VAC_05 - Design of a global multiepitope orthohantavirus vaccine: An Immunoinformatics Approach

Silvia da Silva Fontes[1]; Fernando de Paiva Conte[1]; Jorlan Fernandes[1]; Renata Carvalho de Oliveira[1]; Rodrigo Nunes Rodrigues da Silva[1].
[1]Fiocruz/IOC

Introduction: Hantaviruses, responsible for Hemorrhagic Fever with Renal Syndrome (HFRS) in Europe and Asia, and Hantavirus Cardiopulmonary Syndrome (HCPS) in the Americas, pose a significant public health challenge. Transmission occurs through inhalation of aerosols from infected rodent droppings, yet no FDA- approved vaccine exists. The glycoprotein (GP) on the virion surface, crucial for host invasion and highly immunogenic, is a primary vaccine target. However, GP variability among hantavirus species presents a significant obstacle to vaccine development. Epitope-based vaccines offer a promising route to a universal hantavirus vaccine.

Objectives: The objective is to leverage immunoinformatics to design a universal multi-epitope vaccine that could be effective worldwide against both HFRS and HCPS.

Methodology: Using eight algorithms, GPs of SEOV and PUUV (HFRS) and SNV and ANDV (HCPS) were analyzed to identify B cell epitopes. T cell epitopes were identified using the TepiTool algorithm. These epitopes underwent allergenicity, toxicity, and hemotoxicity evaluations, along with conservation analysis and population coverage assessment using the IEDB server. Two vaccine designs were then proposed, incorporating different adjuvants (β-defensin and 50S ribosomal protein L7/L12), and analyzed for physicochemical properties, antigenicity, and allergenicity. Tertiary structures were predicted, and TL4 affinity was assessed through molecular docking.

Results: Eleven sequences combining B and T cell epitopes, found to be non-allergenic, non-toxic, and highly conserved among HFRS and HCPS hantaviruses, were selected for the vaccine composition. Predicted to cover 100% of the global population, both vaccine designs showed promise in antigenicity, stability, and solubility. Molecular docking demonstrated stable structures with a higher affinity for β-defensin. Immunization simulations indicated an effective immune response and memory cell persistence over a year.

Conclusion: This approach presents potential multiepitope vaccine candidates against hantavirus infection diseases, demonstrating the utility of immunoinformatics in vaccine design.

Keywords: Immunotherapy; Bioinformatics; Hantavirus; Epitopes