

Surveillance of Hepatitis C Virus Genotype Circulating in North India

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Abstract : Introduction: The hepatitis C virus (HCV) is a major public health problem and a leading cause of chronic liver disease. Injection drug use and individuals receiving blood and blood products are the primary modes of HCV transmission. Our study aims to establish the prevalent genotypes/ subtypes of HCV circulating in Uttar Pradesh, North India, as reported from a tertiary care hospital. Methods: It is a retrospective observational analysis of consecutive 404 HCV RNA positive cases referred to our hospital during September 2014 to April 2017. The study was approved by an institutional ethics committee. Written informed consent was taken from each participant. Clinical and demographic details of these patients were recorded using predesigned questionnaires. All the laboratory testing was carried on stored serum sample of enrolled cases. Genotyping of all 404 strains was done by Sanger's sequencing of the core region. The phylogenetic analysis of 179 HCV strains with high - quality sequencing data was performed. Results: The distribution of prevalent genotypes/ subtypes as noted in the present study was; Genotype (GT)1a [n-101(25%)], GT1b [n-12(2.9%)], GT1c [1(0.25%)], GT3a [275(68.07%)], GT3b [9(2.2%)], GT3g [2(0.49%)], GT3i [3(0.74%)], and GT4a [1(0.24%)]. HCV genotypes GT2, GT5 and GT6 were not detected from our region. Sequence analysis showed high genotypic variability in HCV GT3. Phylogenetic analysis showed that HCV GT3 and GT1 circulating in our region were related to Indian strains reported earlier. Conclusions: HCV genotypes 3a and 1a are commonest circulating genotypes in Uttar Pradesh (UP), India.

Keywords : Hepatitis C virus, genetic variation, bioinformatics, genotype, HCV

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