

A NOVEL IMMUNOINFORMATICS METHOD FOR SCREENING AND IDENTIFYING SUB MUCOSAL VACCINE CANDIDATES

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Several problems were reported with conventional, sub-subunit, inactivated, recombinant and sub-mucosal vaccines. Developing conventional vaccines is labour intensive, expensive and time-consuming. Identifying the most suitable antigens to stimulate the immune system is the limitation with subunit vaccines. The inability to induce cellular immunity is the drawback related to inactivated vaccines and recombinant vaccines. Identifying antibody response for gastric pathogen is the problem with sub-mucosal vaccines. The problem interconnected with specificity of the vaccine is genetic diversity of the pathogen and ethnicity of the patient's population diversity. Therefore, identifying a suitable antigen as a vaccine candidate which can stimulate the immune system, induce cellular immunity, sub-mucosal response against diverse pathogen and population is a challenging task. In this connection, a novel immuno-informatics method is proposed against the above known problems by minimizing the cost of both human and financial resources, without losing efficiency and time. The method includes retrieving the coding regions of the genome and translating them to their respective proteome. Then, the proteome is screened for immuno-pathogenic factors which are non-homologous, non-allergenic, and with helices ≤ 3 . Further, epitopes which are conserved, non-homologous, elicit both T-cell and B-cell response, interact with MHC alleles and IgA antibody, and elicit response in wide range of ethnic populations are identified as suitable antigens. The above approach is a comprehensive immuno-informatics method that enables rapid identification of sub mucosal vaccine candidates with immense potential for therapeutic intervention of pathogens.

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