

Letter to Editor

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Epitope finding in 2019 novel coronavirus (2019–nCoV): The first world report

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Wuhan coronavirus infection is a new emerging disease that started in China and presently spread into many countries[1,2]. The disease is an acute illness with respiratory manifestation caused by 2019 novel coronavirus (2019-nCoV) as designated by the World Health Organization (WHO). Until the present, there is no specific antiviral treatment. For prevention, standard infection control is necessary. Similar to any new emerging infectious diseases, finding new vaccine against the virus is the hope. In vaccinology, the first step for finding new vaccine is identifying the epitope of the pathogen. Based on the new bioinformatics technology, the bioinformatics approach is useful for epitope finding. The good example is the previous epitope finding within emerging Zika virus molecule[3]. Based on the same technique as used in the previous study on Zika virus[3], the authors hereby report the primary data on epitope finding in Wuhan novel coronavirus.

Referencing to previous publications[3,4], the standard bioinformatics technique[5], namely BCEPred was used. Based on the bioinformatics technique, epitope prediction is by computational analysis of physicochemical properties of the molecule. Public available sequence of 2019-nCoV (NCBI Reference Sequence: NC_045512.2) from PubMed was used as template in the present study. According to the analysis, the peptide 929EDEE932 is the area with the highest epitope property (the highest value = 2.714). The model of the identified epitope is presented in Figure 1.

Here, with use of the bioinformatics, it can minimize the total number of required tests to find the possible proper epitopes for further vaccine development. Further confirmation by *in vitro* synthesis of the determined peptide and *in vivo* experimental study to verify the efficacy are necessary further processes for vaccine development against 2019-nCoV.

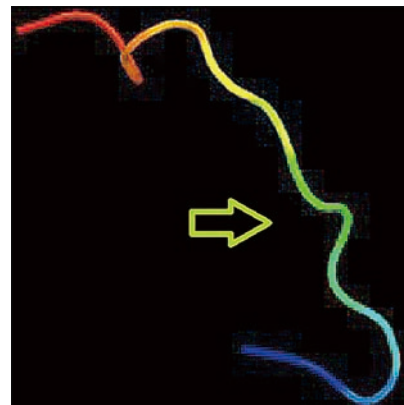


Figure 1. The model of the identified epitope 929EDEE932 (generated by Pyre2 tool).

Conflict of interest statement

We declare that we have no conflict of interest.

Authors' contributions

JB and WV conceived and drafted the manuscript. JB and WV were responsible for literature search and analyses, as well as data interpretation.

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