

What is the ethnicity-specific impact of genetic polymorphisms on the response to hepatitis C treatment in an admixed population of Brazilian patients?

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Dear Editors,

We read with great interest the article by Angelo et al. in *CLINICS* (1). This study revealed interesting points regarding the impact of different genetic polymorphisms on hepatitis C treatment efficacy in 181 Brazilian patients. The evaluation of multiple genetic polymorphisms in this study encouraged us to appreciate the authors' attempt to show the impact of host genetics on the treatment response in hepatitis C virus (HCV)-infected Brazilian patients of admixed ethnicity. Although the statistical analysis in this study was comprehensive in its assessment of the association between different genetic polymorphisms and treatment response, we have several concerns about this statistical analysis. We believe that the frequencies of the polymorphism genotypes should have been reported for the response groups instead of the polymorphisms genotypes that were reported throughout the article. As a result, the presentation of the frequencies of the polymorphism genotypes in Table 2 would be preferable in vertical order instead of in horizontal order (2). Additionally, the protective genotype frequencies in the sustained virological response group, which were presented in the abstract, should be considered in the following manner: 44.2% rs4969170 G/G; 17.3% rs2853744 T/T; 69.2% rs11730582 T/T; 76.9% rs2071430 G/T; and 45.5% rs12979860 C/C. On the other hand, data on the rs12979860 genotype were included for 139 individuals in Table 2, and it appeared that the data on the rs12979860 genotyping was missing for 42 patients in this study. The authors reported that the frequency of

rs12979860 C/C was 18.8% in the study population, which seems to be incorrect; considering the missing data in the statistical calculation, we found the rs12979860 C/C genotype frequency to be 24.5%. Another point that we would like to address in this letter is that a multivariate analysis should have been considered by the authors to clarify the adjusted impact of each polymorphism alongside other factors, such as liver fibrosis, on the response to hepatitis C treatment (3). Finally, because the impact of genetic factors on the HCV treatment response in populations with admixed ethnicity has been not well studied, a study on a large sample of different ethnicities in regions with an admixed population, such as Brazil, is highly recommended. Each genetic marker could have an ethnicity-specific influence on the response to hepatitis C treatment, which should be investigated in a population-based setting.

■ REFERENCES

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