Network for Genomic Surveillance in South Africa (NGS-SA)

SARS-CoV-2 Sequencing Update
14 January 2022

Supported by the DSI and the SA MRC
Msooi 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 14 January 2022 at 08h20

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 gives weekly proportion testing positive rates, 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 39 [2021] – 2 [2022]). Genomes and cases presented as provincial total (percentage of national total) for epiweeks 39 (2021) – 2 (2022).

PTP: percentage testing positive in week 1 (2 Jan 2022 – 8 Jan 2022); the arrow indicates direction of change since the previous week (26 Dec 2021 – 1 Jan 2022).

583 genomes deposited in the past week.
Number of South African genomes deposited on GISAID, by specimen collection week, 2020 – 2022

(N=27,293*)

Total genomes: 27,293
2020 genomes: 6,451
2021 genomes: 20,783
2022 genomes: 59

Sequencing data ending epi week 2 (ending 15 January 2022)
Currently in epi week 2 (ending 15 January 2022)

*This represents the cleaned, de-duplicated dataset of unique National Surveillance sequences. This dataset will be used for all further figures.
All provinces, apart from GP, NC and WC, have comparable percentages of overall cases and overall sequenced genomes.
Omicron sub-lineage spike mutation profiles

BA.1 21K

Lineage definitions based on https://github.com/cov-lineages/pango-designation/issues/367
Images from https://covdb.stanford.edu/page/mutation-viewer/

BA.2 21L

Lacks 69-70del
Not detectable by S-Gene Target Failure

BA.3 21M
Omicron 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, but may be linked to immune escape

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![Mutation impact key]
- Unknown or unconfirmed impact
- Known/predicted immune escape
- Enhanced infectivity

Only lineage-defining mutations are pictured here. Low prevalence mutations can be seen on the following slide.
Mutational profile of Omicron is largely shared amongst all sequences. Low mutation frequencies for N417N, N440K, G446S and N764K are most likely a result of poor coverage due to primer drop off.
Omicron has been detected in 139 countries across the globe (detections based on GISAID).
Delta dominated in South Africa until October at >80%. Omicron dominated November and December at >95%.

Sequencing data ending epi week 2 (ending 15 January 2022)

Currently in epi week 2 (ending 15 January 2022)
Omicron dominated in November, at 86% (1252/1579) and continued to dominate in December (99%, 1361/1377). Omicron appears to continue dominating in January (98%, 58/59), although more sequencing data is needed to confirm this trend and the BA.2 increase.
Detection Rates: Beta, Delta, C.1.2 and Omicron

C.1.2 has been detected at ≤ 4% of sequences monthly since May 2021. Beta prevalence increased slightly in October but has since remained at low levels in November and December. Omicron has been dominant since November (>80% in November, >98% in December and January).
Eastern Cape Province, 2021-2022, n = 1798

**Clade key (bar graph)**

- Omicron (21L)
- Omicron (21M)
- Beta (20H. V2)
- Delta (21A)
- Delta (21I)
- Delta (21J)
- Kappa (21B)
- Eta (21E)
- 20A
- 20B
- 20C
- 20D
- unassigned
- 19A
- 19B

**Weekly proportion testing positive key (line graph)**

- ≤ 5
- 6 - 10
- 11 - 20
- 21 - 30
- 31 - 40
- 41 - 50
- 51 - 55
Free State Province, 2021-2022, n = 1071

(Bar graph) Clade key

(Line graph) Weekly proportion testing positive key
Gauteng Province, 2021-2022, n = 5732

Clade key (bar graph)

Weekly proportion testing positive key (line graph)
KwaZulu-Natal Province, 2021-2022, n = 2696

Clade key (bar graph)
- Omicron (21K)
- Omicron (21M)
- Beta (20H.2)
- Delta (21A)
- Delta (21I)
- Delta (21J)
- Kappa (21B)
- Eta (21D)
- 20A
- 20B
- 20C
- 20D
- unassigned
- 19A
- 19B

