

Epidemic dispersion of HIV and HCV in a population of co-infected Romanian injecting drug users

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Co-infections with HIV and HCV are very common among people who inject drugs (PWID), and result in higher levels of mortality and morbidity. However, very few studies comparatively reconstructed the transmission patterns of both viruses in the same population, and none analysed the overlap between HIV and HCV transmission networks. Our objective was to reconstruct the history and the transmission patterns of HIV and HCV, to assess the likelihood of simultaneous transmission of these two viruses in a population of co-infected PWID and to analyse the congruence between HIV and HCV transmission networks.

We have recruited 117 co-infected PWID during a recent HIV outbreak in Romania. Phylogenetic analyses were performed on HIV and HCV sequences in order to characterize and compare transmission dynamics of the two viruses. Phylogenetic analyses were performed using both maximum-likelihood and Bayesian approaches. Transmission clusters were identified in the maximum-likelihood phylogenetic tree and were further confirmed with Bayesian phylogenetic analyses.

Three large HIV clusters and thirteen smaller HCV transmission networks were identified. Eighty patients (65%) were both in HIV and HCV transmission chains and 70 of those patients shared the same HIV and HCV cluster with at least one other patient. Molecular clock analysis indicated that all identified HIV clusters originated around 2006, while the origin of the different HCV clusters ranged between 1980 and 2011. HCV infection preceded HIV infection in 80.3% of cases. Coincidental transmission of HIV and HCV was estimated to be rather low (19.65%) and associated with an outbreak between PWID during detention in the same penitentiary.

This study clarifies and compares the patterns of spread and transmission of HIV and HCV in Romanian PWID, suggesting that a higher rate of transmission of HIV, rather than HCV, is associated with behavioural changes.