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PERSPECTIVE

A Proposal to Refer to Four Coronaviruses of Limited Human Virulence "Common Cold Coronaviruses"

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We propose the term "common cold coronaviruses," or ccCoV, to describe the four human coronaviruses commonly associated with upper respiratory tract disease – coronaviruses 229E, OC43, NL63, and HKU1. This will differentiate these previously described coronaviruses from those causing more severe disease in humans – including the viruses severe acute respiraotry syndrome coronavirus (SARS-CoV), the Middle East respiratory syndrome coronavirus (MERS-CoV) and SARS-CoV-2.

Keywords. common cold; coronaviruses; pneumonia; respiratory tract infection.

The ongoing coronavirus disease 2019 (COVID-19) pandemic has greatly increased interest in all 9 coronaviruses (CoVs) known to infect humans, including the 4 CoVs (human coronaviruses [HCoVs] 229E, OC43, NL63, and HKU1) that are mainly associated with upper respiratory tract infection (URTI) [1]. Although the HCoVs 229E, OC43, NL63, and HKU1 can cause moderate to severe disease, mainly in high-risk individuals, they are most frequently associated with mild URTIs [1]. However, 3 of these 9 HCoVs including the severe acute respiratory syndrome coronavirus (SARS-CoV), the Middle East respiratory syndrome coronavirus (MERS-CoV), and the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), the causative agent of COVID-19, frequently cause lower respiratory tract disease and/or severe pneumonia [2]. The remaining 2 HCoVs, HuPDCoV (human porcine delta coronavirus) and HuCCoV (human canine coronavirus), are variants of 2 CoVs that infect domestic (swine [porcine delta CoV]) or companion (dogs/cats [canine/feline CoV]) animals [3, 4]. These viruses have been isolated from only a few patients with febrile illnesses (HuPDCoV) or pneumonia (HuCCoV) and little is known about their prevalence or complete disease manifestations. Although human populations do not have immunity to these viruses, they have not yet demonstrated interhuman transmissibility and they will not be further considered in this article.

Studies of the 4 CoVs associated with URTIs have proliferated over the past 2 years as part of efforts to understand SARS-CoV-2 biology, epidemiology, and transmission and to gain insight into whether prior infection with any of these viruses was protective (or less likely, pathogenic) in patients with COVID-19 [5–7]. Confusingly, these viruses have been referred to in different publications and settings as "human" coronaviruses, in earlier years as "novel" coronaviruses, and also as "seasonal," "endemic," "common," or "community-acquired" coronaviruses. The nomenclature and strain-specific diseases associated with the coronaviruses differs substantially from other respiratory viruses, such as influenza virus. To simplify this nomenclature, we, all of whom have worked in the coronavirus field and have been authors of the coronavirus chapters in several widely read textbooks of infectious diseases, propose that these 4 coronavirus strains be referred to, collectively, as "common cold coronaviruses," with the abbreviation "ccCoVs."

We feel that the name "human coronaviruses," which is often used, particularly in contexts where non–human coronaviruses are being discussed, is now not accurate, since SARS-CoV, MERS-CoV, and SARS-CoV-2 are "human coronaviruses" as well. Similarly, while the modifier "seasonal" usually is accurate for the 4 known common cold coronaviruses, there are places where these viruses are not, in fact, seasonal, and we do not yet know whether in temperate climates SARS-CoV-2 will become seasonal. MERS-CoV already shows endemicity in countries on the Arabian Peninsula [8], and SARS-CoV-2 may before long establish its own endemicity. Finally, SARS-CoV-2, while still causing the ongoing pandemic, is community acquired. While this has been evident throughout the pandemic, circulation of the highly transmissible Omicron variant in both naive, vaccinated and previously infected

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populations has reinforced this point [9]. Clearly there are contexts in which the somewhat cumbersome name "common cold coronaviruses" is not necessary. However, in other contexts where some modifier is needed, "common cold coronavirus" seems more accurate than the others mentioned above. In addition, the abbreviated form of this appellation (ccCoV) is both short and, for the most part, accurate.

We make this proposal in a provisional way, for several reasons. First, although ccCoVs are most often associated with URTIs, they occasionally cause more serious disease including pneumonia and bronchiolitis in infants, pneumonia in healthy adults, and severe pneumonia in aged and immunocompromised populations [10–15]. Second, these viruses are often found in asymptomatic patients and in coinfection with other respiratory viruses in some patients with clinical illness [16]. Thus, the presence of the virus does not necessarily result in a URTI. Third, SARS-CoV-2 may eventually become a ccCoV. The HCoVs 229E, OC43, NL63, and HKU-1 all appeared to cross species from progenitor viruses circulating in bats or rodents at times ranging from 100 to 1000 years ago [17]. Intermediary hosts have been identified for HCoV-OC43 (bovids) and HCoV-229E (camelids) [18, 19] but not for HCoV-NL63, HCoV-HKU-1, or SARS-CoV-2. Of particular note, entry of HCoV-OC43 into human populations at the end of the 19th century coincided roughly with a worldwide respiratory virus pandemic [20]. There has been speculation, but without supporting data, that this pandemic, termed the "Russian flu," was actually caused by HCoV-OC43 [20]. Whether true for the Russian flu or not, we have no understanding of how ccCoVs entered immunologically naive human populations and whether they initially caused more severe disease, with disease attenuation occurring as a consequence of the development of widespread human immunity and possible viral attenuation. Finally, we also recognize that more formal nomenclature committees, such as the International Committee on Taxonomy of Viruses, may or may not agree with us. Nonetheless, we believe a consistent nomenclature for the 4 common coronaviruses previously circulating in humans would be a useful addition to the current literature.

Notes

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