

Genetic variation among Dengue Virus that possibly correlate with pathogenesis

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Abstrak

Penyakit dengue masih merupakan masalah kesehatan penting di sebagian besar Negara tropis dan subtropis. Dalam dua dekade terakhir terjadi lonjakan drastis baik jumlah kasus maupun daerah endemik di samping peningkatan keparahan penyakit (DHF/DSS). Meski telah dipelajari secara intensif, belum dipahami benar bagaimana mekanisme infeksi dengue berkembang menjadi DHF/DSS. Sejauh ini diketahui baik faktor inang maupun virulensi virus terlibat dalam menentukan keparahan penyakit. Studi-studi terbaru melaporkan perbedaan struktural genom di antara virus dengue yang memberikan manifestasi klinis berbeda. Perbedaan ini kemungkinan berhubungan dengan patogenesis penyakit. (Med J Indones 2004; 13: 190-4)

Dengue disease are reemerging disease and major health concern in tropical and subtropical regions because of the increasing number of patients, expanding endemic areas and increased occurrence of severe clinical manifestation (DHF/DSS) in the last two decades. Despite extensive studies, it is not fully elucidated mechanism by which dengue infection progress to DHF/DSS. Information obtained so far indicates that both host-related factor and virus virulence are involved. Recent studies have shown several structural differences of dengue virus genome between those associated with DF only and those with the potential to cause DHF. That genome differences might be correlated with pathogenesis. (Med J Indones 2004; 13: 190-4)