The genomic data presented here are based on South African SARS-CoV-2 sequence data downloaded from GISAID (www.gisaid.org) on 13 May 2022 at 08h25.

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


Bar graphs represent genomes sequenced per epiweek, with lines representing cases by collection date (weeks 39 [2021] – 18 [2022]).

Genomes and cases presented as provincial total (percentage of national total) for epiweeks 39 (2021) – 18 (2022).

PTP: percentage testing positive in week 18 (1 April 2022 – 7 April 2022); arrow indicates direction of change since previous week (24 Apr 2022 – 30 May 2022) if change was significant (P<0.05).

547 genomes added since the previous report.
Number of South African genomes deposited on GISAID, by specimen collection week, 2020 – 2022 (N=39 463*)

Total genomes: 39 463
2020 genomes: 6 657
2021 genomes: 25 811
2022 genomes: 6 995

Sequencing data ending epi week 18 (ending 7 May 2022)

Currently in epi week 19 (ending 14 May 2022)

*This represents the cleaned, de-duplicated dataset of unique National and Pneumonia Surveillance sequences. This dataset will be used for all further figures.
All provinces, apart from GP, KZN, LP, MP, NC and WC, have comparable percentages of overall cases and overall sequenced genomes.
Delta dominated in South Africa until October at >80%. Omicron has dominated from November onwards.

Number and percentage of clades by epiweek in South Africa, 2021 – 2022 (32 719*)

Sequencing data ending epi week 18 (ending 7 May 2022)
Currently in epi week 19 (ending 14 May 2022)

*Excludes sequences missing collection dates, as well as those collected January 1st and 2nd 2021 as they are part of epiweek 53 of 2020.
Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in Feb – Apr 2022

**February (N=1204)**
- Omicron (21L/BA.2.*) (n=1033, 86%)
- Delta (21A) (n=1, 0.08%)
- Delta (21J) (n=1, 0.08%)
- Beta (20H, V2) (n=4, 0.33%)
- C.1.2 (20D) (n=1, 0.08%)
- Omicron (21K/BA.1.*) (n=142, 12%)

**Total Omicron in Feb: 1187 (98.6%)**

**March (N=1461)**
- Omicron (21L/BA.2.*) (n=1135, 78%)
- Omicron (21K/BA.1.*) (n=62, 4%)
- Delta (21J) (n=9, 1%)
- Alpha (20L, V1) (n=6, 0.50%)
- C.1.2 (20D) (n=1, 0.08%)
- Omicron (22A/BA.4) (n=44, 3%)
- Omicron (22B/BA.5) (n=154, 11%)
- Omicron (22B/BA.5) (n=273, 18%)
- Omicron (22A/BA.4) (n=683, 46%)
- Omicron (22B/BA.5) (n=142, 12%)
- Omicron (21K/BA.1.*) (n=25, 2%)
- Delta (21J) (n=1, 0.07%)
- Beta (20H, V2) (n=4, 0.33%)
- Omicron (21K/BA.1.*) (n=62, 4%)
- Omicron (21L/BA.2.*) (n=1135, 78%)
- Omicron (21K/BA.1.*) (n=25, 2%)
- Other (n=5, 0.33%)

**Total Omicron in Mar: 1437 (98.4%)**

**April (N=1499)**
- Omicron (21L/BA.2.*) (n=509, 35%)
- Omicron (21K/BA.1.*) (n=273, 18%)
- Omicron (22B/BA.5) (n=683, 46%)
- Delta (21J) (n=9, 1%)
- Beta (20H, V2) (n=4, 0.33%)
- Delta (21J) (n=1, 0.07%)
- Omicron (21K/BA.1.*) (n=25, 2%)
- Omicron (21K/BA.1.*) (n=62, 4%)
- Omicron (21L/BA.2.*) (n=1135, 78%)
- Omicron (21K/BA.1.*) (n=25, 2%)
- Other (n=5, 0.33%)

**Total Omicron in Apr: 1493 (99.6%)**

Omicron dominated in February (98.6%, 1187/1204), March (98.4%, 1437/1461) and April (99.6%, 1493/1499). BA.2 was dominant in February and March. BA.4 and BA.5 together were dominant in April.
Detection Rates: Beta, Delta, C.1.2 and Omicron

