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Opinion

Novel coronavirus: From discovery to clinical diagnostics

Tung Phan

Division of Clinical Microbiology, University of Pittsburgh and University of Pittsburgh Medical Center, Pittsburgh, PA, USA

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ABSTRACT

A novel coronavirus designated as 2019-nCoV first appeared in Wuhan, China in late December 2019. Dozens of people died in China, and thousands of people infected as 2019-nCoV continues to spread around the world. We have described the discovery, emergence, genomic characteristics, and clinical diagnostics of 2019-nCoV.

1. The study

Coronavirus is an enveloped positive-sense RNA virus, which is characterized by club-like spikes projecting from its surface. Although coronavirus is commonly associated with acute respiratory infections in humans, its ability to infect multiple host species and a variety of diseases makes it a complex pathogen (Fung et al., 2019). The frequent interactions of wild animals with humans make them a common source of zoonotic infections. Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV) and Middle Eastern Respiratory Syndrome Coronavirus (MERS-CoV) are zoonotic pathogens that can cause severe respiratory diseases in humans (Luk et al., 2019; Ramadan and Shaib, 2019).

A novel coronavirus designated as 2019-nCoV is another human pathogen. This new virus was first discovered in 2019 when viral metagenomics was carried out on three bronchoalveolar-lavage specimens from Chinese adult patients with unexplained severe pneumonia (Zhu et al., 2020). Two patients infected with 2019-nCoV recovered and were discharged from the hospital. One patient, a frequent visitor to the seafood wholesale market, died (Zhu et al., 2020). Currently, there is only one complete 2019-nCoV genome (29870-bp, excluding the poly (A) tail) in GenBank (accession number MN908947). Five typical ORFs on the same coding strand were identified, including ORF1ab polyprotein (7096-aa), spike glycoprotein (1273-aa), envelope protein (75-aa), membrane protein (222-aa), and nucleocapsid protein (419-aa). Our pair-wise sequence analysis demonstrated that bat SARS-like coronavirus (Genbank accession number MG772933) was the closest relative to 2019-nCoV, sharing 88% nucleotide similarity (Fig. 1). In addition, 2019-nCoV is the new member of the genus *Betacoronavirus*.

Transmission is a central tenet of disease biology and infectious disease epidemiology, and the mechanism of 2019-nCoV transmission remains unknown. The rapid spread of 2019-nCoV appears to have resulted from human-to-human transmission. As of January 26th 2020, confirmed cases of 2019-nCoV have been reported in many countries, including China, Hong Kong, Macau, Taiwan, Australia, France, Japan, Malaysia, Nepal, Singapore, Thailand, The Republic of Korea, United States, Vietnam (https://www.cdc.gov/coronavirus/2019-ncov/locations-confirmed-cases.html#map). For many viruses, one of the key steps in the emergence process is the jump from animals to humans. Given its close similarity to bat coronaviruses, its origins have been traced back to the seafood wholesale market in Wuhan, China. Bats are known to be hosts for moe that 30 coronaviruses with complete genomes sequenced (Wong et al., 2019). Even the role of bats as the primary reservoir has been suggested, but not yet confirmed. Thus, the zoonotic potential of 2019-nCoV is currently under investigation.

To date, 2019-nCoV has been detected in human clinical specimens by next-generation sequencing, real-time RT-PCR, cell culture, and electron microscopy (Zhu et al., 2020). CDC recommends that clinical virology laboratories should not attempt viral isolation from specimens collected from 2019-nCoV patients under investigation (PUI). At this time, diagnostic testing for 2019-nCoV can be conducted only at CDC (https://www.cdc.gov/coronavirus/2019-nCoV/guidelines-clinical-specimens.html). Because 2019-nCoV is a newly discovered virus, the spectrum of the available diagnostic tools is tight. At present, there are several commercially available multiplex NAAT tests for the detection of pathogenic organisms in respiratory specimens in clinical virology laboratories (Beckmann and Hirsch, 2016; Huang et al., 2018, Babady et al., 2018). They can detect HCoV-229E, -NL63, –OC43, and -HKU1. In addition, the BioFire FilmArray Respiratory Panel 2 plus and the BioFire FilmArray Pneumonia Panel plus can detect MERS-CoV in human clinical specimens. A recent study reported that the RespiFinderSmart22kit (PathoFinder BV, Netherlands) failed to identify 2019-nCoV in the bronchoalveolar-lavage specimens collected from 2019-nCoV infected patients in Wuhan, China (Zhu et al., 2020). Two major FDA-cleared multiplex PCR systems in the United States,

E-mail address: phantg@upmc.edu.

