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Review Article

HEPATITIS C VIRUS (HCV) AND ITS WORLDWIDE DISTRIBUTION

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ABSTRACT

Hepatitis C virus (HCV) infection presents severe health problem worldwide, particularly in the developing countries. HCV is a major cause of chronic liver disease and various associated metabolic disorders, affecting approximately 170 million people worldwide. HCV has been categorized into different genotypes on the basis of atleast 67% similarity of nucleotide sequences. It is very imperative to determine HCV genotypes and its distribution to cope with the clinical management, prognosis and assessment of patients before consideration of interferon therapy. Geographic distribution of HCV genotypes are well documented in different parts of the globe but still more work is required in this direction. The purpose of this short review is to summarize the HCV distribution across the globe.

HCV and Its distribution:

HCV was reported in 1989 by Choo et al [1]. It is a major cause of chronic liver disease and various metabolic disorders with approximately 170 million people being infected in the world [2].HCV is a positive stranded RNA virus and abstractedly related to the flaviviruses and pestiviruses, and has been classified into the genus hepacivirus of the virus family flaviviridae [3]. The whole genome of HCV is 9.5Kb containing highly conserved untranslated regions (UTR) at both the 5’ and 3’ termini, which flank a large translational open reading frame encoding a polyprotein of 3,000 amino acids. Structural proteins are core, highly variable glycoprotein, E1 and E2. Rest of genome encodes nonstructural proteins NS2-NS5 and 3’ UTR [4].

The core protein of hepatitis C virus (HCV) is an important structural element of the virion that affects a number of cellular pathways, including nuclear factor B (NF-B) signaling. NF-B is a transcription factor that regulates both anti-apoptotic and pro-inflammatory genes and its activation may results to HCV-mediated pathogenesis [5].The 5'UTR is uncapped containing the internal ribosomal entry site (IRES) which contains highly conserved structures that are essential for proper binding and positioning of the viral genome inside the host cells [6]. HCV genome is highly mutable because of no efficient proofreading ability during replication. It introduces mutations and changes itself while replicating inside host. So HCV continue to exist as a collection of viral quasispecie [7]. Thesenaturally occurring mutations confer resistance to hepatitis C virus polymerase inhibitors in HCV treatment [8].

Hepatitis c virus (HCV) infection is a well-recognized and pose severe health problem worldwide, especially in the developing countries [9]. The global epidemiology of viral hepatitis A and hepatitis B is well established, although HCV data remain limited. In 2004 it was estimated by the WHO that the annual deaths due to liver cancer caused by HCV and cirrhosis were 308000 and 785000 respectively [10]. HCV prevalence in injection drug users (IDUs) and the multi-transfused population is high, suggesting that the reuse of syringes is common among the injecting drug users, and that blood transfusions are not properly screened in many countries of the world [11].

Hepatitis C virus (HCV) is a major health problem associated with liver steatosis, cirrhosis and hepatocellular carcinoma [2]. It has been categorized into different major groups called genotypes whose members have at least 67% identity with each other on the basis of nucleotides [12].HCV has a highly variable sequence, allowing description of 11 genotypes and above 100 subtypes with different geographical distributions. Clinical outcomes as well as response to antiviral therapy are strongly influenced by HCV genotype [13, 14].

In Pakistan the prevalent genotype is 3 followed by genotype1 and 2 while other genotypes are quite rare[13, 15].Genotype 3 and 1 are also the foremost genotypes in Indian population [16]. HCV subtypes1a, 1b, 2a and 2b are found commonly in Unitesd States [17]. In Italian population genotype 2a predominates [18]. In Taiwan the most common genotype is 1b [19]. Type 4 is found in Middle East countries [20]. Genotype 6 is found in Hong Kong, Thailand, south China and south-east Asian population [21]. Genotype 6 is also the most common genotype in Vietnam [22] while 1b, 1a and 3k is common in Indonesian population [23]. Genotype 1 is exclusively found in the Romanian and Slovenian populations [24, 25]. Also in Mexico and Argentina, HCV genotype 1 is the predominant genotype [26]. Genotype 1 and 4 has been reported to be the common genotypes in African countries [27]. In Sri Lankan population genotypes 1b and 2b are the leading genotypes [28] while in Korean population the most prevalent genotype is 1b followed by 2a [29].

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