

- Variation (Biology) / Virus

## Viral tales told by signature mutations

### Why we must keep track of how highly transmissible lineages evolve over time

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All viruses mutate to survive and thrive in their environment. SARSCoV-2 is no exception. And the highly mutated Omicron is the most recent 'variant of concern', designated by the World Health Organization (WHO).

Preliminary evidence suggests Omicron is more easily transmitted than its predecessors. As scientists learn more about the virus, new information is emerging rapidly about transmission, virulence, effectiveness of existing vaccines, and the impact of mutations on available molecular diagnostic tests.

Robust testing can help detect asymptomatic cases, which result in the inadvertent spread of disease. Currently, all reported cases of Omicron are mild or asymptomatic — stressing the need for more testing. Besides, the variant has been found to include the same mutation of S gene, first identified in the Alpha variant. This mutation causes a dropout of the S-gene target in results. Diagnostics tests that have a multi-target design can be used as an indicator for Omicron, prior to sequencing.

Genomic surveillance will be crucial for identifying new mutations and monitoring their spread. The ability to distinguish between variants may provide insights into SARS-CoV-2's evolution.

The resurgence of new variants reminds us that it is critical to continually characterise virus strains and monitor the spread at the population level. This will help assess the effectiveness of containment strategies.

Detecting the signature mutations in these highly transmissible lineages is important, not only for confirming the lineage but also tracking how it changes over time.

Further, next-generation sequencing (NGS) can be used for validating and detailed analysis of the complete SARSCoV-2 genome. Highly automated NGS makes SARS-CoV-2 epidemiology research accessible and supports local, regional, and global surveillance efforts.

Many questions will be answered as the disease progresses. Meanwhile, we need to keep ourselves safe by tracking the mutations, even as we follow public health guidelines.