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Letter to the Editor

CYP24A1 genetic variants in the vitamin D metabolic pathway are involved in the outcomes of hepatitis C virus infection among high-risk Chinese population★

Dear Editor

We read with interest the article by Fan et al. (2019) reporting the influence of genetic variants of cytochrome (CYP) 24A1 on the outcomes of hepatitis C virus (HCV) infection. In that study, viral factors including the HCV genotype and also host factors such as body mass index, alcohol consumption, and co-morbidities should have been considered as predictors of the hepatitis C course and response to drug treatment. The development of direct-acting antivirals (DAAs) has improved the treatment of chronic HCV infection. However, lower rates of sustained virological response to DAAs have been detected among patients with virus of genotype 3 when compared to other genotypes (Feld et al., 2016). So, in Table 1 of the paper, the analysis of HCV genotypes according to genotype 3 and non-3 would have been informative (Fan et al., 2019). Since, high-risk populations for viral acquisition such as transfusion-dependent individuals, thalassemia and hemophilia patients, and also subjects with high-risk sexual behaviors and prisoners were not been included in the study, the results obtained might not be applicable to all high-risk HCV populations.

Vitamin D is an important modulator of the immune response to viral infection. An association between the level of vitamin D and the course and adverse effects of HCV infection, as well as the response to therapy with peginterferon/ribavirin, has been indicated. In this regard, the vitamin D-related gene polymorphisms could modulate the influence of vitamin D deficiency on HCV infection (Jin et al., 2018). In the vitamin D biosynthesis pathway, CYP2R1 and CYP27B1 encode vitamin D 25-hydroxylase and 1-hydroxylase, respectively (Rezavand et al., 2019; Legarth et al., 2018). The $1,25(OH)_2$-D_3 binds the vitamin D receptor (VDR) and has an influence on gene transcription in target tissues. However, CYP24A1 encodes a 24-hydroxylase enzyme that decomposes the $1,25(OH)_2$-D_3 (Fan et al., 2019). So, studying the gene variants of the pathway of vitamin D metabolism and action (CYP2R1, CYP27B1, CYP24A1, and VDR) along with measurement of the plasma level of vitamin D could be useful to elucidate the impact of this vitamin on the outcome of HCV infection and the response to therapy. In the report, the odds ratios for the minor allele rs6068816 in the three genetic models were <1, indicating its protective role; this should have been considered in both the Results and Discussion sections of the paper. Since the distribution of rs2248359 genotypes in previously infected individuals was not in Hardy–Weinberg equilibrium (Chi-square = 14.79, $p < 0.05$), the results obtained should be interpreted with caution.

Author contributions

Z. Rahimi and B. Sayad wrote the manuscript. Y. Mohassel and K. Yari provided some comments.

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Ethical approval

Ethical approval was not required.

Conflict of interest

The authors declare that they have no conflict of interest.

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