

Molecular network characteristics and drug resistance analysis of 392 newly reported MSM HIV/AIDS cases in Chongqing, China

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Abstract

To comprehensively investigate the molecular transmission patterns of HIV-1 genotypes among men who have sex with men (MSM) in Chongqing, we employed 392 pol sequences of MSM to construct a phylogenetic tree and gene transmission network. The study collected a total of 392 sequences for analysis. Among the viral subtypes, CRF07_BC accounted for 73.2% (287/392) and CRF01_AE accounted for 20.7% (81/392), emerging as the predominant subtypes in this investigation. Additionally, we observed the presence of CRF55_01B, CRF59_01B, subtype B, CRF08_BC and other circulating recombinant forms in consecutive detections. The HIV-1 molecular network was constructed with a gene distance threshold of 1.5%, resulting in an entry rate of 61.4% (241/392). Within the network, we identified a total of 23 molecular clusters, with the largest cluster being the CRF07_BC molecular cluster comprising 148 node values. Transmitted drug-resistance (TDR) mutations were found in 4.34% of the cases, with 1.79% associated with protease inhibitors (PIs), 0.51% with nucleoside reverse transcriptase inhibitors (NRTIs), and 2.55% with non-nucleoside reverse transcriptase inhibitors (NNRTIs). Statistical analysis indicated a higher enrollment rate among infected individuals with the CRF07_BC subtype, those identifying with same-sex sexual roles as “vers,” and individuals with higher education levels. This suggests the need for strengthened investigation and intervention in this population to prevent the formation of larger transmission clusters. Furthermore, continuous monitoring of the HIV-1 molecular dynamics network is necessary to promptly and accurately track changes in molecular epidemic characteristics.

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