O07.3 MOLECULAR INVESTIGATION OF TREPONEMA PALLIDUM STRAINS ASSOCIATED WITH OCULAR SYPHILIS IN THE UNITED STATES

[1]A Pillay*, [1]S Katz, [1]A Debra, [1]C Thurlow, [1]S Joseph, [1]K Vilfort, [1,2]K Workowski, [1]R Barrow, [1]K Chi, [1]D Danavall, [1]E Kersh, [1]C Chen. *[1]Division of STD Prevention, Centers for Disease Control and Prevention, Atlanta, USA; [2]Department of Medicine, Emory University, Atlanta, USA*

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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 polA gene. Genotyping was done using the four-component typing scheme (tpr E, 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.

O07.4 INTERSECTION OF SYPHILIS AND HIV NETWORKS TO IDENTIFY OPPORTUNITIES TO ENHANCE HIV PREVENTION IN NORTH CAROLINA, UNITED STATES

[1]A Dennis, [1]A Cressman, [2]D Pasquale, [3,4]S Frost, [1]E Kelly, [1]J Guy, [5]V Mobley, [5]E Samoff, [1]C Hurt, [6]C McNeil, [1]L Hightow-Weidman, [7]M Carry, [7]M Hogben, [1]A Seña*. *[1]University of North Carolina at Chapel Hill, Chapel Hill, USA; [2]Duke University, Durham, USA; [3]Microsoft Research, Redmond, USA; [4]London School of Hygiene and Tropical Medicine, London, UK; [5]North Carolina Department of Health and Human Services, Raleigh, USA; [6]Wake Forest School of Medicine, Winston Salem, USA; [7]Centers for Disease Control and Prevention, Atlanta, USA*

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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.

O07.5 FREQUENCY AND PREDICTORS OF REPEAT INFECTIOUS SYPHILIS INFECTIONS IN MEN WHO HAVE SEX WITH MEN IN THE NETHERLANDS

[1]L Staritsky*, [1]M Visser, [1,2]H Götz, [3]M Hamers, [1]B van Benthem, [1]F van Aar. *[1]Centre for Infectious Diseases Control, National Institute for Public Health and the Environment, Bilthoven, The Netherlands; [2]Department of Infectious Disease Control, Municipal Public Health Service Rotterdam-Rijnmond (GGD Rotterdam), Rotterdam, The Netherlands; [3]STI AIDS, Amsterdam, The Netherlands*

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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

consultation were included. Age, education level, ethnicity, HIV infection, having symptoms related to syphilis/HIV, being notified for STI, prior STI, condom use and number of partners at first infectious syphilis diagnosis were included in the analysis.

Results There were 184,621 consultations registered among 41,210 MSM who tested repeatedly. Among 3,504 MSM, 4,282 syphilis infections were diagnosed. At first syphilis diagnosis median age was 39 (IQR: 29–49), 32.4% was known HIV positive and 41.4% had 10 or more partners in the past 6 months. Repeat infection occurred in 647 MSM (18.5%; median time to repeat infection: 468 days (IQR: 287–808)). Being HIV positive (aOR: 2.02 [95% CI: 1.69–2.42]) and being notified for STI (aOR: 1.21 [95% CI: 1.01–1.46]) were statistically significant predictors of repeat infection.

Conclusion This study showed that repeat infection was common and that HIV infection and being notified for STI at first syphilis diagnosis were predictors of repeat infection among MSM who tested repeatedly. Preventive strategies, including adequate partner management, for repeat syphilis are needed, especially for HIV-positive MSM.

O07.6 ESTABLISHING A GLOBAL CONSORTIUM FOR SYPHILIS VACCINE DEVELOPMENT: PATIENT ENROLLMENT AND SAMPLE PROCUREMENT FOR TREPONEMA PALLIDUM GENOME AND OMPEOME SEQUENCING

[1]A Seña*, [2]B Yang, [2]L Yang, [2]H Zheng, [1]J Tucker, [3]M Matoga, [1,3]I Hoffman, [4]E Lopez-Medina, [4,5]L Ramirez, [1]J Chen, [1,3]M Owino, [6]J Vigil, [7]D Šmajs, [7]P Pospíšilová, [6]M Caimano, [6,8]K Hawley, [1]J Parr, [9]M Moody, [6,8]J Radolf, [6,8]J Salazar. *[1]University of North Carolina at Chapel Hill, Chapel Hill, USA; [2]Southern Medical University Dermatology Hospital, Guangzhou, China; [3]University of North Carolina Project Malawi, Lilongwe, Malawi; [4]CIDEIM, Cali, Columbia; [5]Universidad Icesi, Cali, Columbia; [6]UConn Health, Farmington, USA; [7]Masaryk University, Brno, Czech Republic; [8]Connecticut Children's, Hartford, USA; [9]Duke University, Durham, USA*

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Background The public health impact of syphilis worldwide underscores the need to develop an effective vaccine. We established a global consortium for syphilis vaccine development, and collected Treponema pallidum (Tp) DNA from well-characterized syphilis patients for whole genome and outer membrane protein (OMP) sequencing.

