

ABSTRAK

Judul : Analisis Polimorfisme Genom SARS-CoV-2 dari Indonesia dan Eropa (Turki)
Nama : Amanda Felicia Gustinaya A
Program Studi : Bioteknologi

Pada akhir tahun 2019, muncul penyakit pneumonia baru yang lebih dikenal sebagai penyakit COVID-19 disebabkan virus corona baru SARS-CoV-2. Penyakit COVID-19 mengalami penyebaran cepat dan menyebabkan masalah kesehatan global, hingga pada bulan Maret tahun 2020 WHO menyatakan wabah penyakit COVID 19 sebagai pandemi. Penulis menganalisis 98 sekuen genom SARS-CoV-2 asal Indonesia karena bertempat tinggal di Indonesia dan 175 sekuen genom SARS-CoV-2 asal Turki karena Turki merupakan negara transit dimana terjadi mobilisasi manusia antar benua. Data sekuen diunduh dari basis data GISAID.

Hasil analisis menggunakan tabel pivot menunjukkan klade L mendominasi sekuen genom virus SARS-CoV-2 asal Indonesia dan klade GR mendominasi sekuen genom virus SARS-CoV-2 asal Turki. Kemudian, hasil analisis filogenetik menunjukkan bahwa sekuen genom virus SARS-CoV-2 asal Indonesia memiliki kekerabatan yang dekat dengan sekuen genom virus-SARS-CoV-2 Wuhan 01, sementara sekuen genom virus SARS-CoV-2 asal Indonesia dan Turki tidak memiliki kekerabatan yang dekat.

Hasil analisis *nextclade* menunjukkan sekuen genom virus SARS-CoV-2 asal Indonesia dan Turki memiliki pola mutasi yang berbeda karena adanya tingkat mutasi, delesi dan perubahan target primer PCR yang berbeda. Pemahaman terhadap pola mutasi virus sangat penting karena berpengaruh pada metode deteksi molekuler dan pembuatan desain primer.

Kata kunci: SARS-CoV-2, GISAID, sekuen genom, mutasi, analisis

ABSTRACT

Title : Polymorphism Analysis of the SARS-CoV-2 Genome from Indonesia and Europe (Turkey)
Name : Amanda Felicia Gustinaya A
Study program : Biotechnology

At the end of 2019, new pneumonia emerged, better known as COVID-19, and research showed new coronavirus SARS-CoV-2 as the infector. The COVID-19 disease emerged due to the existence and rapid transmission of the virus and causing global health problems. In March 2020 WHO declared the COVID-19 disease outbreak as a pandemic disease. The author analyzed 98 sequences of the SARS-CoV-2 genome from Indonesia because she lives in Indonesia and 175 sequences of the SARS-CoV-2 genome from Turkey because Turkey is a transit country, a place with the mass human mobilization between continents. The sequence data were downloaded from GISAID database.

At the end of 2019, pneumonia appeared, better known as COVID-19, caused by the new coronavirus SARS-CoV-2. The COVID-19 disease is experiencing rapid spread and is causing global health problems,

Analysis using pivot table shows the L clade dominates the SARS-CoV-2 virus genome sequences from Indonesia and the GR clade dominates in Turkey. The result of phylogenetic analysis shows that the genome sequences of the SARS-CoV-2 virus from Indonesia is closely related to the SARS-CoV-2 Wuhan 01 virus genome sequence, whereas the SARS-CoV-2 virus genome sequences from Indonesia and Turkey do not have close genetic relationship.

Afterward, the outcome of the nextclade analysis shows that the SARS-CoV-2 virus genome sequences from Indonesia and Turkey have different mutation patterns due to different levels of mutation, deletion and changes in the primary target PCR. Understanding the mutation pattern of the virus is very important because it will influence the molecular detection method and the production of primary design.

Key words: SARS-CoV-2, GISAID, genome sequence, mutation, analysis