Retrovirology

Poster presentation

Antiretroviral therapy targeting HIV-1 viral infectivity factor; *in silico* approach

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Background

The HIV-1 viral infectivity factor (VIF) binds to the host defense factor human APOBEC3G (hA3G) and prevents its assembly with viral particles and mediates its elimination. VIF binds Elongin B/C complex of the ubiquitination machinery and it also forms multimers. Knowledge of the surface accessibility by solvents and other proteins and antigenicity is important in designing B and T cell epitopes that could be used as antiretroviral drugs and vaccine to block the activity of Vif. Inactivation of Vif supports the role of hA3G in inhibiting in vivo replication of the virus.

Methods

The VIF protein sequence was downloaded from NCBI database and blast search was performed against Uniprot and Swissprot databases to get a protein sequence with high expected value (e-value). The protein was analyzed for the following surface properties; Emini surface accessibility by solvents and other proteins, Kolaskar antigenicity and B and T cell epitopes for 42 MHC class I alleles. Online bioinformatics tools available in immuneepitope.org database were used.

Results

VIF protein sequence with e-value of 1e-114 was found to be the best. Four peptides two of nine and the rest 11 and 19 amino acids were shown to have good Emini surface accessibility prediction scores. 11 peptides were found to be antigenic with two of these having the SOCS homology box (SLQYLAL) and the dimerization box (PPLP). 18 T cell epitopes had significant binding to MHC class 1 alleles with IC50 < 20. Top three epitopes had dimerization domain and IC50 value < 5.2. The rest had both dimerization and SOCS homology box residues.

Conclusion

A synthetic peptide with Vif specific amino acids of these sites could induce anti-Vif neutralizing antibodies and stimulate B and T cells. Our In silico analysis suggests that HIV-1 Vif protein surface features can be used as potential anti-HIV drug and vaccine target.