019.3 PARTNER SERVICES FOR GONORRHEA CAN DECREASE NEW HIV AMONG MSM IN KING COUNTY, WASHINGTON: A MATHEMATICAL MODELING STUDY

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Background Partner services (PS) for bacterial STIs has potential to increase STI treatment among infected sex partners and HIV testing among people diagnosed with STIs and their partners. The population-level impact of PS on gonorrhea and HIV incidence has not been estimated.

Methods Calibrated to King County's MSM population, our compartmental gonorrhea-HIV coinfection model captures sexual mixing, gonorrhea and HIV transmission, and scale-up of antiretroviral therapy (ART), pre-exposure prophylaxis (PrEP), and routine STI screening. We assessed incremental impact of PS over 5 and 20 years, and compared gonorrhea and HIV incidence and prevalence without PS, with PS, and with PS that integrates promotion of HIV testing (PS+HIV). In the absence of PS, we assumed that 10%, 10%, and 95% of rectal, pharyngeal, and urethral gonorrhea were treated and 63% of MSM receiving gonorrhea treatment also received HIV testing. With PS, 40% of treated cases received PS, increasing the proportion of partners treated for gonorrhea and tested for HIV by 4%, 4%, and 38% at each site. PS+HIV increased the proportion of gonorrhea-infected MSM tested for HIV to 83%.

Results After 5 and 20 years, PS modestly changed rectal, pharyngeal, and urethral gonorrhea incidence and prevalence (<7%). After 5 years, HIV prevalence decreased 0.1% with PS and 0.5% with PS+HIV. HIV incidence decreased 6.0% (from 187.1 to 176.0 per 100,000 persons) with PS and 14.7% (187.1 to 159.6/100,000) with PS+HIV. After 20 years, HIV prevalence decreased 3.2% with PS and 5.6% with PS+HIV. PS reduced incidence 23.3% (75.2 to 57.7/100,000) and PS+HIV 37.7% (75.2 to 46.9/100,000).

Conclusion Moderate gonorrhea PS coverage had modest impact on gonorrhea, given high rates of STI testing and treatment in King County. However, long-term PS+HIV increased HIV testing opportunities and substantially reduced HIV incidence. PS+HIV is a potential approach for prioritizing HIV testing in high ART and PrEP coverage settings.

Disclosure No significant relationships.

019.4 MOLECULAR EPIDEMIOLOGY OF HIV AMONG FOREIGN-BORN RESIDENTS OF KING COUNTY, WASHINGTON, USA, USING HIV SURVEILLANCE DATA

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Background In King County, one-third of HIV diagnoses occur among foreign-born individuals, a 50% increase since 2010. The extent to which these infections are locally acquired is

unclear, but has important implications for HIV prevention and incidence estimation.

Methods Using HIV surveillance (2010–2018) and partner services (PS) (2010–2016) data from Public Health–Seattle & King County, HIV-1 *pol* gene sequences from routine drug resistance testing were linked to demographic, clinical, and epidemiological information. We identified genetic similarity clusters of 2+ individuals using TN93 pairwise genetic distance with a 0.02 threshold. Belonging to a cluster is suggestive of local transmission, therefore correlates of clustering were identified using logistic regression, adjusted for early infection (CD4 >500 cells/mm at diagnosis). We also calculated the proportion of foreign-born cases with a negative HIV test in the U.S. before diagnosis.

Results From 2010–2018, 2,521 people were diagnosed with HIV in King County: 663 (26%) occurred among foreign-born individuals, primarily from Latin America (N=232), sub-Saharan Africa (SSA) (N=214), and Asia (N=98). Among individuals with a PS interview (75% Latin American, 56% SSA, 69% Asian-born), HIV testing histories suggest that 40% of Latin American, 19% of SSA, and 36% of Asian-born individuals likely acquired HIV locally. Individuals with non-B HIV subtypes similarly varied by region of birth: 2% of US, 5% of Latin American, 93% of SSA, and 46% of Asian-born people. Among 1,754 individuals with an available sequence (70% of U.S. versus 63% of foreign-born), 1,092 (62%) clustered in 304 genetically similar clusters. Odds of clustering, compared to US-born, was 0.44 (95%CI: 0.31,0.60) among Latin American, 0.08 (95%CI: 0.05,0.14) among SSA, and 0.40 (95%CI: 0.24,0.66) among Asian-born.

Conclusion Our results suggest that local HIV acquisition occurs least frequently among SSA-born, followed by Asian-born and Latin American immigrants. Incident estimates that include all diagnoses among foreign-born people may overestimate HIV incidence.

Disclosure No significant relationships.

019.5 THE INFLUENCE OF RISK GROUP TURNOVER IN STI/HIV EPIDEMICS: MECHANISTIC INSIGHTS FROM TRANSMISSION MODELING

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Background Heterogeneity in the risks of STI/HIV acquisition and transmission are central to core group theory. We examined the influence of population turnover among risk groups on group-specific STI prevalence and the contribution of unmet needs among the core group to onward transmission.

