Abstract #1561

Using near real-time molecular surveillance to inform data-to-care in New York City

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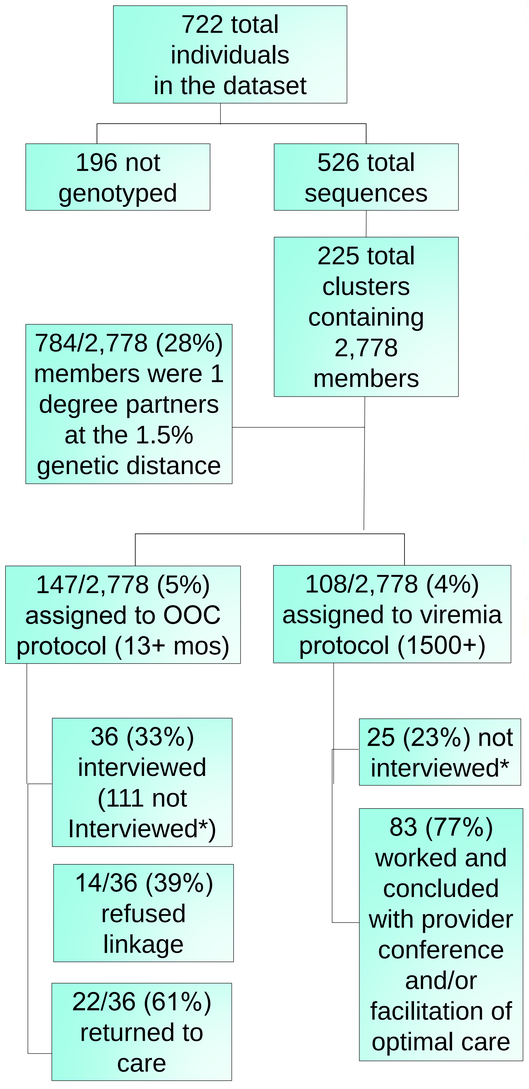
BACKGROUND

Molecular HIV surveillance has been proposed as a tool to augment traditional partner services and data to care (D2C) activities by adding persons with genetically proximate viruses to the pool of named partners and social network members receiving public health intervention after a new diagnosis of HIV.

