Partly 5` Untranslated Region (5` UTR)-Based Phylogenetic Analysis of Three Hepatitis C Virus Isolates from Jakarta, Indonesia: A Preliminary Study

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Abstrak

<i>Currently, we reported results of a nested polymerase chain reaction (PCR) assay specific 5` untranslated region (UTR) region of hepatitis C virus (HCV) genome that showed three different patterns of deoxyribonucleic acid (DNA) fragments (single expected specific DNA band, single DNA band higher in size than an expected band, and multiple DNA bands). Three isolates (Isolate A, B, and C), representing all the three DNA bands, were analyzed by using phylogenetic trees. The results showed that the Isolate A, B, and C were classified into HCV genotypes 2, 1, and 3, respectively. The Isolate A and B were very closely related to viral isolates from Madagascar and Brazil, respectively and were not closely related to other Indonesia isolates. In contrast with the Isolate A and B, the Isolate C was very closely related to another Indonesia isolate. Among all there isolates, the Isolate C was very closely related to an Indonesia isolate detected from a cirrhosis patient, indicating that the Isolate C might be more virulence than the Isolate B and C. However, a complete genome-based comprehensive genetic characterization for all the three isolates needs to be conducted in future research to confirm all findings in this study.</i>