Methods We developed an analytical approach to modeling risk group turnover that leverages demographic data and ensures constant relative risk group size. A deterministic model of STI transmission without disease-attributable mortality incorporated this turnover approach with three risk groups, including: a core group with the highest rates of partner change, a multiple-partnerships group, and a low-risk group. We varied the duration within the core group (3 to 33 years) via turnover among all groups and duration of infectiousness (5 years to lifetime) via a uniform treatment rate. We then compared the influence of turnover on group-specific STI prevalence at different treatment rates. We also calibrated to

group-specific STI prevalence with and without turnover, and compared the fitted partner change rates and transmission population attributable fraction (tPAF) of the core group to cumulative STI infections in the total population.

Results Across the range of turnover and treatment parameters explored, turnover consistently decreased STI prevalence in the core group. In the low-risk group, turnover increased prevalence under low treatment rate, but had the opposite effect under high treatment rate. When calibrating to the same STI prevalence, fitted core group partner change rates were higher with turnover than without. Using these fitted parameters, models with turnover then consistently projected a higher tPAF of the core group versus models without.

Conclusion Modeling of risk group turnover can influence the projected group-specific STI prevalence and fitted risk parameters. Models without turnover may underestimate the contribution of core groups in STI epidemics, and thus the impact of interventions prioritizing these populations.

Disclosure No significant relationships.

019.6 PROFESSIONAL INJECTORS, INJECTION NETWORKS, AND HIV: CASES STUDIES FROM FIVE CITIES IN PAKISTAN

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Background There are large numbers of people who inject drugs (PWID) in Pakistan, with a high and growing HIV prevalence in many cities. Cross-sectional bio-behavioural surveys conducted over fifteen years have shown heterogeneous HIV epidemic trajectories in different cities with inconsistent associations between aggregate and individual measures of behaviour and epidemic trajectories. This study triangulates behavioural, biological, and network data to gain new insights into drivers of local epidemics among PWID.

Methods A questionnaire was administered to 1,439 PWID in five cities in Pakistan in 2014 and dried blood spots were collected for HIV testing and sequencing. The questionnaire collected locations where participants injected recently and these were used to construct place-based injection networks. Demographic, behavioral, geographic, and network structure data were tested for associations with HIV and HIV phylogenetic analysis was conducted to identify transmission clusters.

Results HIV prevalence varied between the cities, from 8.6% to 45.3%. Although aggregate individual behaviours were not strongly associated with HIV, there were differences between cities in injecting practices and network configurations. Injection network configurations differed between cities, ranging from networks with dense sub-regions to widely dispersed networks. A city that experienced an explosive HIV outbreak showed particularly dense geospatial networks and a large phylogenetic cluster (n=52) suggesting a link between

geospatial concentration and rapid HIV transmission. In a city where the use of professional injectors was associated with HIV at the individual level, there were dense network sub-regions and HIV+ individuals were more likely to be more centrally located in networks ($p<0.01$) and in network components with a greater proportion who had used a professional injector ($p<0.05$).

Conclusion Contextual factors shape the injection practices and network configurations among PWID in Pakistan. Factors that influence HIV transmission dynamics are more complex than individual behaviours, and include professional injectors and geographic and network clustering.

Disclosure No significant relationships.

Poster Presentations

PS01 – POSTER VIEWING SESSION – MONDAY

Monday, July 15, 2019

5:45 PM – 7:00 PM

P004 THE NATIONWIDE ANTIMICROBIAL RESISTANCE SURVEILLANCE SYSTEM OF SEXUALLY TRANSMITTED INFECTIONS – SOUTH KOREA, 2017–2018

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Background The Korea Centers for Disease Control and Prevention established the new nationwide surveillance system and conducted the first nationwide surveillance of antimicrobial resistance for three major sexually transmitted pathogens; *Neisseria gonorrhoeae*, *Chlamydia trachomatis*, and *Mycoplasma genitalium*.

Methods The urethral discharge was collected from male patients with urethritis at 20 primary urologic clinics from January 2017 to December 2018. The cervical swab was collected from female patients with cervicitis at 8 primary gynecological clinics from January to December 2018. All specimens were sent to the 4 regional or the central laboratories.

Results A total of 224 *N. gonorrhoeae* isolates were collected. Of these, 90.6% were resistant to tetracycline, 95.3% to ciprofloxacin, and 58.0% to penicillin. None of the strains was resistant to ceftriaxone and spectinomycin. The minimum inhibitory concentration (MIC) range of ceftriaxone was ≤ 0.008 –0.25 $\mu\text{g/mL}$ and the MIC₅₀ and MIC₉₀ were 0.06 $\mu\text{g/mL}$ and 0.12 $\mu\text{g/mL}$. Twenty-two strains were resistant to cefixime (MIC 0.5 $\mu\text{g/mL}$). Most of the penA genotypes were type X. In particular, the proportion of mosaicism in DNA specimens has been steadily increasing, and the spread of penA-34.001 was confirmed in 2018. Reduced azithromycin susceptibility (defined MIC ≥ 1.0 $\mu\text{g/mL}$) increased from 0% in 2017 to 13% in 2018. The MIC range, MIC₅₀ and