Mutations associated with resistance to antiretroviral therapy are a major cause of failure to treatment, and surveillance for the emergence of HIV resistance became a component of all antiretroviral treatment programs. As transmission of resistant viruses to newly infected persons is possible, we aimed to determine the prevalence of primary mutations associated with antiretroviral resistance among treatment-naïve patients, with respect to HIV subtype.

Fourty three plasma samples were collected from treatment-naïve HIV-infected patients, between June 2011 and October 2014. HIV-1 RNA concentrations in the plasma samples of recently diagnosed HIV-1 patients were determined by real-time PCR using the COBAS Amplicor/COBAS TaqMan HIV-1 test v2.0 (Roche Diagnostic Systems, Branchburg, NJ, USA), as manufacturer's instructions. Viral RNA was extracted from plasma samples of 43 treatment-naïve patients. Protease (PR) and reverse transcriptase (RT) regions were amplified and sequenced using the TRUGENE HIV-1 Genotyping Assay. A phylogenetic analysis was performed for HIV subtype assignment.

Complete sequence information could be obtained for 35 patients. A total of ten different HIV-1 subtypes and recombinant forms were found in Kuwait with predominance of subtypes B, C and CRF01_AE (table).

A62V was the only non-polymorphic NRTI resistance-associated mutation (RAM) detected in two patients (5.7%) with HIV-1 subtype A infection. Alone, A62V mutation does not reduce NRTI susceptibility. Three patients (8.6%) with HIV-1 subtype CRF01_AE infection had the non-polymorphic A98G RAM that can be associated with reduced NNRTI susceptibility. Non-polymorphic RAMs in the PR region were not detected in this study.

Our results support continuous surveillance of resistance-associated mutations in newly infected individuals to assess the effectiveness of first-line antiretroviral regimen available in Kuwait.