VARIASI GENETIK GEN *SPIKE SEVERE ACUTE RESPIRATORY SYNDROME CORONAVIRUS-2* (SARS-CoV-2)

TESIS

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UNIVERSITAS ANDALAS
PADANG
2021

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ABSTRAK

Kasus pneumonia akibat infeksi novel korona virus sangat intens dilaporkan sejak Desember 2019. Hampir dua tahun sejak kemunculan virus SARS-CoV-2 di Wuhan China, hingga saat ini belum menunjukkan pandemi ini akan segera berakhir. Laju mutasi yang tinggi teruama pada gen *spike* SARS-CoV-2 memicu terbentuknya varian-varian baru yang memiliki pola transmisi lebih kuat di masyarakat. Tujuan penelitian ini adalah untuk mengetahui mutasi pada sekuens gen *spike* yang berasal dari koleksi Laboratorium Pusat Diagnostik dan Riset Penyakit Infeksi Fakultas Kedokteran Universitas Andalas.

Desain penelitian ini berupa deskriptif eksploratif dengan pendekatan *cross sectional* dimulai dari bulan Maret hingga Juli 2021. Teknik pengambilan sampel dilakukan secara konsekutif dan diperoleh 91 sampel beserta data klinis dari formulir pendaftaran 7, untuk diikutsertakan pada penelitian ini. Sampel berupa cairan *viral transport medium* (VTM) hasil swab nasofaring kemudian diekstraksi, kuantifikasi dan dilanjutkan pada tahapan *libraby preparation. Library* kemudian disekuensing menggunakan mesin miseq. Output mesin berupa FASTQ, *alignment* dan analisa variasi dikerjakan menggunakan *silico tools CLC Genomic Workbench.*

Hasil penelitian menunjukkan 100% sampel yang diaanalisa bioinformatika setidaknya telah memilki satu titik mutasi pada gen *spike* dengan rerata mutasi sebesar 2,53 mutasi gen *Spike* per sampel. Mutasi Asp614Gly, Leu18Phe, Asn439Lys, Pro681Arg dan Pro681his merupakan lima mutasi *nonsynonymous* tersering pada penelitian ini. Gejala klnis yang ditemukan pada penelitian ini umumnya bersifat asimtomatis (68,6%) diikuti batuk (20,2%) dan demam (13,4%).

Kata kunci : SARS-CoV-2, gen Spike, mutasi, manifestasi klinis

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ABSTRAK

Pneumonia that caused by novel coronavirus was reported massively since December 2019. Its almost two years since the pandemic start from Wuhan China but end of this pandemic still unclear. High mutation rate in spike gene SARS-CoV-2 made new variants occur and made transmission around community become higher than before. Main of this research is to detect mutation along spike gene from collection samples in Diagnostic and Research Center of Infectious Disease, Medical Faculty Andalas University

This study design was a descriptive explorative study with cross sectional methode from March to July 2021. The sample were taken using concecutive technique and include 91 samples with clinical manifestation data that taken from form 7. The samples were *viral transport medium* (VTM) from nasopharyngeal swab then extracted, quantificated and include for library preparation. Libraries the sequenced by miseq. FASTQ output, alignment dan variant analysis conducted with *silico tools CLC Genomic Workbench.*

The result from this study shown that 100% samples were at least have one mutation along Spike gene, with average 2,53 mutation each samples. Asp614Gly, Leu18Phe, Asn439Lys, Pro681Arg and Pro681his was the common *nonsynonymous* mutation that found in this study. The most common clinical symptoms in this study were asymptomatic (68,6%) followed by cough (20,2%) and fever (13,4%).

Key word : SARS-CoV-2, Spike gene, mutation, clinical manifestation