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Session: **EPH1**: Friday May 1 – 11:00:12:30 – HIV and HCV Surveillance

Track: Epidemiology and Public Health

Subject: Data and methodological science: use of administrative data, new tools and other novel data sources in HIV surveillance, prevention and control programs

Presentation Type: Oral

Title of Abstract: **A Novel Phylogenetic Approach to Prioritizing HIV-1 Transmission Clusters**

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Abstract

Background

Despite a marked reduction in HIV transmission due to antiretroviral therapy, groups with elevated transmission persist. HIV sequence data can be used to phylogenetically identify groups of individuals at risk of elevated transmission rates, and thus direct optimal allocation of public health resources. However, public health agencies with limited resources require an approach that allows higher resolution prioritization when several clusters of rapid transmission occur simultaneously. We combine phylogenetic clustering with lineage-level phylogenetic diversification rates to form a novel method capable of successfully identifying clusters of urgent concern.

Methods

35760 HIV protease and partial reverse transcriptase sequences collected from 9824 participants between 1996 and 2019 were used to infer 100 approximate maximum-likelihood bootstrap trees rooted by root-to-tip regression. Transmission clusters were inferred using a patristic distance threshold of 0.02 substitutions/site. Lineage-level diversification rates were calculated for all tips in all bootstraps and pooled to generate cluster-level diversification rate summary statistics.

Results

Preliminary results reveal that diversification rates differ significantly between the group of clusters marked as concerning by the current public health prioritization protocol and the remaining clusters, marked as less concerning, when using mean (Mann-Whitney, $p=0.036$) and maximum ($p=0.0496$) diversification rates, but not median rates ($p=0.173$). Mean and maximum diversification rates allowed transmission clusters to be ranked such that the top-ranking clusters matched those marked by public health prioritization as concerning in 2018. Further analyses will compare diversification rates to other commonly used measures for prioritization of transmission clusters and will additionally confirm the effectiveness of this approach on annual sequence subsets for the ten years preceding 2019.

Conclusions

By combining phylogenetic clustering with lineage-level diversification rates, we establish a method capable of distinguishing transmission clusters of urgent concern with increased resolution relative to phylogenetic clustering alone, further optimizing the allocation of limited resources by public health agencies.