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# SARS-CoV-2 variant update: BA.2.87.1

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On 1 February 2024, sequences were uploaded to GISAID of a new highly divergent variant, now designated BA.2.87.1, from South Africa. This update summarizes what we know so far:

*Number and origin of known sequences:*

South Africa: 9 similar sequences from samples taken on 8 dates between 20-9-23 and 29-11-23, from 3 different provinces (not a single cluster)

United States: 1 low quality sample from 12-10-23 from a traveler coming from the UAE

Italy: News reports of detection in Italy are dubious, cannot be verified and cite no sources.

**The appearance of samples, with some genetic diversity, over a 3-month timespan and in different geographic locations suggests community spread**

*Growth*

There is currently too little data to say if it is becoming more prevalent or not. We have only 10 sequences at 9 different time points, no trends can be drawn from this. Specifically, sequencing data are available from South-Africa to assess the growing potential are sparse.

*Mutations*

Relative to BA.2, this new variant has over 100 changes at the RNA level, and over 30 changes at the amino acid level. Many of these changes are known to lead to immune escape, and many have only seen before in cryptic lineages or during chronic infections. The leading hypothesis is that this first emerged from a chronically infected individual (vs undetected community transmission or evolution in animals). Modelling suggests lower ACE2 binding than JN.1, and less immune escape than JN.1 from antibodies raised against BA.2.

*Severity*

There is no data on severity at this time. Of the 10 sequences, 2 come from “pneumonia surveillance”, 7 from “baseline surveillance”, and one from screening of travelers. It is reasonable to assume the cases originating from “pneumonia surveillance” were not mild cases, but no conclusions can be drawn from such sparse data.

*Outlook*

BA.2.87.1 resembles the precursor to JN.1 in many ways. It is likely that it needs to pick up additional mutations to increase ACE2 binding or the population needs to develop substantial immunity against JN.1

before BA.2.87.1 has a chance of replacing JN.1 as the dominant variant. We will continue to monitor this variant and update risk assessments.