



Viral Respiratory Disease: Severe Acute Respiratory Syndrome (SARS)

G. Akshay Kumar*

Department of Pulmonary and Critical Medicine, Oregon Health and Science University, Portland, USA

DESCRIPTION

A coronavirus is the source of the viral respiratory disease known as Severe Acute Respiratory Syndrome (SARS). At the end of February 2003, it was first discovered as part of an outbreak that started in China and quickly expanded to four other nations. With the help of the Global Outbreak Alert and Response Network (GOARN), World Health Organization (WHO) coordinated the global investigation and collaborated closely with the health authorities in the affected nations to provide epidemiological, clinical, and logistical support and contain the outbreak. Similar to the cold and the flu, SARS is an airborne virus that can spread by tiny droplets of saliva.

The first widespread illness to show up in the twenty-first century clearly showed a capacity to spread along the pathways of international air travel. Surfaces touched by a person who is sick with the virus might indirectly spread SARS to others. There have been a few probable SARS cases among youngsters under 15 years old.

The current lower respiratory tract infection outbreak, which includes respiratory distress syndrome, is the third significant epidemic caused by an animal coronavirus spreading to humans in just two decades. The originality of the human pathogen known as 2019-nCoV was evaluated here by the Coronavirus Study Group (CSG) of the International Committee on Taxonomy of Viruses, which is in charge of creating the official classification of viruses and taxa naming (taxonomy) of the *Coronaviridae* family.

The CSG formally recognises this virus as a replicant to Severe Acute Respiratory Syndrome Corona Viruses (SARS-CoVs) of the species severe acute respiratory syndrome-related coronavirus and designates it as severe acute respiratory syndrome coronavirus 2 based on phylogeny, taxonomy, and established practice (SARS-CoV-2).

The independent zoonotic spread of SARS-CoV and SARS-CoV-2 emphasises the importance of researching the complete (virus) species in addition to studies that concentrate on specific pathogenic viruses with immediate relevance. This study will advance our knowledge of how viruses interact with hosts in a dynamic environment and increase our capacity to respond to outbreaks in the future.

The civet and bat SARS-CoV, the human coronavirus NL63, and the human coronavirus HKU1 were all discovered shortly after this virus was first identified. The number of coronaviruses on the list has expanded to at least 36 as a result of coronavirus surveillance in numerous animal species. There was a rush on research into the epidemiological, clinical, pathological, immunological, virological, and other fundamental scientific aspects of the virus and the disease due to the first SARS epidemic's explosive nature, high mortality, brief reemergence a year later, and economic disruptions.

The rapid advance in knowledge of the virus and the illness in such a short period of time has facilitated the creation of diagnostic tools, animal models, antiviral medications, vaccines, and epidemiological and infection control strategies that, should SARS recur, could be tested in randomised control trials.

The discovery that civets are the amplification host and that horseshoe bats are the natural reservoir for the SARS-CoV-like virus emphasises the significance of wildlife and biosecurity in farms and wet markets, which can act as the source and amplification sites for emerging illnesses. The first major sickness to emerge in the twenty-first century was SARS, which spread quickly. Adults between the ages of 25 and 70 who had previously been healthy made up the majority of SARS patients. Hence, for infections that meet the current WHO case criteria for probable and suspected SARS cases about 3%.

Correspondence to: G. Akshay Kumar, Department of Pulmonary and Critical Medicine, Oregon Health and Science University, Portland, USA, E-mail: akshayk@gmail.com

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