Phylogenetic Analysis of HIV from PWID in Eastern Europe and Asia: HPTN 074

Mariya V. Sivay1, Philip J. Palumbo1, Yinfeng Zhang1, Mary Kathryn Grabowski1, Estelle Pikower-Manning1, Xu Guo2, Erica L. Hamilton3, Tran Viet Ha4, Kostyantyn Dumchev5, Zubairi Djoerban6, Brett Hanscom6, Irving Hoffman4, William Miller7, and Susan H. Eshleman1, for the HPTN 074 Study Team

1 Johns Hopkins University School of Medicine, Baltimore, USA; 2 Fred Hutchinson Cancer Research Center, Seattle, USA; 3 FHI 360, Durham, USA; 4 University of North Carolina at Chapel Hill, Chapel Hill, USA
5 Ukrainian Institute of Public Health Policy, Kyiv, Ukraine; 6 University of Indonesia, Jakarta, Indonesia; 7 Ohio State University, Columbus, USA

ANALYSIS OF HIV ENV SEQUENCES

env sequences were analyzed by next generation methodologies.

METHODS

LABORATORY TESTING

HIV diagnostic testing and CD4 cell count testing were performed at study sites. Repeat diagnostic testing, HIV viral load testing, HIV sequencing, and HIV phylogenetic analysis were performed at the HPTN Laboratory Center (Johns Hopkins University, Baltimore, USA).

SAMPLES USED FOR PHYLOGENETIC ANALYSIS

Phylogenetic analysis was performed using samples collected at a second study visit for the seven index-partner pairs. Additional sequences were obtained using samples collected at a second study visit for the seven index-partner pairs.

ANALYSIS OF HIV POL SEQUENCES

HIV pol was sequenced using the ViroSeq HIV-1 Genotyping System v2.0 for samples with viral loads >400 copies/mL. HIV subtypes were determined by analyzing HIV pol sequences with REGA, COMET, and RIP subtyping tools, and were confirmed by phylogenetic analysis using PHYLIP v3.695. Ten background pol sequences most closely related to each study sequence were selected using BLAST. Separate phylogenetic trees were constructed for each study visit using RAxML v8.2.10. Two or more sequences were considered to form a pol sequence cluster if the branch support was >90% and the maximum genetic distance between sequences was ≤1.5%.

RESULTS

Pol sequences were obtained for 467 (98.7%) of 473 index samples and samples from all seven seroconverters; 22 sequences were excluded from analysis due to high sequence ambiguity or interstrain type recombinant. HIV subtypes were A1 (Ukraine) and CRF01_AE (Indonesia and Vietnam). Eighteen pol clusters were identified that included 2-7 sequences per cluster (Table 1, Figure 1).

Genetic linkage was evaluated using phylogenetic methods to evaluate the relationship between HIV strains in the HPTN 074 study.

Figure 1. Phylogenetic analysis of pol sequences from each study site. Blue dots: study sequences; grey dots: background sequences. Purple highlight: index sequences from index-partner pairs (I1-I7); blue highlights: partner sequences from index-partner pairs (P1-P7); grey highlights: sequences from index-index clusters (C1-C15).

Figure 2. Phylogenetic trees of env sequences from index-partner pairs (Panel A) and index-index clusters (Panel B).

Table 1. Characteristics of pol clusters.

Table 2. Characteristics of participants with linked HIV infections.

CONCLUSIONS

• Complex patterns of sequence clustering and genetic linkage were observed, with up to seven participants in a cluster.
• Five (71.4%) of seven injection partners acquired HIV infection from a source other than the corresponding index participant.
• These findings suggest that a comprehensive HIV prevention program that includes interventions for both HIV-infected and HIV-uninfected individuals may be most effective in this population.

The HIV Prevention Trials Network is funded by the National Institute of Allergy and Infectious Diseases (U10AI068629, U10AI068613, U10AI068617), with co-funding from the National Institute of Mental Health, and the National Institute on Drug Abuse, all components of the U.S. National Institutes of Health.

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