



## Emergence of a B/F1 HIV Recombinant in the Philippines: a Potentially New Circulating Recombinant Form

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### Background

The Philippines has one of the fastest growing HIV epidemics globally. This was accompanied by a switch from subtype B to CRF01\_AE. With a large population of returning overseas workers, new subtypes are being introduced regularly. Because diagnosis of HIV in the Philippines is usually late, superinfections can occur and may give rise to new circulating recombinant forms (CRFs). We propose a new CRF from the Philippines.

### Methods

Following institutional board approval, treatment-naïve patients from 2 HIV treatment hubs (San Lazaro Hospital and the Philippine General Hospital) were recruited. Blood samples underwent Sanger sequencing of the PR and RT regions and next generation sequencing (NGS) of near-full length genomes. Sequences were analyzed for recombination using the online tool jumping profile Hidden Markov Model (<http://jphmm.gobics.de/>).

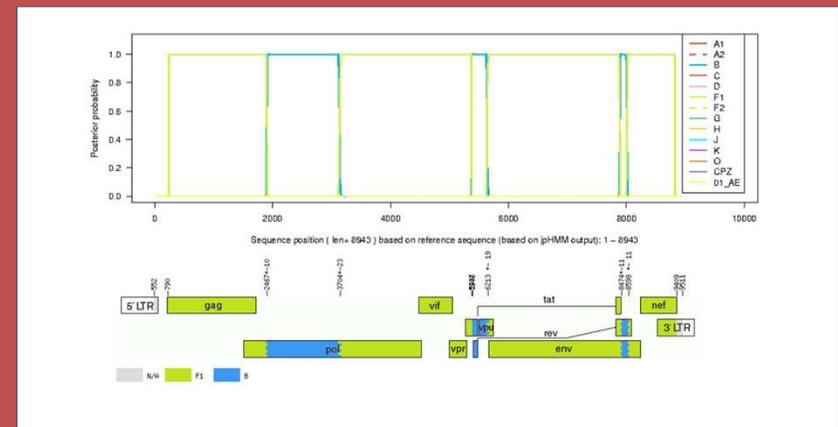
### Results

247 samples underwent Sanger sequencing of the PR and RT regions of the pol gene. Phylogenetic analysis indicated a clustering of 4 of the samples. Further analysis showed all 4 samples had the same breakpoints at nucleotides 2875, 2996, and 3001 (HXB2 numbering). All 4 patients were male, MSM, with a mean age of 28 years old (24-32), and >10 sexual partners. Mean CD4 count was 464 cells/ $\mu$ L and median viral load was  $2.67 \times 10^4$  copies/mL. Two patients had sex with foreigners.

To get a better overall view of subtype composition, we performed NGS using Illumina HiSeq. NGS showed the majority of the genome to be subtype F1 with segments of subtype B inserted in the pol, vpr, and env genes.

A blast analysis of the consensus sequence showed 8932 out of 8943 nucleotides (99%) matched a 1999 sample from Argentina. Phylogenetic analysis of these samples show clustering of the four B/F1 recombinants with some South American sequences. No drug resistance mutations were identified.

Figure 1. New CRF genome showing subtype components..



### Conclusion

Mutation and recombination contribute to the extensive genetic diversity of HIV. Understanding this is important in choosing treatment regimens, developing future vaccines, and pursuing epidemiological investigations. The emergence of a new CRF in the Philippines underlies the importance of conducting routine surveillance for new HIV recombinant forms.

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