

Letter to Hajiani E, Hashemi SJ, Masjedizadeh A, Shayesteh AA, Jalali F.  
Genotypic Analysis of Hepatitis C Virus in Khuzestan Province,  
Southwestern Iran. *Middle East J Dig Dis* 2011;3:126-30

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We have read with interest the recently published article by Hajiani et al.<sup>1</sup> in your journal. The distribution of HCV genotypes can enable clinicians to make better decisions for treatment of HCV-infected cases. In Iran, there is a low endemicity for HCV infections<sup>2,3</sup> the primary high risk groups for acquiring infection are patients on hemodialysis, those with hemophilia and thalassemia, and intravenous drug abusers.<sup>4</sup>

The predominant genotype in this study was genotype 1a (41.7%). The researchers have found an association only between genotype and intravenous drug users (IDUs). We wish to mention that other genotypes might have special risk factors. For instance, genotype 4 is reported in hemodialysis patients in Iran. However it might be related to hemodialysis patients who travel to Saudi Arabia during Hajj as pilgrims, where they receive hemodialysis there. For participation in Haj meeting in Saudi Arabia and receiving dialysis during this period in that country.<sup>5</sup> Genotype 4 is very common in Saudi Arabia and the globalization and travel between countries can change the molecular epidemiology of HCV infection. The distribution of HCV genotype in large numbers of hemophiliacs in Iran is as follows: 1a (58%), 1b (14.7%), 3a (18.5%), mixed (6.2%), and non-typable 0.5%.<sup>6</sup> Similar data has been reported among Iranian patients diagnosed with thalassemia,<sup>7</sup> where genotype 1 is predominant. Thus, it would have been better for Hajiani et al. to present the distribution of HCV genotypes in different groups.

One of the most important points in this report is HCV infection in those who are blood transfusion recipients. The researchers have reported that among 64 patients whose HCV route of infection was proposed to be transfusion,<sup>5</sup> have received transfusions after 1995 when routine screening for HCV infection was implemented in Iran's blood transfusion organization. Although the current screening with only serology might miss some patients with HCV infection, however through strict donor selection strategies and considering the low endemicity of HCV in healthy Iranians, such post-transfusion HCV infections might be unlikely. Another explanation for these cases might be the unapparent inoculation of viruses at the point of care or infection through other routes. The problem of ear piercing, unsafe circumcisions, tattooing and

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other routes of transmission should be ruled out in these patients before pinpointing transfusion as the sole route. Hence, these 5 cases should be reported in detail.

Another view is related to the distribution of HCV genotypes in Iran. Zarkesh-Esfahani et al.<sup>8</sup> have reported the predominance of genotype 3 in 61.2% of enrolled cases from Isfahan. According to Omrani et al,<sup>9</sup> 48.12% of their cases from Tabriz were genotype 3. Other studies from different parts of Iran, such as Shiraz,<sup>10</sup> Tehran,<sup>11</sup> and Kerman,<sup>12</sup> have results comparable to those reported by, as Hajiani et al.

Finally, I would like to mention that 18.84% non-typable HCV in the Hajiani et al. study is related to a limitation in the method of HCV genotyping. If the researchers repeat the study with other methods, such as sequencing, they will find less un-defined genotypes.

#### KEYWORD

Hepatitis C; Genotype; Iran.

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#### CONFLICT OF INTEREST

The authors declare no conflict of interest related to this work.

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