

Review of: "High diversity and transmission dynamics of HIV-1 non-C subtypes in Bangladesh"

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Potential competing interests: No potential competing interests to declare.

The manuscript "High diversity and transmission dynamics of HIV-1 non-C subtypes in Bangladesh" describes the characterization of HIV-1 sequences and transmission in Bangladesh by using phylogenetic analysis. This manuscript provides important data to understand HIV transmission in Bangladesh and where these HIV strains came from. Therefore, this manuscript is worth to be published.

Major points:

The sequence analysis is mostly based on the 400 nt HIV-1 *gag* sequence without the whole genome. Thus, the author does not know if there is a recombination. It is not accurate to conclude that the analyzed sequences are HIV-1 subtype A1, B, or CRFs, such as "Sequence analysis of *gag* gene revealed four subtypes A1, B, D, G and nine CRFs (01_AE, 02_AG, 09_cpx, 10_CD, 15_AE/B, 13_cpx, 14_BG, 22_01_A1 and 25_AGU)." It is better to express like "Sequence analysis of *gag* gene revealed that these sequences are genetically similar to four subtypes A1, B, D, G and nine CRFs (01_AE, 02_AG, 09_cpx, 10_CD, 15_AE/B, 13_cpx, 14_BG, 22_01_A1 and 25_AGU). So the author should be careful to draw a conclusion.

I do not think the title "High diversity and transmission dynamics of HIV-1 non-C subtypes in Bangladesh" is accurate. The manuscript only shows the phylogenetic analysis of HIV-1 sequences in Bangladesh. The transmission dynamics should describe when, where, and how HIV-1 transmitted. But these data are missing in this manuscript.