



NOVEL CORONAVIRUS (2019-NC0V) OUTBREAK: THINGS YOU NEED TO KNOW

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ABSTRACT

Coronaviruses are the RNA viruses, belonging to family Coronaviridae. In past 15 years, 2 highly pathogenic human coronaviruses (HCoVs)—severe acute respiratory syndrome coronavirus (SARS-CoV) and Middle East respiratory syndrome coronavirus (MERS-CoV) have emerged out as threaten. The world is again shaken by the emergence of third more dangerous coronavirus strain - 2019n-CoV. Although, still there are many unknown facts regarding this new virus, but the global community seems more engaged and prepared to battle against this virulent strain this time. As we are still in early stages of emergence of this novel coronavirus, additional research studies are required to study in detail regarding pathogenesis, mechanism of action, transmission rates, treatment guidelines etc. of the HCoVs, because these three attacks of SARS-CoV, MERS-CoV and 2019n-CoV have threatened the global public health and had resulted in higher and higher mortality rate.

INTRODUCTION

Coronaviruses (CoVs) are large, enveloped, positive-strand RNA viruses that can be divided into 4 genera based on sequence comparisons of entire viral genomes. These are alpha, beta, delta, and gamma, of which alpha and beta CoVs are known to infect humans.^[1] Since long, human corona viruses (HCoVs) have been considered the respiratory pathogens. Most people get infected with these viruses at some point in their lives. It usually lasts for a short amount of time.^[2] But in last 15 years, 2 highly pathogenic HCoVs—severe acute respiratory syndrome coronavirus (SARS-CoV)^[3] and Middle East respiratory syndrome coronavirus (MERS-CoV)^[4]—have emerged from animal reservoirs to cause global epidemics with alarming morbidity and mortality of 10% and 37% respectively.^[5,6] Recently, one more highly pathogenic HCoV- 2019 novel coronavirus (2019-nCoV) have come to spotlight in Wuhan, Hubei Province, China.^[7]

To date, seven known HCoVs have been identified. HCoV-229E and HCoV-NL63, belongs to alphacoronavirus genera and HCoV-OC43, HCoV-HKU1, SARS-CoV, MERS-CoV and 2019-nCoV, belongs to betacoronavirus genera. Out of these, first four i.e. HCoV-229E, HCoV-NL63, HCoV-OC43 and HCoV-HKU are responsible for one third of common cold infections in humans. In severe cases, they may lead to life-threatening pneumonia and bronchiolitis especially in elderly, children and immunocompromised patients.^[8] First case of SARS-CoV was identified in 2002 at Guangdong Province, China, which spread

across 29 countries.^[9] Phylogenetic studies suggested bat origin of SARS-CoV based on sequences of SARS-like virus found in bats.^[10] MERS-CoV was first identified from the sputum of a Saudi man, in 2012 at Jeddah, Saudi Arabia.^[11] Although, the clinical features of MERS-CoV were similar to as of SARS-CoV, but presented with higher mortality rate of 37% and the spread was also geographically limited. The natural reservoir of MERS-CoV was presumed to be bats, yet human transmission events had primarily been attributed to an intermediate host, the dromedary camel.^[6,12]

EMERGENCE of 2019-nCoV

On December 31st, 2019, a cluster of pneumonia patients of unknown cause were reported in Wuhan, China. Most of these were exposed to a Human South China Seafood wholesale Market selling many species of live animals suggesting zoonotic transmission. The whole market was shut down the next day i.e. on 1st January, 2020. By January 10, 2020, researchers from the Shanghai Public Health Clinical Center & School of Public Health and their collaborators released a full genomic sequence of 2019-nCoV to public databases, exemplifying prompt data sharing in outbreak response. By far, more than 1000 confirmed cases, including in health-care workers, have been identified in Wuhan, and several international countries like Thailand, Japan, South Korea, and the United States of America (USA).^[13-16] The first travel-related case in USA occurred on January 21 in a young Chinese man who had visited Wuhan. Initial cases were supposed to have zoonotic transmission but increasing

number of cases reportedly have not had exposure to animal markets, indicating person-to-person spread.^[16]

An Indian woman working as teacher in an international school in China is believed to be the first foreigner to have contracted the disease. Around 500 Indian medical students study in the city of Wuhan, the epicenter of the outbreak and therefore are at risk. Because of lunar New Year celebrations, this is the time of maximum international travel for China. To be on safer side, India issued a travel advisory for its citizens too.^[17] In wake of the coronavirus outbreak in China, the Brihanmumbai Municipal Corporation (BMC) created an isolation ward at its Kasturba hospital in Chinchpokali for diagnosis and treatment of two people who returned to Mumbai from China (24 January, 2020) and suspected to have the coronavirus infection.^[18] As per Medical Superintendent at Ram Manohar Lohia (RML) Hospital, on 28 January, 2020, another 3 suspected persons were kept under observation at an isolation ward of RML Hospital in Delhi.^[19] But after investigations at National Institute of Virology (NIV) Pune, these 3 patients were declared free from 2019n-CoV infection and were discharged.^[20] On 30 January, 2020, India confirmed its first novel coronavirus case in Kerala in a student studying in Wuhan University, China.^[21]

