

MD627 893 Seminar in Medical Microbiology

Department of Microbiology, Faculty of Medicine, Khon Kaen University

Seminar title: Proteomic profiling of dengue fever

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Abstract

Dengue virus (DENV) infection is a major mosquito-borne disease worldwide and its pathogenesis is strongly influenced by host immune responses. However, the mechanisms underlying disease progression and severity remain incompletely understood. This seminar report summarizes findings from two proteomic studies investigating changes in host protein expression during different phases of dengue infection.

In the first study, Garishah et al. (2023) performed longitudinal proteomic profiling using a multiplex proximity extension assay (PEA) to analyze inflammatory proteins in plasma samples from dengue patients during the acute and convalescent phases to measure 368 inflammatory proteins in plasma samples. The study identified numerous differentially expressed proteins associated with interferon signaling, cytokine activity, and immune regulation, which were also linked to endothelial dysfunction and vascular permeability.

In the second study, Choudhury et al. (2024) using mass-spectrometry-based analysis to examine plasma samples from dengue patients at different phases of infection and healthy controls. The results revealed differential expression of multiple proteins involved in viral replication, immune regulation, lipid metabolism, and endothelial function that may contribute to severe dengue.

Overall, these findings highlight the importance of proteomic analysis in understanding host responses during dengue infection and identifying potential biomarkers for disease progression.

References

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