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Molecular Dynamics Study of Dengue Pre-Fusion Conformation

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Dengue is caused by one of four related viruses. Even though few vaccines are already available and more are in the stage of the clinical trial, all of them have their drawbacks. Therefore, developing a vaccine against the dengue virus is among the top priorities in the field. The main objective of this research is to study the dynamics of the pre-fusion conformation of the dengue virus envelope protein to design a vaccine candidate using computational methods. For that, the changes in the dengue virus pre-fusion envelope protein were investigated using Molecular Dynamics simulations. The present study focused on the dengue virus envelope protein, serotype 2 (PDB ID: 10KE), and serotype 3 (PDB ID: 1UZG). RMSF, RMSD, experimental B-factor, and secondary structure profile analyses were carried out using NAMD and VMD software packages to investigate the dynamics of the pre-fusion conformation. Mean RMSD, mean RMSF, and B-factor were higher in serotype 3 when compared to serotype 2. Domain Ⅲ displayed higher fluctuations in RMSD when compared to other domains. RMSF of the side chain displayed higher values in the positions where glycans are present. The secondary structure profile revealed that both serotypes contain a higher percentage of β sheets. Our preliminary data indicated that the structural stability of serotype 2 is relatively higher compared to serotype 3. Additionally, the lowest structural deviation was observed within domain Ⅱ of the dengue virus. The observations obtained from this study lays the foundation for the development of a vaccine against the dengue virus.

Keywords: *dengue, molecular dynamic simulations, pre-fusion conformation*