
Conference Abstract**Mutations observed in selected SARS-CoV-2 isolates**

Kugathasan. D, Aruldchelvan. K, Jeyaseelan. T. C., Emmanuel. C. J.*

Department of Botany, Faculty of Science, University of Jaffna, Jaffna 40000, Sri Lanka

*jeyaseelan.ec@univ.jfn.ac.lk

Abstract

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is a single-stranded positive RNA virus. The virus genome is ~ 29.9 Kb in size and comprises 14 open reading frames, which encodes for 27 different proteins. The SARS-CoV-2 virus mutates over time, as all viruses do. It may lead to genetic variation and alteration of biological properties in the population of viral strains. The present study analyses the molecular variation in the amino acid sequences of four structural proteins (spike protein, nucleocapsid protein, envelope protein and membrane protein) in selected SARS-CoV-2 isolates. The sequence of the isolate Wuhan-Hu-1 (GenBank Accession number NC_045512) was used as the reference sequence. Sequences of twenty different isolates, representing ten different countries, were used for the analysis. Two sequences, the first and last sequences reported between 23.12.2019 and 31.12.2020 in each country, were retrieved from GenBank database. The similarities of protein-coding sequences of the selected genes were studied using the sequence demarcation tool (SDTv1.2) [1]. The sequences were aligned using BioEdit (v. 7.2) [2] and modifications were detected. Mutation analysis was performed using an online tool CoVsurver mutations app available in GISAID. In all the selected countries, the amino acid sequences of the isolates vary from the reference sequence. Also, variation was observed between the isolates representing each country. An isolate from the USA had fifteen point mutations, while the isolates reported from Brazil and Egypt had a single mutation. In the isolates of USA, Russia and UK, 31 point mutations were observed in the spike glycoprotein coding gene; about 52% of these mutations are due to the deletion of amino acids or non-conservative mutations. The D614G mutation in spike glycoprotein was detected in all countries. The present study confirms that the recent SARS-CoV-2 isolates have mutated from the first isolate reported in China, and most of the modifications are in the spike glycoprotein.

Keywords: SARS-CoV-2, Mutation, Spike protein.**References**

- [1] B. M. Muhire et al., PLoS One, (2014), 9:e108277
- [2] T. A. Hall, Nucleic Acids Symposium Series, (1999), **41**, 95-98.