MOLECULAR DETECTION, QUANTIFICATION AND CHARACTERISATION OF HEPATITIS C VIRUS STRAINS IN SRI LANKA

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The Hepatitis C Virus (HCV) was first identified in 1989 and since then HCV infection has become an increasing public health concern. The World Health Organization (WHO) estimated that in the year 2000, at least 160 million were infected and over 3 million new cases were reported each year. The global prevalence rates of HCV infection vary with geographic region and according to the WHO, 2.15% of the Asian population is infected. Sri Lanka was one of the few countries in the world which did not have data relating to the occurrence and molecular characterization of HCV. Therefore, the main objectives of this study were to develop and apply molecular methods for the detection, quantification and characterization of HCV strains found in Sri Lanka.

Low-cost in-house RT-PCR based methods were developed for the qualitative and quantitative detection of HCV and determination of the prevalence of HCV Ribonucleic Acid (RNA) among liver disease patients in Sri Lanka. Genetic diversity among the HCV

RNA positive cases was estimated in terms of genotypes by type-specific amplification and sequence analysis. Phylogenetic analyses were performed on HCV sequences to determine the relatedness of Sri Lankan strains to global strains.

Of a cohort of 1933 liver disease patients, 214 (11.07%) were positive for anti-HCV antibodies and 49 (2.5%) were positive for HCV RNA. The data suggests that the occurrence of HCV among the liver disease patients is relatively low in Sri Lanka. Of 49 positively tested patients, 11 (22.44%), 13 (26.53%), 6 (12.24%), 6 (12.24%), 8 (16.32%) and 1 (2.04%) were found to be genotype 1a,1b, 2a, 2b, 3a, mixed infection of genotypes 1b and 2b respectively. Four (8.16%) samples could not be typed with the type-specific PCR assay which was used in this study. The most prevalent genotype among the liver disease patients in Sri Lanka is genotype 1. The type- specific PCR done in this study was found to have concordance 95% in specificity and 96% in sensitivity against the nucleotide sequencing which is the gold standard method for HCV genotyping. According to the phylogenetic analysis of studied sample population it is possible to say that HCV genotypes 1 and 2 found in Sri Lanka are most closely related to HCV strains from western countries such as USA, UK and France and there was a clear segregation of genotype 3 strains which showed a close affinity to strains from Thailand.