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

SHU-HUA WANG[#,+], HUI XING[#], XIANG HE[#], FENG-XIA ZHU[+], ZHE-FENG MENG[#], YU-HUA RUAN[#], AND YI-MING SHAO[#,2]

[#]*State Key Laboratory for Infection Diseases Prevention and Control, National Center for AIDS/STD Control and Prevention, Chinese Center for Disease Control and Prevention, Beijing 100050, China;*
[+]*The General Hospital of Civil Aviation Administration of China, Beijing 100025, China*

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 alter 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 $LTNP_1$(*n*=14), $LTNP_2$ (*n*=16) and slow progressor (SP, *n*=19) groups for mutational analysis of the Nef sequence. The data were obtained by using Bioedit, MEGA, Anthewin and SAS software. **Results** Residues in Nef $TA_{48/49}$ and K_{151} occurred more frequently in the LTNP group while $AA_{48/49}$ was more frequently observed in the SP group. Of the differences observed in the secondary structure comparison using Nef consensus sequences of these three groups, one was roughly corresponding to the $Nef_{48/49}$ mutation site. **Conclusion** $TA_{48/49}$, K_{151}, and $AA_{48/49}$ 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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[2]Correspondence should be addressed to Yi-Ming SHAO. Tel: 010-63166184，E-mail: yshao@bbn.cn

Biographical notes of the first authors: Shu-Hua WANG, female, born in 1982, master at China CDC, majoring in pathogen biology; Hui XING, female, born in 1968, associate professor, majoring in molecular epidemiology, molecular evolution, and pathogenic biology of HIV.

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