Genotypes of Hepatitis C Virus in Kuwait

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Key Words

Genotype · Hepatitis C virus · Kuwait

Abstract

Hepatitis C virus (HCV) genotypes in 144 patients in Kuwait were determined by the Murex Anti-HCV Serotyping Assay. Twenty-nine (38%) of 77 Kuwaiti patients were found to be infected with genotype 4 and 27% with genotype 1 while of the 41 Egyptian expatriate patients 37 (90%) were infected with genotype 4. Results show that although in native Kuwaiti patients the dominant genotype is 4, other genotypes, especially type 1, occur frequently.

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The geographical distribution of hepatitis C virus (HCV) genotypes is important for future vaccine development as well as determining the source of infection [1]. Furthermore, the severity of infection and the effectiveness of interferon therapy may be influenced by genotypes.

Only limited data are available for the Middle East regarding genotype distribution of HCV [2]. Studies thus far have shown that genotype 4 is dominant in Egypt; more than 90% of HCV strains belong to this type. In oth-

er Middle Eastern countries, the pattern is somewhat different: in Syria type 4 and type 1 are predominant, while in Lebanon and Iraq it seems that it is type 1 [3]. In Saudi Arabia, where a relatively large number of samples have been analyzed, it was found that type 4 was represented in 48% of the population. The other rather frequent genotype was type 1 [4]. The most predominant genotypes worldwide are 1, 2 and 3 [3]. Other genotypes are confined to certain areas, such as type 5 for Hong Kong and South Africa. In this study, we report the genotypic distribution among 144 serum samples from HCV antibody-positive patients in Kuwait.

In addition to molecular methods, genotypes of HCV can be determined by serological techniques based on the detection of genotype-specific antibodies to synthetic peptide antigens representing the core and nonstructural (NS) regions of the viral protein [5]. HCV can be classified into 6 major genotypes and several subtypes [6]. ELISA-based assays have also been developed to determine the antibodies to those specific peptide antigens representing the major genotypes. The antigens used in the assay are genotype-specific, showing no cross-reactivity among the 6 major genotypes. Although this serogenotyping is limited to identifying the 6 major genotypes, it gives valuable data on the worldwide distribution of HCV genotypes.

Here in Kuwait we have analyzed 144 HCV antibody-positive samples which were selected from those sent for

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Table 1. Distribution of major HCV genotypes according to nationality in Kuwait

Nationality	Number	Genotype				UT	Mx
		1	2	3	4		
Kuwaiti	77	21 (27)	1 (1.3)	7 (9)	29 (38)	15 (19.5)	4 (5.2)
Egyptian	41	2 (5)	–	–	37 (90)	2 (5)	–
NK	20	1 (5)	–	1 (5)	12 (60)	3 (15)	3 (15)
Syrian	3	3	–	–	–	–	–
Indian	1	1	–	–	–	–	–
Pakistani	2	–	–	2	–	–	–
Total	144	28	1	10	78	20	7

Figures in parentheses represent percentage. Kuwaiti nationality refers to the sector of the Kuwaiti population who are genuine Kuwaiti citizens, having lived in Kuwait for generations. Egyptian nationality refers to Egyptian expatriates who have been working in Kuwait for years. NK refers to non-Kuwaitis. This category includes individuals whose nationality cannot be determined, but are of Middle Eastern origin permanently residing in Kuwait. UT = Untypable genotypes; Mx = mixed genotypes.

hepatitis serology by various hospitals in Kuwait to the Department of Microbiology, Faculty of Medicine, and the Public Health Virology Laboratory, Ministry of Health, Kuwait. Sera were screened first with the Abbott IMx HCV version 3 microparticle immunoassay. The assay is based on recombinant HCV-specific antigens (HCr43 contains sequences of both core structural and nonstructural antigens while c200, c100-3 and NS5 represent antigens related to nonstructural regions of HCV). Sera being HCV-antibody-positive by this assay were retested with (1) Organon LiaTek HCV III line immunoassay, which uses HCV E2/NS1, NS3, NS4, NS5 core proteins on the strip and (2) Genlabs Diagnostics HCV Blot 3.0 Western blot assay, which uses 4 nonstructural and 1 capsid-related antigens on the nitrocellulose strip. The serogenotypic determination of the LiaTek/Genlabs-positive samples was done using Murex Anti-HCV Serotyping Assay version 1–6. This serotyping utilizes a larger number of synthesized HCV-specific, branched peptide antigens, representing the variable regions from NS4 of HCV genotypes 1, 2, 3, 4, 5 and 6. All tests were performed according to the protocol given by the manufacturers.

In Kuwait, 75% of the population of 2 million are expatriates, the majority from South East Asian and Middle Eastern countries. This factor may have an impact on the prevalence of HCV antibodies and the distribution of genotypes. The results are summarized in table 1. Regarding the genotyping distribution of HCV, our data is in agreement with that found in Saudi Arabia [4] where the prevalence of genotype 4 in Saudi nationals was 48% fol-

lowed by type 1 with 28% compared to Kuwaiti nationals of 38 and 27%, respectively. Although genotype 4 seems to be most prevalent in both Saudi Arabia and Kuwait, type 1 is represented with a relatively large percentage. This is definitely in contrast to the pattern which characterizes the expatriate Egyptian population in Kuwait, who are almost exclusively infected with HCV genotype 4. This unique, homogenous pattern was also found among Egyptian health care workers in a Kuwaiti hospital where of the 16 HCV antibody-positive Egyptians, 13 were infected with HCV type 4 [7]. Although many of the Egyptians have been living in Kuwait for longer than 10 years, they are still infected with HCV genotype 4. This may indicate that this infection is acquired in early childhood. On the other hand, there is an example of an Italian who lived in Egypt for approximately 20 years and had an HCV infection of genotype 4 [3]. Genotypes of 20 samples (14.8%) of the 144 tested could not be determined. This figure agrees well with the results of Saudi Arabian (16.8%) and Kuwaiti (17%) studies [4, 7]. Nevertheless, these samples require further study for determining whether new HCV genotypes are present in this part of the world.

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