

## Glycoprotein 120 V2 Amino Acid Sequence Analysis 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:** Characteristics of gp120 V2 amino acid sequence envelope of HIV-1 infected individuals with different rate of disease progression might be useful for prognostic marker and facilitating the development of AIDS vaccine and treatment.

**Objectives:** To investigate and compare the genetic variation in V2 of HIV-1 subtype CRF01\_AE from 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/mm<sup>3</sup>) and twenty slower progressors (SPs; asymptomatic more than 5 years and CD4+ >350/mm<sup>3</sup>) recruited from the North of Thailand were studied. The V2 regions were DNA amplified by nested PCR and sequenced directly from the whole blood of HIV-1 infected individuals. Amino acid sequences were compared for length and potential N-linked glycosylation sites using N-Glycosite.

**Results:** V2 regions displayed few conserved amino acids, but frequent deletions or insertions were observed in both PRs and SPs. The mean length of amino acid in V2 regions of PRs was 43.3 (range 38 – 55) and SPs was 42.5 (range 38 – 55). There was no significantly different between the length of V2 regions in PRs and SPs. The mean numbers of potential N-linked glycosylation sites of PRs and SPs were 2.3 (range 0 – 3) and 2.5 (range 0 – 5), respectively. It did not differ significantly between PRs and SPs.

**Conclusions:** The V2 region of HIV-1 subtype CRF01\_AE from both PRs and SPs demonstrated extensive genetic variation. However, there was no significant difference in length and potential N-linked glycosylation sites of V2 regions between PRs and SPs. Thus, the length and potential N-linked glycosylation in V2 region might not be predictive of disease progression.

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