

## Coronavirus 2020

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Emerging and reemerging infectious diseases are constant challenges for public health worldwide. Recent cases of pneumonia of unknown cause in Wuhan, China, have led to the discovery of a new type of Coronavirus (2019-nCoV), which are enveloped RNA viruses, commonly found in humans, other mammals and birds, capable of causing respiratory, enteric, hepatic, and neurological diseases<sup>(1)</sup>.

To date, there are six known Coronavirus species that cause disease in humans. Four of these (229E, OC43, NL63 and HKU1) cause common flu symptoms in immunocompetent people, and two species (SARS-CoV and MERS-CoV) cause severe acute respiratory syndrome with high mortality rates<sup>(2)</sup>.

Other Coronaviruses are likely to periodically affect humans due to the high prevalence of infections, widespread virus distribution, genetic diversity, frequent Coronavirus recombination and increased human-animal interface<sup>(1-2)</sup>.

2019-nCoV, called Novel Coronavirus-Infected Pneumonia (NCIP), was confirmed through bronchoalveolar lavage, whole genome sequencing, PCR and culture in hospitalized patients in Wuhan, China. The complete analysis of the virus genome framed it in the genus betacoronavirus, which also includes SARS-CoV, discovered in humans, bats and other wild animals<sup>(3)</sup>.

Regarding the epidemiological and clinical characteristics of confirmed 2019-nCoV cases in the city of Wuhan, China, a retrospective cohort of 41 patients demonstrated that 66% (27 patients) had direct contact with a large seafood and animal market. The average age was 49 years, with a male prevalence. Important signs and symptoms of 2019-nCoV were considered: fever (98%), dry cough (76%), dyspnea (55%), myalgia or fatigue (44%), and lymphopenia (63%)<sup>(4)</sup>.

In this context, respiratory secretions were considered the main means of spreading the virus. Culture analysis of human airway epithelial cells, electron microscopy and complete sequencing of the supernatant culture genome were shared with the World Health Organization, aimed at the surveillance and detection of 2019-nCoV infection globally and in China<sup>(1)</sup>.

In summary, 2019-nCoV's viral evolution and pathogenicity are still unknown. Although with a low lethality of around 3%, transmissibility is high<sup>(1)</sup>. However, studies infer the possible animal-human and human-human transmissibility.

Therefore, the absence of vaccine against 2019-nCoV reinforces among the population, in general, the adoption of measures to prevent infection, recommended by WHO, such as hand hygiene, avoiding closed environments and contact with people from the region where the outbreak has started. For health professionals, the use of goggles or face shield, surgical mask/N95, apron, procedure glove and hand washing should be used to provide assistance to suspected or confirmed cases of infection by 2019-nCoV.

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