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Distribusi Serotipe Virus Dengue dan Analisis Variasi Genetik NS5 sebagai Dasar Interaksi Molekuler Kandidat Obat Antiviral
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DISTRIBUSI SEROTIPE VIRUS DENGUE DAN ANALISIS VARIASI GENETIK NS5 SEBAGAI DASAR INTERAKSI MOLEKULER KANDIDAT OBAT ANTIVIRAL

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INTISARI

Infeksi Virus Dengue (IVD) masih menjadi masalah kesehatan masyarakat di Indonesia. Variasi genetik virus dengue (DENV), khususnya pada gen NS5, berpotensi memengaruhi interaksi dengan kandidat obat antivirus. Penelitian ini bertujuan mengidentifikasi serotipe DENV yang bersirkulasi di Kota Surabaya, menganalisis distribusi spasialnya, mengkaji variasi genetik gen NS5 metiltransferase, serta mengevaluasi pengaruh mutasi terhadap interaksi molekuler dengan lovastatin. Penelitian menggunakan desain *cross-sectional* dengan 138 sampel serum pasien suspek dengue yang dikumpulkan dari lima puskesmas di Kota Surabaya pada Januari-Maret 2026. Identifikasi serotipe dilakukan menggunakan *One-Step RT-PCR*, analisis spasial menggunakan QGIS, sedangkan analisis bioinformatika meliputi pensejajaran sekuens, analisis variasi genetik, prediksi struktur protein, identifikasi *binding pocket*, dan *molecular docking*. Hasil penelitian menunjukkan bahwa 114 sampel (84,44%) positif DENV, dengan dominasi DENV-2 (92,10%), diikuti DENV-1 (5,27%), dan koinfeksi DENV-1/DENV-2 (2,63%). DENV-2 terkonsentrasi di Surabaya Timur, dengan beberapa kasus di Surabaya Pusat dan Surabaya Barat. Analisis gen NS5 metiltransferase mengidentifikasi delapan substitusi asam amino, termasuk mutasi N173K dan Y201H pada *binding pocket*. Prediksi struktur menunjukkan model protein berkualitas baik, sedangkan *molecular docking* menunjukkan kedua mutasi tersebut tidak mengubah pola interaksi utama antara protein NS5 dan lovastatin. Penelitian ini memberikan informasi terkait sirkulasi DENV di Surabaya serta karakteristik molekuler NS5 DENV-2 yang mendukung surveilans genomik dan pengembangan kandidat antivirus berbasis inhibitor protein NS5.

Kata Kunci: Multiplex RT-PCR, Oxford Nanopore Technology, protein NS5, serotipe DENV, virus dengue.

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DENGUE VIRUS SEROTYPE DISTRIBUTION AND NS5 GENETIC VARIATION ANALYSIS AS THE BASIS FOR MOLECULAR INTERACTION STUDIES OF ANTIVIRAL DRUG CANDIDATE

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ABSTRACT

Dengue virus infection (DVI) remains a public health problem in Indonesia. Genetic variation in the dengue virus (DENV), particularly in the NS5 gene, has the potential to influence its interaction with antiviral drug candidates. This study aims to identify the DENV serotypes circulating in the city of Surabaya, analyze their spatial distribution, examine genetic variations in the NS5 methyltransferase gene, and evaluate the effect of mutations on molecular interactions with lovastatin. The study employed a cross-sectional design using 138 serum samples from patients with suspected dengue collected from five community health centers in Surabaya from January to March 2026. Serotype identification was performed using One-Step RT-PCR, spatial analysis was conducted using QGIS, while bioinformatics analysis included sequence alignment, genetic variation analysis, protein structure prediction, binding pocket identification, and molecular docking. The results showed that 114 samples (84.44%) were DENV-positive, with DENV-2 being the dominant serotype (92.10%), followed by DENV-1 (5.27%), and DENV-1/DENV-2 co-infections (2.63%). DENV-2 was concentrated in East Surabaya, with a few cases in Central Surabaya and West Surabaya. Analysis of the NS5 methyltransferase gene identified eight amino acid substitutions, including the N173K and Y201H mutations in the binding pocket. Structure prediction revealed a high-quality protein model, while molecular docking showed that neither mutation altered the primary interaction patterns between the NS5 protein and lovastatin. This study provides information on DENV circulation in Surabaya and the molecular characteristics of DENV-2 NS5, which supports genomic surveillance and the development of antiviral candidates based on NS5 protein inhibitors.

Keywords: Dengue virus, DENV serotype, multiplex RT-PCR, NS5 protein, Oxford Nanopore Technology.