

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.

Comments to Author:

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

Overview and general recommendation:

In this manuscript, Safiullah Sarker described the presence of HIV-1 group M non-C subtypes and recombinants in Bangladesh, a country with traditional subtype C epidemic. He identified several non-C lineages including 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). Using demographic information from HIV-infected individuals, he traced the origin of these non-C lineages outside Bangladesh.

I have some major concerns that might limit the impact of this manuscript.

First, the manuscript certainly required a load of work that is beyond one person. Why are other people involved were not mentioned among in the author list?

Secondly, the method used to identify the non-C lineages was not clear. I understand that the author first used HIV genotyping tool (<http://www.ncbi.nlm.nih.gov/projects/genotyping/formpage.cgi>) and then subtrees to subtype and trace the origin of the newly identifies sequenced. How were the references used in those trees selected? Was it randomly or not? If it was randomly, then it is not possible to relate the newly identify sequences based on what they cluster in the trees.

Finally, I am afraid these data were already described in the first published manuscript even partially.

Minor comments.

Please add "group M" to HIV-1 in the title.

Add also a line describing the methodology used in the abstract section.

Page 2: "accordingneedles syringes". Please rephrase this sentence.

Same page. "Bangladesh. HIV prevalence is very low in Bangladesh compared to neighboring countries (India, Nepal, Myanmar". Please give the numbers.

Trees should be standardise. The outlier sequence should be the same in all the trees. Make sure to accurately delimitate the different clades in the trees.