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**Analysis of dengue virus capsid protein for phylogeny and antigenicity:
A computer based approach**

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Capsid (C), the smallest structural protein of Dengue virus (DENV) has been proven to elicit antibody responses during natural infections. However, the detailed antigenic structure of C protein is yet to be revealed. This study aims to characterize the C protein for its antigenicity by available *in-silico* tools, considering their high speed, accuracy and low cost. The C protein sequences of 50 strains of each of the four DENV serotypes with temporal differences and geographical variation were used for the study. The level of conservation was analyzed by IEDB analysis tools. Accordingly, the C protein sequence seems to be highly conserved within each serotype (>80%) with a considerably high conservancy across the serotypes (52%). The highest conservancy (94.7%) was observed within DENV3. This was also evident in the phylogenetic diagram, with lower sub grouping inside the cluster of DENV3. The highest sequence similarity was observed between DENV1 and DENV3 resulting in a close relationship between those two serotypes in the phylogenetic analysis. Sequence analysis showed the two terminal regions (amino and carboxyl) of C protein to be highly hydrophilic, accessible and flexible. These observations are further strengthened by structural analysis depicting two termini as potential sites of B- cell epitopes, which could have important properties for diagnosis and therapeutics of DENV. This subjective statement is to be verified through laboratory experiment during the remaining part of this research study.

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