Author’s response to reviews

Title: Association between KIF1B rs17401966 genetic polymorphism and hepatocellular carcinoma susceptibility: an updated meta-analysis

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The authors’ answer: From a certain point of view, our meta-analysis and Su’s were written, completed and submitted almost at the same time, which can be judged from the range of years used to select the studies and date of submission. However, due to the different submission process, the two meta-analyses encountered different situations now.

Compared the two meta-analyses, we found that the two meta-analyses are similar, but not the same. It is mainly reflected in the selection of phenotype, Su’s team focused on HBV-related HCC whereas ours focused on HCC, as well as selection of original studies, selection of genetic model, final meta results and interpretation of the results. Different concerns directly lead to different results in literature retrieval and inclusion. Finally, we yielded 18 studies, six studies more than Su et al. Three of the six more studies were for association on KIF1B rs17401966 polymorphism with HCC, one for negative-association between HBV-related HCC and KIF1B rs17401966, and the other two studies were focused on the association between KIF1B rs17401966 and HBV-HCC, but not included in Su’s meta-analysis for unknown reasons.

The biggest difference, which is also the highlight of our paper, is that in the selection of genetic model, we did not use all genetic models for analysis like traditional meta-analyses, but selected the optimal genetic model in advance according to Ammarin Thakkinstian’s theory, that is to say if OR1<OR2<1 and OR1<OR3<1, then a co-dominant model is suggested. Then the optimal genetic model was used for analysis. We believe that this can reduce the increase of false positive rate caused by repeated analysis as much as possible, and make the interpretation of the results
more clear in the later stage. This point was not emphasized in the original manuscript. In the revised manuscript, it is emphasized in the Statistical methods section.

In order to express the content more clearly and enhance the aesthetics of the chart, we combined “Table 3-5” into “Table 3”.

Moreover, Ying-ying Luo’s working address has changed because of job transfer.

Based on the above analysis, we made the following amendments to the manuscript.

Author information section, line 8, page 1:
Deleted “Intensive Care Unit, the Second Affiliated Hospital of Chongqing Medical University, Chongqing, China”.
Added “Intensive Care Unit, the Third People’s Hospital of Chengdu, Chengdu, Sichuan, China”.

Background section, line 50-55, page 3:
Deleted “Thus, we have performed a meta-analysis to assess the relationship of KIF1B rs17401966 polymorphism and HCC.”
Added “There were two meta-analyses on the associations between KIF1B rs17401966 polymorphism and HCC. Moreover, a meta-analysis on the associations between KIF1B rs17401966 polymorphism and HBV-related HCC, in which researchers focused on the HBV-related HCC, but not the whole HCC population, were published in the last two years. As new papers published in the last five years, we have performed a updated meta-analysis to assess the relationship of KIF1B rs17401966 polymorphism and HCC.”

Statistical methods section, line 92-95, page 5:
Added “Traditionally, meta-analysis on genetic association studies were based on nearly all genetic models, which not only increase the probability of false-positive rate but also making the explanation of results more confused. According to the Ammarin Thakkinstian’s theory, that is
to say if OR1<OR2<1 and OR1<OR3<1, then a co-dominant model is suggested, we determined co-dominant model is the best genetic model.”

Finally, we appreciate very much for your time in editing our manuscript and the referees for their valuable suggestions and comments. I am looking forward to hearing from your final decision when it is made.