

## ABSTRAK

Virus dengue memiliki empat serotipe yang berbeda dan memiliki masalah kesehatan masyarakat yang cukup serius di daerah tropis dan subtropis. Infeksi dengue dapat menyebabkan spektrum manifestasi klinis yang luas. Faktor virus yang memainkan peran penting dalam patogenesis dengue adalah NS1. Mutasi gen NS1 virus dengue berpengaruh terhadap virulensinya. Informasi mengenai virus dengue di Kota Samarinda belum banyak diteliti. Tujuan penelitian ini menganalisis variasi serotipe DENV pada kejadian Demam Berdarah Dengue, mengetahui variasi distribusi geografi berbagai serotipe dan mengetahui variasi genetik pada nukleotida yang mengkode gen NS1 virus dengue di Kota Samarinda, Kalimantan Timur. Sampel penelitian adalah sampel darah pasien yang terinfeksi Demam Berdarah di Samarinda, Kalimantan Timur. Amplifikasi gen NS1 menggunakan metode *one step* RT PCR. Analisis mutasi nukleotida NS1 menggunakan *software Mega 11* dan *BioEdit 7.2*. Analisis peta menggunakan *ArcMap 10.8*. Terdapat variasi serotipe DENV saat infeksi dengue di Samarinda, dengan serotipe terbanyak adalah DENV3. Distribusi geografi berbagai serotipe DENV terdapat di 9 kecamatan, dengan pola penyebaran mengelompok. Hasil penelitian sebanyak 10 sampel dapat teramplifikasi dan didapatkan sekuensing gen NS1. Perbedaan komposisi gen NS1 pada rentang 0-10%. Hasil penyelarasan menunjukkan adanya perbedaan sekuens gen NS1 dengan sekuens rujukan.

**Kata kunci:** dengue virus; mutasi; gen NS1; distribusi

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The dengue virus has four different serotypes and presents a significant public health issue in tropical and subtropical regions. Dengue infection can cause a wide spectrum of clinical manifestations. A viral factor that plays a crucial role in the pathogenesis of dengue is NS1. Mutations in the NS1 gene of the dengue virus affect its virulence. Information about the dengue virus in Samarinda City has not been extensively researched. This study aims to analyze the serotype variation of DENV in dengue fever cases, determine the geographical distribution of various serotypes, and identify genetic variations in the nucleotides encoding the NS1 gene of the dengue virus in Samarinda, East Kalimantan. The research samples are blood samples from patients infected with dengue fever in Samarinda, East Kalimantan. NS1 gene amplification is performed using the one-step RT-PCR method. Nucleotide mutation analysis of NS1 is conducted using Mega 11 and BioEdit 7.2 software. Map analysis is carried out using ArcMap 10.8. There is a variation of DENV serotypes during dengue infections in Samarinda, with the most common serotype being DENV3. The geographical distribution of various DENV serotypes spans nine districts, with a clustered spread pattern. The study results show that 10 samples could be amplified, and the NS1 gene sequencing was obtained. Differences in the NS1 gene composition range from 0-10%. Alignment results indicate differences between the NS1 gene sequences and the reference sequences.

Keywords: dengue virus; mutation; NS1 gene; distribution