COVID-19 Pandemic: Global overview

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Global epidemiological trends

Previous week
>4.2 million confirmed cases
>65,000 deaths

Cumulative as of 12 August 2021
204,644,849 confirmed cases
4,428,759 deaths

data smoothed with 7-day moving average
Regional epidemiological trends

As of 9 August 2021 10h CET

Cases depicted by bars; deaths depicted by line. Data smoothed with 7-day moving average. Note different scales for y-axes.
Continuous virus evolution

Genomic spread of SARS-CoV-2 variants of concern

Source: Nextstrain based on GISAID data nextstrain.org/ncov/global
# Continuous virus evolution: Variants of Concern

## Variants of Concern (VOC)

**Working definition:**
A SARS-CoV-2 variant that meets the definition of a VOI (see below) and, through a comparative assessment, has been demonstrated to be associated with one or more of the following changes at a degree of global public health significance:

- Increase in transmissibility or detrimental change in COVID-19 epidemiology; OR
- Increase in virulence or change in clinical disease presentation; OR
- Decrease in effectiveness of public health and social measures or available diagnostics, vaccines, therapeutics.

## Currently designated Variants of Concern:

<table>
<thead>
<tr>
<th>WHO label</th>
<th>Pango lineages</th>
<th>GISAID clade</th>
<th>Nextstrain clade</th>
<th>Additional amino acid changes monitored*</th>
<th>Earliest documented samples</th>
<th>Date of designation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Alpha</td>
<td>B.1.1.7</td>
<td>GRY</td>
<td>20I (V1)</td>
<td>+S:484K</td>
<td>United Kingdom, Sep-2020</td>
<td>18-Dec-2020</td>
</tr>
<tr>
<td>Beta</td>
<td>B.1.351 &lt;br/&gt;B.1.351.2 &lt;br/&gt;B.1.351.3</td>
<td>GH/501Y.V2 &lt;br/&gt;20H (V2)</td>
<td>+S:L18F</td>
<td>Brazil, Nov-2020</td>
<td>18-Dec-2020</td>
<td></td>
</tr>
<tr>
<td>Gamma</td>
<td>P.1 &lt;br/&gt;P.1.1 &lt;br/&gt;P.1.2</td>
<td>GR/501Y.V3 &lt;br/&gt;20J (V3)</td>
<td>+S:681H</td>
<td>Brazil, Nov-2020</td>
<td>11-Jan-2021</td>
<td></td>
</tr>
</tbody>
</table>

*Notable spike (S) amino acid changes under monitoring, which are currently reported in a minority of sequenced samples.*

Continuous virus evolution: Variants of Interest

Variants of Interest (VOI)

Working definition
A SARS-CoV-2 variant:

- with genetic changes that are predicted or known to affect virus characteristics such as transmissibility, disease severity, immune escape, diagnostic or therapeutic escape; AND
- identified to cause significant community transmission or multiple COVID-19 clusters, in multiple countries with increasing relative prevalence alongside increasing number of cases over time, or other apparent epidemiological impacts to suggest an emerging risk to global public health.

Currently designated Variants of Interest:

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</tr>
</thead>
<tbody>
<tr>
<td>Eta</td>
<td>B.1.525</td>
<td>G/484K.V3</td>
<td>21D</td>
<td>Multiple countries, Dec-2020</td>
<td>17-Mar-2021</td>
</tr>
<tr>
<td>Iota</td>
<td>B.1.526</td>
<td>GH/253G.V1</td>
<td>21F</td>
<td>United States of America, Nov-2020</td>
<td>24-Mar-2021</td>
</tr>
<tr>
<td>Kappa</td>
<td>B.1.617.1</td>
<td>G/452R.V3</td>
<td>21B</td>
<td>India, Oct-2020</td>
<td>4-Apr-2021</td>
</tr>
<tr>
<td>Lambda</td>
<td>C.37</td>
<td>GR/452Q.V1</td>
<td>21G</td>
<td>Peru, Dec-2020</td>
<td>14-Jun-2021</td>
</tr>
</tbody>
</table>

https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/
Continuous virus evolution: Variants of Concern

Countries, territories, and areas reporting Variants of Concern
(situation as of 10 August 2021)

- Alpha (185)
- Beta (136)
- Gamma (81)
- Delta (142)
- Lineage not specified (2)

*Includes countries/territories/areas reporting the detection of 81,617 without further specification of lineage at this time. These will be reallocated as further details become available.

