Retrovirology

Poster presentation

Homology of HIV-1 Indian subtype C tat gene with other subtypes correlates with the induction of potent cross clade immune responses following immunization with HIV-1 Indian subtype C mutated and codon optimized tat DNA/MVA vaccine in mice

Huma Qureshi*, VVSP Prasad, Bimal K Das and Pradeep Seth

Address: Department of Microbiology, All India Institute of Medical Sciences, New Delhi, India
* Corresponding author

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Presence of anti-Tat immune responses in HIV infected individual's correlates inversely with the progression of disease. Thus, we focused on the phylogeny & immunogenicity of Indian subtype C tat gene. In this study full length HIV-1 tat gene was amplified and sequenced. Based on sequencing data HIV-1 Indian subtype Ctat gene consensus sequence was derived, mutated & codon optimized. This modified tat gene consensus was used to construct tat DNA/MVA vaccine. Immunogenicity of tat DNA/MVA vaccine was studied in mice and immune responses were evaluated by IFNg ELISpot assay and ELISA. Our tat study sequences depicted maximum homology with HIV-1 subtype C. DNA distances of tat study sequences with consensus sequences of subtype M, C, B&A were 8–10%, 4–6%, 19–21% & 11–18% respectively. Mice immunized with tat DNA construct alone developed potent cross clade T cell & antibodyresponses. Magnitude of these immune responses was increased 3 folds in mice immunized with tat DNA/MVA prime boost regimen. Immunogenic regions of Indian subtype CTat protein localize at amino acid (aa)1–20, aa 16–35, aa 31–50, aa 67–86. Core region(aa 31–50) of Indian subtype CTat protein was found to be immunodominant. In this scenario HIV-1 Indiansubtype Ctat gene appears to be a suitable candidate for future multigene HIV vaccine.