

Phylogenetic Analyses of HIV-1 Sequences can be used to Target Prevention Programs in Chicago

Background Analysis of HIV nucleotide sequence data can be used to identify individuals with highly similar HIV strains and understand transmission. We identified and described which subgroups were more highly connected and the extent to which transmission occurred within vs. between geographic areas in Chicago.

Methods We analyzed genetic sequences from the HIV-1 *pol* region collected in Chicago between 2005 and 2011 under the Variant, Atypical, and Resistant HIV Surveillance program. We determined pairwise genetic distance, inferred potential transmission events ('ties') between individuals ($\leq 1.5\%$ genetically distant), constructed clusters of connected individuals (≥ 1 tie to another sequence), and determined demographic and risk attributes associated with degree of connectivity.

Results Of 1,154 sequences, 177 (15.3%) were tied to at least one other sequence. In multivariable analyses, we found that, compared to older individuals, younger individuals were significantly more likely to more highly connected. Race, gender and transmission category were not significantly associated with connectivity. We also found a high degree of geographic heterogeneity among our sample—48 (71.6%) of 67 clusters had individuals from different regions (North, South, or West sides) of Chicago.

Conclusion We found that young persons are the most highly connected individuals, suggesting a need to address the transmission of HIV through these networks. We also found a high level of geographic mixing, which argues for broad delivery of prevention interventions across the Chicago metropolitan area.