

Glycoprotein 120 V3 Amino Acid Sequence Analysis and Predicted Coreceptors Usage of HIV-1 Subtype CRF01_AE from Individuals with Different Rates of Disease Progression in the North of Thailand

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Abstract

Background: Understanding sequence characteristics of gp120 V3 envelope and coreceptor usage of HIV-1 infected individuals with different rate of disease progression are important in facilitating the development of AIDS vaccine and treatment.

Objectives: To investigate the genetic variation in V3 of HIV-1 subtype CRF01_AE and predicted coreceptor usage of HIV-1 subtype CRF01_AE infected individuals with different rates of disease progression in the North of Thailand.

Methods: Twenty four progressors (PRs; symptomatic or AIDS within 5 years and CD4+ <200/mm³) and twenty slower progressors (SPs; asymptomatic more than 5 years and CD4+ >350/mm³) recruited from the North of Thailand were studied. The V3 regions were DNA amplified by nested PCR and sequenced directly from the whole blood of HIV-1 infected individuals. Coreceptor usage was predicted using online tool HIV-1 PhenoPred.

Results: The median CD4+ counts of PRs and SPs are 66 and 510/mm³, respectively. The Envelope sequence analysis showed that V3 motif of SPs were dramatically dominated by GPGQ (16/20) but by GPGQ (14/24) and GPGR (11/24) in PRs. . The predicted coreceptor usage demonstrated, 14 viruses used CCR5 (58.3%), 8 used CXCR4 (33.3%) and 2 used both CCR5 and CXCR4 (8.3%) among the 24 PRs. In 20 SPs, 15 viruses used CCR5 (75%), 1 used CXCR4 (5%), and 4 used both CCR5 and CXCR4 (20%).

Conclusions: These findings demonstrated that most of V3 motif of HIV-1 CRF01_AE in SPs are GPGQ and the predicted coreceptor usage is CCR5. However, most viruses in PRs were R5 and X4. Thus, this study may provide valuable information on CCR5 antagonists therapy and AIDS vaccine development.

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