

## B-cell Epitope Prediction of Dengue Virus Envelope Protein Using BCPRED Prediction Tools

Nurul Ain Abd Jalil<sup>a</sup>, Roziah Kambol<sup>a\*</sup>

**Background:** Dengue virus (DENV) poses a major global health threat, especially in tropical regions, due to its mosquito-borne transmission and the absence of specific antiviral treatments. The existence of four antigenically distinct serotypes (DENV-1 to DENV-4) complicates vaccine development. This study aimed to identify conserved linear B-cell epitopes within the DENV envelope (E) protein using bioinformatics approaches, including epitope prediction and conservancy analysis, to support vaccine and diagnostic development.

**Methods:** Envelope protein sequences of DENV-1 to DENV-4 were retrieved from NCBI and ViPR databases, covering six Southeast Asian countries: Malaysia, Singapore, Indonesia, Thailand, Vietnam, and the Philippines. B-cell epitopes were predicted using the BCPRED tool with thresholds ranging from 0.5 to 0.9. Conservancy analysis was conducted using the IEDB Epitope Conservancy tool, applying a 100% sequence identity threshold. WebLogo 3.0 was used to visualize conserved amino acid residues across predicted epitopes.

**Results:** A total of 48 sequences were analyzed. BCPRED successfully predicted 48, 56, 51, and 71 linear B-cell epitopes for DENV-1 to DENV-4, respectively. Most epitopes had high confidence scores ( $\geq 0.990$ ). Highly conserved epitopes included “LSWFKKGSSIGKMF EATARG” and “AKISNTTDSRCPTQGEATL” in DENV-1, “VEPGQLKLSWFKKGSSIGQM” and “KLTNTTTASRCPTQGEPSLN” in DENV-2, “GDKALKINWYKKGSSIGKMF” in DENV-3, and “ITTATRCPTQGEPYLKEEQD” and “NTNSVTNIELEPPFGDSYIV” in DENV-4. Conservancy analysis confirmed 100% identity for 24 DENV-1, 35 DENV-2, 41 DENV-3, and 6 DENV-4 epitopes across multiple countries. WebLogo visualizations showed dominant letters at conserved positions, indicating minimal sequence variability.

**Conclusion:** In conclusion, this study successfully identified conserved, high-confidence B-cell epitopes across DENV serotypes using BCPRED and validated their conservancy through IEDB tools and WebLogo. These findings support the potential of predicted epitopes as stable targets for vaccine and diagnostic development. Future work should integrate T-cell epitope prediction, population coverage analysis, and experimental validation for practical application.

**Keywords:** Dengue Virus (DENV), B Cell Epitope Prediction, IEDB, NCBI, ViPR

\*Correspondence: [rozhiah1259@uitm.edu.my](mailto:rozhiah1259@uitm.edu.my)

<sup>a</sup> School of Biology, Faculty of Applied Sciences, Universiti Teknologi MARA, Shah Alam, Malaysia