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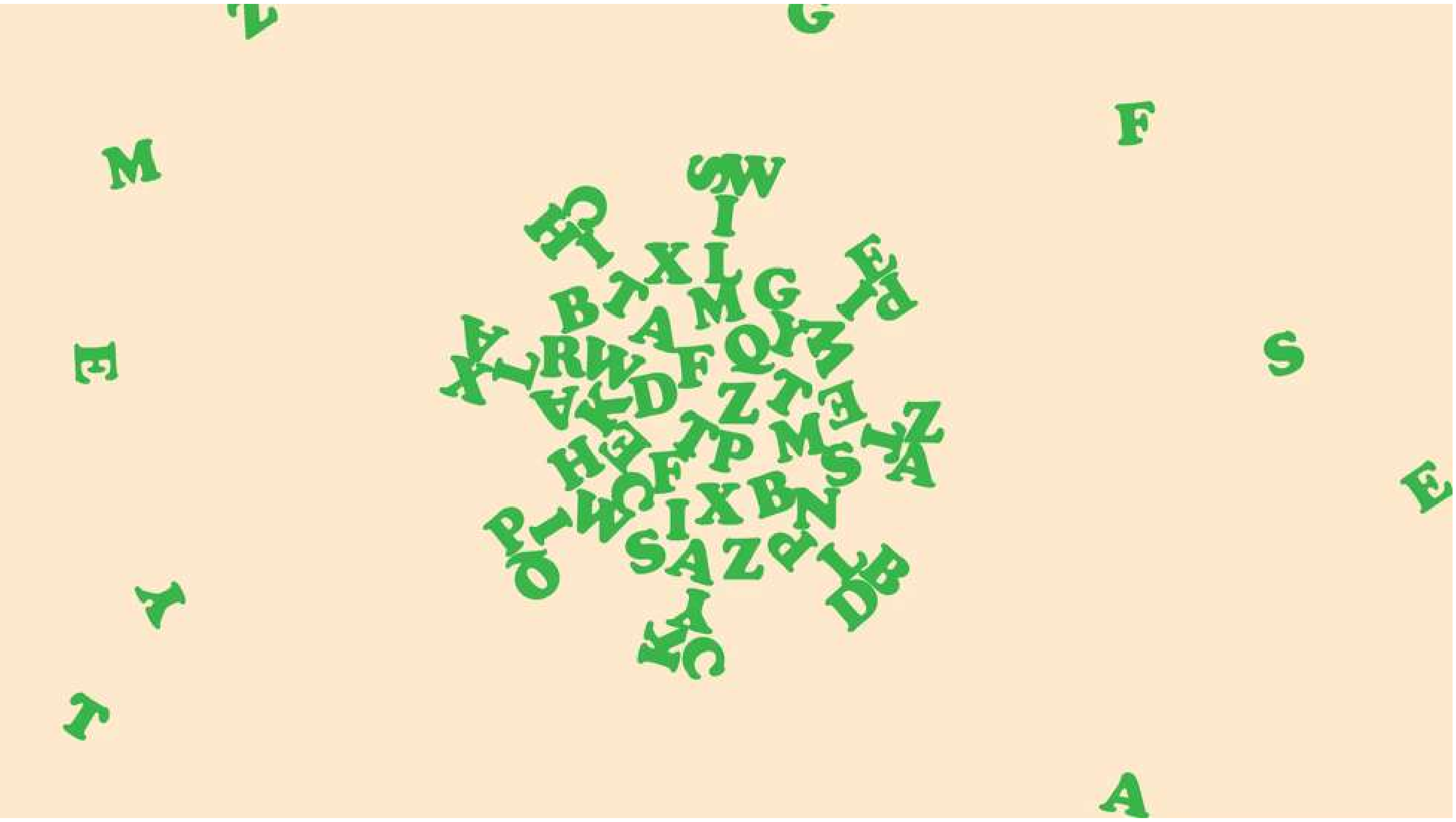
Why Can’t We Just Call BA.2 Omicron?

Whatever happened to the simpler Greek-letter naming system?

By Sarah Zhang



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When coronavirus variants emerged in full force in late 2020, the news suddenly turned into alphanumeric soup. Remember? The U.K. variant, B.1.351, GR/501Y.V3. After this initial period of chaos, the World Health Organization came up with a sanity-preserving system that renamed those variants, respectively, Alpha, Beta, and Gamma. And down the Greek alphabet we went, until we got to Omicron. The system worked.

Lately however, the post-Omicron news landscape is turning into alphanumeric soup again. An Omicron subvariant called **BA.2** is now globally dominant. **BA.4** and **BA.5** have just been discovered. And a cornucopia of new recombinants have names that seem to follow some inscrutable logic: **XD** (a recombinant of Delta and BA.1), **XE** (a recombinant of BA.1 and BA.2), **XF** (a *different* recombinant of Delta and BA.1), and so on, all the way down to **XS** (a recombinant of Delta and BA.1.1).

Would it help if I told you that the names do actually follow a coherent internal logic, which is quite pleasing once you've read and digested all 1,800 words laying out the rules? No? Okay, well, I will instead try to explain where the rules came from and why they are still used, despite the WHO's much simpler Greek-letter system.

