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Immunoinformatic approach for epitope-based peptide vaccine against Lagos rabies virus glycoprotein G

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Background & Aim: Lagos rabies virus belongs to Lyssavirus genus responsible for meningoencephalomyelitis in mammals that affect millions of people around the world and causes thousands of human deaths every year, to the best of our knowledge there is no peptide vaccine designed for Lagos rabies virus. The resulting peptide vaccine is expected to be more immunogenic and less allergic than conventional biochemical vaccines. The aim of this study was to design an in silco peptide vaccine for Lagos rabies virus using immunoinformatic tools.

Methods & Materials: Sequences of glycoprotein G of Lagos rabies virus was retrieved from NCBI, the retrieved sequences were then treated using different immunoinformatic tools for B cell to find out the most conserved, surface and antigenic epitopes, and for T cell to find conserved peptides and to test their binding affinity to different MHC1 and MHC11 alleles. Then population coverage analysis and homology modeling was performed for most promising epitopes to show their structural positions in glycoprotein G.

Results & Conclusion: B cell tests were conducted for BepiPred with 22 conserved epitopes, Emini surface accessibility prediction with 12 conserved surface epitopes and Kolaskar and Tongaonkar antigenicity test with only three conserved epitopes being antigenic. 23 conserved epitopes were interacted with different MHC-1 alleles with (IC50) ≤500 while 39 conserved epitopes interacted with MHC-II alleles with IC50≤ 1000. Among all the tested epitopes for world population coverage the epitope FVGYVTTTF binding to both MHC1 and MHC11 alleles was 97.30% and it was found to bind 13 different alleles that indicate strong potential to formulate peptide vaccine for Lagos rabies virus.

Biography

Omar Hashim Ahmed is lecturer at University of Gazira, faculty of pharmacy, pharmacology department, with considerable teaching and research experience. Interested research areas are Immunoinformatics(Insilco designing and *in-vivo* evaluation of peptide vaccines), translation bioinformatics and pharmacogenitics with many published papers in high impact journals and contributing as speaker in many local and international conferences. Eager for gaining new knowledge, connections and collaborations with researchers having common research interests around the globe.

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