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The distribution of hepatitis c virus genotypes in US population. Data from NHANES 2006-2016

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Background

Unlike other non-hepatitis c viral infection, hepatitis c viral infection is a non-vaccine preventable disease. Thus, effective treatment is an important part in the prevention of complication of chronic hepatitis c infection. The viral genotype plays a significant role in the choice of treatment regimen.

Objectives

To estimate the prevalence of hepatitis c viral infection and the distribution of viral genotype in the US population

Methods

Diagnosis of Hepatitis C viral infection was made by assaying the blood specimen collected from the study participants using Ampiclor monitor (Roche Diagnostic System, Inc Branchburg NJ), and genotype determined from the NS5b region. The data is from NHANSE 2006-2016. SAS v 9.4 software was used to perform the analysis.

Results

Of the 356 participants (2006-2016) who tested positive to Hepatitis C virus-RNA, 205 persons had genotype 1a, 1b (n=66), other forms of genotype 1 (n=1), genotype 2(n=41), genotype 3 (n=30), genotype 4 (n=1), genotype 6(n=1), undetermined genotype (n=8). Based on weighted analysis of person infected with genotype 1, 2, 3; genotype 1 was highest across all ages and gender (78.2%). Of 271 participants infected with genotype 1, there were 5.09% Mexican Americans, 3.94% other Hispanics, 56.58% non-Hispanic whites, 28.74% non-Hispanic black, and 5.65% other races including multiracial population. Subjects aged 50 years or above was 27.7% less likely being infected with HCV genotype 1 vs 2 and 3, compared with younger individuals (adjusted Odds Ratio (95% confidence interval) (aOR): 0.72 (0.72-0.73)). Non-Hispanic black were about 13 times (aOR: 13.1 (13.0-13.2)) as likely to be infected with genotype 1 vs 2 and 3 as non-Hispanic white.

Table 1. Distribution of Genotype Among Infected with Hepatitis C Virus Genotype 1, 2 and 3 According to Demographic Characteristics

| Characteristics | Weighted Percentage by Genotype (%) | | |
|-----------------------------|-------------------------------------|-------|-------|
| | 1 | 2 | 3 |
| Total (n=342) | | | |
| Age | | | |
| 6-29 (n=8) | 83.4 | 0 | 16.6 |
| 30-39 (n=12) | 44.28 | 35.7 | 20.02 |
| 40-49 (n=72) | 87.21 | 10.51 | 2.28 |
| 50-59 (n=92) | 76.36 | 16.76 | 6.88 |
| >59 (n=87) | 79.87 | 15.81 | 4.33 |
| Sex | | | |
| Male (n=226) | 77.79 | 17.07 | 5.14 |
| Female (n=116) | 79.06 | 12.17 | 13.79 |
| Race | | | |
| Mexican American (n=36) | 62.53 | 11.45 | 26.02 |
| Other Hispanics (n=27) | 81.59 | 8.29 | 10.12 |
| Non Hispanic Whites (n=121) | 72.34 | 22.14 | 5.52 |
| Non Hispanic Black (n=144) | 96.89 | 1.84 | 1.28 |
| Multiracial (n=14) | 79.72 | 10.86 | 9.43 |

Conclusions

Hepatitis C virus genotype 1 is predominant among those infected with hepatitis c virus in the US population. Improvement in therapy targeting genotype 1 is essential to reduce the burden and complication of chronic hepatitis C in the United States.

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