

# Corona Viral Epidemic: A Review

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## ABSTRACT

Viruses are both living and non-living organisms; living when found inside the host cell as they proliferate and grow, whereas, on occasions when they do not find any host cell, they are inactive or in a dormant stage. The virus can replicate itself and their genetic material mostly consists of either DNA or RNA. Different viral species spread in different ways. For example, plant virus spreads from plant to plant by insects and other organisms, some viruses are spread by body fluids of humans: influenza virus spread by aerosol droplets when people sneeze or cough. HIV is transmitted through body fluids; Dengue is propagated by mosquito bite. SARS virus is a respiratory disease that is spread by animals and humans.

Keywords: Coronavirus; Influenza; SARS; Public health; WHO

## INTRODUCTION

The latest virus which is terrifying mankind is Coronavirus (CoV) and is considered as one of the most dangerous viruses that affected humans. Coronavirus belongs to the same virus family as SARS (Severe Acute Respiratory Syndrome). It belongs to Coronaviridae family.

Coronaviruses commonly occur in animals but have the potential to infect people like MERS, SARS showed and now the latest 2019-nCoV, where 2019 stands for the year of detection, n stands for novel and CoV stands for Corona Virus. The latest name for the virus as per WHO is COVID-19.

The virus has been spotted primarily in Wuhan city of China. The outbreak of this infection is spreading its wings to different parts of the world so much so that WHO has declared this as "Public Health Emergency of International Concern". The Coronavirus propagates through animals and human beings. This virus is also airborne which spreads through infected respiratory droplets of cough and sneeze. The main source for CoV is yet to be identified. Whether transmission takes place by touching the objects (having surface viral particles) and then mouth/nose/eyes are not yet clear. This virus is challenging the global public health system causing an epidemic. In one month time, the spread of the virus to neighboring countries indicated human to human transmission. The neighbouring countries of China are on high alert because of this virus as the passengers

who are traveling from China may potentially bring this virus to their homeland. There are a lot of screening centres at the International borders and at all the airports where International travelers are entering the countries.

Confirmed cases of viral infection have been reported in Western Pacific, South-East Asia, USA, Canada, France, Finland, Germany, and UAE. Japan, Singapore, Republic of Korea, Australia and Thailand reported more than 20 cases. The symptoms can occur from 2 to 14 days after exposure. The clinical symptoms would be cold, running nose, cough, fever, sore throat. If these symptoms are neglected then it may lead to fatal pneumonia. As per the current stats, it is estimated that the deaths are approximately 2595 with a mortality rate of around 3% in China. The mortality rate outside China was 2% as per the latest statistics. In the Western Pacific region, the highest number of confirmed cases was recorded in the Republic of Korea followed by Japan. In European regions, Italy remains worst affected with 124 confirmed cases.

Mortality-wise the Corona was observed to be milder compared to SARS but definitely outnumbered its transmission rate and prevalence. For the implementation of public health measures for supporting countries to prepare and respond to the epidemic is USD 675 million. Accurate diagnosis is based on a molecular study that is cost and resource-intensive. Currently, Reverse Transcription-Polymerase Chain Reaction protocol can detect and identify 2019-nCoV in serum and respiratory clinical

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samples. Prevention is always better than cure. The prevention practices include washing and sanitization of hands, avoid touching of eyes, nose, and mouth; isolation when in sick condition, covering a cough and sneeze with tissues and disposing of in trash and disinfection of object surfaces. Table 1 provides updated information on virus isolation, identification, transmission, symptomatology, and genetic resemblance.

Yang et al. [1] conducted a single centred retrospective observational study on the clinical outcomes of 52 critically ill adult patients in Wuhan, China. Based on the demographic data, symptoms, laboratory recording and comorbidities, the author along with his team compared the clinical characteristics in surviving and non-surviving patients. The results revealed that patients had organ failures while hospital-acquired infections were noted in 13% of patients. They have observed that older patients with co-morbidities were at increased risk of mortality.

WHO has given certain specific recommendations and advice to the general public in order to reduce the risk of transmission. These measures include avoiding close contact with people affected with acute respiratory symptoms, frequent hand washing, covering of cough and sneeze with disposable tissues or clothing.

Table 1: Recent studies on novel Coronavirus.

Referenc e	Finding	Methods			
Zhu et al. [2]	Novel coronavirus 2019- nCoV isolated from human airway epithelial cells were found to be different from MERS-CoV and SARS-CoV	Viral diagnostics, viral isolation, electron microscopy, viral genome sequencing			
Li et al. [3]	Average incubation time was found to be 5.2 days; human to human transmission; the epidemic doubled every 7.4 daysDemographics, ex history, illness time among 425 patien confirmed coronavirus pneumonia (NCIP)				
Huang et al. [4]	2019-nCoV infection caused severe respiratory illness highly associated with mortality	Real-time PCR, next- generation sequencing, cytokine and chemokine measurements			
Li and De Clercq [5]	Emphasized on development of broad-spectrum antiviral agents and depicted potential drug targets for beta-corona virus	Review study			
Holshue et al. [6]	Reported first confirmed case of 2019-nCoV infection in the United States in a 35- year-old man	Specimen collection, 2019- NCOV diagnostics, gene sequencing			
Wang et al. [7]	Emphasized on novel antiviral drugs, monoclonal	Review study			

	and polyclonal neutralising antibodies	
Zhou et al. [8]	The sequence of novel CoV share 79.5% similarity with SARS-CoV and at whole- genome level, 2019-nCoV is 96% identical with bat coronavirus. Novel CoV uses the same cell entry receptor, ACE2, as SARS-CoV.	Full-length genome sequencing from five patients' bronchoalveolar lavage fluid,
Song et al. [9]	Have observed that consolidation lesions could serve as a marker of disease progression or more severe disease; emphasized that positive nucleic acid testing is the golden standard in diagnosis; patients with fever and/or cough and with GGO prominent lesions in the peripheral and posterior part of lungs combined with normal or decreased white blood cells and a history of epidemical exposure should be highly suspected of the 2019-nCoV pneumonia.	Thin section CT scans of the 2019-CoV infected patients as well as the study of clinical and laboratory parameters
Lu et al. [10]	The novel Coronavirus 2019- nCoV showed 88% similarity with bat derived SARS-like coronavirus and was found to be distant to SARS-CoV and MERS-CoV; 2019-CoV had similar receptor binding domain structure to that of SARS-CoV with amino acid variation at key residues; 2019-nCoV might be able to bind to the angiotensin- converting enzyme 2 receptors in humans.	Viral genome analysis including sequencing and phylogenetic analysis
Corman et al. [11]	Have observed that the methodology and workflow mentioned, reliably detects 2019-nCoV, and further discriminates 2019-nCoV from SARS-CoV	RNA extraction, real-time reverse transcription
Chan et al. [12]	The study supports person-to- person transmission in hospital and family setting, old patients had extensive radiological lung changes and biochemical parameters; found the closest similarity to the bat severe acute respiratory syndrome (SARS)- related coronaviruses found in Chinese horseshoe bats.	Respiratory and diarrhoeal pathogen detection, RT- PCR and sequencing, whole-genome sequencing and genome analysis by bioinformatics, phylogenetic tree analysis,

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Backer et	Mean	incubation	time	was	Incubation	period	
al. [13]	estimated to be 6.4 days			distribution analysis, travel			
					history, symptom onset,		

#### CONCLUSION

Surveillance, epidemiological assessment, prediction modeling, medical preparedness, diagnostics, precaution, clinical care, and quarantine have great significance and importance in preventing the spread of the virus, particularly in the context of the growing density of urban populations.

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