P204

SERODISCORDANCE AND SEX PARTNER CONCURRENCY: EVIDENCE FOR RACIAL DISPARITIES IN HIV AMONG GAY AND BISEXUAL MEN (MSM)

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Background There are extreme racial disparities in HIV infection among MSM in the U.S. These disparities may in part be explained by racial differences in the transmission potential (i.e. mixing between infected and uninfected individuals) and structure (i.e. density) of sexual networks. The objective was to determine whether the association between HIV serodiscordance and sex partner concurrency differed by race among MSM sex partner dyads.

Methods Data came from the Understanding Sexual Health in Networks Study, an ongoing longitudinal cohort among MSM ages 18–45. Participants completed an egocentric sexual network survey with questions about 3 most recent sex partners in the past 3 months. An HIV serodiscordant partnership was defined as a dyad with a positive status index and a negative or unknown status partner or vice versa. Summary statistics, chi-squared tests, and logistic regressions adjusted for the nested structure of the data were used for hypothesis testing.

Results 163 MSM reported on 354 (median: 3, range: 0–3) sex partnerships. MSM were 63.2% Black (BMSM), on average 29.4 (SD 5.96) years old, and 33.6% reported condom use at last sex. There were no differences in age or condom use by race. Among partnerships, index BMSM (vs. non-BMSM) were more likely to report serodiscordant partnerships (48.8% vs. 14.4%, p -value<0.001) but not sex partner concurrency (87.4% vs. 77.8%, p -value 0.29). Among BMSM, sex partner concurrency was significantly associated with 4.97 higher odds (95% CI: 2.26, 10.91) of having a serodiscordant partnership, and this association was not significant among non-BMSM.

Conclusion Among BMSM dyads, we found evidence of the necessary and sufficient causes for HIV transmission including mixing between infected and uninfected individuals (i.e. serodiscordance) combined with dense sexual network structures (i.e. sex partner concurrency) and we did not find this evidence among non-BMSM dyads. These factors may help explain persistent racial disparities in HIV.

Disclosure No significant relationships.

P205

HIV NON-B SUBTYPES IN SAN FRANCISCO: MIGRATION BUT LITTLE LOCAL TRANSMISSION

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Background Several HIV non-B subtypes and recombinants have been documented at low frequencies in the US. We

characterized the viral diversity, epidemiology, and extent of local transmission and migration of non-B subtypes in San Francisco.

Methods Viral sequences from patients in care at local public and private health providers (2000–2016) were matched to the San Francisco Department of Public Health HIV/AIDS case registry. Phylogenies were reconstructed for the *pol* region of subtypes A1, C, D, G, CRF01_AE, CRF02_AG, and CRF07_BC sequences, with reference sequences from the LANL HIV database. Local transmission and global migration frequencies were compared based on phylogenetic topology. Epidemiologic associations between non-B subtypes and patient characteristics were assessed by multivariate logistic regression.

Results Of the 11,382 viral sequences subtyped, 10,669 were matched to 7,236 registry cases. Fourteen non-B subtypes and CRFs were observed. Among registry cases, 141 (2%) had non-B subtypes or CRFs, and 72 (1%) had unnamed recombinant forms. The proportion of non-B subtypes increased over time. Of the 146 non-B transmission linkages identified, 104 (71%) appeared to represent migration from outside the study dataset, of which 86 (83%) had no close linkage to US reference strains. Twenty-six cases (18%) appeared to be local transmission, clustering with other sequences in this analysis. Of the 77 registry cases born outside of North America, 54 (70%) were phylogenetically linked to the case's region of birth. Cases with non-B subtypes or CRFs were associated with Asian/Pacific-Islander race/ethnicity ($aOR=3.17$; $p<0.001$), non-US birth country ($aOR=11.02$; $p<0.001$) and HIV diagnosis after 2009 ($aOR=4.81$; $p<0.001$).

Conclusion Non-B subtypes were present at low but increasing frequency in San Francisco. Local transmission of non-B subtypes appeared to be limited, as most non-B infections were likely acquired outside the US. Knowledge of subtype diversity can provide a better understanding of HIV global migration patterns, and inform treatment and prevention efforts.

Disclosure No significant relationships.

P206

THE SPECIFIC CONTRIBUTION OF EACH DATA SOURCE IN A POPULATION-BASED ADMINISTRATIVE DATA COHORT FROM MANITOBA, CANADA

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Background In the development of administrative data case-definitions for HIV, it is important to understand the contribution of each data source to prevalence estimates, especially as it pertains to generalizability of methods.

Methods HIV case-definitions were constructed from four population-based databases available in Manitoba: physician claims, hospital discharge, pharmaceutical dispensations, and provincial laboratory tests. Performance was assessed using sensitivity, specificity, positive/negative predictive value (PPV & NPV), and Youden's index (YI). Cases identified by HIV case-definitions, and those reported to public health surveillance