

***AFINITAS FILOGENETIK VARIASI GENETIK VIRUS SARS-COV-2
DELTA DAN OMICRON PADA POPULASI INDONESIA***

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INTISARI

Pandemi COVID-19 menjadi masalah serius di seluruh dunia beberapa tahun silam. COVID-19 adalah penyakit pernapasan yang mudah menular, dan pertama kali ditemukan di Wuhan, Cina pada tahun 2019. Penyakit ini dengan cepat menyebar ke seluruh dunia, disebabkan oleh infeksi Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2). Indonesia terkena dampak negatif yang cukup besar dari virus tersebut. Hingga 29 Maret 2022, total ada 6 juta kasus COVID di Indonesia. Varian genetik baru terus muncul seiring berjalannya waktu, sehingga menghambat upaya untuk mengakhiri pandemi. Minimnya penelitian tentang varian genetik virus COVID-19 di Indonesia, menghambat upaya pemulihan saat itu. Memahami variasi genetik virus COVID-19 akan membantu upaya pencegahan munculnya kembali penyakit tersebut. Penelitian ini bertujuan untuk memperoleh dan mengetahui variasi genetik virus COVID-19 dengan menggunakan analisis filogenetik dan distribusinya di Indonesia. Hasil penelitian ini menunjukkan bahwa virus COVID-19 strain asli dan varian Delta tidak memiliki perbedaan genetik yang signifikan. Di sisi lain, pohon filogenetik varian Omicron menyajikan nilai bootstrap yang tinggi, menunjukkan perbedaan genetik yang signifikan. Varian Omicron juga terbukti menjadi varian paling dominan di Indonesia, disusul dengan varian Delta.

Kata kunci: COVID-19, Delta, Filogeni, Indonesia, Omicron, SARS-CoV-2, Variasi Genetik.

**PHYLOGENETIC AFFINITIES OF SARS-COV-2 VIRUS GENETIC
VARIATION DELTA AND OMICRON IN THE INDONESIAN
POPULATION**

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ABSTRACT

The COVID-19 pandemic was a significant issue all around the world. Caused by Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), COVID-19 was an easily transmittable respiratory disease first identified in Wuhan, China in 2019, and quickly spread around the globe. Indonesia was negatively impacted by the virus. By March 29th, 2022, there were 6 million covid cases in Indonesia. New genetic variants kept emerging as time passed, hindering efforts to end the pandemic. The lack of research about the genetic variant of the COVID-19 virus in the Indonesian population further undermines the attempts to recover. Understanding the genetic variation of the COVID-19 virus in Indonesia will help the preventive measures and treatments for the disease. This study aims to acquire and determine the genetic variation of the COVID-19 virus using phylogenetic analysis and its distribution in the Indonesian population. This research shows that the original strain and the Delta variant of the COVID-19 virus in the Indonesian population do not have any significant genetic differences. On the other hand, the Omicron variant phylogenetic tree presented a high bootstrap value, indicating significant genetical distinction. The Omicron variant is also proven to be the most predominant variant in the Indonesian population, followed by the Delta variant.

Keywords: COVID-19, Delta, Genetic Variation, Omicron, Phylogeny, Indonesi