

Coronavirus: Basic Understanding

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Coronavirus infections were first reported from Wuhan China. Although there is controversy about numbers of affected patients, it is assumed that millions of population have been affected already in China.

Keywords: 2019-nCoV, Wuhan, Coronavirus, Severe acute respiratory syndrome coronavirus, China

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Tentatively termed as 2019-nCoV, which was initially reported in Wuhan, China generated triggered responses from the various Public Health Department of China, in association with many major scientific societies to distinguish the prospective between the clinical and epidemiological scenario of the infection. Initial cases reported were linked with the exposure to the seafood market in Wuhan, however, within a short span of time, several epidemiological data indicated the risk of the person to person transmission [1-4]. 2019-nCoV causes similar respiratory problems such as two other pathogenic human coronaviruses, i.e. Severe acute respiratory syndrome coronavirus [SARS-CoV] and Middle East respiratory syndrome coronavirus [MERS-CoV]). As reported, Zhu N [2] and Researchers have identified and characterized 2019-nCoV. The sequencing of the viral genome indicated 75%-80% identical

Patterns with the SARS-CoV, in addition to several bat coronaviruses, which can be proliferated in the equivalent cells that are useful in the growth of SARS-CoV and MERS-CoV. A notable feature of 2019-CoV is the better growth observed in the primary human airway epithelial cells in comparison to the standard tissue culture cells, which is in contrast to SARS-CoV or MERS-CoV. The identification of the virus holds the key to address the unknown issues which will eventually lead to the development of the antiviral therapies. The three key factors which have emerged from the identification of the virus are:

- The assessment of the infection in humans through serological assays.
- Observing the patterns of the viral genome facilitates the detection of the virus through the use of quantitative-reverse transcriptase PCR reactions.

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- The virus will lead to attempts to develop antiviral therapies and experimental animal models.

The degree of human transmission and the clinical spectrum about the disease is yet to be explored. The implication of transmission of 2019-nCoV is rapid, similar to both SARS-CoV and MERS-CoV, however, the comparative outburst is yet to be determined. Intrapulmonary epithelial cells in comparison to the cells of the upper airways are more prone to infection by both SARS-CoV and MERS-CoV. It is assumed as of now that 2019-nCoV utilizes the same cellular receptor as SARS-CoV (human angiotensin-converting enzyme 2 [hACE2]), so the transmission is expected develop only after signs of lower respiratory tract disease develop [3]. 2019-nCoV is assumed to behave similarly to SARS-CoV with a more profound binding affinity to hACE2. Clinical isolates from cases that are temporarily and geographically unrelated are important to be obtained in order to assess the mutation pattern and further the adaptation nature to the human host. Another important aspect to be considered if the assumption that 2019-nCoV behaves similarly to SARS-CoV is the systemic proliferation of the virus. The pathological pathway of the infection can be elucidated with the analysis of the patient's samples at autopsy, which directly influences the deviations in the therapeutic interventions, in addition to revalidation of the results derived from the experimental infections of laboratory animals.

Determination and identification of the zoonotic origin of the virus is another important aspect that is to be considered in regard to 2019-nCoV. In the case of SARS-CoV and MERS-CoV, the ancestral hosts were probably bats, which are considered as the primary reservoir for 2019-nCoV. The transmission of 2019-nCoV is from bats or by many different means of the host will be useful in defining the zoonotic patterns of the transmission.

Transmission of 2019-nCoV probably occurs by means of large droplets and contact and less so by means of aerosols and fomites, based on the previous experience with SARS-CoV and MERS-CoV. Public health measures, including quarantining in the community as well as timely diagnosis and strict adherence to universal precautions in health care settings, were critical in controlling SARS and MERS. All these measures need to be replicated in a more stringent manner in order to reduce the transmission of 2019-nCoV. In declaring a global

Health emergency, the WHO's director-general, Tedros Adhanom Ghebreyesus, said his main concern was that the outbreak could spread to countries with fragile health systems.

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