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GENETIC DRIFT OF SARS-COV-2 MUTATIONS IN QATAR POPULATION

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Introduction. COVID-19 pandemic remains a pressing issue as a consequence of its new emerging variants of concern (VOCs) among population of Asian countries. Therefore, a one of the important priority of modern medicine toward pandemic management is to elucidating viral genome characteristics and its influence on disease severity and clinical outcome.

The aim was to assess the prevalence of mutations SarS-CoV-2 genome among Qatar population.

Material and method: COVID-19 epidemiology trends in Qatar were obtained on the web platform Google Public Data. Analysis of SARS-CoV-2 genomes in 4300 samples from patients with COVID-19 of Qatar population were detected on GISAID database platform from 2020 to 2021. Genome evolution and transmission analysis were performed on the Nextstrain platform.

Results: Epidemiology data shown that there have been 365,191 infected persons with COVID-19 and 677 coronavirus-related deaths reported in the Qatar since the pandemic began. It was reported on 7 January 2022 a 3% of the peak – the highest daily average of illness.

During pandemic period was sequenced ten SARS-CoV-2 strains in the country. Among the mutations of the Sars-CoV-2 virus in Qatar, the most numerous are the strains Delta and Omicron during 2020 -2021, GK (according to WHO as Delta; 36.71%) and GH (according to WHO as Beta; 33.71%). It was detected than in man more often than in woman present GK strain (21.91% against 14.8%, respectively), GR strain (according to the WHO as Gamma, 3.79% against 1.51%, respectively), GH strain (24.05% against 9.64%, respectively). GK strain more often detected in population from 25 to 34 years (8.81%) and from 35 to 44 years (9.5%). Transmission ways were detected for the Alpha, Delta and Omicron strains was detected from 16 Asian countries to Qatar.

Conclusion: Thus, our study provides integrative insights about Sars-CoV-2 virus mutations, which significantly associated with a gender and sex factors, phylogeny and ways of transmission between Asian countries, its global presence, and its possible effects at the structural level to understand the role of mutations in driving the COVID-19 pandemic in Qatar.

Keywords: SARS-COV-2, strains, mutation, Qatar.

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