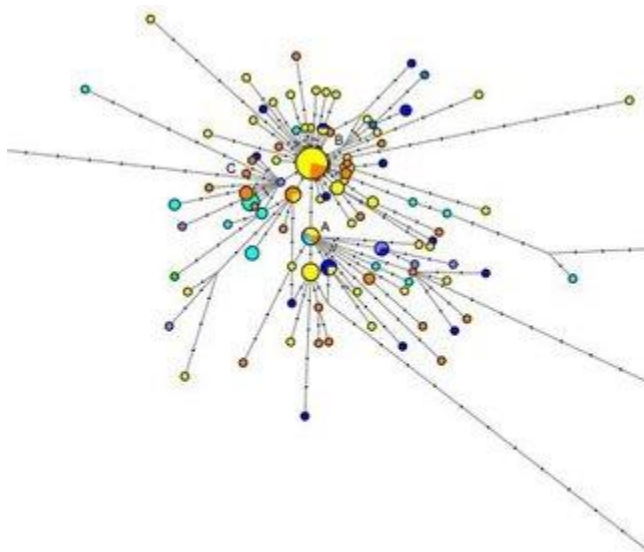
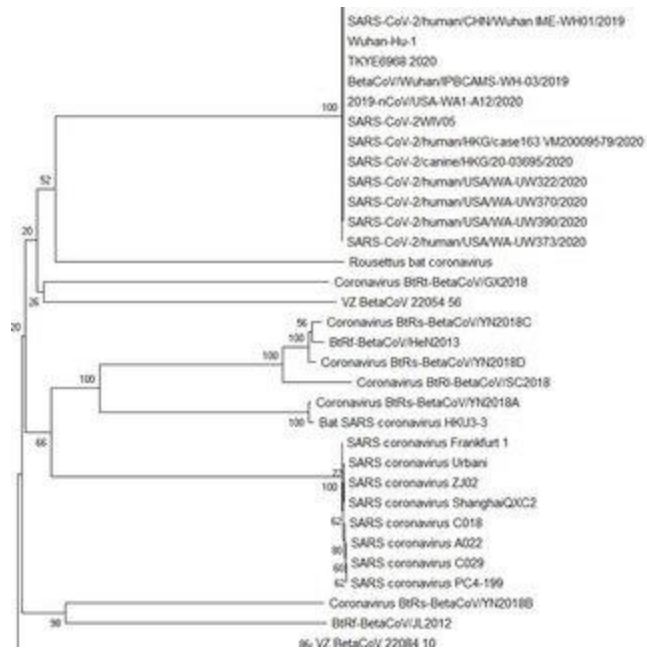


SARS-CoV-2 Molecular Clock and Zoonosis.

Abstract and figures

SARS-CoV-2 (Severe Acute Respiratory Syndrome Coronavirus 2), associated with Corona Virus Disease 2019 (COVID-19) coined by World Health Organization, belongs to single stranded RNA viruses (ssRNA Viruses) under Betacoronaviruses. The virus' molecular dynamics are necessary in the wake of human-human transmissions globally with mortality cases on the rise, thusly the race for a vaccine. As the viral genome expresses more human-biased mutations, the coronavirus disease 2019 continues to infect people in their millions, with the available detection kits limiting the numbers detected out of the population. Understanding the molecular basis of the virus through bioinformatics would speed up the viral diagnostics, management and vaccine generation. Currently, the scientific community seeks to give varied perspectives of what is known of the virus at a cellular level. The knowledge is scattered and requires a consolidated flow on thematic understanding in order to ensue further build up towards curbing the disease. The structure and function of the virus, genome and revealed mutations are critical in directing the SARS-CoV-2 virus and disease understanding. Here, we analyze and review published knowledge on the virus in relation to the molecular specs and evolutionary relationships of the virus.





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