Author’s response to reviews

Title: HBV/HIV co-infection and APOBEC3G polymorphisms in a population from Burkina Faso

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Author’s response to reviews:

Dear Editor

We are pleased to answer the reviewers’ questions about our manuscript submitted for consideration and publication in your journal. We are very grateful to the reviewers for their valuable comments and suggestions to improve our article.
Response to Reviewers:

Reviewer #1: Current study evaluates the associations between three APOBEC3G polymorphisms and HIV-1/HBV co-infection. Authors show, that the rs3522853 minor allele T, rs3522853TT genotype, and rs6001417 GG genotype are protective against HIV-1/HBV co-infection. In addition, GGT haplotype is associated with protection against HIV-1/HBV.

Since the first submission, a lot of changes have been made and the manuscript has been improved. However, multiple issues still need to be addressed.

My comments are following:

1. The APOBEC3G polymorphisms of 100 study subjects with HIV-1 or HBV mono-infections have been added to the paper. However, baseline data of these patients is still missing from Table 1.

The remarks have been taken into account.

2. APOBEC3G polymorphisms of 100 study subjects with HIV-1 or HBV mono-infections should be added to Table 2. For more comprehensive analyses (from Tables 4 and 5). It is not clear, if the data has been corrected for multiple comparisons. This aspect should be clarified in the paper.

Table 2 was revised.

3. The number of HBV positive subjects with detectable viral load should be added to Table 1.

The number of HBV positive subjects with detectable viral load was added to Table 1.

4. In Table 1, the percentages of male and female subjects still do not add up to 100% (20.02 and 79.80).

The line was removed
5. The study population should be described in more detail in the paper, as mentioned in the previous review.

The remark has been taken into account.

6. A sentence stating that all study subjects were HCV negative, should be added to the paper.

All study subjects, tested negative for HCV.

7. The discussion part has not been revised, only new results and one limitation have been added. The Discussion still needs revising.

The heterozygote genotype CG of rs6001417 and the heterozygote genotype AG of rs8177832 were more frequent in HBV mono-infected patients, but were not significant in HIV-1/HBV co-infected patients and in HIV-1 mono-infected patients.

Both heterozygous genotypes may favor HBV infection which in turn is a risk factor for the development of hepatocellular carcinoma (HCC). Indeed, a previous study has suggested that the expression of APOBEC3G is a risk factor for HCC development and survival [35]. Furthermore, heterozygote genotype of a gene could influence a susceptibility to an infection, such as that of TAP1 which may decrease a susceptibility to HPV infection but can increases susceptibility to the development of esophageal cancer among the Kazakh populations [36].

Minor remarks

1. There are still some lack of uniformity issues, that need to be addressed (p-Value in Table 2 and +/- or -/+ in Table 1).

The remarks have been taken into account.

2. In the Materials and methods section in paragraph 1 words "we" and "our" have been used. The rest of the section passive voice has been used.

The sentences were corrected.
3. In Table 1, there are empty rows or issues with line spacing.

This issue was corrected

Reviewer #2: Comments to the Authors,

1) The number of HIV-1 mono-infected patients is much small, which might cover the truth of the relationships of the minor alleles of A3G variants between HIV-1 mono-infected patients and healthy controls.

This statement is correct.

2) No one in the case group was infected with HCV. It is very rare and interesting. If possible, it is better to point out the transmission of HIV-1 and/or HCV, because HCV co-infection is very common in HIV-1-infected intravenous drug users.

HCV infection was not found in our study group, although HCV co-infection is very common in HIV-1-infected intravenous drug users especially in most parts of Europe and USA, but not so much in Sub-Saharan Africa.

3) Again, Table 1 "Mean Age +/- SD" is not in line with the note under the table, and the authors should correct the space sign before and after equal sign in the manuscript.

These remarks have been taken into consideration.

4) The authors found the minor genotype CG of rs6001417 and the minor genotype AG of rs8177832 were more frequent in HBV mono-infected patients, but were not significant in HIV-1/HBV co-infected patients. Whether HIV-1 co-infection has an influence on the associations.

We do not think that HIV co-infection does not affect the host genotype.
5) The authors examined the relationships of the minor alleles of A3G variants among four groups subjects: HIV-1 mono-infection, HBV mono-infection, HIV-1/HBV co-infection and healthy control. It would be interesting to discuss the difference in the minor alleles of A3G variants between mono- and co-infection.

We compared the A3G minor alleles between mono and co-infection and found no significant difference.