

**CHARACTERIZATION AND GENOTYPING OF HEPATITIS C  
VIRUS ON CORE AND NS5B REGIONS IN VIETNAMESE  
BLOOD DONORS**



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M.Sc. (TROPICAL MEDICINE)

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**ABSTRACT**

This study aimed to determine the prevalence of Hepatitis C virus genotype and characterize HCV genome on core and NS5B regions in Vietnamese blood donors. A total of one hundred and three HCV antibody-positive plasma samples were collected from blood donors at the National Institute of Hematology and Blood Transfusion, Hanoi, Vietnam. All specimens were subjected to RT-PCR of the 5'UTR to confirm the presence of HCV RNA. The core and NS5B regions of positive samples were subsequently amplified by RT-PCR followed by direct sequencing and phylogenetic analysis.

Of seventy (68.0%) RNA positive samples, core and NS5B were successfully amplified and sequences were obtained for seventy and sixty-five samples, respectively. Phylogenetic analysis revealed that genotype 6a was the most common, accounting for 37.1% (26/70), followed by genotype 1a with 30.0% (21/70) and genotype 1b with 17.1% (12/70). Two genotype 6 variants, 6e and 6l, were detected with a prevalence of 8.6% and 1.4%, respectively. The analysis of nucleotide and amino acid sequences exhibited a higher sequence variation in NS5B region than that in core region. The homology among same subtypes of NS5B sequences varied from 93.3 % to 97.7% while those percentages of core sequences ranged from 96.7% to 99.0 %. In NS5B amino acid sequences, the differences between genotypes were 12-27% while the dissimilarity among those of core was 5-10%.

The high prevalence of genotype 6a presented a difference from previous studies in Vietnam. These findings, along with recent studies, showed the geographic distribution of genotype 6 mainly in south China and on the mainland of SEA including Vietnam, Laos, Thailand, and Myanmar. The characteristics of HCV genome confirmed the high variability in NS5B region compared to the core region.

**KEY WORDS: HEPATITIS C VIRUS/ GENOTYPE/ CHARACTERIZATION/ CORE/ NS5B**

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