Back in March 2020, scientists who study viral evolution began tracking how the novel coronavirus was changing. They ran into a very basic communication problem: What to call a new lineage after its genome was sequenced? "People in the U.S. were calling it one thing; people in Europe were calling it another," says Áine O'Toole, a postdoctoral researcher at the University of Edinburgh. So O'Toole's adviser, Andrew Rambaut, and a group of collaborators came up with a naming system. They called it Pango. And O'Toole, who is now the chair of Pango's lineage-designation committee, worked on a piece of software called pangolin, which allowed scientists to assign a likely Pango name to any viral genome.

(Yes, *Pango* is a tongue-in-cheek reference to pangolins, which were briefly suspected to have had a role in the coronavirus's origin—several of the team's computational tools are named after animals—and yes, this became confusing when *pangolin lineage* could be used to mean either viral lineages found in pangolins or lineages assigned by the pangolin tool. Again, scientists talking among themselves didn't quite anticipate how their jargon might be interpreted by others.)

At this point, no one yet knew the dramatic role that variants would play in the pandemic. Scientists were mostly interested in tracking lineages to see how the virus spread from country to country. And there were only two main lineages of the coronavirus at first: A and B. As the virus accrued different mutations in different places around the world, scientists used the Pango system to name sublineages by adding numbers. B.1.1.7, for example, is the seventh sublineage to be discovered of B.1.1, which in turn is the first sublineage discovered of B.1. You might know B.1.1.7 better as "Alpha." O'Toole remembers overhearing the BBC talk about "B.1.1.7" over Christmas in 2020. "It was very surreal for me," she told me. "I remember saying to my sister, 'Oh, you know that name there?' And she's like, 'Yeah, it's awful.'" These names were designed for scientists tracking lots and lots of different variants. For the general public, she said, "we hadn't considered how difficult it would be to tell apart B.1.1.7, B.1.351, and B.1.128."

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Until late 2020, though, the general public didn't really need to tell different lineages apart. Alpha was the first variant to truly change the pandemic's trajectory. The world now needed a system that distinguished "variants that are epidemiologically important" from "variants that simply exist." The WHO Greek-letter system is meant to do the former, the Pango system the latter.

This division of responsibility has worked fairly well, though Omicron has made things a little more complicated. The variant that the WHO originally designated as Omicron is called B.1.1.529 under Pango. Scientists then quickly found further subvariants of Omicron, which you might know as BA.1, BA.2, and BA.3. This is because when names get too long under the Pango nomenclature system, the first part of the name gets replaced with a new letter—or a pair of letters if all the single letters are taken. When the Omicron subvariants were described, the next available pair of letters was *BA*. So instead of B.1.1.529.2, we have BA.2. By chance, we ended up with some relatively easy-to-remember Omicron subvariant names.

BA.1 and BA.2 have caused big, successive waves in parts of Europe. The two subvariants are actually quite distinct from each other, almost as evolutionarily divergent as Alpha was from Delta. But the WHO decided back in February that BA.2 should still be considered Omicron, and more recently, it decided BA.4 and BA.5 should be too. Could an Omicron subvariant look and behave so differently that it actually should get a new Greek letter? In retrospect, BA.2 falls in a somewhat debatable zone: The BA.2 wave got as big, if not bigger, than the original BA.1 wave in some European countries, but it's not looking to be quite as dramatic yet in the U.S. There's a balance, O'Toole said, between giving a lineage a name as soon as possible and giving it a name when you know its epidemiological importance. The earlier we try to designate variants with Greek-letter names, the less we know about what they're potentially capable of. The WHO has also designated many variants of interest—Epsilon, Eta, Iota, and Lambda, to name a few—that did not end up making a big epidemiological impact.

In recent months, more recombinants have appeared too, and this is not a coincidence. This coronavirus, like other coronaviruses, has always been capable of recombination. But early on, different lineages were so similar to one another that recombination just meant swapping very similar sequences—in other words, it didn't mean much. Recently, however, parts of the world have seen a Delta wave followed by a BA.1 wave followed by a BA.2 wave. High co-circulation of several distinct lineages means more potential for recombination. The Pango system anticipated recombinants from the beginning, reserving the letter *X* for recombinant lineages. Then you just go down the alphabet and keep adding letters or numbers as usual. The WHO is monitoring one recombinant, XD, and if any recombinants start driving cases upward, they too could get a Greek-letter name. That new lineages with confusing

Pango names are making it into the news even before we understand their importance reflects a truly unusual level of media and public interest in the nitty-gritty of viral evolution.

A naming system that follows the Greek alphabet might seem to imply a linear progression of new variants. But viral evolution is more like watching a tree branch and grow. And you don't know which branches will become stunted and which will go on to grow long and dense with twigs. Nor can you know which distant branches might fuse with one another into a recombinant branch that itself grows long and dense. The Greek-letter system is meant to highlight the most important branches in this tree of viral evolution. But it doesn't cover everything—not even close. The Pango system now encompasses more than 2,000 lineages, the majority of which are consigned to obscurity. And in all likelihood, most of the alphanumeric-soup names in the news today will go back to obscurity soon too. If they don't, well, then we'll probably all have a new Greek letter to learn.

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