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**ANALYSIS OF THE HIV-1 SUBTYPE C ENVELOPE BY BIOLOGICAL METHODS IN
HIV-POSITIVE INDIVIDUALS**

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ABSTRACT

HIV is a member of the Lentivirus genus, which is part of the retrovirus family. Cytopathic or lentiviruses, like HIV, are responsible for sickness in the body by attacking cells, whereas oncogenic or transforming retroviruses are responsible for tumour development. Lentiviruses are enclosed, single-stranded, positive-sense RNA viruses. Once the virus particle enters the host cell, an enzyme called reverse transcriptase (RT) transforms the RNA genome into DNA. Two subtypes of HIV, HIV-1 and HIV-2, have been defined based on serologic features and sequence analysis of molecularly cloned viral genomes. Before being known as LAV and HTLV-III, the virus was known as HFV-1. More infectious and virulent than the original HIV, it is responsible for the great majority of new HIV infections worldwide. There are a lot of people with subtype C in India, China, and South Africa. And there are HIV-1 strains that don't fit into any of these subtypes since their mosaic genomes aren't the same as any of the known ones. In places where numerous different HIV-1 subtypes are circulating, they have been seen. When two different HIV-1 subtypes infect the same cell and undergo recombination, these variations emerge. The recombination happens because the reverse transcriptase enzyme switches templates during reverse transcription. HIV-1 recombination has been documented between and amongst different populations, subtypes, and recombinant strains (Peeters, Toure-Kane, et al. 2003; Lai, Chakrabarti, et al. 2005; Yang, Li, et al. 2005). There are currently 19 identified CRFs, several of which, like CRF01_AE and CRF02_AG, have played critical roles in the global dissemination of specific epidemics.

Keywords: HIV-1 Subtype C Envelope, Biological Methods, HIV-Positive Individuals.