'A bloody mess': confusion reigns over naming of new COVID variants

As more lineages emerge, researchers are struggling with a patchwork of nomenclature.

Would a virus by any other name spread so fast? As scientists identify more and more potentially worrying variants of the coronavirus SARS-CoV-2, they are grappling with what to call them. At a 12 January World Health Organization (WHO) meeting devoted to coronavirus variants, health officials and researchers started hashing out a new naming system.

"I think all of us are becoming very confused by the different variant names," said Maria Van Kerkhove, an infectiousdisease epidemiologist and COVID-19 technical lead for the WHO in Geneva, Switzerland, at the meeting.

That much is clear - there is no one-size-fits-all approach for naming variants of SARS-CoV-2. When a fast-spreading variant was identified in the United Kingdom in late 2020, Public Health England initially named it Variant Under Investigation 202012/01 (VUI 202012/01 for short); then, after a risk assessment, it was dubbed Variant of Concern 202012/01 (or VOC 202012/01).

One naming system that researchers developed to indicate the evolutionary relationships between SARS-CoV-2 lineages calls the same variant B.1.1.7. whereas another with the same goal dubs it 201/501Y.V1. 'The UK variant' is popular in the media. Variants identified in South Africa and Brazil have received similar monikers. Terms such as 'variant', 'lineage' and 'strain' add to the confusion, because they have no unambiguous definitions.

Because of the relevance to the public, "I can see the need for a more straightforward way of naming the variants of concern", says Oliver Pybus, an evolutionary biologist at the University of Oxford, UK, who co-developed a naming system that describes the relationships between the various early lineages of SARS-CoV-2 and their evolutionary descendants (A. Rambaut et al. Nature Microbiol. 5, 1403-1407; 2020). This is the source of the name B.1.1.7, in which each successive character denotes a subgroup of the preceding one. "There are already naming schemes for all these lineages, but they're mostly of relevance to phylogenetics geeks like me," says Pybus.



New variants of the coronavirus SARS-CoV-2 are being identified around the world.

Experts also want to do away with names that associate a variant with the country or region in which it was identified. "We want to remove any of the geopolitical issues," Van Kerkhove said. "We are trying to avoid 'the UK variant', 'the South African variant', 'the Brazil variant' — and there will be more."

Avoiding stigma

Variants are not necessarily identified in the country where they emerged, and fast-spreading ones such as B.1.1.7 that are spotted in one nation will eventually spill out into the wider world. Geographical associations could also stigmatize countries and so discourage surveillance, Pybus adds. "The last thing we want to do is dissuade any particular place from reporting they've got a new concerning variant - in fact, we want to do the opposite."

When South African researchers identified a worrying variant, they avoided including the country in its name at the request of South Africa's president and health minister, savs team member Tulio de Oliveira, a bioinformatician at the University of KwaZulu-Natal in Durban. They called it 501Y.V2 (H. Tegally et al. Preprint at medRxiv https:// doi.org/fqth; 2020); it is now also called B.1.351 under the system that Pybus's team developed. De Oliviera expects that until researchers agree on a less confusing naming system, the

media and public will continue to use 'the South African variant'. "The nomenclature is a bloody mess at the moment," he adds.

Some scientists also want to do away with names that flag individual mutations. De Oliveira's team called the variant that it identified 501Y.V2, because it carries a substitution in the 501st amino acid site of the virus's spike protein that changes the residue there from an asparagine to a tyrosine (denoted Y in biochemical shorthand). That name helped connect hundreds of researchers in disparate fields studying the effects of the mutation, says de Oliveira, but it also omits other important changes in the variant.

Researchers did not settle on a new naming system for concerning variants at the WHO meeting. Pybus, who is part of a working group tackling the issue, thinks a new system should go hand in hand with identification criteria. As evidence such as epidemiological or laboratory studies builds up, a name could reflect the heightened (or allayed) concerns surrounding a particular variant, he says.

Emma Hodcroft, a molecular epidemiologist at the University of Bern, agrees that there is confusion over naming, but she isn't sure that another system will solve the problem. "We need to be cautious."

By Ewen Callaway