Molecular analysis of HIV-1 integrase sequences among Pre-HAART patients in the Eastern Cape, South Africa

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Background: The HIV 1 integrase catalyses the chromosomal integration of newly synthesized double stranded RNA into the host genomic DNA. Some countries have incorporated integrase inhibitors as components of antiretroviral drug in curtailing the replicative proclivity of the AIDS virus. The aim of this study was to analyse the complete HIV 1 integrase gene obtained from newly diagnosed HIV 1 pre-HAART patients from selected clinics in the Eastern Cape South Africa.

Methods: Sequencing of the HIV 1 integrase region from plasma samples of 45 newly diagnosed drug naive patients were carried out using ABI PRISM genetic analyser and edited with the Geneious 10.3 software while complete sequenced results were obtained from the HIV sequences in 32 patients. Drug resistance mutation to the integrase was inferred from the HIV 1 Stanford drug resistance database while phylogenetic analysis was done to classify the viral sequences into subtypes.

Results: No major resistance to the integrase sequence was observed. Only 1(3.1) case of polymorphic accessory E157Q mutation was observed. Another minor mutation (L74M/L) which is a highly polymorphic accessory mutation was identified in 1(3.1%). Phylogenetic analyses classified all the sequences as HIV 1 subtype C.

Conclusion: The present study indicates that no major integrase mutation was observed and the data obtained will contribute to the relevance of integrase polymorphism and improve resistance interpretation algorithm among the subtype C. Apparently more sample size and additional studies may be essential to evaluate the impact of these mutations on integrase inhibitors prior to their introduction into South Africa in the nearest future.

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