SARS-CoV-2 基因突變與演化分布

SARS-CoV-2 mutations, evolution and spatiotemporal distribution

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SARS-CoV-2 continues to cause widespread morbidity and mortality all over the world nearly two years after its recognition. While much progress has been made with our understanding of its transmission, associated control measures and vaccination. Stumbling block of persuade people to receive vaccine and to fairly distribute vaccine worldwide have hampered our efforts. The SARS-CoV-2 pandemic's trajectory is controlled by the competition between public health intervention and viral evolution. SARS-CoV-2's mutation rate enables it to adapt to its host at a breakneck speed. The steady evolution of SARS CoV-2 into clinically important variants highlight the need to better understanding the underlying drive and mechanisms in order to control this virus. The fast dissemination and development of different SARS-CoV-2 mutations have been the major concern globally. In less than one year, the SARS-CoV-2 population has acquired over 75 heritable mutations, a rapid rate on the evolutionary scale. Studies of mutations, both those that occurred spontaneously in COVID-19 patients during the last year and those that were produced artificially in the laboratory, led us to better understand the interplay among mutations, adaption and host/therapy response. In the talk we will describe the SARS-CoV-2 and its attributes, the factors driving development of SARS-CoV-2 variants and the implications to therapy and important mutations, variants and their clinical impact. In December 2020, a novel variation (B.1.17) was identified in the United Kingdom, characterized by several spike protein mutations. This variation would not be linked with more severe illnesses or impact a particular age group more than previously circulating viruses, but due to its increased contagiousness, it resulted in the greatest death rate in the UK. Although it is unlikely that the B.1.1.7 variant will escape recognition by antibodies generated during prior infection or vaccination, some suggested that the complete set of Spike mutations present in the B.1.1.7 variant may reduce the neutralizing activity of vaccine. Another variation, B.1.351 (501Y.V2), was first identified in South Africa in December 2020; it has eight distinct mutations in the spike protein and may enhance transmissibility, although no change in disease severity has been shown to far. It has been seen in a number of European nations. Important mutation might be the driving force of pandemic. For example, the E484K mutation presented in several variants and occurs in fast succession throughout the world, most notably in the South Africa and South America. The E484K mutation was first discovered in the South African Beta variation (B1.351) and has since been found in

the United Kingdom's Alpha variant (B.1.1.7) and Brazil's Gamma variant (P.1), both of which are classed as SARS-CoV-2 variants of concern. The mutation is associated with increasing transmissibility, severity and a significant decrease in effectiveness of vaccines, therapy and other health measures by the WHO. E484K escape a variety of monoclonal antibodies, convalescent plasma, and post-vaccine sera. Numerous investigations have shown that the E484K mutation decreases the neutralization of convalescent sera, as demonstrated by a pseudoviral test. Monoclonal antibodies obtained from convalescent patients were further studied, and class 2 antibodies were shown to be resistant to the E484K mutation. The virus's evolution is accompanied by continuous adaptive diversification within and across geographic areas. Understanding the pandemic's development is critical for controlling and eventually eradicating it.