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# Origin, Epidemiology, and Transmission of Pandemic *Corona Viruses* (SARS-Cov, MERS-Cov, 2019-NCoV): A Review



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#### **ABSTRACT**

The prevalence of COVID-19 has become a pandemic infection. The term 'coronavirus' was first coined in 1968, from showing crown-like morphology when observed in an electron microscope. Coronaviruses (CoVs) infect humans and a huge variety of animals with the progression of diseases in hepatic, enteric (intestines), respiratory and neurological systems with different severity potentials. The family Coronaviridae comprises two subfamilies including Letovirinae and Orthocoronavirinae. CoVs are summarized into four genera-Alphacoronavirus, Betacoronavirus, Gammacoronavirus, and Deltacoronavirus. Betacoronavirus was further classified into four lineages A, B, C and D. As per W.H.O, since mid of December 2019, a pneumonia-like disease with symptoms fever, difficulty in breathing, cough, invasive lesions on lungs, of unknown etiology emerged in the central Chinese city of Wuhan. After the pathogenesis of SARS, SARS-CoV was identified and also anti-SARS-CoV antibodies were seen in masked palm civets and animal handlers- in markets. Moreover, in camels, MERS-CoV-specific antibodies have been seen from the Middle East (the United Arab Emirates, Kingdom of Saudi Arabia, Oman and Jordan) Africa and Asia (South Korea and Thailand). Bats have been a natural reservoir of all discovered coronavirus lineages and believed as an ancestor for all coronavirus lineages. As of 13 March 2020, a total of 81 cases of COVID-19 have been reported in India. This review will help out in understanding, origin, and epidemiology with the transmission of novel coronavirus worldwide. It encourages fellow researchers to focus on insights into designing a novel vaccine or treatment for eradicating it on the planet.

#### **INTRODUCTION**

The term 'coronavirus' was first coined in 1968, from showing crown-like morphology when observed in an electron microscope. The RNA is bound with basic nucleocapsid (N) protein, forming a helical capsid within the virus's membrane [1]. Coronaviruses (CoVs) infect humans and a huge variety of animals with the progression of diseases in hepatic, enteric (intestines), respiratory and neurological systems with different severity potentials [2]. CoVs are summarized into four genera- Alphacoronavirus, Betacoronavirus, Gammacoronavirus, and Deltacoronavirus. Betacoronavirus was further classified into four lineages A, B, C and D. Later, they renamed as Embecovirus (previously lineage A), Sarbecovirus (previously lineage B), Merbecovirus (previously lineage C) and Nobecovirus (previously lineage D). Continuous outbreaks of MERS-CoV have become life-threatening to humans. Both, Alphacornonavirus and Betacoronavirus have been detected from bats (mode of transmission) in Asia, Africa, Europe, Australia, North and South America [3]. A total of six species of human coronavirus has been discovered including OC43, 229E, NL63, HKU1, SARS-CoV, and MERS-CoV. Human coronaviruses OC43 and 229 E were identified approx. 51 years ago which cause common cold in humans [4]. The coronavirus belongs to the family Coronaviridae- the largest family in Nidovirales order. The family Coronaviridae comprises two subfamilies including Letovirinae and Orthocoronavirinae. All four genera are parts of Orthocoronavirinae subfamily that include alphacoronavirus, betacoronavirus, gammacoronavirus and delta coronavirus. Mammals are habitats for alphacoronavirus and betacoronavirus, and birds for gammacoronavirus and delta coronavirus. In 1967, HCoV-229E was first identified and found circulating in humans; spread by bats. Over 200 novel coronaviruses have been detected in bats till now [5].

## **Origin of Human Coronaviruses**

As per W.H.O, since mid of December 2019, a pneumonia-like disease with symptoms fever, difficulty in breathing, cough, invasive lesions on lungs, of unknown etiology emerged in the central Chinese city of Wuhan. The outbreak in Wuhan was released and informed by a consortium of researchers, government and institutes, on Global Initiative on Sharing All Influenza Data (GISAID) and on virological.org. Chinese authorities declared causative agent a novel coronavirus (2019-nCoV). The UN Health Agency has urged China to identify the source, reservoirs and possible intermediate hosts of the new virus [6].

