

Which is more accurate SARS-CoV + MERS-CoV = SARS-CoV2 or SARS-CoV + MERS-CoV = MERS-CoV2?

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Abstract

The functions of existing proteins are explained based on the proteins of previously known coronaviruses. While the role of most non-structural proteins in viral replication has been defined, the role of some is still not fully explained. Four structural proteins have an essential role in combining virion and being a target for coronavirus infection pathogenesis and drug development.

Keywords: SARS-CoV; MERS-CoV; covid-19

Introduction

E protein

This protein activates protein by interacting with other proteins in the cell. The E protein is an important virulence factor that plays a role in bud's separation from the cell. The assembly of viral parts plays a role in pathogenesis and virus release. Even though its role in pathogenesis is not fully known, the oligomerization of E proteins causes ion channel structure. If there is no E protein in the virus, the viral load in the host was found to be lower [1-23].

S protein

It is in the form of protrusions on the surface of the virus, on the viral envelope, and allows the virus to attach to the host cell by binding to the membrane and receptor fusion. It is an essential viral protein that determines host cell tropism. S protein has S2, and S1 loops, primarily S2 protein is responsible for membrane fusion, and S1 protein is responsible for binding to the host cell receptor. The S2 protein of 2019-nCoV is 93%, similar to bat-SLCoVZXC21 and bat-SL-CoVZC45. In S1 protein, this similarity is approximately 68%. Both the C and N terminal parts of the S1 loop can bind to the host cell receptor. Even though SARS-CoV and 2019-nCoV are among separate tribes, both viruses have 50 protected proteins in the S1 protein. This result; offers that the new coronavirus can use angiotensin-converting enzyme 2 (ACE 2) as a receptor as in SARS-CoV [1-23].

N protein

It plays a role in the regulation of transcription and replication of viral RNA. The N protein also acts as an interferon antagonist, thereby preventing the virus from being destroyed by the immune system. Along

with M protein, they are envelope proteins that have a critical role in virus release and structure. It includes two domains that can bind the viral genome through various mechanisms. This protein binds to the nsp3 protein to provide contributes to the virion structure and binds the genome to RTK [1-23].

M protein

It plays a vital role in the cry of viral intracellular balance. This protein is essential for the host cell to become susceptible to the virus, enabling the activation of the Interferon-beta (IFN-beta) pathway through the Toll-like receptor-dependent mechanism [1-23].

Along with N protein, they are envelope proteins that have a significant role in virus release and structure. It has three transmembrane shapes virions (Virion = full virus particle), and sections, increases binds to the nucleocapsid, and the membrane curve. It helps the stabilization of the nucleocapsid protein. Hence, it helps the continuation and structure and the nucleocapsid-RNA complex [1-23].

Hemagglutinin Esterase Protein

It is found on the envelope, more privately, a protein located in beta coronaviruses. It permits the virus to link to the receptors, including sialic acid [1-23].

The natural host of coronaviruses are bats, and their growth is shaped in bats. It is confirmed that most coronaviruses in humans are derived from bat reservoirs. Bat belongs to SARS-CoV-2 and subgenus Sarbecovirus by various research groups. The genetic similarity of betacoronavirus has been confirmed. At the same time, MERS-CoV (roughly this degree of similarity with the genomes of 50%) or SARS-CoV (about 79%) was not found (**Figure 1-3**) [1,2,4,5,9,24-28].



Figure 1. There are four options for the intermediate host of COVID-19 [29].

