

[Paper Research]

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

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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.