

عنوان مقاله:

In silico identification and validation of OspA 3D structure and its topology as a candidate for lyme disease vaccine

محل انتشار:

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خلاصه مقاله:

Borrelia burgdorferi is a bacterial species of the spirochete class of the genus *Borrelia* and is the predominant causative agent of Lyme disease that is a multi-system inflammatory disease involving the skin, joints, heart, and nervous system. Recently, however, it was demonstrated that purified OspA lipoprotein (L-OspA) is profoundly more immunogenic than nonlipid acylated OspA (NL-OspA), even in the absence of adjuvant. The protective role of antibodies to *B. burgdorferi* has been explored in animal models of Lyme disease. Findings indicated that antibodies against OspA were protective, making this antigen a likely candidate for a vaccine. Early clinical trials demonstrated that recombinant OspA was immunogenic and well tolerated, even in subjects with a history of Lyme disease. A dose-ranging study showed that as compared with doses of 1, 5, and 10 μg , a dose of 30 μg of the OspA vaccine elicited an optimal antibody response without causing an increased rate of symptomatic reactions. Evidence suggests that OspA protein is a useful antigen for inclusion in an effective vaccine, hence the identification of its structure is very important. The present study was designed to in silico resolving the major obstacles in the control or in prevention of the lyme disease. We exploited bioinformatic tools to better understanding and characterizing the OspA structure

کلمات کلیدی:

Borrelia burgdorferi, OspA, Bioinformatic

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