Title: Impact of Y181C and/or H221Y Mutation Patterns on HIV-1 Phenotypic Resistance to Available Non-Nucleoside and Nucleoside Inhibitors in China

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Author's response to reviews: see over
Dear Editor:

I, along with my coauthors, would like to ask you to consider the attached manuscript entitled “Impact of Y181C and/or H221Y Mutation Patterns on HIV-1 Phenotypic Resistance to Available Non-Nucleoside and Nucleoside Inhibitors in China” for publication in BMC Infectious Diseases (Section: HIV and co-infections) as an original article.

HIV-1 resistant virus may accumulate resistances to all the available drugs and recent studies have identified novel mutations emerging with different patterns. Here, we focused on defining impact of Y181C and/or H221Y mutation patterns on HIV-1 phenotypic resistance to available non-nucleoside and nucleoside inhibitors in China. Moreover, K101Q was considered as a background mutation emerging with Y181C and/or H221Y. Also, we analysed the interaction between 181 and 221 at the background of K101Q by statistical method. We observed K101Q/Y181C/H221Y mutation patterns significantly increase NVP and EFV resistance. K101Q/Y181C mutation patterns only significantly increase NVP resistance. K101Q/H221Y significantly change the three NRTIs resistance and EFV resistance. The interactions between 181 and 221 were significant in four used agents.

In the work, there are 3 aspects that will be of interest to the general readers. First, we obtained recombinant HIV-1 viruses hiding mutations which were unclarified in HIV Stanford Drug resistance database in different patterns in china. Second, K101Q/H221Y patterns was remarkable. Last, we analysed the interaction between 181 and 221 at the background of K101Q by statistical method.

All of these features from our research will complement the HIV-1 resistance research.

We believe that the findings of this study are relevant to the scope of your journal and will be of interest to its readership.

This manuscript has not been published or presented elsewhere in part or in entirety, and is not under consideration by another journal. All study participants provided informed consent, and the study design was approved by the appropriate ethics review boards. All the authors have approved the manuscript and agree with submission to your esteemed journal. There are no conflicts of interest to declare.

Thank you for your consideration. I look forward to hearing from you.

Sincerely,

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