



Original Article

Peptide vaccine prediction against Hepatitis-C virus causing hepatocellular cancer using immunoinformatics

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Abstract: The prime objective of this study is to predict peptide HCV that might be a part of combination therapy. We used bioinformatics to identify the T cell and B cell epitopes having high antigenicity from the envelope protein of HCV. For the analysis, HLA-A1, HLA-A*01:01, HLA-A3, HLA-B*27:01, HLA-B8, HLA-Cw*0702, HLA-DRB1*1101, HLA-DRB1*03:01, DRB1*04:01 were selected for the prediction of T cell epitopes. Consequently, potent protein were predicted *i.e.*, ALYVGMCGA, VNYRNVSGIY, GAAVYVGMCGA. Likewise, T cell peptide epitopes having potential to bind with HLA-A1 were identified *i.e.*, AWAKVVVIL, VRYVGATTA, VAPTLAVRY, AVKWEYVVL and WEYVLLFL. Further, T cell epitope capable of binding with HLA-B8 molecule was identified *i.e.*, VAIIMVMFS, LVLAQVMRI, VVASATLCS, LLADARVCA, IQLINTNGS, LQLINTNGS and VRYVGATTA. These are potential candidates for design of vaccine.

Keywords: Hepatitis C virus; Peptide Epitopes; Vaccine prediction

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1. Introduction