

Virology, Emerging Diseases & vaccines

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Virus is living and its treatment

The objective of the study was to characterize the Untenable HCV isolates from various geographical areas of Pakistan by sequencing and phylogenetic analysis of their 5' UTRs. The emergence of large number of HCV Untypable isolates among chronically infected Pakistani subjects pose challenges to accurate diagnosis, optimal regimen, dose and duration of antiviral therapy as well as for estimating the response rate. During the course of this study, a total of 415 Untenable HCV strains were detected from different parts of the country in which 50 (12%) randomly selected serum samples were used for sequence analysis of 5' UTR of HCV. The derived consensus sequences in case of all the 50 isolates were later used for genotype prediction using NCBI BLAST (ncbi.nlm.nih.gov) and online HCV genotype prediction tools. The results indicated that all the 50 samples (100%) were very close to HCV 3a. Self-alignment of all the 5' UTR sequences identified 10 diverse types circulating in Pakistan. Most common sequence variations were conserved (*), deletion (-) and transversion. Phylogenetic analysis of HCV Untypable isolates based on the 5' UTR sequences indicated that most of these isolates were genetically closer to Pakistani HCV 3a isolates with high bootstrap value as compared to some regional isolates. However, One Untypable isolate PK3 clustered with isolates from other regions and was distant from the Pakistani isolates which indicates that HCV 3a of different origins are distinctly evolving in Pakistan. The genetic diversity and phylogenetic analysis point towards the rise of variants of HCV 3a in this region in the form of the untenable strains which need through characterization.

Biography

Dr. Kunal Joon has as a Student rom Quaid-i-Azam University in Molecular Virology.I.



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