

EVOLUTION OF ENVELOPE SEQUENCES IN HIV-1 SUBTYPE CRF01_AE INFECTED THAI PATIENTS WITH DIFFERENT RATES OF DISEASE PROGRESSION

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ABSTRACT

Background: To understand the relationship between disease progression and amino acid variations of envelope region of HIV-1 subtype CRF01_AE and to determine whether sequence changes on env due to selective immune pressure.

Methods: We obtained and analyzed sequences of the V1-V5 region of the HIV-1 env gene from nine HIV-1 subtype CRF01_AE (E) infected Thais. Five are progressors (PR; follow-up CD4+ cells < 200/mm³ and progression to AIDS) and four are slower progressors (SP; asymptomatic and/or follow-up CD4+ cells > 350/mm³ at the end of follow-up). HIV-1 DNA from two time points per individual were sequenced. They were followed at least 16 months. Selective pressure at the amino acid level was measured by using the synonymous/nonsynonymous base substitutions (ds/dn) ratio and ds/dn ratio of PR and SP were compared between early and late time points.

Results: In V3 region, GPGQ motifs were found in all SP, while V3 region of RP evolved more rapidly. There was deglycosylation of env V3 sequence of HIV-1 subtype CRF01_AE infected progressors, whereas it was conserved in slower progressors. Positive selective pressure operated only on env V3 region in RP and this reflected nonsynonymous substitution accumulation on env V3 region in PR.

Conclusions: These finding showed that the host immune responses may be one selective pressure driving sequence changes in V3 region, where antibodies, cytotoxic T lymphocytes and helper T lymphocytes epitopes are common

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2) 15th International AIDS Conference, Bangkok, Thailand, July 11-16, 2004 [Abstract number TuPeA4392, Poster presentation]