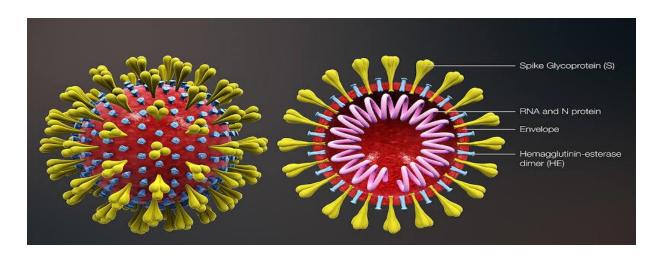


Figure No. 1: Structure of Novel Coronavirus (2019-nCoV)

In 2002, severe acute respiratory syndrome coronavirus (SARS-CoV) was detected in China. After the pathogenesis of SARS, SARS-CoV was identified and also anti-SARS-CoV antibodies were seen in masked palm civets and animal handlers- in markets. Later, investigations showed that SARS-CoV strains seen in markets were transmitted from diverse animals to them (humans) [1]. In 2005, the discovery of novel coronaviruses was come in nature being related to human SARS -CoV and named as SARS-Like coronaviruses in horseshoe bats. Various strains of SARS-Like coronaviruses were discovered in bats in different states in China, European, African and Southeast Asian countries. The genome (genetic sequence) of human SARS-CoVs is almost identical to the genome of SARS-CoVs from market civets. In 1983, MERS-CoV was detected in camel serum remaining almost identical to human coronaviruses. Moreover, in camels, MERS-CoV-specific antibodies have been seen from the Middle East (the United Arab Emirates, Kingdom of Saudi Arabia, Oman and Jordan) Africa and Asia (South Korea and Thailand) [7]. Coronaviruses genetic sequences are made up of one continuous RNA strand (positive polarity) ranges between 27000 to 32000 nucleotides- the largest continuous RNA genomes (genetic sequences) among mammalian viruses. Only a small fraction of mammalian coronaviruses are found to be originated from primates, carnivore and rodent hosts. Bats showed itself as a mammalian host and cause of diverse viruses. Betacoronavirus 1 has been found in cows, dogs, horses, deer, humans, camels, waterbucks, and giraffes worldwide [8]. In research held in 1983, declares that many human coronaviruses (HCV) have been reported for their isolation to cause upper respiratory tract infections in both children as well as adults. These were classified into 1 of 2 distinct antigenic groups and named HCV 229E and HCV OC43. These coronaviruses cause wheezing in young asthmatic children but rarely in normal children. In

children with respiratory infections, an enzyme-linked immunosorbent assay (ELISA) technique was implemented for the detection of HCV antigens in nasal secretions [9].

## **Global Epidemiology**

As of 13 March 2020, a total of 81 cases of COVID-19 have been reported in India: 64 identified as Indian nationals, 17 foreign nationals, 3 recovered and 1 died. Death was reported for a 76-year-old male from Karnataka, with a history of travel to Saudi Arabia (Feb 2020)- WHO, India.

In late December 2019, several patients were found admitted to hospitals with pneumonia-like health problems having unknown etiology. It predicted the onset of a potential new (novel) coronavirus outbreak and named as COVID-19 or 2019-nCoV (by W.H.O. on Feb 11, 2020). Till January 2, 2020, 41 patients were found hospitalized and infected by COVID-19, less than half of these patients had underlying medical conditions such as diabetes, hypertension and cardiovascular diseases [10].

A study in 2013 suggests that in over 30 countries, SARS coronavirus has been leading cause behind the sum of 774 deaths among more than 8000 infected individuals due to severe acute respiratory syndrome (SARS). The world is facing a new challenge by 'SARS-Like' infection spread by another novel coronavirus in the Middle East; originally named as human coronavirus EMC/2012 (HCoV-EMC), after Coronavirus Study Group of International Committee for Taxonomy of Viruses as Middle East respiratory syndrome coronavirus (MERS-CoV). MERS-CoV was reported as a zoonotic agent because of having the ability to replicate in bat, porcine, rabbit, goats, camels, sheep, and civet cell lines [11].

