

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.

My caveat to this manuscript would be that the data/seqs should be carefully interpreted because the seqs are very small gag genes.

The authors should consider NGS or, at the very least, seq any of the pol genes and/or the env gene.

In the abstract, there is no indication of the fragment length in which part of the gag gene was sequenced. this should be clear from the very outset.

The method section is also missing

what primer seqs were used to amplify.??

"All study participants provided informed, written agreement prior to blood collection, and in the instance of the one child who tested HIV positive, parental consent was also acquired. For those who couldn't read, the summary of the consent form was read, and for those who couldn't sign, a left thumbprint was taken." Authors should clarify what they meant by obtaining consent - were consent obtained for diagnosis purposes? and waived for research? or was it obtained for both research and diagnosis? If the latter, why use leftover samples? If the former, was consent waived?

Authors should consider renaming subtyping to methods because there is no mention of how subtyping was achieved under this sub-heading.

Phylogenetic analyses are flawed, and there is no indication of what was used as a control. for the experiment.

the genes are too small.

"Analysis of only one gene may fail to accurately characterize the recombinant subtypes. Since our findings are based on only the *gag* gene sequence, we might have failed to characterize some recombinant strains accurately." - Perhaps analysing small genes could also be a misrepresentation, and the strains might not be recombinant when you do the whole genome analyses.

The discussion refers to an "African strain" - this is a discriminatory statement that has no place in science - there is no such thing as African strains.

Refs in the discussion were missing & the lit review was insufficient

Our study provides evidence that many migrant workers sampled here were primarily infected with strains while buying sex from female sex workers in Saudi Arabia, however, these strains were genetically very close to African strains. - again no refs

Where is ref"Our study provides evidence that many migrant workers sampled here were primarily infected with strains while buying sex from female sex workers in Saudi Arabia, however, these strains were genetically very close to African strains."

For this paper to be published, I would strongly recommend that more genes should be amplified for further analyses, not only the gag gene.

In summary, the genes are too small, and further amplification is required. The discussion needs more refs and robust arguments. The introduction needs more work; therefore, I recommend this manuscript is not publishable in its current state.