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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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doi:10.1111/apt.12589

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 (r² = 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.

ACKNOWLEDGEMENT
The authors wish to thank Prof. Thomas O’Brien for his helpful comments.

Declaration of personal and funding interests: None.

REFERENCES