

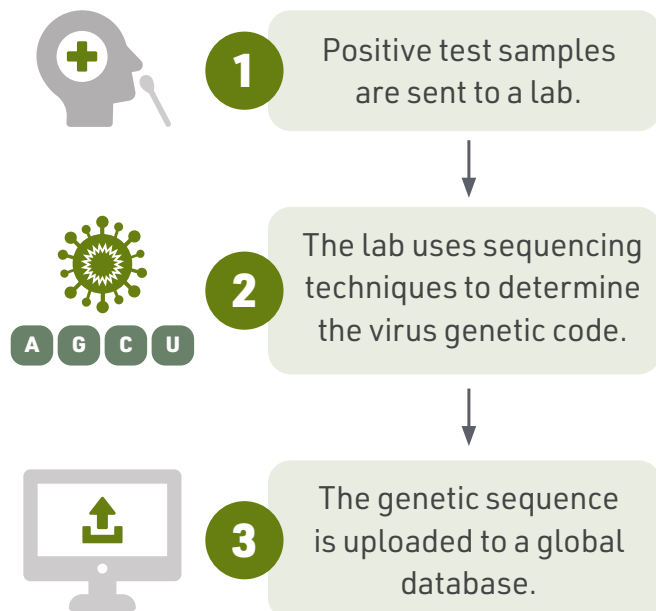
18 DEC
2020

CHEM VS. COVID TIMELINE

Alpha variant designated as a variant of concern

Tracking variants

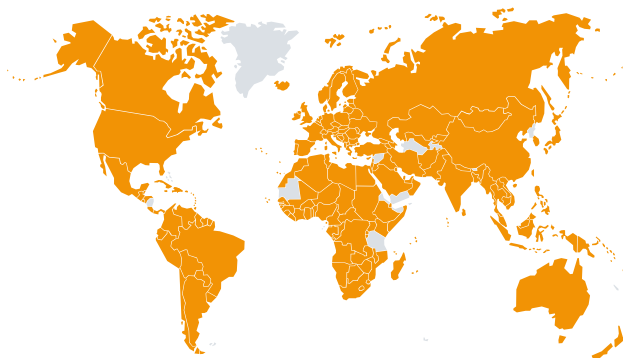
Coronavirus variants arise from mutations in the virus RNA, its genetic code. These mutations occur over time as the virus copies itself. The mutations can be used to identify variants and track their spread.



As of December 2021, over 6,000,000 SARS-CoV-2 genome sequences have been submitted to the shared GISAID database, from most of the countries in the world (as highlighted on the map)



Alpha (B.1.1.7) was the first SARS-CoV-2 variant identified as a variant of concern. Subsequently, several other variants of concern have been identified. Genomic sequencing helps monitor their spread.



How is variant tracking helping?



Understanding the virus

Tracking mutations in the virus and how it affects its characteristics helps scientists understand which mutations are significant and which are benign.



Outbreak control

Being able to track the development, course and spread of new variants allows scientists to understand how quickly they are spreading and their effects.






Sharing sequences

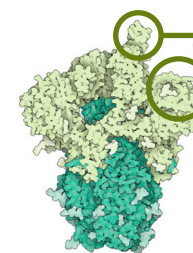
Sharing sequences in online repositories allows advanced warning of new variants, as seen with the work of South African scientists on the Omicron variant.

Variant consequences

Most mutations in the virus genome have little or no effect on the characteristics of the virus. But some mutations in the code cause more meaningful changes, such as those affecting the spike protein.

| | Mutations | Spike protein mutations |
|---|-----------|-------------------------|
|  Alpha variant | 21 | 9 |
|  Delta variant | 20 | 8 |
|  Omicron variant | 51 | 33 |

The spike protein helps the virus enter cells. It's the main target of vaccines and our body's immune response. Changes to the spike protein's structure may increase the virus's infectivity and ability to evade immune responses.



Receptor-binding domain

Mutations here can affect the virus's transmissibility.

N-terminal domain

Mutations here can affect the virus's infectivity.