

Voice from China: nomenclature of the novel coronavirus and related diseases

Since early December 2019, the novel coronavirus has caused an outbreak of pneumonia that has claimed over 2000 lives, with more than 77,000 confirmed cases of infection by February 23, 2020 in China.^[1] The World Health Organization (WHO) recently named the disease caused by this new coronavirus as “coronavirus disease 2019 (COVID-19)”. The International Committee on Taxonomy of Viruses (ICTV) has named the new virus “severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)”.^[2] However, questions have been raised by different academic and professional bodies regarding whether the nomenclature is appropriate. In view of the lack of consensus, the *Chinese Medical Journal* invited Chinese scientists, epidemiologists, and virologists to submit their comments and provide references for establishing an acceptable nomenclature.



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Comments:

Evidence from many aspects such as comparative genomics, viral origin, epidemiology, and clinical manifestations suggests that the coronavirus is a new kind of virus distinct from the severe acute respiratory syndrome coronavirus (SARS-CoV). According to scientific conventions, any new virus and associated disease can be named through expert consensus while taking into consideration existing public knowledge about the disease at the same time. Naming the new coronavirus SARS-CoV-2 is problematic. First, it may be misleading, especially for the general public who have a lack of virological knowledge. Second, the new name for the virus is not

consistent with the disease name COVID-19. Third, the government and the general public may become complacent, believing that the disease caused by the new coronavirus, similar to the severe acute respiratory syndrome (SARS), will not recur after this outbreak. Therefore, the new coronavirus should have a unique name. I would like to suggest that the virus be named human coronavirus 2019 (HCoV-19) instead of SARS-CoV-2. The name HCoV-19 ensures that the new virus is distinct from SARS-CoV and is consistent with the name of the disease COVID-19.



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Comments:

An ICTV work group suggested naming the new coronavirus SARS-CoV-2, which was temporarily referred to by WHO as “2019 novel coronavirus (2019-nCoV)”. Discussions are needed for the nomenclature of the novel coronavirus until wide consensus is reached by science community.

Currently, there are no standardized nomenclature guidelines for coronaviruses. Looking back in history, the first two human coronaviruses (HCoVs) were named after 229E and OC43. In recent years, two seasonal HCoVs have been named NL63 and HKU1 according to the country (e.g., NL = the Netherlands) or the organization (eg, HKU = Hong Kong University) in which they were identified. The two highly pathogenic viruses, that is, SARS-CoV and Middle East respiratory syndrome coronavirus (MERS-CoV), were named primarily according to the key features of disease caused.^[3]

The genomic sequences of the new coronavirus are distinct from those of SARS-CoV (approximately 79% identity).^[4] Most individuals (approximately 80%) infected with

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2019-nCoV develop mild or moderate symptoms and signs and asymptomatic individuals may also be infectious.^[5,6] These may make it hard to control the epidemic. It is highly possible that COVID-19 will eventually evolve into a seasonal epidemic. Thus, the virus causing COVID-19 is largely different from SARS-CoV. To avoid conceptual confusion and considerable public fear associated with SARS, the new coronavirus should not be named SARS-CoV-2.

On the basis of the historical nomenclature procedure, I suggest establishing a standardized nomenclature process for coronaviruses. One approach may be to name the new coronavirus under the four existing genus, that is, α , β , γ , and δ .^[3] For example, the current new name suggested for HCoV-OC43 is betacoronavirus 1. Alternatively, the new coronavirus can be named to reflect the WHO's naming of the disease (COVID-19). We can differentiate the new coronavirus according to the year of discovery, for example, human coronavirus-19, which is similar to the naming of the influenza virus subtype A/H1N1/2009pdm.



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Comments:

Recently, the ICTV suggested that the new coronavirus be named SARS-CoV-2 because the genomic sequences of the two coronaviruses appear to be similar (approximately 80% homogeneity).^[7,8] In addition, this new coronavirus and SARS-CoV of 2003 share similar pathogenesis, both primarily affecting the respiratory system.

This nomenclature is controversial. Several significant discrepancies between these two viruses should be noted. First, although both viruses may have originated from bats, the intermediate host involved is likely to be different, indicating that the transmission paths are distinct. Second, SARS-CoV results in more than 40% of patients developing severe acute respiratory syndrome (SARS) and 10% of patient deaths.^[9,10] In contrast, the new coronavirus only leads to SARS in approximately 10% of cases and death in 3% of cases respectively,^[11-13] including all the cases from Hubei province. Third, treatment regimens or vaccines for SARS are not indicated for the new coronavirus. Altogether, there exist significant differences in transmission, pathogenesis, clinical treatment, and vaccine development between these two viruses.

Traditionally, human viruses in the same family or genus are typed based on serological tests, as the results help with the diagnosis of the infection, guide medications used for treatment, and assist in the development of a vaccine. In

more recent times, genetic sequence-based tests have advanced, and such genotyping tests have been able to provide a more rapid and precise typing approach than serological tests. Genotyping provides a new clinical diagnostic tool for directing the use of drugs and the development of vaccines. Based on genotyping, SARS-CoV-2 is unlikely to be significantly linked to SARS-CoV. Rather, SARS-CoV-2 may lead to the misunderstanding of the pathogenesis of the new coronavirus, which is less pathogenic compared with SARS-CoV.

Human coronavirus (HCoV) is commonly referred to coronaviruses of low pathogenicity, with human beings being their primary natural host, as exemplified by HCoV-OC43, 229E, NL63, and HKU1. In contrast, SARS-CoV and MERS-CoV are used to refer to coronaviruses that are highly pathogenic, with non-human animals as their primary natural host. When considering pathogenicity and natural hosts, the new coronavirus fits in between but shares more similarity with the latter. Hence, I would suggest the new coronavirus be referred to as the "2019 acute respiratory syndrome coronavirus (TARS-CoV)". TARS-CoV uniquely identifies the new coronavirus from SARS-CoV and is also different from human coronavirus. Accordingly, the disease caused by TARS-CoV should be named 2019 acute respiratory syndrome (TARS).

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