Centers for disease control and prevention (CDC) is closely monitoring this situation and is working with WHO and state and local public health partners to respond to this emerging public health threat. DC established a 2019-nCoV Incident Management Structure on January 7, 2020. On January 21, 2020, CDC activated its Emergency Response System to better provide ongoing support to the 2019-nCoV response. On January 27, 2020 CDC issued updated travel guidance for China, recommending that travelers avoid all nonessential travel to all of the country. CDC has developed a real time Reverse Transcription-Polymerase Chain Reaction (rRT-PCR) test that can diagnose 2019-nCoV in respiratory and serum samples from clinical specimens.^[22] On January 30, 2020, the International Health Regulations Emergency Committee of the World Health Organization declares the outbreak a “public health emergency of international concern external icon” (PHEIC). A PHEIC is declared if an event poses a public health threat to other nations through the spread of disease and potentially requires a coordinated international response.^[23]

Incubation period of 2019-nCoV is 2-14 days after exposure, which is similar to the incubation period of MERS-CoV.^[24] As of 27 Jan 2020 reported by WHO, 2798 patients have been confirmed to have infection by the 2019-nCoV, out of which, 2761 are from China with 80 associated deaths. Among the 37 cases identified outside of China, three were detected without the onset of symptoms, while among the remaining 34 patients, there is information on date of symptom for 28 individuals. The median age of cases detected outside of

China is 45 years ranging from 2 to 74 years, 71% of cases were male (information was missing on age for 6 cases, and on sex for 4 cases). Of the 27 cases for whom we have detailed information on date of symptom onset and travel date from China, 8 cases had symptom onset in China, 5 had onset on the same day as travel, and 14 developed symptoms after leaving China. 36 cases had travel history to China, of whom 34 had travel history in Wuhan city, or had an epidemiological link to a confirmed case with travel history to Wuhan. For the remaining two, investigations into their travel histories are ongoing. One additional case was the result of human-to-human transmission among close family contacts in Viet Nam.^[25] Since 31 December, 2019 and as of 30 January, 2020 reported by European center for disease prevention and control (ECDC), 7824 patients have been laboratory confirmed to have infection by the 2019-nCoV, including 16 healthcare workers and 170 deaths, details of which have been shown in table 1.^[26]

HCoV is an enveloped RNA virus belonging to coronaviridae family. It works on the principal of virus-host interaction. At present, there is very limited clinical information of the 2019-nCoV. United States has laid criteria to evaluate patients under investigation (PUI) for 2019-nCoV.^[27] According to Leung GM et al, based on data from the first 41 patients reported by Chaolin Huang and colleagues (admitted before Jan 2, 2020), 98% (40) patients infected with this virus presented with fever, 76% (31) with dry cough, 55% (22) with dyspnoea and 3% (1) with diarrhea. 8-9% patients required ventilator support. All the patients were in age range 21-76 years with M:F ratio 2.7:1.^[28] After outbreak of SARS-CoV in 2003, China had adapted an efficient system for monitoring and responding to infectious disease outbreaks and the 2019-nCoV pneumonia has been quickly added to the Notifiable Communicable Disease List and given the highest priority by Chinese health authorities.^[29] Chen N et al conducted a single center study including 99 real time RT-PCR confirmed cases of 2019-nCoV in Wuhan Jinyintan Hospital from Jan 1 to Jan 20, 2020. Patients had clinical manifestations of fever (82 [83%] patients), cough (81 [82%] patients), shortness of breath (31 [31%] patients), muscle ache (11 [11%] patients), confusion (nine [9%] patients), headache (eight [8%] patients), sore throat (five [5%] patients), rhinorrhoea (four [4%] patients), chest pain (two [2%] patients), diarrhea (two [2%] patients), and nausea and vomiting (one [1%] patient).^[30] In severe cases pneumonia, severe acute respiratory syndrome and kidney failure have been reported. Deaths have been reported in mostly the patients who were elderly or had underlying health conditions.^[31]

Table 1: Distribution of confirmed cases of 2019-nCoV by country and region.

Continent	Country / Territory / Area	Confirmed cases	Deaths
America	United States of America	5	0
America	Canada	3	0
Asia	China	7734	170
Asia	India	1	0
Asia	Japan	11	0
Asia	Republic of Korea	4	0
Asia	Taiwan	8	0
Asia	Thailand	14	0
Asia	Singapore	10	0
Asia	Vietnam	2	0
Asia	Nepal	1	0
Asia	Malaysia	8	0
Asia	Philippines	1	0
Asia	Sri Lanka	1	0
Asia	Cambodia	1	0
Asia	United Arab Emirates	4	0
Europe	France	4	0
Europe	Germany	4	0
Europe	Finland	1	0
Oceania	Australia	7	0
TOTAL		7824	170

CONCLUSION

As we are still in early stages of emergence of this novel coronavirus, current clinical and epidemiological data are insufficient to understand the full extent of the transmission potential of the epidemic. Transmission rates are still unknown; however, there is evidence of human-to-human transmission. Additional research studies are required to study in detail regarding pathogenesis, mechanism of action, transmission rates, treatment guidelines etc. of the HCoV, as last three attacks of SARS-CoV, MERS-CoV and 2019n-CoV have threaten the global public health and had resulted in higher and higher mortality rate.

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