



OMICRON SUB-LINEAGE BA.2

We need to optimise genome surveillance and tracing of SARS-CoV-2 variants

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Whole genome sequencing has been crucial in studying the evolution and genetic diversity of SARS-CoV-2 during the pandemic, and it had an important role in identifying the omicron variant.^{1,2}

Earlier in the pandemic, the alpha variant was found to result in an undetectable S gene on reverse transcription polymerase chain reaction (S gene target failure (SGTF))—a feature of considerable diagnostic value.^{3,4} The South African investigations that led to announcement of the omicron variant of concern found SGTF in more than 50% of all tested specimens, supporting SGTF as a proxy for this variant too.⁵ This aligns with the World Health Organization's recommendations for early detection of the omicron variant, which calls for diagnostic test kits containing two confirmatory genes, at least one of which is the S gene, pending sequencing confirmation.²

Now the SARS-CoV-2 omicron (B.1.159) lineage is thought to be split into two sub-lineages: BA.1 and BA.2 (www.gisaid.org). These sub-lineages share several common defining mutations and seem to be co-circulating, but the BA.2 sub-lineage does not carry the del69-70 mutation in the spike region, and recently sequenced cases belonging to the BA.2 sub-lineage have not been flagged by SGTF.⁶ The UK Health Security Agency⁷ and the American Medical Association⁸ have expressed concerns over this new “stealth” sub-lineage, which also seems to be more transmissible, a trait likely to affect the current trend of declining cases.

Detection of SGTF seemed to be an effective strategy to contain omicron through targeted contact tracing and isolation, but the rapid evolution of variants and sub-lineages, and the unfolding data regarding their genetic profiles, need to be incorporated into our diagnostics tools if we are to succeed in overcoming SARS-CoV-2.

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All authors contributed equally to this letter.

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