ANALISIS POLIMORFISME GEN *NUCLEOCAPSID* (GEN N) *SEVERE ACUTE RESPIRATORY SYNDROME CORONAVIRUS-2* (SARS-COV-2) PADA VARIAN DI SUMATRA BARAT

TESIS

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Abstrak

Penelitian ini bertujuan untuk mengetahui distribusi varian SARS CoV-2, variasi nukleotida pada gen N serta untuk mengetahui pola mutasi gen N pada varian SARS-CoV-2 yang ditemukan di Sumatera Barat. 268 sekuens SARS-CoV-2 digunakan dalam penelitian ini yang merupakan bahan biologis yang tersimpan dalam *Viral Transport Medium* (VTM) koleksi sampel dari Pusat Diagnostik dan Riset Penyakit Infeksi (PDRPI) Fakultas Kedokteran UNAND. Peneliti melakukan analisis 268 sekuens genom yang dikumpulkan pada awal pandemi periode April 2020 hingga Maret 2022. Semua sekuens penelitian diunduh dari .org kemudian di*alignment* dengan sekuens referensi NC_45512 menggunakan CLC *Workbench app*. Untuk konfirmasi kembali jenis varian yang ditemukan dari penelitian dicek dengan website *Pangolineage*. Hasil analisis 20 *lineages* dengan mayoritas B.1.466.2 n = 85. 31,72%) diikuti varian Delta 52 sampel yang terbagi 2 *lineage* AY.23 dan AY24, arian Omicron 38 sampel (14.18%), B.1.36.19 sebanyak 27 sampel (10.67%), B.1.1.398 berjumlah 24 (9.32%), B.1.468 berjumlah 17 (6.34%) dan varian kecil lainnya (B.1, B.1.459, B.6, B.1.1, B.1.1.216, B.1.470 dan terakhir B.1.456. Pada gen N ditemukan mutasi unik dari varian yang ditemukan di Sumatera Barat. Mutasi unik dapat dilihat pada varian B.1.466.2 perubahan asam amino T205I, Delta perubahan asam amino D64G, R203M dan G215C, varian Omicron perubahan asam amino P13L, DEL 31/33, R203K dan G204R serta B.1.36.19 dan B.1.398 karna jumlah sekuens yang diamati banyak dan sesuai dengan varian global. Dari 268 sekuens gen N ditemukan 12 sekuens gen N yang tidak ada mutasi (*wild type*). Hasil ini memberikan data tambahan mengenai variasi gen N di Indonesia.

Kata Kunci: SARS CoV-2, gen nukleokapsid, mutasi unik varian B.1.466.2, Delta, Omicron

POLYMORPHISM ANALYSIS OF THE NUCLEOCAPSID (GEN N) SEVERE ACUT RESPIRATORY SYNDROME CORONAVIRUS-2 (SARS-COV-2) IN VARIANTS IN WEST SUMATRA

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Abstract

This study aims to determine the distribution of the SARS-CoV-2 variant, the nucleotide variations in the N gene and to determine the mutation pattern of the N gene in the SARS-CoV-2 variant found in West Sumatra. 268 sequences of SARS-CoV-2 were used in this study which are biological materials stored in the Viral Transport Medium (VTM) sample collection from the Center for Diagnostics and Infectious Disease Research (PDRPI), Faculty of Medicine, UNAND. Researchers analyzed 268 genome sequences collected at the pandemic's start for the period April 2020 to March 2022. All research sequences were downloaded from Gisaid.org and aligned with the reference sequence NC_45512 using the CLC Workbench app. To confirm again the types of variants found from research, check with the Pangolineage website. The results of the analysis of 20 lineages with the majority B.1.466.2 n = 85. 31.72%) followed by the Delta variant 52 samples divided into 2 lineages AY.23 and AY24, Omicron arian 38 samples (14.18%), B.1.36.19 as many as 27 samples (10.67%), B.1.1.398 totaling 24 (9.32%), B.1.468 totaling 17 (6.34%) and other small variants (B.1, B.1.459, B.6, B.1.1, B .1.1.216, B.1.470 and finally B.1.456. In the N gene, a unique mutation was found from a variant found in West Sumatra. Unique mutations can be seen in variant B.1.466.2, a change in the T205I amino acid, Delta, a change in the D64G amino acid, R203M and G215C, Omicron variants, changes in amino acids P13L, DEL 31/33, R203K and G204R as well as B.1.36.19 and B.1.398 because the number of sequences observed was large and in accordance with global variants. Of the 268 N gene sequences, 12 gene sequences were found N which has no mutations (wild type). These results provide additional data regarding the variation of the N gene in Indonesia.

Keywords: SARS CoV-2, nucleocapsid gene, unique mutation variant B.1.466.2, Delta, Omicron