SYNOPSIS

02/03/2020

Review of “A novel coronavirus from patients with pneumonia in China, 2019”


One-minute summary

- Characterization of a novel coronavirus (2019-nCoV) isolated from bronchoalveolar-lavage samples from three patients admitted to hospital on December 27, 2019 in Wuhan, China. One was a retailer in the seafood market, the other a frequent visitor to the market and no information is available on the third patient.

- Whole genome sequencing and phylogenetic analysis showed that the three isolates clustered together and fell into the genus betacoronavirus, which includes coronaviruses found in humans, bats and other wild animals.

- 2019-nCoV is similar to bat SARS-like CoV, with 86.9% sequence identity (compared to one sequence), but is distinct from SARS-CoV and MERS-CoV.

- Viral culturing showed that cytopathic effects were observed 96 hours after inoculation on primary human airway epithelial cells, but not until six days in cell lines.

- Electron microscopy showed that 2019-nCoV has typical coronavirus morphology.

Additional information

- The 2019-nCoV genome shows typical betacoronavirus organization (consisting of: a 5’ UTR, orf1ab, S gene, E gene, M gene, N gene, 3’ UTR, and several unidentified non-structural open reading frames).

- Based on the genomic analyses, the authors developed diagnostic assays to specifically detect 2019-nCoV. The protocol has been shared on the WHO website.
Citation

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