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Short Communication

Clinical Application of COVID-19 and its Viral Variants

Cairo Urbi*

Department of Microbiology, Tanta University, Tanta, Egypt

DESCRIPTION

In May 2022, the SARS-CoV-2 Omicron BA.2.75 variant emerged. BA.2.75 is a BA.2 descendant but is phylogenetically distinct from BA.5, the dominant BA.2 descendant at the moment. BA.2.75 has a higher effective reproduction number and a different immunogenicity profile than BA.5. BA.2.75 was tested for sensitivity to vaccine and convalescent sera, as well as a panel of clinically available antiviral drugs and antibodies. The potency of antiviral drugs was mostly preserved, but antibody sensitivity varied depending on several key BA.2.75-specific substitutions. The BA.2.75 spike had a far greater affinity for its human receptor, ACE2. Furthermore, BA.2.75 had higher fusogenicity, growth efficiency in human alveolar epithelial cells, and intrinsic pathogenicity in hamsters than BA.2. Our multilevel investigations indicate that BA.2.75 acquired virological properties independent of BA.5, and that BA.2.75 poses a greater risk to global health than BA.5. Metagenomic next-generation sequencing (mNGS) is an untargeted technique for determining microbial DNA/RNA sequences in a wide range of infectious syndrome samples [1].

mNGS is still in its early stages of widespread clinical application. The European Society for Clinical Virology (ESCV) Network on Next-Generation Sequencing (ENNGS) has been established to further support the development, implementation, optimization, and standardization of mNGS procedures for virus diagnostics. ENNGS's goal is to bring together professionals involved in mNGS for viral diagnostics in order to share methodologies and experiences, as well as to develop application guidelines. Pursuing the ENNGS publication in this journal Recommendations for the introduction of mNGS in clinical virology, part I: wet lab procedure, the current manuscript aims to provide practical recommendations for the bioinformatic analysis of mNGS data and the reporting of results to clinicians. Since its discovery in early 2020, the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has been wreaking havoc. Despite its similarities to several Betacoronavirus strains, including SARS-CoV-1 and bat-derived SARS-related Coronaviruses (SARSr-CoVs), SARS-CoV-2 has several distinguishing characteristics that contribute to its pathogenesis and transmission. Clinically, Coronavirus Disease 2019 (COVID-19) exhibits a wide range of symptoms, from asymptomatic to mild/moderately symptomatic to critical illness with Acute Respiratory Distress Syndrome (ARDS) and death. Furthermore, presymptomatic transmission has significantly aided SARS-CoV-2 community spread. Asymptomatic, pauci-symptomatic, and presymptomatic transmission made it difficult to trace and contain its spread, resulting in a global pandemic that has lasted more than two years, with over 330 million confirmed cases and 5.5 million reported deaths, though the COVID-19 pandemic's attributable mortality has been estimated to be 12 to 22 million by January 2022. 5 The authors discuss key aspects of SARS-CoV-2 virology that contribute to the virus's varied clinical manifestations, evolution, replication dynamics in the respiratory tract, and systemic dissemination in this review [2].

SARS-CoV-2 is a member of the Betacoronavirus and Sarbecovirus subgenera. It is a 29.9-kilobase (kb) single-stranded, positive-sense RNA virus. This virus is 96.2% identical to a bat SARSr-CoV strain RaTG13 and 79.6% identical to SARS-CoV-1. SARSr-CoV has also been recovered from pangolins (Manis javanica) and various bat species (e.g., RpYN06 from Rhinolophus pusillus in southern China and RshSTT182/RshSTT200 from Rhinolophus shameli in Cambodia), with varying degrees of recombination detected in different regions of the genome. Chronic Hepatitis B (CHB) is a major public health issue that affects more than 250 million people worldwide. Cirrhosis and Hepato Cellular Carcinoma (HCC) are more likely in these patients [3].

The goal of antiviral therapy for CHB patients is to achieve sustained suppression of Hepatitis B Virus (HBV) and, ideally, clearance of Hepatitis B Surface Antigen (HBsAg), which is associated with functional remission of CHB and better long-term outcomes. However, the relapse rate for HBV remains high, and HBsAg loss occurs infrequently following current antiviral therapy. SARS-CoV-2 is a highly transmissible pathogenic coronavirus that emerged in late 2019 and caused a pandemic of acute respiratory disease known as "coronavirus disease 2019". It has spread rapidly throughout the world, posing a significant

Correspondence to: Cairo Urbi, Department of Microbiology, Tanta University, Tanta, Egypt, Email: urbro@uni.il.eg

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threat to global public health. There are seven human coronaviruses in addition to SARS-CoV-2. The mild pathogens are 229E, OC43, NL63, and HKU1, while the pathogenic ones are SARSCoV, MERS-CoV, and SARS-CoV-2 [4].

CONCLUSION

Coronaviruses are spherical in shape and have club-shaped spikes on their surfaces. It contains a large positive sense, single stranded RNA genome with helical symmetry within the nucleocapsid. It has been shown to infect a wide range of mammalian hosts, including humans, cats, bats, civets, dogs, and camels. The viral genome contains four major structural proteins: the Spike (S), Membrane (M), Envelope (E) and Nucleocapsid (N) protein, all of which are encoded at the 3's end of the genome. The S protein of the virus binds to a specific receptor on the host cell. Following receptor binding, the virus enters the host cell cytosol and fuses the viral and cellular membranes, followed by viral genomic RNA translation. The mature virus is formed following viral replication and sub-genomic RNA synthesis. The virions are then delivered to the cell surface in vesicles and exocytosed.

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