Detection rates of variants being monitored in South Africa

Omicron has been dominant since November (>85% in November, >98% in December – May). BA.2 made up 43% of genomes in January, 86% in February, 78% in March and 34% in April. BA.4 and BA.5 together dominated in April, at 46% and 18% respectively, and appear to be dominant in May.
South Africa, 2021-2022, n = 32719*

*Excludes sequences missing collection dates, as well as those collected January 1st and 2nd 2021 as they are part of epiweek 53 of 2020.
Free State Province, 2021-2022, n = 1476

FS number of genomes, cases, and PTP per epiweek (N=1476)

FS percentage of genomes, number of cases, and PTP per epiweek (N=1476)

Clade key (bar graph)

Weekly percentage testing positive key (line graph)
Gauteng Province, 2021-2022, n = 9102

GP number of genomes, cases, and PTP per epiweek (N=9102)

GP percentage of genomes, number of cases, and PTP per epiweek (N=9102)

Clade key (bar graph)

Weekly percentage testing positive key (line graph)
KwaZulu-Natal Province, 2021-2022, n = 3649

KZN number of genomes, cases, and PTP per epiweek (N=3649)

KZN percentage of genomes, number of cases, and PTP per epiweek (N=3649)

Clade key (bar graph)

Weekly percentage testing positive key (line graph)
Limpopo Province, 2021-2022, n = 2421

LP number of genomes, cases, and PTP per epiweek (N=2421)

LP percentage of genomes, number of cases, and PTP per epiweek (N=2421)

Clade key (bar graph)

Weekly percentage testing positive key (line graph)
Northern Cape Province, 2021-2022, n = 1750

NC number of genomes, cases, and PTP per epiweek (N=1750)

NC percentage of genomes, number of cases, and PTP per epiweek (N=1750)
Western Cape Province, 2021-2022, n = 7183

WC number of genomes, cases, and PTP per epiweek (N=7183)

WC percentage of genomes, number of cases, and PTP per epiweek (N=7183)

Clade key (bar graph)

Weekly percentage testing positive key (line graph)
Summary

• **Variant of Concern Omicron in South Africa**
  • Dominates 2022 sequencing data at >98% of genomes.
  • While BA.1 (and sub-lineages) was the predominant lineage in January (55%), BA.2 dominated in February (86%) and March (78%).
  • Omicron lineages BA.4 and BA.5 increased in prevalence in March (16%), and together are dominant in April (64%).
  • BA.4 and BA.5 make up 96% of May sequences, but more data is needed to determine prevalence.
  • BA.3 continues to be detected at low levels.
• NGS-SA teams are monitoring sequencing data for recombinants.
• Low frequency of previously circulating variants such as Delta still detected in recent data.

1 [https://github.com/cov-lineages/pango-designation/releases/tag/v1.3](https://github.com/cov-lineages/pango-designation/releases/tag/v1.3)
BA.4 and BA.5 spike mutations

Frequency of spike SNVs for BA.4 (n = 820)

Frequency of spike SNVs for BA.5 (n = 240)
BA.4 whole genome mutation prevalence over time
BA.5 whole genome mutation prevalence over time
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.

Known/predicted immune escape
Enhanced infectivity
Unknown or unconfirmed impact
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DSI
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SA MRC
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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.
## Currently circulating 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>
</table>


• Includes all descendant lineages. See the cov-lineages.org and the Pango network websites for further details.

° Only found in a subset of sequences
# Previously circulating Variants of Concern

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<tr>
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</tr>
</thead>
<tbody>
<tr>
<td>Alpha</td>
<td>B.1.1.7</td>
<td>GRY</td>
<td>20I (V1)</td>
<td>United Kingdom, Sep-2020</td>
<td>VOC: 18-Dec-2020</td>
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<td>Previous VOC: 09-Mar-2022</td>
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<td></td>
<td></td>
<td>Previous VOC: 09-Mar-2022</td>
</tr>
<tr>
<td>Gamma</td>
<td>P.1</td>
<td>GR/501Y.V3</td>
<td>20J (V3)</td>
<td>Brazil, Nov-2020</td>
<td>VOC: 11-Jan-2021</td>
</tr>
<tr>
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<td></td>
<td></td>
<td></td>
<td></td>
<td>Previous VOC: 09-Mar-2022</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.)