Methods Patients with primary, secondary or early latent syphilis were enrolled from four sites located in Chapel Hill (United States), Cali (Colombia), Lilongwe (Malawi) and Guangzhou (China) beginning November 2019. Inclusion criteria included age ≥18; early syphilis based on symptoms/signs, sexual history; positive darkfield microscopy, nontreponemal and treponemal antibodies. Patient demographics, clinical presentation, syphilis staging, HIV co-infection, and nontreponemal antibody titers were recorded. Ulcer swabs and skin biopsies were collected for DNA extraction, and blood was obtained for rabbit infectivity testing (Guangzhou site). Tp burdens in specimens were quantitated by qPCR for polA (tp01021).

Results To date, 833 patients have been screened and 94 enrolled across all sites (median age of 27, range: 18–59). Among enrolled participants, 31% are female, 22% are men who have sex with men, and 20% are HIV-coinfected. Primary syphilis was confirmed in 43 persons by darkfield microscopy, and all syphilis cases were confirmed by serology. Nontreponemal titers ranged from 1:1–1:256. Twenty-one Tp strains have been isolated from rabbits, building upon recently published genomes. Tp qPCR assays have been performed on 79 specimens so far, providing a range of copy numbers based on specimen type and stage. Twenty specimens have been sequenced to-date, and analysis for structural variability in OMP targets is underway.

Conclusion We established a global clinical research consortium and have begun to characterize Tp genomic sequences and catalog Tp's global repertoire of OMPs based on strains circulating in affected populations across sites. Our findings will enable us to identify vaccinogens with broad protective capacity against circulating Tp strains.

Gonorrhoea epidemiology

O08.1 OROPHARYNGEAL GONORRHOEA INFECTIONS AMONG FEMALES AND HETEROSEXUAL MALES WITH GENITAL GONORRHOEA ATTENDING A SEXUAL HEALTH CLINIC IN MELBOURNE, AUSTRALIA

[1,2]C Allen*, [1]C Fairley, [1,2]M Chen, [1]K Maddaford, [1,2]J Ong, [3]D Williamson, [1,2]E Chow. *[1]Alfred Health, Melbourne Sexual Health Centre, Melbourne, Australia; [2]Central Clinical School, Monash University, Melbourne, Australia; [3]University of Melbourne, Microbiology and Immunology, Melbourne, Australia*

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Background There is limited evidence about the transmission and prevalence of oropharyngeal gonorrhoea in heterosexuals. From August 2017, Melbourne Sexual Health Centre (MSHC) began testing for oropharyngeal gonorrhoea among heterosexuals with untreated genital gonorrhoea. This study aims to determine the positivity of oropharyngeal gonorrhoea among heterosexuals diagnosed with genital gonorrhoea at the MSHC between August 2017 and May 2020.

Methods We conducted a retrospective analysis including individuals who had oropharyngeal gonorrhoea testing within 30 days of initial genital gonorrhoea testing. We report oropharyngeal gonorrhoea positivity, stratified by gender and reported contact with gonorrhoea. Chi-square test was performed to compare oropharyngeal gonorrhoea positivity between groups.

Results Of 617 individuals with untreated genital gonorrhoea, 424 (68.7%) were tested for oropharyngeal gonorrhoea. Oropharyngeal gonorrhoea positivity was 38.9% (95% CI 34.2% to 43.7% [165/424]), and was higher in females than males (45.6% [115/252] vs 29.1% [50/172], p=0.001). Furthermore, oropharyngeal gonorrhoea positivity was higher among individuals reporting contact with gonorrhoea compared to those who did not (65.9% [29/44] vs 35.8% [136/380], p<0.001). There was no significant difference between females who were sex workers and those who were not (38.5% [30/78] vs 48.9% [85/174], p=0.126).

Conclusions Our data suggests oropharyngeal gonorrhoea infection was common among females and heterosexual males with untreated genital gonorrhoea. The high proportion of unrecognised oropharyngeal gonorrhoea suggests routine oropharyngeal testing will identify a significant proportion with previously undetected oropharyngeal infections. These findings bear important public health implications for preventing the transmission of gonorrhoea by elucidating the necessity for routine screening and treatment among such individuals.