

Stationary and non-stationary mutagenesis in the SARS-CoV-2 genome

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The pandemic of the coronavirus infection COVID-19, which began at the end of 2019 and caused by the SARS-CoV-2 virus, has led to unprecedented consequences in the world. By the end of March 2022, in the world there were 450 million infected and 6 million died directly from infection [1]. SARS-CoV-2 is known to be a betacoronavirus, so it shares many properties with other viruses in this family, including mutation patterns and conserved fragments [2]. Since the beginning of the spread of COVID-19, the issues of research the SARS-CoV-2 virus have been to discover its evolutionary variability, active points or standard mutation patterns, including those common with other betacoronaviruses.

This report examines the stationarity of mutations present in the SARS-CoV-2 genome, comparing both located in conserved RNA fragments of the genome and in coding regions. For this, a phylogenetic tree provided by the UShER project was used [3]. Hot spots of genome mutations, stationary and non-stationary mutations, their relationship with conservative and other functional fragments of the genome were characterized.

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References

1. Roser M., Ritchie H., Ortiz-Ospina E., Hasell J. Coronavirus Pandemic (COVID-19). 2020. Published online at
2. Rangan R., Zheludev I.N., Hagey R.J. et al. RNA genome conservation and secondary structure in SARS-CoV-2 and SARS-related viruses: a first look. *RNA*. 2020;26(8):937-959. doi: 10.1261/rna.076141.120.
3. Turakhia Y., Thornlow B., Hinrichs A.S. et al. Ultrafast Sample placement on Existing tRees (UShER) enables real-time phylogenetics for the SARS-CoV-2 pandemic. *Nat Genet* 2021;53:809-816. doi: 10.1038/s41588-021-00862-7.