**Supplemental Digital Content**

**Table.** Characteristics of sequence clusters.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Cluster | Sequence type | City, State | Sampling year | Protease/RTa | | Integraseb | |
| Resistance mutations | Genetic distancec | Resistance mutations | Genetic distancec |
| 1 | Study | Atlanta, GA | 2017 | K103N | 0.18% | None | 0.36% |
|  | Study | Birmingham, AL | 2017 | K103N | None |
|  | Background [1] | Nashville, TN | 2015 | K103N | - | - | - |
|  | Background [1] | Nashville, TN | 2015 | K103N | - | - | - |
| 2 | Study | Atlanta, GA | 2016 | M184V, T215C/Y | 2.06% | E138K, S147G, Q148R | 1.99% |
|  | Study | Birmingham, AL | 2017 | T215C | None |
| 3 | Study | Atlanta, GA | 2016 | None | 2.66% | None | 1.76% |
|  | Study | Atlanta, GA | 2017 | None | None |
|  | Background [2] | Unknown | 2002 | None | - | - | - |
|  | Background [3] | Unknown | 2005 | None | - | - | - |
| 4 | Study | Boston, MA | 2016 | None | 2.50% | None | 2.82% |
|  | Study | Boston, MA | 2016 | None | None |
|  | Background [4]d | Boston, MA | 2010 | None | - | - | - |
| 5 | Study | Atlanta, GA | 2016 | - | - | None | 2.70% |
|  | Study | Boston, MA | 2016 | - | - | None |

Footnotes for Table.

The table shows results of cluster analysis of HIV sequences from individuals screened for participation in HPTN 078 (study sequences). Background sequences from a public database were included in the analysis. Cluster analyses were performed separately for protease/reverse transcriptase (RT) sequences and integrase sequences. Clusters were identified if the genetic distance between the sequences was <4.5% and the bootstrap value was >90%; a genetic distance threshold of <0.5% was used to identify recent transmission clusters. The table shows characteristics for the five clusters that included at least two study sequences. Clusters 3 and 4 included individuals from the same study site (Atlanta and Boston, respectively). All four of these individuals were recruited through deep-chain respondent-driven sampling (DC-RDS); however, two individuals in each cluster were not in the same recruitment chain. Cluster 5 was only identified in integrase analysis.

a Sixteen additional protease/RT clusters that included only one study sequence are not shown.

b Six additional integrase clusters that included only one study sequence are not shown.

c Genetic distance values were determined for study sequences only.

d This background sequence was from an individual recruited at the same study site in Boston that recruited the two individuals with study sequences included in this cluster.

References for Supplemental Digital Content.

1. Dennis AM, Volz E, Frost A, Hossain M, Poon AFY, Rebeiro PF, et al. **HIV-1 transmission clustering and phylodynamics highlight the important role of young men who have sex with men**. *AIDS Res Hum Retroviruses* 2018; 34:879-888.
2. Bonhoeffer S, Chappey C, Parkin NT, Whitcomb JM, Petropoulos CJ. **Evidence for positive epistasis in HIV-1**. *Science* 2004; 306:1547-1550.
3. Viani RM, Peralta L, Aldrovandi G, Kapogiannis BG, Mitchell R, Spector SA, et al. **Prevalence of primary HIV-1 drug resistance among recently infected adolescents: a multicenter adolescent medicine trials network for HIV/AIDS interventions study**. *J Infect Dis* 2006; 194:1505-1509.
4. Chen I, Connor MB, Clarke W, Marzinke MA, Cummings V, Breaud A, et al. **Antiretroviral drug use and HIV drug resistance among HIV-infected Black men who have sex with men: HIV Prevention Trials Network 061**. *J Acquir Immune Defic Syndr* 2015; 69:446-452.