A recent survey done by W.H.O., states that novel coronavirus (2019-nCoV) and other known species of coronaviruses are more specifically found in Rhinolophus sub-species of the bat. These sub-species are abundantly and broadly distributed in Southern China, South and Middle East Asia, Africa and Europe. In China, more than 500 CoVs have been identified in bats. Globally total confirmed cases- 72469, new cases-10955, death- 2531 and new deaths- 333 on COVID-19, confirmed by W.H.O. on March 15, 2020.

Table No. 1: Globally presence and deaths by a novel coronavirus (2019-nCoV)

WHO Region	Country/Territory	Confirmed Cases	New Cases	Total Deaths (new)
	China	81048	27	3204 (10)
Western Pacific	Singapore	212	12	0 (0)
	Republic of Korea	8162	76	75 (3)
	Japan	780	64	22 (1)
	Malaysia	238	41	0 (0)
	Australia	249	52	3 (0)
	Viet Nam	53	5	0 (0)
	Philippines	111	47	6 (4)
	Cambodia	7	0	0 (0)
	New Zealand	6	0	0 (0)
	Mongolia	1	0	0 (0)
	India	107	25	2 (0)
	Thailand	75	0	1 (0)
South-East Asia	Nepal	1	0	0 (0)
	Sri Lanka	11	5	0 (0)
	Bangladesh	3	0	0 (0)
	USA	1678	0	41 (0)
America	Canada	244	68	1 (0)
	Italy	21157	3497	1441 (173)
Europe	Germany	3795	733	8 (2)
	France	4469	829	91 (12)
	The United Kingdom	1144	342	21 (11)
	Spain	5753	1522	136 (16)
	Belgium	689	90	0 (0)
	Finland	210	101	0 (0)
	Sweden	924	149	0 (0)
	Russian Federation	34	0	0 (0)
	Iran	12729	1365	608 (94)
Middle East	Qatar	337	75	0 (0)
	Bahrain	211	1	0 (0)
	Kuwait	112	12	0 (0)
	Saudi Arabia	103	41	0 (0)
	UAE	8	1	0 (0)

In the 21<sup>st</sup> century, the whole world has seen globally spreading of two previously unrecognized and being highly pathogenic coronaviruses, severe acute respiratory syndrome coronavirus (SARS-CoV) and Middle East respiratory syndrome coronavirus (MERS-CoV).

At the beginning of November 2002 in China, the transmission of SARS-CoV, from person to person was resulted in high fatality rates. Also, zoonotic transmission of SARS from the end of 2003 to the beginning of 2004, researchers came into the origin of this new coronavirus. After, certain 'SARS-Like' viruses came in knowledge in bats with the ability to spread and infect the human cells without prior and enough adaptation which indicates the possibility of re-occurrence of SARS-CoV or 'SARS-Like' coronaviruses [12] [5].

Table No. 2: Cell line sensitivity, prevalence and biological features of SARS-CoV and MERS-CoV [12] [5]

Feature	SARS-CoV	MERS-CoV	
Origin	Guangdong province, China	Arabian Peninsula	
Natural reservoir	Bat	Bat	
Intermediary host	Palm civet	Dromedary camel	
Genus	Beta-CoVs, (lineage B)	Beta-CoVs, (lineage B)	
Total no. reported to WHO,	More than 8437 people	2494	
Al Jazeera	More than 8437 people		
Affected countries	30	27	
Number of deaths (WHO, Al	016	858	
Jazeera)	HU <sup>916</sup> AN		
Mortality	More than 10%	More than 35%	
Transmission region	Globally	Regionally	
Transmission mode	From animal to human,	From animal to human,	
Transmission mode	from human to human	from human to human	
	Human angiotensin-	Human dipeptidyl peptidase 4 (UPP4 or CZ26)	
Predominant receptor	converting-enzyme 2		
	(ACE2)		
		Liver, Kidney, Neurons,	
Cell line sensitivity	Liver, Kidney	monocyte, lymphocyte,	
Cen fine sensitivity	Respiratory tract	histiocytic cells, respiratory,	
		intestinal & genitourinary tract	
Replication efficiency	High	Higher	

#### Transmission and outreach- worldwide

A research published on 27 February 2020, WHO confirms that when COVID-19 infected person cough or exhales and fluid fall on objects such as desks, tablets or telephones and other persons get the same infection by touching contaminated surfaces. It spreads even if a person is standing one meter apart through droplets of exhaling or ventilation. COVID transmits in a similar way to the flu. Most persons (infected with COVID-19) experience mild symptoms and easily recovered but some get hospitalized and require extensive care. The severity of infection increases with age: people over 40 years are more vulnerable than those got infection under 40 years. Persons suffering from medical conditions such as diabetes, heart disease, lung disease, and weak immune system remain more vulnerable to involve in serious illness: WHO. Bats have been a natural reservoir of all discovered coronavirus lineages and believed as an ancestor for all coronavirus lineages [13].

