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SYNOPSIS

02/03/2020

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

Article citation: Zhu N, Zhang D, Wang W, Li X, Yang B, Song J, et al. A novel coronavirus from patients with pneumonia in China, 2019. N Engl J Med. 2020 Jan 24 [Epub ahead of print]. Available from: https://www.nejm.org/doi/full/10.1056/NEJMoa2001017

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

Ontario Agency for Health Protection and Promotion (Public Health Ontario). Review of “A novel coronavirus from patients with pneumonia in China, 2019”. Toronto, ON: Queens’s Printer for Ontario; 2020.

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