Karakteristik Protein Spike-1 SARS-CoV-2 Strain Jakarta sebagai Dasar Pengembangan Vaksin DNA = Characteristics of SARS-CoV-2 Spike-1 Protein Jakarta Strain as a Basis for DNA Vaccine Development

Munawir Umakaapa, author

Abstrak

SARS-CoV-2 sebagai virus penyebab COVID-19 yang berikatan dengan reseptor ACE-2 untuk masuk ke dalam sel inang melalui protein spike-1. Protein spike-1 dapat menjadi target pencegahan COVID-19 melalui pengembangan vaksin. Vaksin berbasis DNA merupakan kandidat vaksin yang menjanjikan untuk dikembangkan. Spesimen naso-oro faring pasien COVID-19 yang telah dikonfirmasi dengan RT-PCR, diekstraksi dan diamplifikasi dengan menggunakan primer kloning terhadap plasmid pUMVC4a. Hasil sekuensing dianalisis dengan SeqScape 3.0 dan MEGA 11. Analisis epitop sel B dilakukan dengan berbagai piranti lunak berbasis web. Konstruksi DNA vaksin dilakukan melalui analisis in silico menggunakan SnapGene 6.0 serta in vitro melalui teknik DNA Rekombinan. Gen spike-1 teramplifikasi dengan ukuran 2.265 bp, namun ligasi ke pUMVC4a dan transformasi ke E.coli strain DH5Î± belum berhasil. Berdasarkan analisis, seluruh sekuen memiliki mutasi D614G dengan isolat A dan B memiliki PNI yang dekat dengan varian Wuhan wt sementara 5 isolat (C-G) termasuk dalam varian Omicron. Berdasarkan sifat antigenisitas, toksisitas, alergenisitas, topologi dan hidrofobisitas, empat belas sekuen asam amino (pada posisi 68-678 protein S-1) diajukan sebagai epitop terpilih. Terdapat 14 sekuens asam amino pada protein spike-1 SARS-CoV-2 yang dapat diajukan sebagai domain epitop sel B dalam pengembangan vaksin COVID-19 berbasis DNA.

.....SARS-CoV-2 as the virus that causes COVID-19 binds to the ACE-2 receptor to enter host cells via the spike-1 protein. Spike-1 protein can be a target for preventing COVID-19 through vaccine development. DNA-based vaccines are promising vaccine candidates to be developed. Naso-oropharyngeal specimens of COVID-19 patients confirmed by RT-PCR were extracted and amplified using clone primers against the plasmid pUMVC4a. The sequencing results were analyzed with SeqScape 3.0 and MEGA 11. B cell epitope analysis was performed with various web-based software. Vaccine DNA construction was carried out through in silico analysis using SnapGene 6.0 and in vitro using Recombinant DNA techniques. The spike-1 gene was amplified with a size of 2,265 bp, but ligation to pUMVC4a and transformation to E.coli strain DH5Î± were not successful. Based on the analysis, all sequences have the D614G mutation with isolate A and B having a PNI that is close to the Wuhan wt variant while 5 isolates (C-G) belong to the Omicron variant. Based on antigenicity, toxicity, allergenicity, topology and hydrophobicity, fourteen amino acid sequences (at positions 68 - 678 of protein S-1) were proposed as selected epitopes. There are 14 amino acid sequences in the SARS-CoV-2 spike-1 protein that can be proposed as B cell epitope domains in the development of a DNA-based COVID-19 vaccine.