

A total of 33 individuals with acute (n=15) and chronic (n=18) stages, 23 (acute, n=12 and chronic, n=11) were successfully sequenced. Only HBV genotype A subgenotype A1 were detected among the study groups. Rates of the A1 genotypes were 6.4%, 1.9%, 2.2% and 3.1% in HIV-1 infected IDUs, HIV-1 uninfected IDUs, HIV-1 infected non-IDUs, and HIV-1 uninfected non-drug users, respectively. In addition, phylogenetic analysis of the 23 isolates indicated minimal diversity.