Author’s response to reviews

Title: Diversity of HIV-1 genotypes and high prevalence of pretreatment drug resistance in newly diagnosed HIV-infected patients in Shanghai, China

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Author’s response to reviews:

Dear Editor,

Thanks for your reply. Please see a detailed response to the comments below. We hope that you find the manuscript improved and acceptable for publication.

With regards,

Hongzhou Lu (on behalf of the authors)

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Response to comments:

1. Part of the title “..high prevalence of pretreatment drug resistance at a potential low level” – it is hard to understand what “a potential low level” is referring to in this context since it is staring with “high”, what does it refer to? Could you please clarify this and change the title accordingly?
Response: The “high prevalence” refer to that the overall prevalence of patients with PDR was high among the newly diagnosed HIV-infected patients; however, “a potential low level” refer to that the degree of resistance to antiretroviral drugs was classified as a potential low-level for about half of the HIV-1 strains with mutation. In order to have a better understanding of study results, we change the title to “Diversity of HIV-1 genotypes and high prevalence of pretreatment drug resistance in newly diagnosed HIV-infected patients in Shanghai, China”.

2. Please submit sequences to Genbank. You may want to consider submitting only a representative subset of you N=317 sequences (as this will require less work), and as discussed in section 2.5 in https://academic.oup.com/ve/article/2/1/vew010/1753512 and references found there. We will allow sufficient time for you to do this. Please also include a short statement in the manuscript if you choose not to submit all sequences.

Response: We have submitted a total of 80 pol sequences as a representative subset of all the sequences to GenBank. The accession numbers were MK573428 - MK573507. We also included a short statement in the manuscript on the reason why we choose not to submit all the sequences. (the method section, line 159-161)

3. Line 95: change to uppercase “C” in China

Response: We changed “c” to uppercase “C” in China. (introduction part, line 93)

In addition, thank you for your additional comments about the recommendation method for HIV genotyping analysis. We would consider using maximum-likelihood phylogenetic method in our future analysis.

Other amendments to the manuscript:

1. In the Funding section, we add another project “Shanghai Municipal Key Clinical Specialty”. (line 337)

2. In the Availability of data and materials section, we included the following statement

“A proportion of sequences is accessible via GenBank (accession numbers, MK573428 - MK573507).” (line 341-342)

3. In the Reference section, we add a reference (no. 11) (line385-387), and revised other reference numbers (11-22) accordingly in the manuscript.