

# 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.

This is an HIV-1 molecular epidemiology study carried out in Bangladesh. It reveals the importance of HIV-1 molecular epidemiological surveillance, especially in countries where migratory activities are high. There is a great HIV-1 genetic diversity, which, as the author reports, can generate implications for the dynamics of transmission and antiretroviral resistance.

However, I have some doubts:

- 1- Why was it chosen to sequence the HIV-1 gag region, since the pol region would be more conserved and with previously described recombination points for the main recombinants described (01AE and 02AG)?
- 2- Please, better detail the process of choosing reference sequences for phylogenetic analyses.
- 3- I suggest performing recombination tests (eg simplot) for confirmation and placing the results as supplementary material.
- 4- Figure 1 lacks bootstrap support for CRF02AG. Maybe, because it is lower than 70. Hence, the need to better evaluate these sequences.
- 5- In figure 5, could it be said that the sequence 04BD067 is a 10BD recombinant, since there is no good bootstrap support?