

## Evolution & Behavior

# The evolution of the new coronavirus: what the past teaches us for a better future

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### ABSTRACT

*The new coronavirus which is causing the ongoing global crisis is evolutionarily related to SARS-CoV: the very same which induced the SARS outbreak in the early 2000s. Accordingly, scientists named this novel virus SARS-CoV-2, and here we report the steps they took to classify it.*



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As we are writing, the world is facing the global crisis of [the coronavirus disease 2019 \(COVID-19\)](#). Since the beginning of the outbreak, scientists have been struggling with establishing standards to overcome this challenging situation. Unlike for the common cold or the seasonal flu, treatments, antibodies, or vaccines are not available. That is because the virus causing the COVID-19 is a new virus.

When a new disease manifests itself, the first thing to do for the scientific community is to identify its causing agent, and, if new, classify it. In this case, COVID-19 is caused [by the "severe acute respiratory syndrome coronavirus 2" \(SARS-CoV-2\)](#). As you may guess from this name, the new virus is closely related to the SARS coronavirus (SARS-CoV) that caused [the](#)

[SARS outbreak in the early 2000s](#). Therefore, SARS-CoV-2 is a novel virus, but this doesn't mean that it originated from an unknown planet! In this article, an international team of authorities in virology explains how they named this new virus reviewing its "evolution" process. The authors also describe how helpful is its classification within the virus families to define priorities of future research and public health.

The Coronaviridae Study Group (CSG) of [the International Committee on Taxonomy of Viruses](#) is responsible for classifying and naming the family of coronaviruses. When they started, the new virus was initially called "2019-CoV", hence, the group assessed the new virus, to give it a more accurate name.

A [virus](#) is a tiny infectious agent that can only reproduce within host organisms. A virus has its own [genome](#) that is the core of life enabling replication. The virus genome is protected being packaged within [a shell \(called capsid\)](#). Since a virus cannot reproduce by itself, first, it enters within the host cell. Then it releases the genetic materials inside to hijack the host cell, forcing it to replicate the virus genome. As a result of the virus spreading, the virus genome can include partial modification ([mutation](#)), which may, in turn, give a new, perhaps useful, features to the virus. This process drives evolution. In other words, how similar is a novel virus compared to other known viruses can be estimated based on how related their genomes are. For example, a human is genetically close to chimpanzee more than a mouse, which is also true regarding their different biological characteristics.

The CSG took the recently sampled genome data of the novel virus and compared it to an established genome database. This extensive database includes 2505 coronavirus from all known 49 coronavirus species. The in-depth analysis allowed them to position the new virus within [the evolutionary tree](#) of the coronavirus family. Importantly, the researchers discovered that it is a close relative of the (in)famous SARS-CoV that causes SARS. However, the new virus does not descend directly from the SARS-CoV. This new virus differs from SARS-CoV and any other coronaviruses, so that the CSG eventually named this novel virus SARS-CoV-2. Of note, this naming was reasoned based on evolutionary features, not disease-related.

The available yet limited data for SARS-CoV-2 suggest that the disease symptoms and its transmission speed differ from those reported for SARS-CoV. To accommodate the full range of outcomes of SARS-CoV-2 infection (from asymptomatic to severe or even fatal in some cases), the World Health Organization (WHO) recently introduced a rather unspecific name: coronavirus disease 19 (COVID-19). Moreover, the diagnostic methods to test SARS-CoV-2 infections are different from those of SARS-CoV. This is reflected by the specific recommendations for public health practitioners and laboratory diagnostic staff for SARS-CoV-2.

Having now established different names for the causative virus (SARS-CoV-2) and the disease (COVID-19), the CSG has promoted this clear distinction between these two. This will help to improve the outbreak management and reduces the risk of confusing virus and disease. The same approach in the past has been equally helpful with SARS-CoV (the causative virus) and SARS (the disease).

To promote informative scientific exchange, the CSG recommends researchers to use a standardized format for public databases and publications. The proposed format includes a reference to the host organism, the geographic location, the time, etc., which provides critical information on the major characteristics of each particular virus. The study focusing on individual virus will help our understanding of virus-host interactions in an ever-changing environment and get us prepared for future outbreaks.