

# SHOULD VIRUS-NAMING RULES CHANGE DURING A PANDEMIC?

Some virologists say there is an urgent need for standardization; others say it is a bad time.

By Smriti Mallapaty

**V**irologists are debating whether to establish a standardized system for naming virus species later this year. Some researchers say that the current way in which viruses are named is disorganized and that there is an urgent need for standardization. But others say that now is not the time to engage in an academic discussion over naming conventions, when virologists are focused on fighting the pandemic.

Virologists currently name species – the most basic taxonomic rank – in several ways, often on the basis of where the virus is found, the animals that host it or the disease it causes. Many argue that the lack of conventions is frustrating for researchers who identify new viruses regularly. It also creates confusion when the virus's common name is the same as its species name, as with variola virus (*Variola virus*), which causes smallpox.

The International Committee on Taxonomy of Viruses (ICTV), a body that oversees naming of virus taxa, has proposed a system that will be put to a vote in October (S. G. Siddell *et al. Arch. Virol.* **165**, 519–525; 2020). If it is implemented, it could change how almost all of the more than 6,500 known viral species are named.

“It is obviously good and correct to have a standardized classification scheme for naming virus species, as the current ‘system’ is utterly chaotic and a major source of frustration for those of us that regularly identify novel viruses,” says Edward Holmes, a virologist at the University of Sydney in Australia. But the effort “can hardly be classed as ‘urgent’ compared to a global pandemic”, he says.

Other researchers think now is the perfect time for such an exercise. There has been an acceleration in the number of viruses and species being identified over the past 15 years, thanks to genome-sequencing technology, says Eric Delwart, a virologist at the University of California, San Francisco. “This is the golden age of virus discovery. It is a good time to start organizing the deluge of viral genomes,” he says.

## Time pressure

The debate comes amid discussions about another naming issue: how to classify the tens of thousands of genomes of SARS-CoV-2, the virus that causes COVID-19, being sequenced around the world. Groups of evolutionarily related viruses of the same species are often described as lineages. It is important to track them in case mutations emerge that make the virus more infectious or more dangerous. The

ICTV sets rules only down to the level of the species, but Holmes and other virologists independent of the ICTV have proposed a method for naming the SARS-CoV-2 lineages (A. Rambaut *et al. Nature Microbiol.* <http://doi.org/gg47xd>; 2020).

Currently, the only requirements for a viral species name are that it is italicized (with the first word capitalized) and appropriately unambiguous, and that it uses as few words as possible – although some names are long, such as *Tomato yellow leaf curl Indonesia virus*. On 3 December, members of the ICTV's executive committee published a paper in *Archives of Virology* proposing a new format in which species names would be limited to two words.

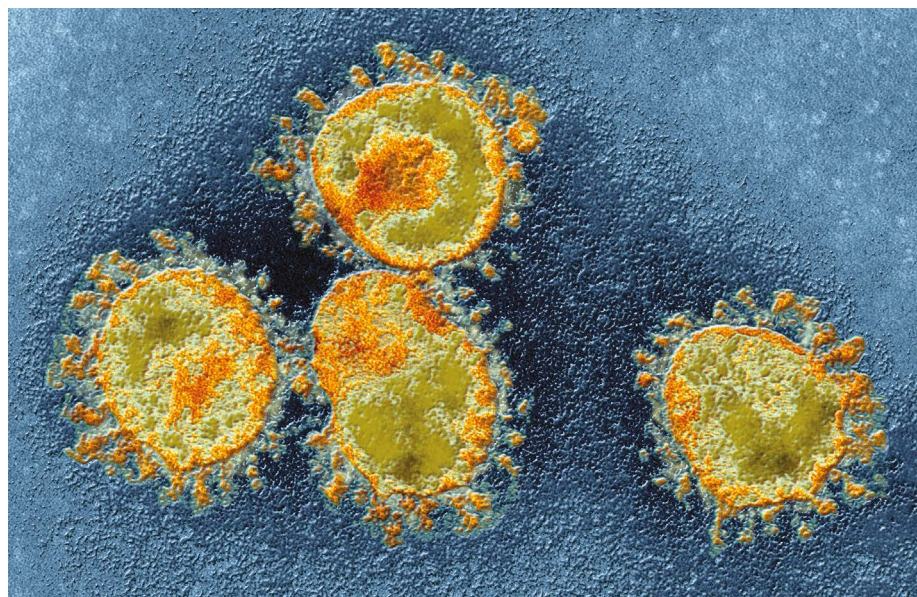
The first word would be the genus (ending in *-virus*), which is defined as a group of species that share some common characteristics. The paper proposes three options for the second word. Option one is always to use a Latinized term, in line with similar rules for naming biological organisms, such as *Homo sapiens*. The second option would restrict the second word to numbers or letters, as in *Alphacoronavirus 1*, and the third would open it up to any set of characters. So, existing names would be condensed to either a single, potentially Latinized, word, or numbers or letters.

The paper, which is the result of several years of public deliberation, called on researchers to provide feedback by 30 June, ahead of a decision at the committee's next meeting, in October. That decision would then be put to a vote by all ICTV members.

## Community concern

But several virologists say they did not notice the paper at the time, and were then swept up in the coronavirus response. “In an ideal world, we would all be looking at these journals, but the amount of literature we have to keep up with has mushroomed,” says Katherine Spindler, a virologist at the University of Michigan in Ann Arbor and secretary-treasurer of the American Society for Virology (ASV) – one of the world's largest virology communities, with more than 3,000 members in some 20 countries. “Taxonomy doesn't affect what I do. It only happens to come up when I write a paper,” says Spindler, who learnt of the consultation after the 30 June deadline. She and the rest of the ASV executive committee wrote to the ICTV committee on 9 July, stating that their members had not had sufficient time to consider the issue.

