

ANALISIS SEKUEN GEN PENYANDI NS1 VIRUS DENGUE SAMPEL KLINIS ASAL KOTA SALATIGA, JAWA TENGAH

INTISARI

Latar belakang: Virus dengue terdiri dari empat serotipe dan menjadi masalah kesehatan masyarakat di daerah tropis dan subtropis. Infeksi dengue dapat menyebabkan spektrum manifestasi klinis yang luas. Faktor virus yang memainkan peran penting dalam patogenesis dengue salah satunya adalah NS1. Mutasi gen NS1 virus dengue berpengaruh terhadap virulensinya. Kasus infeksi dengue di Kota Salatiga mengalami KLB pada tahun 2019 dan 2022. Informasi mengenai virus dengue di Kota Salatiga belum banyak diteliti.

Tujuan: Penelitian ini bertujuan untuk mengetahui karakteristik gen NS1 virus dengue di Kota Salatiga pada kejadian KLB tahun 2019 dan 2022 dan hubungannya dengan keparahan penyakit serta melihat sebaran serotipe virus dengue.

Metode: Penelitian ini merupakan penelitian deskriptif observasional. Sampel penelitian adalah sampel darah tersimpan pasien positif dengue yang sebelumnya dilakukan genotiping dan serotiping oleh Joharina *et al*, (2022). Amplifikasi gen NS1 menggunakan metode *One step* RT-PCR. Analisis hubungan perubahan gen NS1 dengan keparahan penyakit dianalisis menggunakan SPSS 26. Analisis peta menggunakan QGIS 3.28.

Hasil: Sebanyak 21 sampel berhasil teramplifikasi dan didapatkan sekuensi gen NS1. Perbedaan komposisi nukleotida gen NS1 pada rentang 0-10%, sedangkan asam amino <5%. Hasil penyelarasan menunjukkan adanya perbedaan sekuens gen NS1 dengan sekuens rujukan. Ditemukan mutasi K272R pada DENV2, yang berpotensi menyebabkan keparahan penyakit. Terdapat lima mutasi gen NS1 pada DENV1, 11 mutasi pada DENV2, tujuh mutasi pada DENV3, dan 10 mutasi pada DENV4. Beberapa mutasi ditemukan pada epitope yang sudah diidentifikasi. Hasil prediksi struktur tersier protein NS1 tidak menunjukkan perbedaan. Analisis statistik antara mutasi gen NS1 dengan DENV2 menunjukkan P value=0,228 (OR=0,220; 95%CI=0,025-1,946) dan DENV3 menunjukkan nilai P value=0,881 (OR=0,949; 95%CI=0,480-1,878).

Kesimpulan: Terdapat perbedaan sekuens gen NS1 virus dengue isolat Salatiga dengan sekuens pembandingan, meskipun ditemukan beberapa mutasi namun struktur tersier protein NS1 tidak menunjukkan perbedaan. Mutasi gen NS1 tidak berhubungan dengan derajat keparahan penyakit. DENV 3 tersebar di seluruh kecamatan di Kota Salatiga.

Kata kunci: virus dengue, mutasi, gen NS1, keparahan penyakit

SEQUENCE ANALYSIS OF NS1 GENE DENGUE VIRUS IN A CLINICAL SAMPLE FROM SALATIGA CITY, CENTRAL JAVA

ABSTRACT

Background: Dengue virus consists of four serotypes and is a public health problem in tropical and subtropical regions. Dengue infection can cause a wide spectrum of clinical manifestations. One of the viral factors that play an important role in dengue pathogenesis is NS1. Mutation of the NS1 gene of dengue virus affects its virulence. Cases of dengue infection in Salatiga experienced outbreaks in 2019 and 2022. Information on dengue virus in Salatiga has not been widely studied.

Objective: This study aims to determine the characteristics of the NS1 gene of dengue virus in Salatiga during outbreaks in 2019 and 2022 and its relationship with disease severity as well as the distribution of dengue virus serotypes.

Methods: This study was a descriptive observational study. The study samples were stored blood samples of dengue positive patients who were previously genotyped and serotyped by Joharina *et al*, (2022). NS1 gene amplification using One step RT-PCR method. Analysis of the relationship between NS1 gene changes and disease severity was analyzed using SPSS 26. Map analysis using QGIS 3.28.

Results: A total of 21 samples were successfully amplified and NS1 gene sequences were obtained. NS1 gene nucleotide composition differences in the range of 0-10%, while amino acids <5%. Alignment results showed differences in NS1 gene sequences with reference sequences. The K272R mutation in DENV2 was found, which has the potential to cause disease severity. There were five NS1 gene mutations in DENV1, 11 mutations in DENV2, seven mutations in DENV3, and 10 mutations in DENV4. Some mutations were found in epitopes that had already been identified. The prediction results of the tertiary structure of NS1 protein showed no difference. Statistical analysis between NS1 gene mutations and DENV2 showed P value=0.228 (OR=0.220; 95%CI=0.025-1.946) and DENV3 showed P value=0.881 (OR=0.949; 95%CI=0.480-1.878).

Conclusion: There are differences in the NS1 gene sequences of Salatiga dengue virus isolates with the comparator sequences, although some mutations were found, the tertiary structure of the NS1 protein showed no differences. NS1 gene mutations are not associated with disease severity. DENV 3 is distributed in all sub-districts in Salatiga.

Keywords: dengue virus, mutation, NS1 gene, disease severity