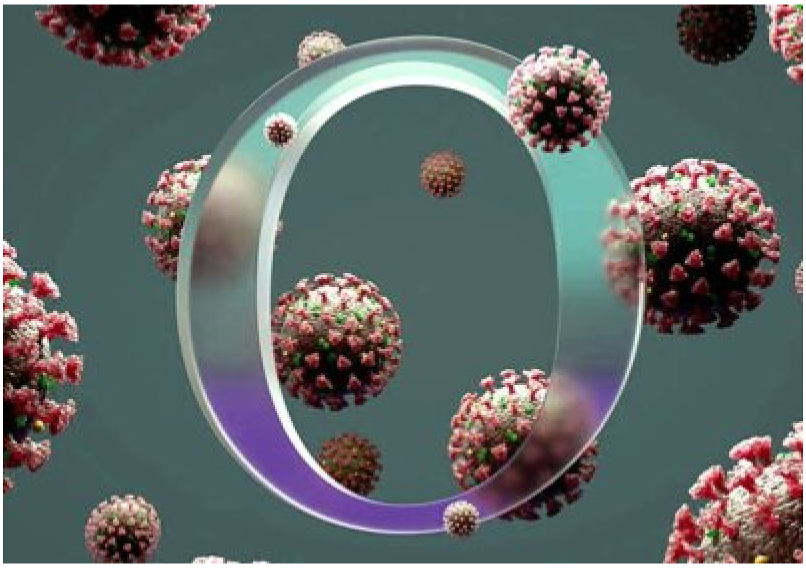
Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is an enveloped, positive-sense, single-stranded RNA virus. Its genome encodes four structural proteins, namely the spike (S), envelope (E), nucleocapsid (N), and membrane (M) protein. The emerging variants of the SARS-CoV-2 are characterized by increased viral fitness and each shows multiple mutations predominantly localized to the S protein. In this study, two Japanese authors investigated the evolutionary processes that led to the formation of the Omicron variants of SARS-CoV-2. They focused on Omicron variants with many amino acid mutations in the spike (S) protein.

The researchers compared the sequences of 129 isolates related to Omicron BA.1, 141 isolates related to BA.1.1, and 122 isolates related to BA.2 to determine the order of mutations leading to the formation of the SARS-CoV-2 Omicron variants. They sought to elucidate the evolutionary process of the Omicron variant, which has twice as many amino acid mutations in the S protein as other variants, by examining the order of introduction of amino acid mutations in the S protein.



The examination of 35 recombinant isolates of the Omicron variants BA.1 and BA.2 revealed that the Omicron variant of SARS-CoV-2, first reported to WHO by the Network for Genomics Surveillance in South Africa on November 24, 2021, was already endemic in Puerto Rico in 2020.

According to the results of this study, the scientists concluded that the formation of the Omicron isolates BA.1, BA.1.1, and BA.2 was not the result of genome evolution, such as the accumulation of mutations and homologous recombination, as it is common in nature.

They emphasized that the SARS-CoV-2 isolates are formed by a completely new mechanism that cannot be explained by previous biology and that it is highly unlikely that these viruses arose spontaneously.

This study has been published on a preprint server and is currently being peer-reviewed.

Journal Reference

Tanaka, Atsushi, & Miyazawa, Takayuki. (2023). Unnaturalness in the evolution process of the SARS-CoV-2 variants and the possibility of deliberate natural selection (1.0). Zenodo. https://doi.org/10.5281/zenodo.8216373