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ANALYSIS OF HIV-1 ENVELOPE GENES IN HIV-POSITIVE INDIVIDUALS

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ABSTRACT

The prevalent subtype of HIV-1 in India, known as clade C, has been the primary cause of new infections globally from the onset of the epidemic, with transmission occurring predominantly through the CCR5 receptor (Cecilia et al., 2000). While there have been reports of other subtypes and recombinant forms (Lakhashe et al., 2008; Lole et al., 1999; Tripathy et al., 2005), the predominant focus of published data on viral subtypes in India indicates that subtype C is responsible for the majority of HIV infections in the country (Mandal et al., 2002; Siddappa et al., 2004). Throughout the extended duration of infection, the HIV-1 env gene experiences significant variation from the env sequence acquired from the transmitted virus (Coetzertai, 2008). When HIV-1 is able to persist in the presence of significant humoral immunological pressure, there is a notable increase in the variety of the virus's envelope protein. Individuals infected with human immunodeficiency virus type 1 (HIV-1) commonly harbour a diverse array of quasispecies, which exhibit distinct genetic characteristics corresponding to various stages of disease progression. Mukhopadhyay et al. The hypothesis posits that these changes contribute to the progression of sickness by either evading the immune system or developing resistance to antiretroviral treatment. Despite the ongoing presence of host-selective pressure, particularly from autologous neutralizing antibodies, the envelope protein (Env) of the human foamy virus (HFV), which engages with cellular receptors and coreceptors during the process of viral entry, remains accessible on the surface of the virus. The ongoing mutational evolution of viral quasispecies poses a challenge to the effective recognition by virus-specific cellular and humoral immune systems.

Keywords: HIV-1 Envelope Genes, HIV-Positive Individuals