Typical clinical symptoms were observed as fever, dry cough, dyspnea, headache, and pneumonia. The onset and severity of disease determine respiratory failure due to alveolar damage and even death. The condition was named viral-induced pneumonia by physicians according to the manifestation of clinical symptoms such as increasing body temperature (fever), decreasing lymphocytes and white blood cells, new pulmonary infiltrates and no common improvement upon antibiotics treatment [14].

Swine acute diarrhea syndrome coronavirus (SADS-CoV) recently emerged and spilled over from bats to pigs. Bats serve as major natural reservoirs of alpha coronaviruses as well as beta coronaviruses [7]. In 2012, MERS-CoV (2c  $\beta$ - coronavirus) was firstly identified in Saudi Arabia; a causative agent (in a series of) of highly pathogenic in lower respiratory tract infections. In the Middle East, it became the reason for high mortality (20% to 40%); also outbreaks in South Korea in 2014 [4].

After 15 years outbreak of MERS-CoV, another severe acute diarrhea syndrome coronavirus (SADS-CoV)- causing fatal diseases in pigs was identified. CoVs have enveloped with crown-like viral structure, for that, it named so. Compared with other RNA viruses, the replication of coronaviruses is much rapid, and it's believed due to expanded/large genome (genetic sequence) size. CoV being the second largest of all RNA virus genomes contains a positive sense, single-stranded RNA (+ssRNA) [15].

Feline infectious peritonitis (FIP) is a fatal-immune mediated disease seen in domestic cats as a result of infection by an immunogenic coronavirus called FIP virus (FIPV); with a positive-stranded RNA genetic sequence. Since 1963, the original description came in knowledge but still, its etiology is unknown. Three clinical forms of FIP's disease are known: i) wet/effusive, which is characterized by fatal pleuritis or fibrinous peritonitis; ii) dry/non-effusive, which does not contain fluid but has fatal fibrinous peritoneal deposition; iii) subclinical enteritis, which contains mild symptoms only. Research in 1990, has reported the occurrence of coronavirus infection in captive and free-ranging cheetah in North America, Europe, and Africa. Coronavirus earlier has been confirmed in domestic cats, too [16]. HCoV-HKU1 is probably transmitted through the exchange of respiratory secretions; reported worldwide. The incidence of infection remains more susceptible in winter. A seropositive result for HCoV-HKU1 was 59.2%, significantly lower than those for HCoV-OC43 (90.8%), HCoV-229E (91.3%), and HCoV-NL63 (91.8%) [17].

A study in 2004, reported that SARS-Like-CoV found in horseshoe bats. Four species of horseshoe bats were found in different regions of mainland people's- Republic of China. All four species demonstrated, the infection by SARS-Like-CoV: Two species (*R. pearsoni, R. macrotis*) had diagnosed and confirmed by both serologic and PCR tests and the last 2 species (*R. pussilus, R. ferrumequinum*) confirmed either by serologic or PCR tests. Genetic codon of all SARS-Like-CoV is almost identical to that of SARS-CoVs isolated from humans and civets [18]. Coronavirus like particles was detected in feces of diarrheic foal and adult horses by electron microscopy- negative stain. The coronavirus N protein has been demonstrated as a highly variable in amino acid composition [19].

#### **SUMMARY**

The present study is going to describe coronaviruses comprehensively to know well. It has become essential to be familiar and aware of causes, modes of transmission from one living to another by any means and mechanisms. The crowd acts as a spreading tool of COVID-19 but not originate site of this novel virus. This review will help out in understanding, origin, and epidemiology with the transmission of novel coronavirus worldwide. As there is not any specific vaccine or treatment strategy to terminate its pathogenesis, so it encourages fellow researchers to focus on insights of designing a novel vaccine or treatment for eradicating it from the planet.

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Nil

#### CONFLICT OF INTEREST

None

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