

The BMJ

Cite this as: *BMJ* 2023;382:p1964 http://dx.doi.org/10.1136/bmj.p1964 Published: 24 August 2023

Covid-19: Scientists sound alarm over new BA.2.86 "Pirola" variant

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A new SARS-CoV-2 subvariant with a high number of mutations that could help it neutralise the immune system has emerged in four countries, raising alarm among scientists.

"BA.2.86 is the most striking SARS-CoV-2 strain the world has witnessed since the emergence of omicron," said Francois Balloux, professor of computational systems biology and director of University College London's Genetics Institute.

Genetic sequencing has found BA.2.86 in six covid cases so far, the earliest being in Denmark on 24 July. The other cases were from Israel, the UK, and the US. None of the cases seem linked. The UK Health Security Agency said that the UK case was in a person with no recent travel history, suggesting a degree of community transmission within the UK.

The genetic diversity suggests that BA.2.86 has been in circulation for months, said Balloux. "Interestingly, all 30-plus mutations on that long branch are found in the spike protein—through which the virus gains entry to cells—which is the target of neutralising antibodies."

BA.2.86, which some media outlets have nicknamed "Pirola," is another subvariant of the omicron variant, this one descending from the BA.2 strain that led to widespread covid cases at the start of 2022. The new strain has 34 more mutations than BA.2 and 36 more than XBB.1.5 (dubbed "Kraken" in the media¹ and the strain recommended for vaccination), said an early analysis by Jesse Bloom, a computational virologist at the Fred Hutchinson Cancer Research Institute in Seattle, USA.²

BA.2.86 has "at least as much" antibody escape as XBB.1.5 did when compared with BA.2, meriting high priority monitoring for signs of spread, Bloom wrote. The World Health Organization has labelled BA.2.86 a "variant under monitoring"—its second tier of notable covid variants.

The mutations give BA.2.86 "all the hallmark features of something that could take off," said Kristian Andersen, an immunologist at the Scripps Research Institute in the US, writing on the social media platform X (formerly Twitter). He added, "Our immunity landscape is now complex so it's too early to say it will. I think it might."

Transmissibility and severity

At the time of writing, little is yet known about the transmissibility of BA.2.86 or whether it may cause more severe disease, but scientists do not expect it to be much different from previous omicron strains currently in circulation.

Bloom wrote, "While neutralising antibodies (which are partially escaped by highly mutated variants like BA.2.86) provide best protection against infection, there are also broader mechanisms of immunity elicited by vaccination and infection that provide some protection against severe disease even for very heavily mutated variants. So even if [it] starts to spread, we will be in a better place than we were in 2020 and 2021, since most people have some immunity to SARS-CoV-2 now."

Balloux said, "Even in the worst case scenario where BA.2.86 caused a major new wave of cases, we are not expecting to witness comparable levels of severe disease and death [as] we did earlier in the pandemic when the alpha, delta, or omicron variants spread."

The discovery of BA.2.86 comes soon after public concern over the EG.5/EG.5.1 "Eris" subvariant³ that has become dominant in the US and accounted for 17.4% of cases worldwide in the week ending 23 July.

Balloux added that, unlike EG.5, the BA.2.86 subvariant is much more warranting of attention. "The most plausible scenario [accounting for its appearance] is that the [omicron] lineage acquired its mutations during a long term infection in an immunocompromised person over a year ago and then spread back into the community," he said. "BA.2.86 has since then probably been circulating in a region of the world with poor viral surveillance and has now been repeatedly exported to other places in the world. Over the coming weeks we will see how well BA.2.86 will be faring relative to other omicron subvariants."

Bloom said that, in order to be successful, BA.2.86 would need to combine its antigenic advantage with inherent transmissibility of the kind seen in the XBB subvariants. He told *Nature*, "The most likely scenario is that this variant fizzles out, and in a month, nobody other than people like me even remember that it existed."⁴

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