Nef Mutations in Long-term Non-progressors from Former Plasma Donors Infected with HIV-1 Subtype B in China

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Objective To study the specific amino acid variation in Nef that may be related to disease progression after infection with HIV-1 subtype B, a predominant strain circulating in China, and to determine whether changes in Nef secondary structure may influence different stages of AIDS development based on the concept that the Nef gene of HIV infection dramatically alters the severity of viral infection and virus replication and disease progression, and that long-term non-progressors (LTNP) of HIV infection are commonly associated with either a deletion of the Nef gene or the defective Nef alleles. Methods The study subjects were divided into LTNP (n=14), LTNP2 (n=16) and slow progressor (SP, n=19) groups for mutational analysis of the Nef sequence. The data were obtained using Bioedit, MEGA, Anthewin and SAS software. Results Residues in Nef TA48/49 and K151 occurred more frequently in the LTNP group while AA48/49 was more frequently observed in the SP group. Of the differences observed in the secondary structure comparison using Nef consensus sequences of three these groups, one was roughly corresponding to the NefLTR mutation site. Conclusion TA48/49, and AA48/49 in the Nef gene might be associated with the different stages of HIV infection, and there may be a link between the Nef secondary structure and the progression of HIV-1 infection.

Key words: HIV-1; Nef; Long-term nonprogressors; Sequence mutations; Secondary structure prediction

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