COMPARISON OF V3 ENVELOPE SEQUENCES OF HIV-1 SUB-TYPE CRF01_AE BETWEEN R5 VIRUSES FROM PROGRES-SORS AND R5 VIRUSES FROM SLOWER PROGRESSORS

Chuenchitra T[1], Ruangpung A[1], Dettrairat S[2], Viputtikul K[1], Chaitaveep N[1], Sukwit S[1], Tabprasit S[1], Srisurapanon S[3], Khorianudom S[4], Sutthent R[5], Sirisopana N[1] and Nitayaphan S[1]

[1]Armed Forces Research Institute of Medical Sciences, Bangkok, Thailand [2]Chiang-Mai University, Chiang-Mai, Thailand [3]SrinakharinWirot University, Bangkok, Thailand [4]Ministry of Public Health, Nonthaburi, Thailand [5]Siriraj Hospital, Mahidol University, Bangkok, Thailand

Abstract

Background: Switching HIV-1 coreceptor usage from CCR5 to CXCR4 is correlated with disease progression. However, approximately 50% of HIV-1 infected individuals who progress to AIDS maintain R5 viruses.

Objectives: To compare the V3 envelope sequences of HIV-1 subtype CRF01_AE R5 viruses from slower progressors and R5 viruses from progressors.

Methods: The sequences of the V3 regions of the HIV-1 envelope gene from twenty nine HIV-1 subtype CRF01_AE infected Thais were analyzed. Fourteen are R5 viruses from progressors (PRs; symptomatic or AIDS within 5 years and $CD4^+ < 200$/mm3) and fifteen are R5 viruses from slower progressors (SPs; asymptomatic more than 5 years and $CD4^+ >350$/mm3). The V3 regions were DNA amplified by nested PCR and sequenced directly from the whole blood of HIV-1 infected individuals. Coreceptor usage and cell tropism was predicted using online tool HIV-1 PhenoPred. The amino acid net charge of the V3 region for each sequence at pH 7.0 was determined by using online peptide-property calculator from Innovagen. The V3 region N-linked glycosylation site was assessed by using N-GlycoSite program.

Results: The median $CD4^+$ counts of PRs and SPs are 60 and 545/mm3, respectively. We found that V3 motif of R5 virues from HIV-1 CRF01_AE infected PRs were dramatically dominated by GPGQ (10/14) but by GPGR (4/14). All V3 motif of SPs were GPGQ (15/15). The significant difference of V3 motif sequences between PRs and SPs was found ($p = 0.026$). Both R5 viruses from PRs and SPs were non-syncytium inducing (NSI). Net charge of V3 of both R5 from PRs and SPs were +3. There was no difference in the sequon motif NNT within the V3 loop of both populations.

Conclusions: This study shows that no difference in net charge and N-glycosylation sites of V3 regions of HIV-1 subtype CRF01_AE envelope sequences from R5 viruses of both PRs and SPs. However, V3 motif GPGQ in R5 of SPs was conserved.

Microbicide 2010, Pittsburg, Pennsylvania, USA, 22-25 May 2010, Poster presentation

38th Phramongkutklao Hospital Annual Scientific Meeting, Bangkok, Thailand, 24-26 November 2010, Abstract no. 58, Poster presentation (2nd Award poster presentation contest)