



Name: Haidy Essam Elhamady
Prof: Dr/Sara elmetwaly

[Paper Research]

about Insights on early mutational events in SARS
CoV-2 virus reveal founder effects across
geographical regions

ABSTRACT

In this study, we characterized the early mutational events across 50 illumina high-quality datasets publicly available on the sequence read archive repository. A total of 30 out of 50 samples (60%) contained at least a single founder variant and most of the variants across samples are missense (over 63%). SARS-CoV-2 founder variants in WA State and USA are dissimilar to Australian SARS-CoV-2 founder variants, which were found to be heterogeneous. However, a mutational signature from USA mutations was found in an Australian sample, suggesting a world-wide spread of this molecular signature consisting of five-point variants. Remarkably, mutations in the helicase and ORF1ab proteins of the virus were found more frequently than others, suggesting that these regions continue to actively evolve. As proof of the latter.

Introduction

Coronavirus disease (COVID-19) is an infectious disease caused by a newly discovered coronavirus .Most people who fall sick with COVID-19 will experience mild to moderate symptoms and recover without special treatment. positive-stranded RNA virus with a large genome belonging to the family Coronaviridae, order Nidovirales .It is rapidly spreading worldwide, greatly surpassing the 8,000 total cases of the 2002–2004 SARS coronavirus outbreak (SARS-CoV-1) after 1 month of the initially identified case in China. The virus that causes COVID-19 is mainly transmitted through droplets generated when an infected person coughs, sneezes, or exhales.it is a threat to the global population. It is critical to understand SARS-CoV-2 characteristics to deal with this ongoing pandemic and to develop future treatments.

Releted work

The COVID-19 pandemic caused by a novel 2019 SARS coronavirus, known as SARS-CoV-2, is rapidly spreading worldwide, greatly surpassing the 8,000 total cases of the 2002–2004 SARS coronavirus outbreak (SARS-CoV-1) after 1 month of the initially identified case on 31 December 2019, in Wuhan ([Wilder-Smith, Chiew & Lee, 2020](#))

A SARS-CoV-2 virus is an enveloped, positive-stranded RNA virus with a large genome (29.9 kb) belonging to the family Coronaviridae, order Nidovirales ([De Wit et al., 2016](#))

One of the striking genomic features of this novel virus is the presence of a novel furin-like cleavage site in the S-protein of the virus, which differs from SARS-CoV-1.

([Coutard et al., 2020](#); [Wu et al., 2020a](#))

(Firstly, it was suggested that SARS-CoV-2 is relative of the RaTG13 bat-derived coronavirus rather than of SARS-CoV-1).(in the early beginning of the outbreak in China, sequencing the virus from nine patients from Wuhan in China revealed 99.9% similarity among samples. That finding suggests 2019-nCoV originated from one source within a very short time, supporting clonality of spreading) ([Lu et al., 2020](#))

Due to this association with bat coronaviruses, it was also argued that SARS-CoV-2 virus has the potential to spread into another species, as bat coronaviruses do ([Hu et al., 2018](#))

Although bats are likely natural reservoir hosts for SARS-CoV-2, it was recently demonstrated that SARS-CoV-2 is closely related to a pangolin coronavirus (Pangolin-CoV), the closest relationship found so far for SARS-CoV-2 .

([Zhang, Wu & Zhang, 2020](#))

In that study, genomic analyses revealed that the S1 protein of Pangolin-CoV is related closer to SARS-CoV-2 than to RaTG13 coronavirus. Also, five key amino acid residues involved in the interaction with the human ACE2 receptor are maintained in Pangolin-CoV and SARS-CoV-2, but not in RaTG13 coronavirus. ([Zhang & Holmes, 2020](#))

Recently, thousands of GenBank sequences from SARS-CoV-19 available at the NCBI virus database were trackable by region, suggesting that the transmission occurred mainly through clonal events due to clustering of the available sequences.

([Chen, Allot & Lu, 2020](#); [Kupferschmidt, 2020](#))(https://www.ncbi.nlm.nih.gov/labs/virus/vssi/#/virus?SeqType_s=Protein&VirusLineage_ss=SARS-CoV-2,%20taxid:2697049)