METHODS

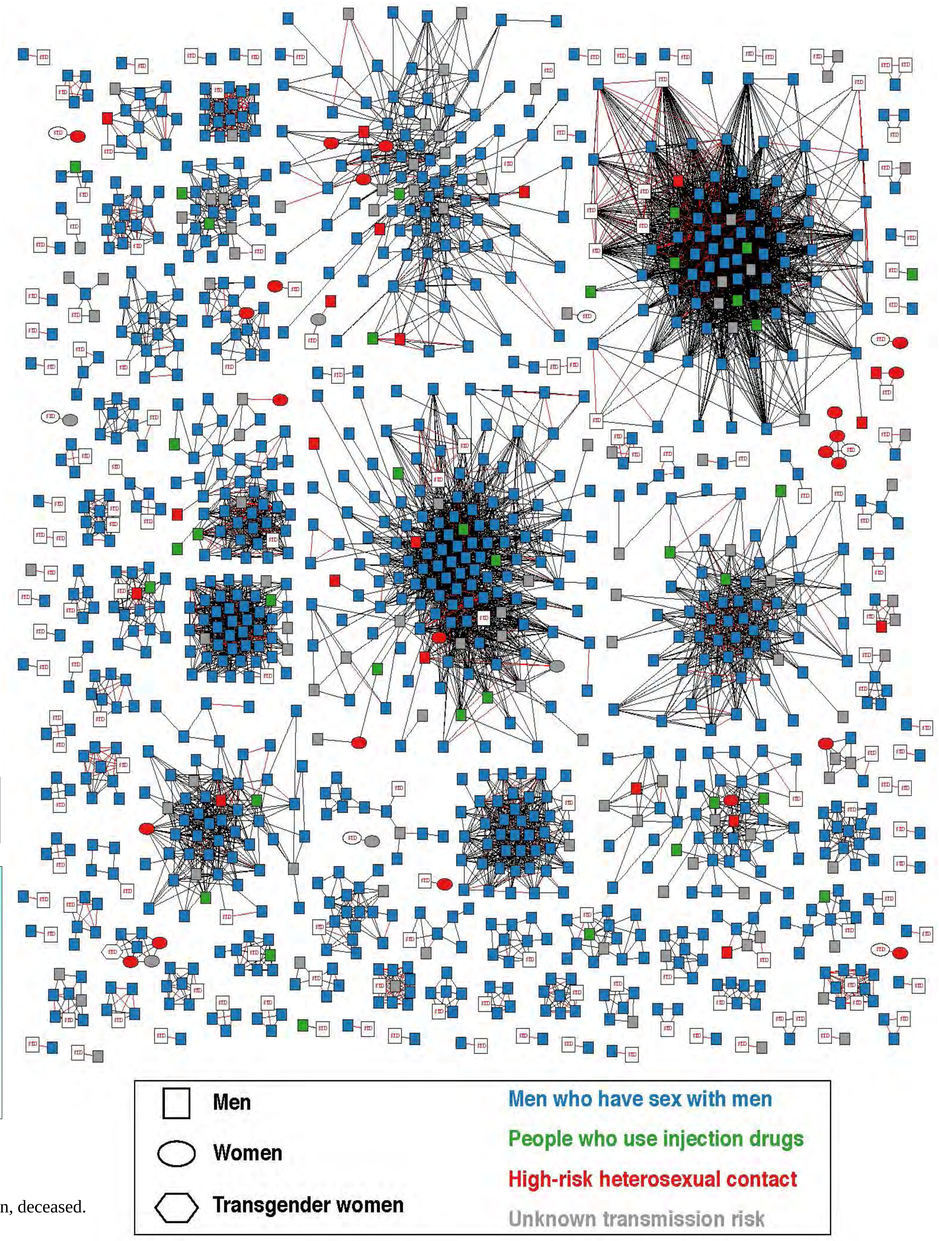
The New York City Department of Health and Mental Hygiene conducted a demonstration project to determine whether early ascertainment of viral genetic proximity between newly diagnosed and prevalent cases was feasible and resulted in timely identification of and outreach to persons in transmission clusters identified by HIV-Trace, a genetic distance-based clustering tool. Persons newly diagnosed with HIV at the city's 8 sexual health clinics (SHC) were the Index cases; their partial *pol* sequences were analyzed for pairwise concordance to those of 71,189 prevalent cases using a 1.5% genetic distance threshold. Clusters were inferred, and cluster members that were out of care for ≥13 months (OOC) or in care but viremic (>1500 copies/mm^3) and their viruses genetically linked to the Index virus were identified and prioritized for assistance with partner services and reengagement in optimal care.

Molecular Surveillance Data-to-care Work Flow



*Current to care, not viremic, unable to locate, moved/out of jurisdiction, deceased.

Molecular Network



RESULTS

Between June 1, 2016, and June 25, 2018, whole blood specimens from 722 persons testing preliminary positive on point-of-care rapid HIV screening were submitted to the NYC Public Health Laboratory for confirmation and resistance testing, resulting in 526 interpretable genotypes. SHCs received resistance reports and sequences were posted a median of 10 days (IQR 8-15) after specimen draw date. Pairwise concordance analysis of the Index virus against the prevalence pool yielded a total of 225 clusters containing 2,778 unique members. Clusters ranged in size from 2-155 persons with diagnosis dates from 1981-2018, of whom 147 (5%) were deemed to be potentially eligible for OOC and 108 (4%) for viremia services. 91% of cluster members were MSM; clusters were homogeneous with respect to age at diagnosis (median 26) and race/ethnicity but not by neighborhood of residence.

CONCLUSION

Despite our optimized scenario (genotype ordered on day of diagnosis), cluster data were not available at the time of the Index partner services interview. However, analysis performed as soon as the sequence was posted allowed us to identify and prioritize for outreach previously diagnosed, genetically proximate OOC and in-care but viremic cluster members on a monthly basis, making it possible to achieve "near real-time" D2C for genetic partners.

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