MD627 893 Seminar in Medical Microbiology

Title: Molecular epidemiology of Dengue in Thailand and Laos

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Abstract

Dengue fever is a mosquito-borne viral disease that causes a major public health problem in tropical and subtropical regions. In recent years, outbreaks have become more frequent and larger with spread into non-epidemic areas (1). Limited vaccine availability together with climate change and rapid urbanization, has further increased the risk of dengue transmission. Under these conditions, effective outbreak prevention and early prediction remain the most practical and impactful approaches for dengue control.

In the first study, Nyathi et al. (2023) investigated the molecular epidemiology and evolutionary characteristics of DENV-2 circulating in Kenya and East Africa using near- and whole-genome sequences generated in the study and retrieved from GenBank. Phylogenetic and phylodynamic analyses revealed the co-circulation of multiple DENV-2 lineages, with evidence of repeated introductions followed by local expansion and regional diversification. Most East African strains were closely related to Asian lineages indicating Southeast Asia as a likely source of viral introduction (2).

In the second study, Chem et al. (2024) examined the molecular epidemiology of dengue virus in Malaysia based on envelope gene sequences. The results revealed high genetic diversity with multiple co-circulating lineages and frequent lineage replacement reflecting sustained endemic transmission and episodic introductions. Phylogeographic analyses indicated extensive viral dispersal within South and East Asia and across Malaysian states, particularly highly urbanized and populated cities as major hub of DENV emergence and spread in Malaysia (3).

Prevention of viral spread and early outbreak prediction based on molecular epidemiological and evolutionary analyses are key strategies for dengue control. Integrating viral genomic data with spatiotemporal surveillance provides critical insights into transmission pathways, lineage replacement, and cryptic circulation, thereby improving outbreak preparedness and public health response.

References

1. WHO, 2024. Dengue - Global situation [Internet]. [cited 2026 Jan 28]. Available from: https://www.who.int/emergencies/disease-outbreak-news/item/2024-DON518

2. Nyathi S, Rezende IM, Walter KS, Thongsripong P, Mutuku F, Ndenga B, et al. Molecular epidemiology and evolutionary characteristics of dengue virus 2 in East Africa. Nat Commun. 2024 Sep 7;15(1):7832.

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