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BRIEFING

Covid-19: What do we know about omicron sublineages?

On 26 November 2021 WHO designated omicron a variant of concern. With its sublineage BA.2 now widespread, **Elisabeth Mahase** looks at what science has found out about the variant and its three (so far) variations

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BA(B.1.1.529.1)

The original SARS-CoV-2 omicron variant is B.1.1.529.1, the version that most people think of when omicron is referred to and that currently makes up more than nine in 10 omicron cases. BA.1 has so far spread to more than 130 countries and is characterised by a significant number of mutations, including 37 on the spike protein.

The World Health Organization says BA.1 is more likely than delta to infect and replicate in the upper respiratory tract, whereas delta targets the lower respiratory tract. This difference may be behind the transmission advantage that BA.1 has shown but could also be the reason for its seeming to lead to less severe disease than delta.¹

However, although BA.1 infection is generally associated with lower severity, its increased transmissibility has resulted in high numbers of patients being admitted to hospital, putting a big strain on healthcare systems. It is also associated with a 5.4-fold higher reinfection risk than delta.²

Current covid vaccines seem to provide strong protection against severe disease and death from BA.1 infection. Early reports indicated that the two dose covid vaccine schedule had reduced effectiveness against milder disease caused by BA.1 than previous variants. Administration of a third “booster” dose was found to provide greater protection.³

Looking at treatments, ronapreve (a combination of the monoclonal antibodies casirivimab and imdevimab) has been found to have reduced efficacy against BA.1. Another antibody treatment, sotrovimab, seemed to retain activity against the BA.1 spike protein in laboratory experiments and is likely to be added to the Recovery trial for clinical examination. The antiviral molnupiravir has also been found to remain active against BA.1 in six preclinical studies, although it has not yet been assessed in clinical studies.⁴

BA(B.1.1.529.2)

BA.2 has fewer mutations than BA.1, with 31 on the spike protein. WHO reported that by 30 January it had reached at least 57 countries,⁵ while nearly 50 000 cases had been confirmed up to 3 February.⁶

The UK Health Security Agency has reported that across England BA.2 has an “increased growth rate” in comparison with BA.1 and that, although growth rates can be overestimated in early analyses, the “apparent growth advantage is currently substantial.” Meanwhile, contact tracing data show that people infected with BA.2 are more likely than people with BA.1 to infect household contacts. The agency has said there are currently no data on the severity of BA.2.⁷

Wendy Barclay, head of infectious disease at Imperial College London, said that much was still unknown about BA.2 but that it did have the same “double whammy ability” as BA.1, with many changes in the spike protein meaning that the antibodies the population has made against vaccines or previous infection were not able to “see the virus very well.” She suggested that BA.1 may have compromised its own ability to infect and reproduce because of the vast number of changes it has accumulated. BA.2, with fewer changes, may have “struck a better balance with the escape from antibodies, while maintaining good transmissibility.”⁸

Preliminary investigations by the UKHSA found no evidence of decreased vaccine effectiveness against symptomatic disease for BA.2 when compared with BA.1. At least 25 weeks after two doses, vaccine effectiveness against symptomatic infection was reported as 13% for BA.2 (versus 9% for BA.1). At two weeks after a third booster dose this increased to 70% (versus 63% for BA.1).

BA(B.1.1.529.3)

Even less is known about BA.3. As at 3 February fewer than 400 cases of this sublineage had been detected around the world, although it has still reportedly reached at least 19 countries.⁹ Early investigations showed that BA.3 has 33 mutations in the spike protein, of which it shares 31 with BA.1. It shares the other two mutations with BA.2. Researchers have speculated that the reason behind BA.3’s slow spread could be that it lacks the six additional mutations that BA.1 has.¹⁰

Nothing is yet known about BA.3’s disease severity or vaccine effectiveness.

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