

February 26, 2022

Dear Editor,

Name of journal: *World Journal of Clinical Cases*

Manuscript NO: 73015

Title: Distribution and changes in hepatitis C virus genotype in China from 2010 to 2020

Author: Jia yang, Huixin Liu, Ying-Ying Su, Zhisheng Liang, Hui-Ying Rao

We revised the manuscript in accordance with the reviewers' comments, and carefully proofread the manuscript to minimize typographical, grammatical, and bibliographical errors.

The first reviewer's composition comment on the manuscript and my answer

This study reveals the distribution of HCV genotype in China in recent 10 years, G1 and G2 consistently decreased and G3 and G6 become the new challenge for the moment. The two genotypes are mainly associated with IDU. We should focus on the management of this population in the future regarding prevention and therapy to achieve the goal of WHO elimination in 2030. The main limitation of our study is that part of the samples is from patients in hospitals which may not reflect the situation of the general population.

Answer: Although some samples of our study came from the hospital records, a large number of the data was based on surveys and screening data and we tried to include all the available literatures involving distribution to reduce this kind of bias.

The second reviewer's composition comment on the manuscript and my answer

No special comment, thank you.

Scientific Quality: Grade B (Very good)

Language Quality: Grade B (Minor language polishing)

Answer: We sent our manuscript to a professional English language editing company to polish the manuscript further to avoid language errors.

The Science editor's composition comment on the manuscript and my answer

Respected authors, this is a well-written paper and covers an interesting topic. However, the author uses literature retrieval, not a large database, which is a great pity.

Answer: HCV is a silent disease without symptoms, so it is very difficult to discover the infected population. Besides, genotyping is not available in every region, and methods of genotype are varied as well. There are no such databases to describe the distribution of genotype information across the nation and it is also very costly to build such a database. Thus, literature retrieval would be the most cost-effective way to learn about the information at present. We are also looking forward to a database regarding HCV genotype being built in the future to provide us with more accurate knowledge.

Thank all the reviewers and editors for the kind advice.

Sincerely yours,

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