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Identification of antigenic properties of Acinetobacter baumannii proteins as novel putative vaccine candidates using reverse vaccinology approach

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Multidrug-resistant *Acinetobacter baumannii* (*A.baumannii*) infections are becoming more prevalent all over the world. As a cost-effective and preventative method, vaccination seems to be required against this bacterium. In the present study, subtractive proteomics along with reverse vaccinology approaches was used to predict suitable therapeutics against *A.baumannii.* Using the Vaxign online tool, we studied over 35 genomes of A.baumannii strains and chose outer membrane and secreted proteins of *A.baumannii* 1656- 2 as possible vaccine candidates. Then, investigations were performed on the immunogenicity, antigenic characteristics, physicochemical properties, B-cell and MHC class I, and MHC class II molecules epitope densities of proteins. After optimizing the codon of the proteins, the pcDNA3.1(+) expression construct was designed and the immunogenicity, allergenicity, and physicochemical properties of the vaccine construct were predicted.

Hcp and OmpC proteins were predicted as extracellular and outer membrane proteins, respectively. These proteins interact with 10 other proteins to form a network of protein interactions with virulence properties. Immunoassays of Hcp and OmpC proteins showed antigenicity of 0.88 and 0.79, respectively. These proteins have 5 structural cell epitope points and 5 linear B epitope points. They are also able to bind to different HLA alleles of MCH- class I / class II as selected immunogenic proteins and designed non-allergenic structures with Solubility of 0.650 and immunogenicity score of 0.91. The results of "In-Silico" of this study indicate high specificity and the development of a significant humoral and cellular immune response. It can be concluded that the Hcp and OmpC dual vaccine construct is one of the promising candidates against *A.baumannii.* The findings of this "In-Silico" study show excellent specificity and the emergence of a substantial humoral and cellular immune response. This is a computer-based study that needs to be tested *in vitro* and *in vivo* to corroborate the conclusions of the vaccine design procedures.

Biography

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