GENOTYPIC DISTRIBUTION OF HEPATITIS C VIRUS IN VOLUNTARY BLOOD DONORS OF NORTHERN THAILAND

Prapan Jutavijittum1, Yupa Jiviriyawat1, Amnat Yousukh1, Chansom Pantip2, Niwat Maneekarn2 and Kan Toriyama3

1Department of Pathology, 2Department of Microbiology, Faculty of Medicine, Chiang Mai University, Chiang Mai, Thailand; 3Department of Pathology, Japanese Red-Cross Nagasaki Atomic Bomb Hospital, Nagasaki, Japan

Abstract. The purpose of this study was to determine the prevalence and distribution of HCV genotypes among voluntary blood donors in northern Thailand. From 1998 to 2000, 167 serum samples which tested positive for anti-HCV antibodies in the screening of voluntary blood donors from 5 provinces in northern Thailand were selected for genotyping. Viral RNA was extracted from the sera. The core-E1 region of the HCV-RNA genome was amplified using a OneStep RT-PCR kit. The core-E1 amplicon was sequenced and the HCV genotype was assigned by comparing with the reference sequences available in the GenBank database. Of 167 anti-HCV positive serum samples, 126 (75.4%) contained HCV RNA as detected by PCR. HCV genotype 3 was the most predominant genotype (39.6%), of which 33.3% belonged to genotype 3a and 6.3% to 3b. Genotype 6 was detected in 31%, and genotype 1 was detected in 27.8%. Of the genotype 1 isolates, 14.3% were 1a, 12.7% were 1b, and 0.8% were 1c. Two HCV isolates detected in the present study were untypeable. About 75% of anti-HCV positive blood donors had chronic HCV infection. In northern Thailand, genotype 3a was the most predominant genotype, while genotype 6, 1a and 1b were also commonly found. The genotypic distribution of HCV isolates from various regions of Thailand were more or less similar. Nevertheless, in this study, the prevalence of HCV genotype 6 (31%) was higher than previously reported by others (8-18%). Phylogenetic analysis of the HCV isolates detected in the present study was also performed.