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5th Annual Conference on TOXICOLOGY AND ENVIRONMENTAL HEALTH

August 05-06, 2024 | Paris, France

Subtractive proteomics and reverse-vaccinology approaches for novel drug target identification and chimeric vaccine development against Bartonella henselae strain Houston-1

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Bartonella henselae is a Gram-negative bacterium causing a variety of clinical symptoms, ranging from cat-scratch disease to severe systemic infections, and it is primarily transmitted by infected fleas. Its status as an emerging zoonotic pathogen and its capacity to persist within host erythrocytes and endothelial cells emphasize its clinical significance. Despite progress in understanding its pathogenesis, limited knowledge exists about the virulence factors and regulatory mechanisms specific to the B. henselae strain Houston-1. Exploring these aspects is crucial for targeted therapeutic strategies against this versatile pathogen. Using reverse-vaccinology-based subtractive proteomics, this research aimed to identify the most antigenic proteins for formulating a multi-epitope vaccine against the B. henselae strain Houston-1. One crucial virulent and antigenic protein, the PAS domain-containing sensor histidine kinase protein, was identified. Subsequently, the identification of B-cell and T-cell epitopes for the specified protein was carried out and the evaluated epitopes were checked for their antigenicity, allergenicity, solubility, MHC binding capability, and toxicity. The filtered epitopes were merged using linkers and an adjuvant to create a multiepitope vaccine construct. The structure was then refined, with 92.3% of amino acids falling within the allowed regions. Docking of the human receptor (TLR4) with the vaccine construct was performed and demonstrated a binding energy of −1047.2 Kcal/mol with more interactions. Molecular dynamic simulations confirmed the stability of this docked complex, emphasizing the conformation and interactions between the molecules. Further experimental validation is necessary to evaluate its effectiveness against B. henselae.

Biography

Sudais Rahman, a dedicated researcher at Abdul Wali Khan University, propelled by a fervent passion for impactful contributions in proteomics, vaccine development, and drug design. His studies in Mardan, Pakistan, empower me to explore innovative approaches to address pressing global health challenges. With extensive hands-on experience as a Research Assistant, Intern at a Biomedical Research Institute, Teaching Assistant in Molecular Biology, and Administrative Intern at a Hospital Research Center.