Detection and Characterization of HIV Clusters Using HIV-TRACE among a Cohort of Persons
Living with HIV in Washington, DC

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Background
• Washington, DC has a 2% HIV prevalence and approximately 400 incident cases annually.
• HIV phylodynamic analyses are being used to inform and direct public health prevention interventions to interrupt HIV transmission.

Combining molecular sequence data with behavioral and clinical data may improve our ability to detect high priority clusters in a high prevalence city.

Objective
To characterize clusters and identify clinical and behavioral predictors of clustering that might lead to transmission among a large cohort of persons living with HIV (PLWH) in DC.

Methods
DC COHORT MOLECULAR EPIDEMIOLOGY SUBSTUDY
Prospective Sequence and Behavioral Data Collection
• Participants were recruited from the DC Cohort study, an ongoing longitudinal observational cohort of persons infected with HIV who reported mostly MSM risk (Table 1).
• Eligible participants were diagnosed with HIV within the prior 12 months or had longstanding infection and were viremic (i.e., viral load (VL) >1500 copies/ml).
• Collected behavioral data and plasma samples which were sequenced using Next-Gen sequencing (n=111 participants).

Retrospective Sequence Collection
• Data were abstracted from DC Cohort participants’ electronic medical records manually and through electronic exports.
• Molecular sequences collected by LabCorp® using Sanger sequencing from 2011–2017, among participants diagnosed from 1980–2017, were transferred to the DC Department of Health (DC DOH) (n=3,132 participants).

Per study protocol, matching was conducted with the DC DOH to identify sequences from Cohort participants.

Analysis
Demographic, clinical, and HIV sequence data were linked, as was self-reported behavioral data for those participants with prospective data.

HIV-TRACE used to identify molecular transmission clusters using a pairwise genetic distance threshold ≤0.015 substitutions/site from the RT or PR/RT region.
Conducted uni- and bivariate analyses comparing demographic characteristics and clinical outcomes by clustering.

Results
Figure 1. Prospective and Retrospective Clusters of Three or More Participants, N=28

Table 1. Characteristics of Participants by Cluster Status (N=3,243)

Table 2. Characteristics of Participants in Five Largest Clusters, N=35

Figure 2. Five Largest Clusters, No 35

Figure 3. Risk Behaviors of Participants in Prospective Only Clusters, N=9

Results (continued)
• Among 3,243 participants for whom we analyzed sequences, 86% were Black, 68% were male, the median age was 44 (31-53), and 48% were infected through male-to-male sexual contact (Table 1).

• HIV-TRACE found 207 genetic links connecting 267 individuals.

• The five largest clusters comprised of all males whom reported mostly MSM risk.

• One cluster included a prospectively sequenced PLWH who was resequenced in 2012.

Conclusions
• Combining HIV-1 sequences, clinical, and behavioral data revealed risky behaviors and high levels of viremia among known PLWH that could potentially lead to ongoing transmission.

• A number of relatively large clusters were identified, they did not include recently diagnosed PLWH, which might be more useful for cluster prioritization.

• The strength of our analysis include the ability to triangulate data from multiple sources to comprehensively describe the behaviors and risks of cluster members.

• These analyses can complement active HIV surveillance efforts with the future goal of providing real-time HIV phylodynamic analyses to interrupt HIV transmission among defined populations and geographic areas.

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