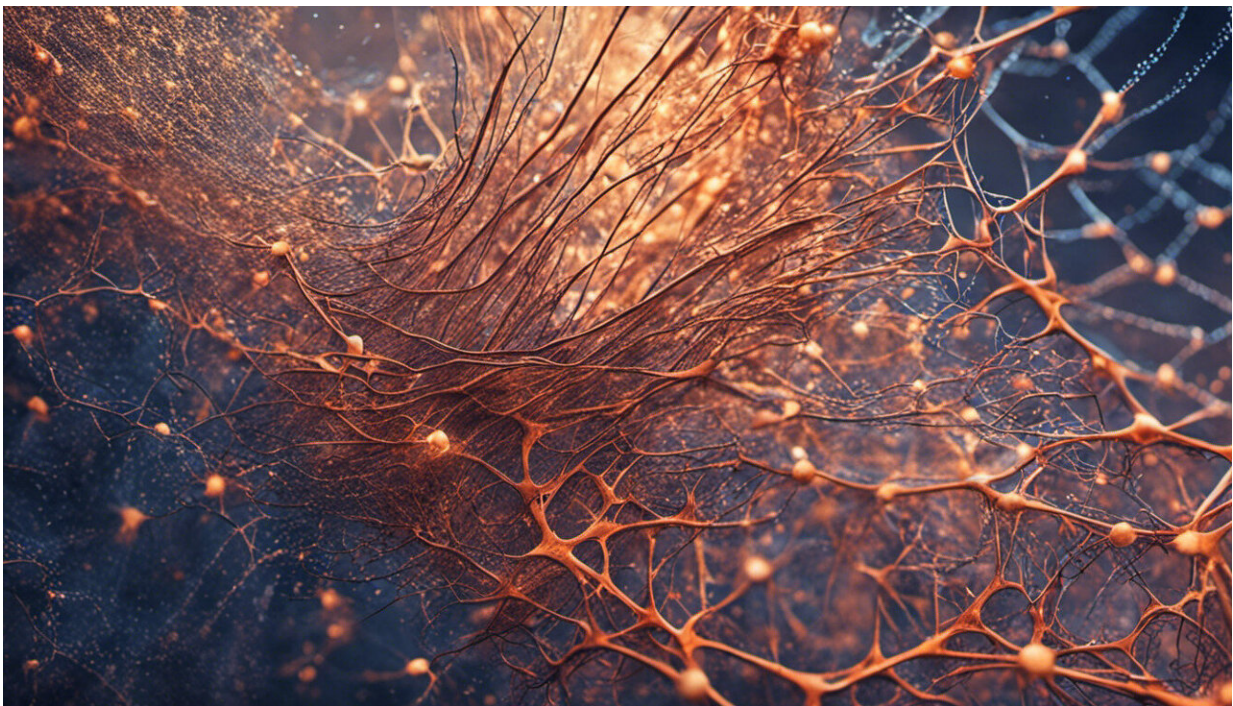# Open platform SARS-CoV-2 naming system to harness international scientific collaboration

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Credit: AI-generated image (disclaimer)

Researchers at the Universities of Oxford and Edinburgh have announced the formalization of the Pango Network, an international team of experts to oversee the identification and naming of different lineages of SARS-CoV-2 virus.

The team behind the widely used virus names such as B.1.1.7 and P.1 have published the details of their managing committees and the rules that govern the naming of variants on their new website.

Founded by Oliver Pybus at the University of Oxford and Andrew Rambaut at the University of Edinburgh, and supported by the Oxford Martin School, the Pango Network is a resource for scientists, public health specialists, journalists, and other stakeholders worldwide who need to communicate clearly about the different genetic types and variants of SARS-CoV-2.

The lineages and their names are decided by a small team in two committees, made up of experts from around the world who analyze virus genomic information and make a judgment about whether a new lineage is warranted. Members of the team, and the rules they use to designate new lineages, can be found on the Pango Network website.

Most scientists studying the pandemic believe that we will not be able to completely eliminate COVID-19, and that vaccines will be key to the long-term management of the virus. The Pango nomenclature has been created with this future in mind and provides a consistent system for tracking various SARS-CoV-2 outbreaks across the world. By using Pango to categorize different lineages, professionals can better understand virus transmission and spread and make informed decisions about public health responses.

Pango was inspired by the influenza virus naming system which is an established system that informs vaccination plans and public health decisions. However, the Pango team introduced a number of innovations, including a flexible set of designation criteria to adapt to changing circumstances. Further the Pango nomenclature limits lineage names to a maximum of four levels of ancestry, to ensure lineage names don't get too long.

Many of the lineages reported in the media start with the letter B. This is because B is one of two lineages that emerged during at the start of the pandemic in early 2020. The first named lineage that evolves from this strain is then called B.1—the dot is important because it identifies the next generation in the chain. When chain of ancestry gets too long the lineage names are given an alias to shorten them again. For example, the variant of concern spreading in Brazil is known as P.1 rather than B.1.1.28.1.

Prof Oliver Pybus said: "It's great that the Pango system has proved useful to researchers around the world. We're pleased to announce our new committee structure and website that explains clearly and openly how the nomenclature works."

Áine O'Toole, chair of the Lineage Designation Committee said: "We're very excited to expand the Pango Network. Having a dedicated committee will allow us to track the development of SARS-CoV-2 transmission into the future. We invite researchers from around the world to contribute by submitting suggestions so that the Pango system continues to reflect the global diversity of circulating virus."

More information: Andrew Rambaut et al, A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology, *Nature Microbiology* (2020). DOI: 10.1038/s41564-020-0770-5

Pango Network website: pango.network/

Provided by University of Oxford