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Immunoinformatics predication and in silico modeling of epitope-based peptide vaccine against virulent Newcastle disease viruses

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Newcastle disease virus (NDV) is negative sense single stranded RNA belongs to the *Avulavirus* genus of the *Paramyxoviridae* family which can be transmitted by inhalation or ingestion. Birds infected shed these viruses in feces as well as respiratory secretions. The aim of this study is to analyze fusion (F) protein of all virulent Newcastle strains reported in NCBI database using *in silico* approaches to select all possible epitopes that can be used as a therapeutic peptide vaccine. A total of 56 virulent NDV fusion protein variants retrieved from NCBI database. The conserved regions were introduced into IEDB analysis resource to predict B and T cell epitopes, as well as predicting the binding affinity of the conserved epitopes with BF2 21:01 from the predominantly expressed chicken MHC I molecule. Epitopes with high scores in both B and T cell epitopes predicting tools were suggested. Peptide vaccine against virulent NDV is strongly supersedes the conventional vaccines, as it is designed to cover variant virulent mutated strains which will reduce the recurrent outbreaks and their huge accompanied economical loss to a minimum.

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