Contribution ID: **109**   Type: **Paper**

Identifying sources of new HIV diagnoses in southern Uganda

Thursday, July 18, 2024 10:20 AM (20 minutes)

Despite expansion of HIV treatment and prevention programs in Uganda, new HIV diagnoses continue to occur. Identifying sources of new HIV diagnoses following the scale-up of HIV interventions may provide insights into the HIV transmission dynamics in declining African HIV epidemics. Here, we investigated sources of new diagnoses using HIV sequence and survey data from the Rakai Community Cohort Study (RCCS), an open population-based HIV surveillance cohort. HIV gag genome sequence from RCCS (1994-2019) and background sequence datasets were aligned. Phylogenetic trees were reconstructed, and transmission chains were inferred in BEAST. A Negative Binomial branching process model was used to estimate the number and origin of unobserved transmission chains. The majority of sequences were either singletons or in clusters of less than 5 (94.4%), and only 1.8% of clusters were of a size greater than 10. An estimated 94.4% of subtype A1 chains originated from outside Rakai communities, while only 9.3% of subtype D chains were due to importation. Between 2016 and 2019, 447 participants were newly diagnosed and 202 had sequence data available. Of these, 32.7% were singletons, while 67.3% were part of local transmission chains. Newly diagnosed singletons were more likely to be from outside the communities, younger, and had a recent migration history than individuals in local transmission chains. This study reveals that both importations and ongoing within-community transmission chains play a critical role in shaping the dynamics of HIV epidemics. Intervention strategies that address local transmission dynamics as well as broader regional influences may be necessary.

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Session Classification: Paper Presentations

Track Classification: Global Health: Infectious Diseases