SARS-CoV-2 Sequencing Update
26 November 2021

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Msimi N. Milisana K. et al. Lancet Microbe 2020

Prepared by the National Institute for Communicable Diseases (NICD) of the National Health Laboratory (NHLS) on behalf of the Network for Genomics Surveillance in South Africa (NGS-SA)
The genomic data presented here are based on South African SARS-CoV-2 sequence data downloaded from GISAID (www.gisaid.org) on 25 November at 16h01.

Data license: https://www.gisaid.org/registration/terms-of-use/


Case data is based on specimen collection date. Cases from https://www.nicd.ac.za/diseases-a-z-index/disease-index-covid-19/surveillance-reports/weekly-epidemiological-brief/ Test data from https://www.nicd.ac.za/diseases-a-z-index/disease-index-covid-19/surveillance-reports/weekly-testing-summary/
Bar graphs represent genomes sequenced per epiweek, with lines representing cases by collection date (weeks 18 – 46).
Genomes and cases presented as provincial total (percentage of national total) for epiweeks 18 – 46.
PTP: percentage testing positive in week 46 (14 Nov – 20 Nov); the arrow indicates direction of change since the previous week (7 Nov – 13 Nov).
Number of South African genomes deposited on GISAID, by specimen collection week, 2020 and 2021
(N=23 623*)

Total genomes: 23 623
2020 genomes: 6 308
2021 genomes: 17 315

Sequencing data ending epi week 47 (ending 27 November 2021)
Currently in epi week 47 (ending 27 November 2021)

*This represents the cleaned, de-duplicated dataset of unique sequences. This dataset will be used for all further figures.
All provinces, apart from GP, KZN, NC and WC, have comparable percentage of overall cases and overall sequenced genomes. The majority of November sequencing data is from Gauteng.
B.1.1.529 lineage mutation profile

- 45-52 amino acid changes (including deletions) across the whole GENOME
  - 26-32 changes in SPIKE

- Does not possess the RdRp G671S change associated with a decrease in Ct value for Delta variants
- Does possess the Δ69-70, which causes the S-Gene Target Failure (SGTF) and was previously seen in the Alpha VOC
- Sequences identified from Botswana, Hong Kong and South Africa
B.1.1.529 spike mutations compared to other VOC/VOIs

- Multiple changes within the two immunogenic regions in S1 (NTD and RBD)
  - including a three amino acid insertion

- Accumulation of mutations surrounding the furin cleavage site
  - Including combination of N679K and P681H

- Effect of most spike S2 subunit changes have not been defined

![Mutations with unknown or unconfirmed impact](Image)
Delta dominated South Africa’s third wave with >90% frequency in October, with C.1.2 detection remaining <6%. B.1.1.529 dominates November sequencing data but estimates are based on <100 sequences, with the majority of these sequences from Gauteng.
The Delta variant dominated in August, September and October in South Africa. B.1.1.529 was first detected in South Africa in November, comprising 76% (66/87) of sequences.
Detection Rates: Beta, Delta, C.1.2 and B.1.1.529

C.1.2 has been detected at ≤ 6% of sequences monthly.

B.1.1.529 was first detected in South Africa on November 14th. It makes up 76% (n=66/87) of November sequences released on GISAID.
Free State Province, 2021, n = 930
Gauteng Province, 2021, n = 4581
KwaZulu-Natal Province, 2021, n = 2119

KZN (N=2119)

Number of genomes

Percent of genomes

Epiweek
Mpumalanga Province, 2021, n = 1021

![Graph showing the number of genomes and cases over time for Mpumalanga Province, 2021, with data points for each week and a breakdown of different virus variants.](image-url)
Northern Cape Province, 2021, n = 1187
Western Cape Province, 2021, n = 3482
Summary

• Delta variant dominated in all provinces until end October
  • The Delta sub-lineages vary by province

• C.1.2 lineage detected in all provinces of South Africa with prevalence of <6% of genomes, with increases detected in KZN and NC in November

• New B.1.1.529 lineage first detected from specimens collected in Gauteng on 12 November
  • B.1.1.529 dominates November sequencing data at 76% of genomes (n=66/87). However, total number sequences for November are low.
  • Sequencing is ongoing to determine prevalence of B.1.1.529 in other provinces.
  • Additional detections reported in Botswana and Hong Kong
  • B.1.1.529 has been assigned as NextStrain clade 21K
  • More information can be found at https://www.nicd.ac.za/frequently-asked-questions-for-the-b-1-1-529-mutated-sars-cov-2-lineage-in-south-africa/
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Multiple labs from NGS-SA and collaborating private laboratories are contributing to the sequencing effort.

NGS-SA Labs
CERI: Centre for Epidemic Response and Innovation
KRISP: KZN Research Innovation and Sequencing Platform
NICD: National Institute for Communicable Diseases
NHLS: National Health Laboratory Service
SU: Stellenbosch University
UCT: University of Cape Town
UFS: University of the Free State
UP: University of Pretoria

*NGS-SA laboratories
## Variants of Concern (VOC)

<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 +S:452R</td>
<td>United Kingdom, Sep-2020</td>
<td>18-Dec-2020</td>
</tr>
<tr>
<td>Gamma</td>
<td>P.1</td>
<td>GR/501Y.V3</td>
<td>20J (V3)</td>
<td>+S:681H</td>
<td>Brazil, Nov-2020</td>
<td>11-Jan-2021</td>
</tr>
</tbody>
</table>


*Notable spike (S) amino acid changes under monitoring, which are currently reported in a minority of sequenced samples
*Includes all descendant lineages.
#Includes all Q.* lineages in the PANGO nomenclature system.
§Includes all AY.* lineages in the PANGO nomenclature system.
Currently designated Variants of Interest (VOI)

<table>
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</thead>
<tbody>
<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>
<tr>
<td>Mu</td>
<td>B.1.631</td>
<td>GH</td>
<td>21H</td>
<td>Colombia, Jan-2021</td>
<td>30-Aug-2021</td>
</tr>
</tbody>
</table>


*Includes all descendant lineages.
Submission of routine specimens for sequencing

- representative of multiple geographic regions (provinces/districts/health facilities) from individuals of
  - all ages
  - over as many time periods during the SARS-CoV-2 epidemic in South Africa

- requested that testing laboratories in both the private and public sectors, submit respiratory samples to their closest NGS-SA sequencing laboratory on a routine basis (ideally every week) as follows, depending on the capacity of the testing laboratory:
  - All positives samples should be sent every week (NGS-SA laboratory will perform random sampling as described below) OR
  - A weekly selection of approximately 10%-20% of randomly selected positive samples should be sent every week. Number of selected samples will depend on the size of laboratory and how many other laboratories are drained by the submitting laboratory.
Submission of special interest specimens for sequencing

In addition to routine samples mentioned above, please send specimens separately to above and clearly marked if:

• Suspected vaccine breakthrough (≥14 days after vaccine), especially if hospitalised and clinically severe
• Suspected re-infection (≥90 days after previous episode), especially if hospitalised and clinically severe
• Prolonged shedding with high SARS-CoV-2 viral loads (i.e. Ct values less than 30 for more than 1 month post-primary diagnosis) in immunocompromised individuals
• Possible animal-to-human transmission
• Suspected cases of importation from another country, especially countries known to harbour SARS-CoV-2 variants of concern or countries with little available information
• Clusters of “unusual” cases (e.g., in terms of disease presentation, patient groups affected, etc.)