Abstract

The development of vaccines and diagnostic tools for SARS-CoV-2 heavily relies on identifying conserved epitopes across various virus strains. BLASTp is a pivotal bioinformatics tool for comparing protein sequences to unveil regions of similarity, aiding in understanding evolutionary relationships and functional conservation. The current study used bioinformatics methods to highlight the conserved epitopes on SARS-CoV-2 genomes isolated in Moi Teaching and Referral Hospital. To achieve this objective, the genomes were divided into their constituent genes using NCBI ORFfinder and translated to proteins using EXPASY. BlastP was then used to identify the proteins. Meanwhile, epitopes from the Wuhan genome were downloaded from IEDB and a BlastP analysis was done to identify matching epitopes. From the IEDB databank, 12,285 Wuhan genome epitopes were found and on conducting BlastP analysis, 5154 epitopes were isolated. These epitopes were deemed conserved as they had not changed despite numerous mutations. The identification and analysis of the conserved epitopes in the SARS-CoV-2 genome are crucial for the development of effective vaccines and diagnostic tools. Further laboratory experiments are however recommended to ascertain them to be conserved epitopes.