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Identification of vaccine target through CTL epitope prediction and structure modeling of capsid protein from dengue virus 3 of Indian isolates

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Dengue virus is a member of the family *Flaviviridae* and a positive-sense RNA virus. Epidemics caused by the 4 DENV serotypes have emerged as major public health problems in tropical and subtropical regions over the past 20 years. The World Health Organization (WHO) estimates that 50 million cases of dengue occur every year, and 500,000 (1%) require hospitalization. The capsid (C) protein of dengue virus is necessary for specific encapsidation of the RNA genome, but little structural information on the C protein is available. No dengue vaccine is currently available, and dengue control relies solely on vector control. In present investigation, attempts have been made to study epitope prediction, molecular modeling and structural aspect of capsid protein. A 3-dimensional model (3D) was developed for the capsid protein of the dengue virus, a major vector of Dengue Fever. A homology modeling method was used for the prediction of the structure. For the modeling, capsid proteins were obtained by ITASSER, and mGenTHERADER, by using high-resolution X-ray crystallography structure as template. By comparing the template protein a rough model was constructed for the target protein using MODELLER, a program for comparative modelling. Results will be discussed during presentation. The predicted 3-D model may be further used in characterizing the protein in wet laboratory.

Biography

A. G. Ingale obtained Ph.D. in Biotechnology from Sant Gadge Baba Amravati University, Amravati (India). He was the founder Head, Department of Biotechnology, Dr. Babasahed Ambedkar Marathwada University, Aurangabad (MS) India. He is the president of Society for Biotechnology and Bioinformatics, India. He is also the editor in-chief of the Journal of Biotechnology and Bioinformatics (JBB) and International Journal of Modern Biotechnology. He has received the award as a Fellow of Society of Sciences (FSSc), Dumka. His primary field is immunology with research emphasis on CD antigens and the structure-function prediction using Bioinformatics approach. He has recently entered the developing field of lectin biosensor and glyco nanobiotechnology research. In Genomics research area he has been working on constructions of transgenic okra against pest (*Lipidopteron*) and pigeon pea against bollworm. In proteomics research area he is working on proteomics of lectin and other plant and microbial proteins. Finally, His main research area is bioinformatics. In this, he has developed a database of CD markers and toxin database is on completion. He has published several research papers in national and international journal of repute. He has submitted protein and nucleotide sequences on NCBI and viral protein models are being submitted in PDB database. Currently, he is holding Major research projects as a Principal Investigator and Head Department of Biotechnology, North Maharashtra University, Jalgaon (MS) India. Recently he has been awarded by MIF fellowship by Matsuame International foundation, Japan.

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