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خلاصه مقاله:

Background: The arboviruses Zika virus (ZIKV) is a pathogen that threatens human health. Scientists have warned that a single mutation in the mosquito-borne ZIKV could spark another major outbreak of the disease in humans. Therefore, designing a suitable vaccine for this virus seems necessary. This study aimed to predict the protective epitopes of envelope protein from the Zika virus with bioinformatics methods for multi-epitope vaccine development. Materials and Methods: Computational studies including the identification of potential B-cell and T-cell epitopes were used. For generating a multi-epitopic vaccine construct (MEVC), selected epitopes are connected by suitable linkers. To enhance protein immunogenicity, Maltosebound protein was added to the MEVC after the prediction and refinement of the ۳D structure of the designed vaccine. The binding mode of the MEVC with toll-like receptor was investigated by molecular docking technique. Finally, molecular dynamics and in silico cloning were performed for the designed vaccine. Results: This study showed that this recombinant vaccine is nontoxic, nonallergenic, and thermostable and elicits immune responses against the Zika virus. Conclusion: The computational data suggest that the MEVC has appropriate characteristics and a high-quality structure.

کلمات کلیدی:

In-silico, Zika, multi-epitopic-vaccine-construct, Virus, Immunoinformatics, Vaccine