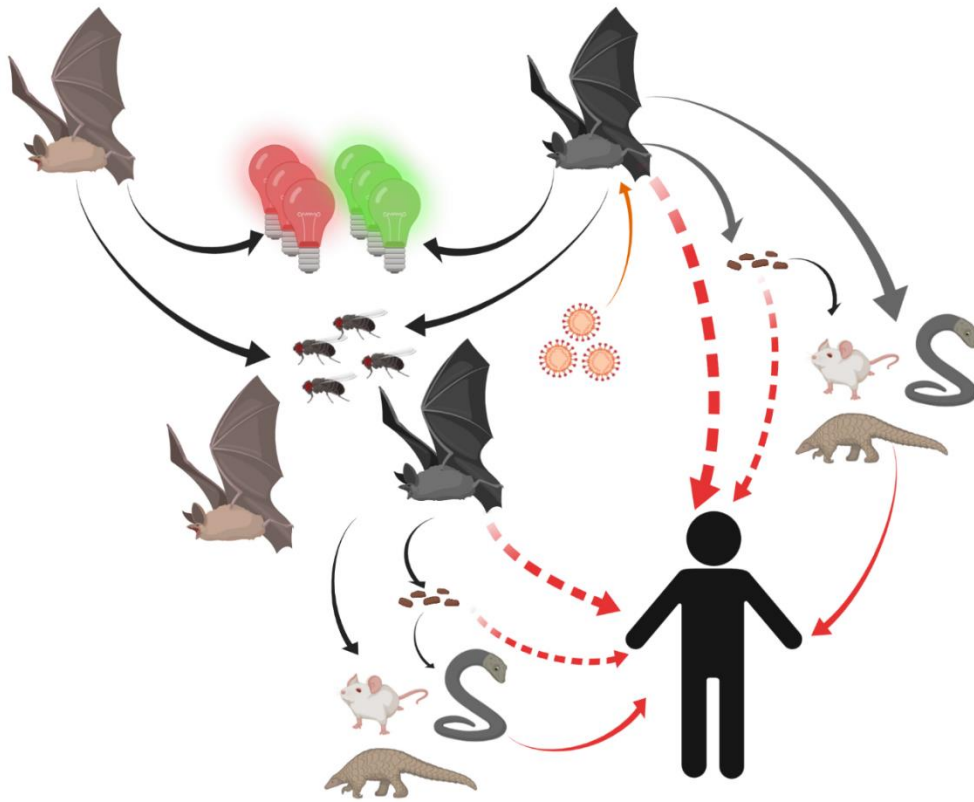


Figure 2. Possible COVID-19 transfer paths[30].

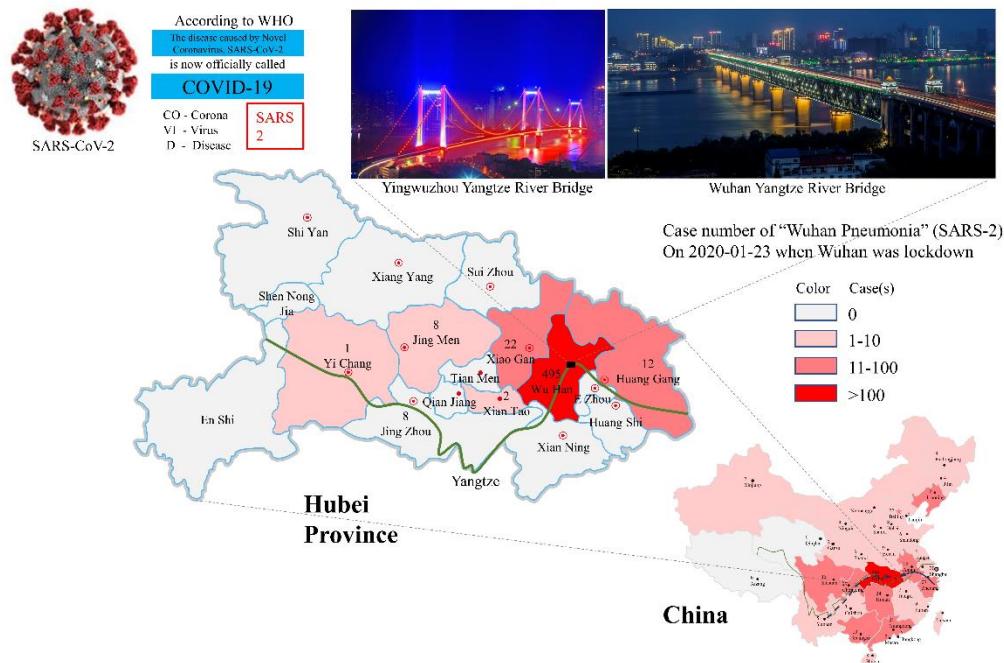


Figure 3. SARS-2 outbreak map for China, and Hubei Province[30].

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