Weekly proportion testing positive key (line graph)
- ≤ 5
- 6 - 10
- 11 - 20
- 21 - 30
- 31 - 40
- 41 - 50
- 51 - 55
Limpopo Province, 2021-2022, n = 1234

Clade key (bar graph)

Weekly proportion testing positive key (line graph)
Mpumalanga Province, 2021-2022, n = 1202

Clade key (bar graph)
- Omicron (21K)
- Omicron (21M)
- Beta (20H, V2)
- Delta (21A)
- Delta (21I)
- Delta (21J)
- Kappa (21B)
- Eta (21D)
- 20A
- 20B
- 20C
- 20D
- unassigned
- 19A
- 19B

Weekly proportion testing positive key (line graph)
- ≤ 5
- 6 - 10
- 11 - 20
- 21 - 30
- 31 - 40
- 41 - 50
- 51 - 55
Northern Cape Province, 2021-2022, n = 1377
Western Cape Province, 2021-2022, n = 4295

**Clade key (bar graph)**

**Weekly proportion testing positive key (line graph)**
Summary

• **Variant of Concern Omicron**
  - Detected in 139 countries and dominating globally
  - Split into three lineages based on different mutational profiles: BA.1 (21K), BA.2 (21L), BA.3 (remains in 21M with parent lineage B.1.1.529 as does not meet requirements for new clade)
    - New sub-lineage has been designated: BA.1.1. This contains lineage-defining BA.1.1 + spike:R346K

• South Africa (detected in all provinces):
  - Dominated November sequencing data at 86% of genomes (n=1252/1579) and December sequencing data at 99% of genomes (n=1361/1377)
  - Limited sequence data for January shows continued dominance of Omicron (n=58/59)
  - BA.1 dominant in SA, with BA.2 increase recently observed and to be confirmed by additional data

• Low frequency of previously circulating variants such as Delta and C.1.2 still detected in recent data
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GIZ/BMBF: African Network for Improved diagnostics and epidemiology of common and emerging infectious agents (ANDEMIA)
G7 Global Health fund, Robert Koch Institute, Dr Fabian Leendertz

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Multiple labs from NGS-SA and collaborating public and private laboratories are contributing to sequencing, both as originating and as submitting (pictured here) laboratories.

**South African genomes submitted per submitting lab, 2020 and 2021 (N=27 293)**

<table>
<thead>
<tr>
<th>Submitting lab</th>
<th>Number of genomes submitted</th>
</tr>
</thead>
<tbody>
<tr>
<td>NICD</td>
<td>12173</td>
</tr>
<tr>
<td>KRISP*</td>
<td>7152</td>
</tr>
<tr>
<td>UCT</td>
<td>2880</td>
</tr>
<tr>
<td>NHLS/UCR/CRERI*</td>
<td>2397</td>
</tr>
<tr>
<td>UFS*</td>
<td>1803</td>
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<tr>
<td>NHLS*</td>
<td>758</td>
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<tr>
<td>VIDA</td>
<td>97</td>
</tr>
<tr>
<td>UW</td>
<td>20</td>
</tr>
<tr>
<td>UP*</td>
<td>11</td>
</tr>
<tr>
<td>UP*</td>
<td>2</td>
</tr>
</tbody>
</table>

*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
## Variants of Concern (VOC)

<table>
<thead>
<tr>
<th>WHO label</th>
<th>Pango lineage•</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>


• Includes all descendant lineages. See the cov-lineages.org and the Pango network websites for further details.
* See TAG-VE statement issued on 26 November 2021
° Only found in a subset of sequences
Currently designated Variants of Interest (VOI)

<table>
<thead>
<tr>
<th>WHO label</th>
<th>Pango lineage*</th>
<th>GISAID clade</th>
<th>Nextstrain clade</th>
<th>Earliest documented samples</th>
<th>Date of designation</th>
</tr>
</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. See the cov-lineages.org and the Pango network websites for further details.
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.)