SARS-CoV-2 Sequencing Update
27 September 2021

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 27 September at 08h56

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


Case data is based on collection date. Case from https://www.nicd.ac.za/diseases-a-z-index/disease-index-covid-19/surveillance-reports/weekly-epidemiological-brief/
Number of South African genomes deposited on GISAID, by specimen collection week, 2020 and 2021 (N=18 802*)

Total genomes: 18 802
2020 genomes: 6 077
2021 genomes: 12 723

Sequencing data ending epi week 37 (ending 18 September 2021)
Currently in epi week 39 (ending 2 October 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, and WC, have comparable percentage of overall cases and overall sequenced genomes.
Delta came to dominate by end June at >65%, in July at >85% and in August and September at >90%

C.1.2 present at <3% frequency since March
Prevalence of Variants of Concern (VOC) and Variants of Interest (VOI) in May and June 2021 sequences, South Africa

Beta variant dominated in May, but the Delta variant started to dominate in June

May (N=1147)
- Beta (20H, V2) (n=750, 65%)
- Delta (21A) (n=189, 16%)
- Other (n=53, 5%)
- Eta (21D) (n=10, 1%)
- C.1.2 (20D) (n=2, 0.17%)
- Alpha (20I, V1) (n=66, 6%)
- Kappa (21B) (n=1, 0.09%)
- unassigned (n=76, 7%)

June (N=2931)
- Delta (21A) (n=1932, 66%)
- Other (n=88, 3%)
- C.1.2 (20D) (n=32, 1%)
- Alpha (20I, V1) (n=104, 4%)
- Kappa (21B) (n=11, 0.38%)
- unassigned (n=233, 8%)
- Beta (20H, V2) (n=531, 18%)
The Delta variant dominated in July and August in South Africa.
Genomes sequenced from specimens collected in May to mid-August 2021 (epiweeks 18 – 39) from KwaZulu-Natal, Gauteng, Western Cape Provinces

Following its detection in week 18, Delta rapidly replaces Beta and begins to dominate in all three provinces by mid-June. Delta continues to dominate in July to September.
Genomes sequenced from specimens collected in May to mid-August 2021 (epiweeks 18 – 39) from Eastern Cape, Limpopo and North-West Provinces

Delta variant dominates the third wave in Eastern Cape, Limpopo and North-West Provinces
Genomes sequenced from specimens collected in May to mid-August 2021 (epiweeks 18 – 38) from Free State, Mpumalanga and Northern Cape Provinces

Delta dominates the third wave in Free State, Mpumalanga and Northern Cape provinces
Gauteng Province, 2021, n = 3562
KwaZulu-Natal Province, 2021, n = 1897

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**KZN (N=1897)**

**Number of genomes**

- Epiweek 1: 50
- Epiweek 2: 61
- Epiweek 3: 45
- Epiweek 4: 16
- Epiweek 5: 27
- Epiweek 6: 53
- Epiweek 7: 51
- Epiweek 8: 83
- Epiweek 9: 81
- Epiweek 10: 73
- Epiweek 11: 144
- Epiweek 12: 81
- Epiweek 13: 37
- Epiweek 14: 30
- Epiweek 15: 26
- Epiweek 16: 15
- Epiweek 17: 13
- Epiweek 18: 10
- Epiweek 19: 39
- Epiweek 20: 37
- Epiweek 21: 78
- Epiweek 22: 143
- Epiweek 23: 164
- Epiweek 24: 125
- Epiweek 25: 87
- Epiweek 26: 75
- Epiweek 27: 54
- Epiweek 28: 59
- Epiweek 29: 52
- Epiweek 30: 39
- Epiweek 31: 6
- Epiweek 32: 36

**Percent of genomes**

- Epiweek 1: 100
- Epiweek 2: 90
- Epiweek 3: 80
- Epiweek 4: 70
- Epiweek 5: 60
- Epiweek 6: 50
- Epiweek 7: 40
- Epiweek 8: 30
- Epiweek 9: 20
- Epiweek 10: 10
- Epiweek 11: 0
- Epiweek 12: 0
- Epiweek 13: 0
- Epiweek 14: 0
- Epiweek 15: 0
- Epiweek 16: 0
- Epiweek 17: 0
- Epiweek 18: 0
- Epiweek 19: 0
- Epiweek 20: 0
- Epiweek 21: 0
- Epiweek 22: 0
- Epiweek 23: 0
- Epiweek 24: 0
- Epiweek 25: 0
- Epiweek 26: 0
- Epiweek 27: 0
- Epiweek 28: 0
- Epiweek 29: 0
- Epiweek 30: 0
- Epiweek 31: 0
- Epiweek 32: 0

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**Legend**
- **cases**
- Delta (21A)
- Beta (20H, V2)
- Alpha (20I, V1)
- C.1.2 (20D)
- Kappa (21B)
- Eta (21D)
- 20A
- 20B
- 20C
- 20D
- unassigned
- 19B

**Network for Genomic Surveillance in South Africa**
Western Cape Province, 2021, n = 2553

WC (N=2553)

Number of genomes

Number of cases

Epiweek

Percent of genomes

Epiweek

cases Delta (21A) Beta (20H, V2) Alpha (20I, V1) C.1.2 (20D) Kappa (21B) Eta (21D) 20A 20B 20C 20D unassigned 19B

