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Decoding Covid-19 with the SARS-CoV-2 Genome Analysis and

Visualization: Development and Usability study

Introduction

In December 2019, a pneumonia illness of unknown aetiology surfaced in Wuhan, China, with an animal meat market at the epicentre. The causative agent was quickly discovered and initially termed by the World Health Organization (WHO) as the 2019 novel coronavirus (2019-nCoV). Genetic analysis identified strong similarities between the severe acute respiratory syndrome (SARS) coronavirus (CoV) that was discovered in 2003 and it was renamed SARS-CoV-2. Infection with SARS-CoV-2 produces a clinical syndrome known as 2019 novel coronavirus disease (Covid-19).

Abstract.

SARS-CoV-2, the recently emerged coronavirus (CoV) that is responsible for the current global pandemic Covid-19, first appeared in late 2019 in Wuhan, China. Here, we summarise details of the SARS-CoV-2 genome to assist understanding of the emergence, evolution and diagnosis of this deadly new virus

Recent Findings:

Based on high similarities in the genome sequences, the virus is thought to have arisen from SARS-like CoVs in bats but the lack of an intermediate species containing a CoV with even greater similarity has so far eluded discovery. The critical determinant of the SARS-CoV-2 genome is the spike (S) gene encoding the viral structural protein that interacts with the host cell entry receptor ACE2. The S protein is sufficiently adapted to bind human ACE2 much more readily than SARS-CoV, the most closely related human CoV