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.

1. Positive test samples are sent to a lab.

2. The lab uses sequencing techniques to determine the virus genetic code.

3. The genetic sequence is uploaded to a global database.

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).

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.

<table>
<thead>
<tr>
<th>Variant</th>
<th>Mutations</th>
<th>Spike protein mutations</th>
</tr>
</thead>
<tbody>
<tr>
<td>Alpha variant</td>
<td>21</td>
<td>9</td>
</tr>
<tr>
<td>Delta variant</td>
<td>20</td>
<td>8</td>
</tr>
<tr>
<td>Omicron variant</td>
<td>51</td>
<td>33</td>
</tr>
</tbody>
</table>

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.

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.

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.