Letter to the Editor

Letter: the rs12979860 and ss469415590 polymorphisms of *IFNL4* gene are in strong linkage disequilibrium in Caucasian patients with chronic hepatitis C

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Sirs, We read the article by Stattermayer *et al.* with great interest and we believe that the quality of their study regarding the design, sample size and results is remarkable.[1] They found that *IFNL4* ss469415590 single nucleotide polymorphism (SNP) had a significant role in treatment response of hepatitis C virus (HCV) genotype 1- and 4-infected patients. Also, they concluded that as *IFNL4* ss469415590 had a strong correlation with rs12979860 SNP, there was no additional benefit to test *IFNL4* ss469415590 for prediction of treatment response in Caucasian patients.[1]

We also assessed the rs12979860 and ss469415590 SNPs in 183 Iranian patients with hepatitis C by DNA sequencing.[2] In our study population, we found the frequency of ss469415590 TT/TT, TT/ΔG and ΔG/ΔG to be 38.8%, 45.4% and 15.8%, respectively, and the distribution of rs12979860 C/C, C/T and T/T genotypes to be 38.8%, 45.4% and 15.8%, respectively, which resulted in strong linkage disequilibrium (r^2 = 1.0) between the ss469415590 and rs12979860 SNPs. The perfect correlation of these two genetic variants in Caucasian Iranian patients was similar to that in the study by Stattermayer *et al.*[1]

Similarly, given the perfect correlation of these two genetic variants in our population, these variants will be equally informative in prediction of spontaneous and treatment-induced clearance among Iranian patients with HCV infection. Also, we would like to remind Stattermayer and colleagues that as Prokunina-Olsson *et al.*[3] found the rs12979860 SNP to be located within intron 1 of *IFNL4* gene, it is preferred to refer the rs12979860 as the SNP of *IFNL4* instead of *IL28B*.

In conclusion, different studies including that by Stattermayer *et al.* confirm that the significance of *IFNL4* ss469415590 and rs12979860 SNPs are equal in Caucasian patients with HCV infection.[1, 3] However, if we accept the argument that *IFNL4* ss469415590 is the functional variant in the process of HCV spontaneous and treatment-induced clearance, then it would seem to make sense to base clinical decisions on ss469415590 SNP, rather than a correlated variant such as rs12979860 SNP, even if the correlation is high.

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