**Countries/territories/areas highlighted include both official and unofficial reports of VOC detections, and do not presently differentiate between detections among travellers (e.g., at Points of Entry) or local community cases. Please see Annex 2 for further details.

WHO Weekly Epidemiological Update on COVID-19: 10 August 2021
https://www.who.int/emergencies/diseases/novel-coronavirus-2019/situation-reports
## Continuous virus evolution: Variants of Concern

Summary of phenotypic impacts* of Variants of Concern (as of 10 August 2021)

<table>
<thead>
<tr>
<th>WHO label</th>
<th>Alpha</th>
<th>Beta</th>
<th>Gamma</th>
<th>Delta</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Transmissibility</strong></td>
<td>Increased transmissibility and secondary attack rate⁷</td>
<td>Increased transmissibility⁸</td>
<td>Increased transmissibility⁹</td>
<td>Increased transmissibility and secondary attack rate¹⁰ Similar transmissibility between vaccinated and unvaccinated individuals¹¹ - ¹³</td>
</tr>
<tr>
<td><strong>Disease severity</strong></td>
<td>Increased risk of hospitalization¹⁴, possible increased risk of severity and mortality¹⁵</td>
<td>Not confirmed, possible increased risk of in-hospital mortality¹⁶</td>
<td>Not confirmed, possible increased risk of hospitalization¹⁷</td>
<td>Increased risk of hospitalization¹⁸</td>
</tr>
<tr>
<td><strong>Risk of reinfection</strong></td>
<td>Neutralizing activity retained¹⁹, risk of reinfection remains similar²⁰</td>
<td>Reduction in neutralizing activity reported; T cell response elicited by D614G virus remains effective²¹</td>
<td>Moderate reduction in neutralizing activity reported²²</td>
<td>Reduction in neutralizing activity reported²³ - ²⁵</td>
</tr>
<tr>
<td><strong>Impacts on diagnostics</strong></td>
<td>Limited impact – S gene target failure (SGTF); no impact on overall result from multiple target RT-PCR, No impact on Ag RDTs observed²⁶</td>
<td>No impact on RT-PCR or Ag RDTs observed²⁷</td>
<td>None reported to date</td>
<td>None reported to date</td>
</tr>
</tbody>
</table>

*Generalized findings as compared to previously/co-circulating variants. Based on emerging evidence, including non-peer-reviewed preprint articles and reports, all subject to ongoing investigation and revision.
Delta has the highest estimated transmissibility of all variants

All VOCs and some VOIs demonstrate increased effective R
- Beta: 25% (20% – 30%)
- Alpha: 29% (24% – 33%)
- Gamma: 38% (29% – 48%)
- Delta:* 97% (76% – 117%)

*Estimate subsequently revised to 75% based on shorter serial interval
B.1.617.2 Delta variant

Replacement effect of Delta

Source: WHO Epi Analytics Group
Delta is outcompeting all variants in all countries with data

- Delta has significantly higher effective R than other VOCs
- Expected to become dominant lineage in coming months if trends continue

Source: WHO Epi Analytics Group
B.1.617.2 Delta variant

- Increased transmissibility – $R_0$ likely around 5
- Higher transmissibility for both very close (e.g. household) and more casual contacts (community SAR)
- Lower Ct values/higher viral load, potentially for earlier/longer period
- Decreased latent period and shorter serial interval
- Limited data on contact events and duration of infectiousness
- Healthcare outbreaks noted to be smaller and shorter in duration