The Australasian Virology Society (AVS), representing some 700 members in Australia and New Zealand, sent its own letter to the ICTV on 4 July. “We believe that 2020, the year of COVID-19, is not an appropriate time to undertake a major change of naming virus species. Our members are stretched to the limit with other tasks, and many have not had time to properly consider this matter,”



Particles of a coronavirus, seen under a transmission electron microscope.

the letter stated.

In response to concerns about the timing, ICTV president Andrew Davison, a virologist at the University of Glasgow, UK, says that a version of the proposal has been on the ICTV agenda for nearly two years, but he expects the committee to consider all the relevant factors at its meeting. "I agree that these are unusual times," he says.

In their letters, the ASV and AVS also state that they oppose the idea of mandating Latinized names, because that would require virologists to learn Latin grammar, and would be cumbersome to implement. Both groups prefer the option in which any word can be used as the species name, although the AVS's top preference would be to maintain the status quo, its letter states. "There is no need to overhaul the whole system," says AVS president Gilda Tachedjian, a virologist at the Burnet Institute in Melbourne, Australia.

But when naming a species, virologists would need to know only the appropriate Latin suffix, says Jens Kuhn, a virologist at the Integrated Research Facility at Fort Detrick, Maryland, and a member of the ICTV executive committee. Latin terms would also be universal, not requiring translation in papers published in languages other than English, he says.

### SARS-CoV-2 diversity

Virologists are less conflicted about the urgent need for coherence in naming the many SARS-CoV-2 lineages, which are being labelled in an ad hoc manner. "We are clearly going to end up with more than 100,000 complete genome sequences of SARS-CoV-2, which is staggering. It is obviously important to come up with a simple, rational and widely adopted scheme to classify all this diversity," says Holmes.

No official body decides how to name viral lineages. "We've stepped in to try and sort this out. Whether people will adopt it is another matter: it's really up to the users," says Holmes.

He and his colleagues have proposed a dynamic method that prioritizes naming lineages that have seeded an epidemic. The lineages would be labelled active, unobserved or inactive depending on how recently they have been isolated; these labels would be reassessed regularly, on the basis of whether the lineages are still spreading. The researchers described the method in their *Nature Microbiology* paper on 15 July, and seem to have gained support among virologists. They have also developed online tools to help users identify which lineage their sequence belongs to.

Such a system could make it easier to monitor lineages with unique pathogenic properties when they arise, says Elliot Lefkowitz, a virologist at the University of Alabama at Birmingham and member of the ICTV executive committee.

Q&A



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## The mathematician who helped to reshape physics

**In 1983, mathematical physicist Barry Simon uncovered a surprising connection between a phenomenon in materials and a branch of mathematics called topology. Topology is the study of physical shapes that deform continuously. But the field has now proved crucial to understanding the shapes of quantum waves formed by the electrons inside certain materials. These waves can form topological shapes such as vortices, knots and braids, and create a variety of exotic properties. Simon's work explained a strange phenomenon related to resistance called the quantum Hall effect, first described in a semiconductor by German physicist Klaus von Klitzing 40 years ago this month. Under certain conditions, the electrical resistance in a material jumps predictably, rather than moving continuously, because of the topological behaviour of the electrons. With collaborators, Simon showed that the equations created to describe the quantum Hall effect were a manifestation of topology. Researchers are now using ideas from this field to predict more physical phenomena, and hope these behaviours could be applied in fields such as quantum computing. *Nature* spoke to Simon to ask how it all started and about the relationship between mathematics and physics.**

**What made you think there was a connection between the quantum Hall effect and topology?**

The thing that's surprising about the quantum Hall effect is that something that appears to be continuous is quantized — it comes in discrete units. When I saw [theoretical physicist] David Thouless's quantum Hall formula, I immediately thought of a topological concept called homotopy. The simplest example to think of is how a circle can continuously map to itself. In the case of the circle to a circle, there is a key issue: one circle winds around the other an integer number of times. And if you continuously deform the map, you're not going to change that number.

**So in your papers, you showed that this topological effect, called the winding number, made the resistance of the semiconductor jump between discrete**

**values. Did you imagine that the discovery would be so successful?**

I knew it would make a splash because it would appeal to high-energy physicists, who were already accustomed to ideas from topology. I didn't realize it would have this long-lasting impact in solid-state physics.

**As a mathematician, do you think in a different way from theoretical physicists?**

There is a sharp dividing line between physicists and mathematicians: whether you really 'prove' things in the mathematical sense of proving things. It's the difference between demonstration and proof. There is a very different style.

**How would you describe the relationship between the two communities?**

It depends on the subfields. The condensed-matter physicists were so used to being looked down on by the high-energy physics community — particle physicist Murray Gell-Mann described condensed matter as "squalid-state physics" — that they didn't look down on other people. There's a tradition among high-energy physicists and string theorists that's not very positive towards maths. Sometimes there's a lack of mutual respect.

**Is that bad for research?**

It's certainly bad for life — it makes life less pleasant. Is it bad for business? Would science progress more without it? I don't know. To the extent that these cultural things prevent collaboration, it's very bad. Although sometimes it's not clear, even if people were more accepting of each other, that they could successfully collaborate.

**Have interactions between the two communities improved since the 1980s?**

There are still separate camps, but the landscape has changed enormously. There is much more attention in both directions now than there was 40 years ago. It amazes me what has happened to the use of topological ideas in condensed-matter physics. It's really, really striking.

**Interview by Davide Castelvecchi**

This interview has been edited for length and clarity.