Author's response to reviews

Title: Genotypic Distribution and Hepatic Fibrosis Among HIV/HCV Co-infected Individuals in Southern China: A Retrospective Cross-sectional Study

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Author's response to reviews: see over
Dear BMC Infectious Diseases Editors:

I am pleased to resubmit the MS: 1055366814156401 “Genotypic Distribution and Hepatic Fibrosis Among HIV/HCV Co-infected Individuals in Southern China: A Retrospective Cross-sectional Study.” We thank the reviewer for his comments and believe the changes we made have resulted in a stronger manuscript. We have addressed any concerns as outlined below.

REVIEWER COMMENTS:
MINOR COMPULSORY REVISIONS
1. The authors have improved the manuscript considerably by revising it. However, they do not mention the major limitation of the study, which should be stated clearly as the most important limitation: for an epidemiological study and the scale of the problem in southern china, patient numbers are small. Furthermore, the co-infected patients are not representative of the whole population, because they took part in an interventional study. The selection of the mono-infected patients was done at random and not matched to the co-infected cohort. (minor compulsory revision)

We agree with the reviewer that the sample size as well as unmatched cohort are major limitations to our manuscript. We have edited the limitations section of the discussion to reflect your comments.

Please refer to page 11 of the manuscript for the section copied below:
“Several limitations of this study should be noted. First, our sample size is small compared to the scale of HIV/HCV co-infection in China. All participants came from a single clinic in Guangzhou and co-infected patients were enrolled in an interventional study; as such, participants in this study may not be representative of HCV-infected individuals from the region. However, the HCV/HIV co-infection genotypes we identified in our cohort are consistent with literature; moreover, the subjects we studied came from a broad, province-wide catchment area. Second, there may be significant selection bias present in our analysis due to 1) missing demographic data from the mono-infected cohort and 2) lack of matching between the mono-infected and co-infected cohorts.”