

Genome evolution of SARS-CoV-2 and its virological characteristics

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Coronavirus disease of 2019 (COVID-19), which originated in China in 2019, shows mild cold and pneumonia symptoms that can occasionally worsen and result in deaths. severe acute respiratory syndrome (SARS) coronavirus 2 (SARS-CoV-2) was reported to be the causative agent of the disease and was identified as being similar to SARS-CoV, a causative agent of SARS in 2003. In this symposium, I first mention the phylogeny of SARS-CoV-2, covering various related studies, in particular, focusing on viruses obtained from horseshoe bats and pangolins that belong to *Sarbecovirus*, a subgenus of *Betacoronavirus*¹. We also describe the virological characteristics of SARS-CoV-2 by comparing them with other coronaviruses. More than 155,000 genome sequences of SARS-CoV-2 are available in the GISAID database (<https://www.gisaid.org>) as of October 22, 2020. Using SARS-CoV-2 genome sequences including closely related coronavirus genomes, the genomic characteristics and evolution of SARS-CoV-2 were extensively studied. And several studies including ours² identified genetic mutations that affect characteristic of SARS-CoV-2. I will also present the such mutations we know to date.

References

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