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## Emergence of COVID-19 –ground for its evolutionary success

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To prevent the spread of SARS-CoV-2, many countries adopted strict non-pharmacological interventions such as non-essential businesses or complete lockdowns. All these measures seem to be of little effectiveness. This is unlike its predecessors, SARS –CoV and MERS-CoV, that affected limited populations and disappeared shortly after they had emerged. High virulence of these viruses, severity of disease and death toll reduced transmissibility since the hosts had been too sick to expose others. COVID-19 found its intermittent evolutionary niche due to its high transmissibility by vast majority of non-symptomatic cases and lack of pre-existing immunity.

Social media are flooded with arousing trepidation speculations on 'dangerous mutations'in the new virus. Looking into the history of epidemiology, we shouldn't worry when a virus mutates during disease outbreaks. Most RNA virus populations are complex mixtures of genetic variants, resulting from the high RNA polymerase error rate. Usually multiple genes are likely involved in the primary evolution of an emerging virus. Mutations are requisite for 'spill over'from an animal reservoir or use a new vector for transmission. The continuous pandemic may enable accumulation of immunologically relevant mutations. Immunological response durability to SARS-CoV2 is doubted and the genetic drift may influence the future vaccines utility.

Favored mutations constitute the backbone for further genetic variants but the latent usually are not 'gamechangers'in a current epidemic. It is unusual to find viruses that have changed or expanded their mode of transmission over short time-scales despite high rates of mutation. Unfortunately, the role of natural selection in virus evolution is not easily predicted. This opens the field for speculation around the evolutionary trajectory of a virus during a newest COVID-19 outbreak.

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