national SHC surveillance data between July 2014 and December 2019. A unique identifier enabled individual level analysis of repeat consultations and infections. Infectious syphilis (syphilis) included primary, secondary and early latent syphilis diagnoses. Repeat infection was defined as having two syphilis diagnoses during the study period. Multivariable logistic regression analyses were used to explore predictors of repeat syphilis infection. MSM with at least one syphilis diagnosis and one following