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In silico design of a hexavalent protein, a potential candidate vaccine against Staphylococcus aureus E L R ¿ O P U H O D W H G L Q I H F W L R Q

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Staphylococcus aureus possessing a pool of virulence factors is responsible for the signi cant and increasing number of hospital and community-acquired infections worldwide. Developing a potential vaccine to prevent these life-threatening and drug-resistant infections would have many advantageous impacts on global healthiness. In this study, considering the bio lm mode of growth and polymicrobial nature of S. aureus and Candida albicans infections, a multivalent protein vaccine was designed. In the rst phase, the prediction of putative antigenic targets of S. aureus and C. albicans was conducted based on data mining and bioinformatic characterization of their proteins. Various properties of the proteins were evaluated such as subcellular localization, hydrophilicity, repeat containing modules, beta turns, surface accessibility and number of antigenic determinants. Eventually, 6 proteins AlS, ClfA FtmB, SdrE, Spa and Bap were selected. e second phase included various immunoinformatics analyses on their sequences leadin to design of a novel sub-unit hexavalent candidate vaccine. Several potential T cell and B cell epitopes are present in this synthet construct and it is expected to strongly induce IFN-gamma production. In conclusion, the amino acid sequence introduced here is expected to enhance T cell-mediated and humoral responses against S. aureus bio lm-related infections to clear bio lm communities of S. aureus and intracellular colonies of pathogen as well as planktonic cells and thus reducing colonization and persistence.

Biography

Maryam Shahbazi has completed her PhD program in Bacteriology from Shiraz University in 2016 with the thesis entitled “Design and Synthesis of a Protein Candidate Vaccine against S. aureus % L R ¿ O P 5 H O D W H G , Q I H F W L R Q V ´ 6 K H L V D 5 H V H D U F K H U Q G K D V S X E O L V K H G D U W L F O H V L Q

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