HEPATITIS C VIRUS GENOTYPES IN IRAQ

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ABSTRACT
This study included 210 Hepatitis C Virus(HCV) infected patients 150 males and 60 females with an range of 3-50 years, they are 100 patients from thalassemic HCV infected, 100 patients from chronic liver disease HCV infected, and 10 persons from blood donors HCV infected. The study show 94(94%), 85(85%), 80(80%) from thalassemic and chronic liver disease and blood donors HCV infected carrier the HCV, genotype (4) respectively, and 5(5%), 10(10%). 20(20%) respectively carrier 1b genotype and 1(1%), 5(5%) from thalassemic and chronic liver disease HCV infected respectively carrier mixed genotype (1b and 4). While 2(20%) from blood donor HCV infected HCV carrier 1b genotypes.

Key words: HCV, Genotype, Iraq

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النمر الوراثي لفايروس التهاب الكبد نمط C في العراق

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الخلاصة

شملت الدراسة 210 مريضاً بالتثاب الكبد الفايروسي نمط C، 150 ذكراً و 60 إناثاً والتي تراوحت أعمارها بين 3-50 سنة، منهم 100 من مرضى الثلاسيميا و100 من المصابين بالتثاب الكبد المزمن و10 من مبتعلي الدم ومصابيهم و Faivrus انتصاب الكبد نمط C، وأظهرت الدراسة (94%, 85%, 80%) على التوالي من مرضى الثلاسيميا والتثاب الكبد المزمن ومبتعلي الدم المصابين بالتثاب الكبد نمط C يحملون النمر الوراثي 4، (5%, 10%, 20%) على التوالي يحملون النمر الوراثي b1b، (1%)، 5% على التوالي من مرضى الثلاسيميا والتثاب الكبد المزمن يحملون النمر الوراثي المختلط b1b بينما 20% من مبتعلي الدم المصابين بفايروس التهاب الكبد الفايروسي نمط C يحملون النمر الوراثي b1b.
INTRODUCTION
The term genotype refers to different genetic variations or strains of hepatitis C virus (HCV) (19). The variance in genetic differences is approximately 113 between the different genotypes (10). There are six major groups or genotypes numbered 1 to 6 although some experts believe that there may be as many as 11, and within each genotype there are further divisions called subtypes (for example 1a and 1b) and quasispecies (18). The virus constantly changes and mutates as it replicates more than 1 trillion hepatitis C virions replicate each day and, the HCV will make up of the newly replicated virus (9). The process of constant mutation helps the virus evade the body's immune response when the dominant quasi-species is eradicated, another quasi-species emerges (8). HCV genotype and subtype are distributed differently in different part of the world, and certain genotypes predominate in certain areas, Genotypes 1-3 are widely distributed throughout the world, genotype 4 in middle east and Africa, genotype 5 in south Africa, while genotypes 6 is widely distributed in south east Asia (2,20).
HCV genotype information is important because of the role it plays in predicting HCV medical treatment response, treatment duration and the dose of ribavirin (7,17).

Aims of study: To determine hepatitis C virus genotype in Iraq.

MATERIALS AND METHODS

Subject
Human HCV positive serum samples from 210 HCV infected patients were collected from thalassemic and chronic liver disease and blood donors. The selection of the studied population was based on the following criteria: presence of HCV RNA in plasma confirmed by nested reverse transcription polymerase chain reaction (nRT-PCR): absence of other concomitant liver disease; negative HIV test, no prior interferon and/or ribavirine treatment, and neither habitual alcohol nor active intravenous drug user.

Anti - Hcv Elisa
All serum samples were screened for anti-HCV antibodies using ELISA (Biokit, Espania). The results of the assay were expressed quantitatively as the ratio of the optical density of the test sample to the calculated cut off absorbance as recommended by the manufacturer. Serum samples with OD values ≥0.30 were considered to be positive, while those with OD values <0.30 were considered negative.
Positive and indeterminate serum samples, were re-tested with another ELISA assay, Innotest AbIV (Innogenetics NV HCV, Gand, Belgium). Sample were confirmed as anti-HCV antibody positive when they were tested positive using both ELISA sets.

Hcv Rna Detection
HCV RNA preparation and cDNA synthesis performed as described previously (11). The extracted RNA was used as a template and was amplified by nested RT-PCR with primers specific for the 5UTR (5 non coding region) of HCV (12,13).
PCR product were re-amplified using the same cycling program, negative controls lacking template were included for each pair of primer. If a control was found positive, all of the PCR products in that set were considered to be contaminated and we are
discarded. Amplified cDNA was electrophoresed by 2.0% agarose gel and stained with ethidium bromide.

Genotyping Of Hcv

HCV genotypes were determined by amplification of the core region with genotype-specific primers that distinguished between genotypes 1, 2, 3 and 4 (15,16). Part of the HCV core gene (272 bp) was amplified from HCV cDNA with universal primers. A portion of the product was then amplified by PCR with universal sense primers and a mixture of five antisense primers deduced from HCV core (HCV-C) gene sequences specific for genotypes 1, 2, 3 and 4 (14,15). The four genotypes were distinguished from one another by the size of PCR products: 123 bp for genotype 1; 211bp for 2; 240bp for 3 and 188bp for 4.

RESULTS AND DISCUSSION

The results in table (1) show that the HCV genotype among thalassemic and chronic liver disease and blood donors infected HCV were mainly type 4 (94%,85%,80%) respectively, followed by type 1b (5%,10%,20%) respectively, other genotype were rare.

| Table(1):The percent age of HCV genotype among hepatitis C patients. |
|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|
| No (%) of samples of Hepatitis C virus genotypes | No. of samples | 1 | 1a | 1b | 2a/ab | 3 | 4 | 5 | 6 | Unknown | Mixed genotypes |
| Thalassemic hepatitis C patients | 100 | 0 | 0 | 5 (5%) | 0 | 0 | 94 (94%) | 0 | 0 | 0 | 1 (1%) |
| Chronic liver disease hepatitis C patients | 100 | 0 | 0 | 10 (10%) | 0 | 0 | 85 (85%) | 0 | 0 | 0 | 5 (5%) |
| Blood donors hepatitis C patients | 10 | 0 | 0 | 2 (20%) | 0 | 0 | 8 (80%) | 0 | 0 | 0 | 0 |

This study agree with Abimbola and Osaba, 2002 in Kingdom of Saudi Arabia (KSA) to determine the prevalence of HCV genotype in various population group in KSA. The prevalence of each genotype in population, genotype 4 was recorded as the most common genotype ranging from 40%-74% among the various group of patients studied genotype of HCV strain important in epidemiological studies and clinical practice, in particular, examination of sequence diversity can help understand the different patterns of serological reactivity, response to treatment (17).

There is substantial evidence that HCV possesses different pathogenic potentials, since different responses to interferon treatment depending on the HCV type/subtype have been reported (5). Furthermore, association between some HCV types and the severity of liver disease has been noted in some reports (1). Some of these have suggested that genotypes 2 and 3 are predictive of favorable response to therapy than genotype 1(6). There is a considerable variation in the natural history of HCV more severe liver pathology has been reported to depend not only on viral factors such as genotype viral load, level of heterogeneity of HCV quasi species but also on host factor
such as age, sex, use of alcohol and length of time of HCV infection in infected patients (4).

CONCLUSION
The predominant of HCV genotype in Iraqi patients was genotype (4) followed by genotype (1b).

REFERENCE