

Answering reviewers - 39208

Dear Editor-in-Chief of *World Journal of Gastroenterology*,

We have revised our manuscript according to the comments and suggestions of the reviewers. Below are the point-by-point changes we have made.

Sincerely yours.

Reviewer code: 03656572

... This editorial review is described in detail, which, as valuable information, could help the readers that have better understand the first-hand knowledge of this topic to start novel studies.

Thank you very much for your assessment.

Reviewer code: 00183339

This paper reviews "Host genetic factors affecting hepatitis B infection outcomes". The manuscript is well presented and of interest and can contribute to increase the knowledge of this topic.

Thank you very much for your assessment.

Reviewer code: 00032933

... 1. Many researchers were unable to find a consistent gene that related to advance liver diseases. The authors may consider whether non-genetic roles are important in the outcome of chronic persistent infection. For examples: transmission route, maternal status and generation.

We have mentioned in Conclusion (paragraph 2) the non-genetic factors that contribute to the clinical heterogeneity of chronic HBV infection. We now emphasize more strongly that these confounders might be the reason why

GWAS for advanced liver diseases were unable to identify consistent genes. We now also include transmission route and maternal status in our list of non-genetic confounders.

2. HBV is an important global infection. Only one GWAS study conducted in south Asia (Saudi Arabian) and none in African. A global perspective on HBV-related SNPs and evolution during human migration was reported. The authors may make a discussion on this issue.

In the 3rd paragraph of Conclusion, we now mention that susceptible alleles of *HLA-DP/DQ* identified in GWAS are more frequent in Asian populations, and might be the reason for higher prevalence of chronic HBV infections in Asia. Allele frequency distributions across human populations might give important insights into human-HBV co-evolution. Thank you very much for your assessment.

Reviewer code: 01800523

The manuscript is well written, and I have nothing to comment.

Thank you very much for your assessment.