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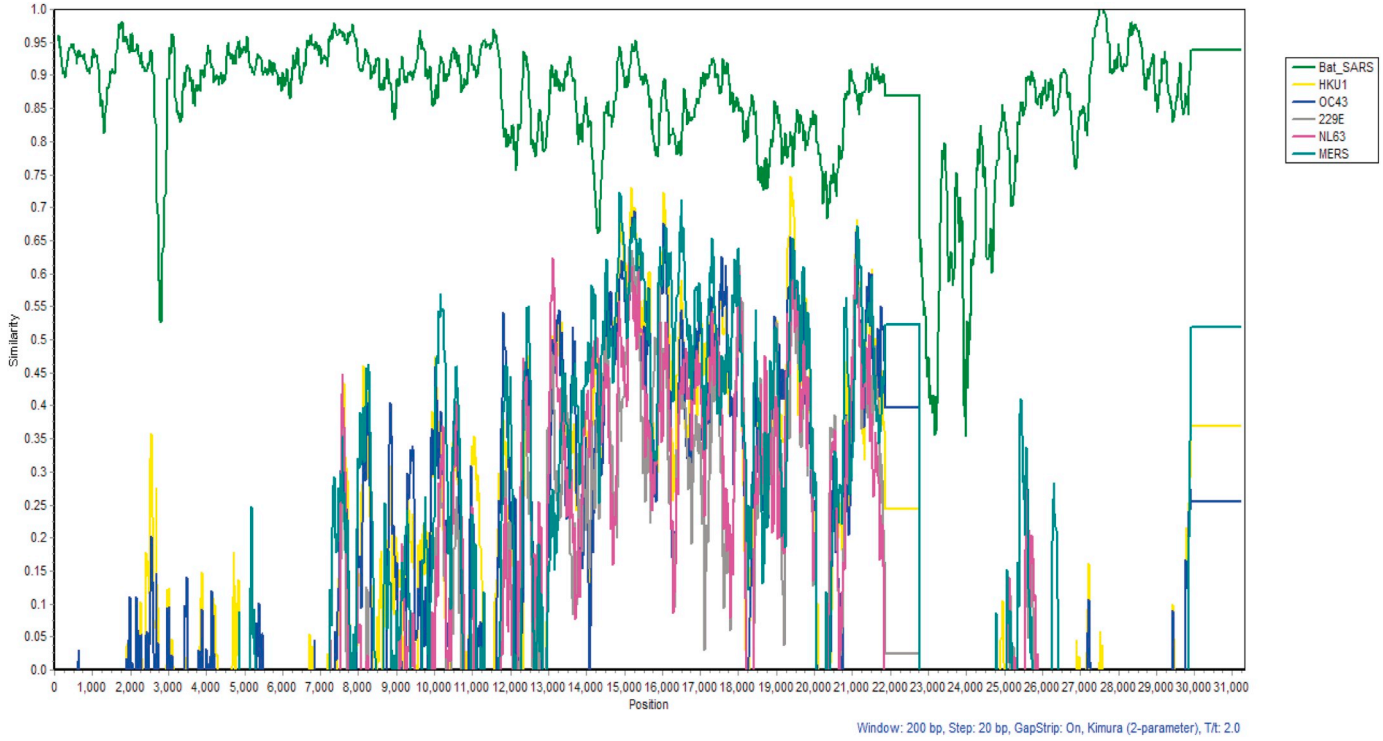

Fig. 1. Pairwise sliding window of percent nucleotide similarity of 2019-nCoV (GenBank accession number MN908947) aligned with bat SARS-like coronavirus (Genbank accession number MG772933), MERS-CoV (Genbank accession number KT006149), HCoV-229E (Genbank accession number KF514433), HCoV-HKU1 (Genbank accession number KF430201), HCoV-NL63 (Genbank accession number KF530112), and HCoV-OC43 (Genbank accession number KF530098).

including the ePlex Respiratory Pathogen Panel (GenMark Diagnostics, Carlsbad, CA) and the FilmArray Coronavirus Assays (BioFire Diagnostics, Salt Lake City, UT), are predicted no cross-reactivity with 2019-nCoV. Our pair-wise sequence analysis demonstrated that 2019-nCoV shared very low nucleotide similarity, less than 50%, to HCoV-229E, -NL63, –OC43, -HKU1, and MERS-CoV (Fig. 1).

While we know relatively little about 2019-nCoV, we do know that it is a highly pathogenic human pathogen, possibly a zoonotic agent. Challenges will remain in several key areas. Additional studies are needed to gain further insights about its origin, tropism, and pathogenesis.

Declaration of Competing Interest

The author declares no competing financial interests.

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