ABSTRACT

The COVID-19 pandemic has been going on for three years, and research on preventive and curative measures is continuously being made. Belonging to the same coronavirus family, human common cold coronaviruses (CCCs) like 229E, NL63, HKU1, and OC43 have been around for decades. However, unlike SARS-CoV-2, they do not manifest serious signs and symptoms. Reports on T-cell cross-reactivity against SARS-CoV-2 epitopes in unexposed individuals have been linked with prior exposure to the human CCCs. Still, no clear conclusion can be drawn from current research, in particular, whether the cross-reactivity means cross-protection. This study aims to identify potential cross-reactivity between SARS-CoV-2 and human CCCs in the context of T-cell epitopes peptides presented by HLA alleles of the Indonesian population through epitope analysis. Primarily by utilizing immunoinformatics tools, SARS-CoV-2 derived T-cell epitopes were predicted and assessed for their conservancy, variability, and population coverage. A total of two fully conserved 9-mer epitopes with 100% homology shared by SARS-CoV-2 and all four human CCCs were identified. An additional nine heterologous epitopes with identical TCR-contact residues were also identified. All presented by at least one major Indonesian HLA allele and some have been reported in IEDB. Overall, showing the cross-reactivity could indeed arise due to sequence homology shared between the SARS-CoV-2 and human CCCs. Furthermore, all of the identified epitopes were observed to belong to ORF1ab, further suggesting the vital role of ORF1ab in the coronaviruses family. Thus, establishing its potential role as a candidate for the universal coronavirus vaccine target. Despite several limitations, this study collectively gathered data that support further understanding of SARS-CoV-2 T-cell cross-reactivity and its potential contribution to vaccine construction.

Keywords: cross-reactivity, SARS-CoV-2, human common cold coronaviruses, Indonesian HLA, ORF1ab