Network for Genomic Surveillance in South Africa
Limpopo Province, 2021, n = 764
Northern Cape Province, 2021, n = 675
Free State Province, 2021, n = 716

NGS-SA
Network for Genomic Surveillance in South Africa
The majority of C.1.2 sequences have been detected in Gauteng (n=86), followed by Limpopo (n=19) and the Northern Cape (n=15).
12 C.1.2 sequences have been detected in KwaZulu-Natal, 11 in the Free State, and 7 in Mpumalanga.
C.1.2 (n=166 in SA) in May – August 2021 by epiweek

The Western Cape has 8 sequences, the North West has 4, and the Eastern Cape has 4 detections of C.1.2.
C.1.2 is being continually monitored and is currently only detected at low levels
Summary

• Delta continues to dominate in all provinces from specimens collected in September

• Overall diversity of lineages decreased as Delta became dominant

• Mutated C.1.2 lineage has now been detected in all provinces of South Africa
  • The frequency of C.1.2 at less than 3% of genomes from May through September

• Lambda and Mu variants not detected in South Africa
UKZN-Inkosi Albert Luthuli Central Hospital

Dr Khanyi Msomi
Dr Kerusha Govender
Dr Pravi Moodley
Dr Aabida Khan
Dr Lili Gounder
Dr Kerri Francois
Dr Cherise Naicker
Dr Joedene Chetty
Dr Neli Ngcaba
Dr Tshepiso Mosito
Mr Malcolm Ellapen
Mr Kubendran Reddy
The COVID-19 Bench team

University of KwaZulu-Natal & Africa Health Research Institute

KRISP at UKZN:
Tulio de Oliveira
Richard Lessels
Houriiyah Tegally
Eduan Wilkinson
Jennifer Giandhari
Sureshnee Pillay
Emmanuel James San

AHRI
Alex Sigal
Sandile Cele
Willem Hanekom

University of Stellenbosch & NHLS Tygerberg Virology

Susan Engelbrecht
Wolfgang Preiser
Gert van Zyl
Tongai Maponga
Bronwyn Kleinhans
Shannon Wilson
Karabo Phadu
Tania Stander
Kamela Mahlakwane
Mathilda Claassen
Diagnostic laboratory staff
University of Cape Town, NHLS & WCG

NHLS-UCT
Carolyn Williamson
Nei-yuan Hsiao
Diana Hardie
Kruger Marais
Stephen Korsman
Ziyaad Valley-Omar

WCG-UCT
Mary-Anne Davies
Hannah Hussey
Andrew Boulle
Masudah Paleker
Theuns Jacobs
Erna Morden

UCT, IDM and CIDRI-Africa
Deelan Doolabh
Arash Iranzadeh
Lynn Tyers
Innocent Mudau
Nokuzola Mbhele
Fezokuhle Khumalo
Thabang Serakge
Bruna Galvão
Arghavan Alisoltani (U. California)

University of the Free State

UFS
Dominique Goedhals
Armand Bester
Martin Myaga
Peter Mwangi
Emmanuel Ogunbayo
Milton Mogotsi
Makgotso Maotoana
Lutfiyya Mohamed

NHLS Division of Virology
Sabeehah Vawda
Felicity Burt
Thokozani Mkhize
Diagnostic laboratory staff
National Institute for Communicable Diseases

Centre for Respiratory Diseases & Meningitis
Jinal Bhiman
Anne von Gottberg
Thabo Mohale
Daniel Amoako
Josie Everatt
Boitshoko Mahlangu
Noxolo Ntuli
Anele Mnguni
Amelia Buys
Cardia Fourie
Noluthando Duma
Linda de Gouveia
Jackie Kleyhans
Nicole Wolter
Sibongile Walaza
Mignon du Plessis
Stefano Tempia
Mvuyo Makhasi
Cheryl Cohen

Centre for HIV and STIs
Cathrine Scheepers
Constantinos Kurt Wibmer
Thandeka Moyo
Tandile Hermanus
Frances Ayres
Zanele Molaudzi
Bronwen Lamson
Tandile Hermanus
Masudu Madzivhandila
Prudence Kgagudi
Brent Oosthuysen
Penny Moore
Lynn Morris

Sequencing Core Facility
Zamantungwa Khumalo
Annie Chan
Morne du Plessis
Stanford Kwenda
Phillip Senzo Mtshali
Mushal Allam
Florah Mnyameni
Arshad Ismail

NICD Groups
NICD COVID-19 response team
NICD SARS-CoV-2 Sequencing Group

Zoonotic arbo and respiratory virus program
Centre for Viral Zoonoses
Department Medical Virology/ NHLS
Tshwane Academic division
University of Pretoria

ZARV research program/UP
Marietjie Venter (Head: ZARV)
Adriano Mendes (Postdoc)
Amy Strydom (Postdoc)
Michaela Davis (MSc, intern medical scientist)

NHLS Tshwane
Prof Simnikiwe Mayaphi (HOD)

Funders:
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
Additional support and collaborators

NHLS
Koeleka Mlisana
Zinhle Makatini
Eugene Elliot
Florette K. Teurnicht
Kathleen Subramoney
Oluwakemi Laguda-Akingba
Shareef Abrahams
Greta Hoyland
Gloria Selabe
Elias Bereda
Jeannette Wadula

Hyrax Biosciences
Simon Travers

Cape Town HVTN Laboratory
Erica Anderson-Nissen
Anneta Naidoo

Ndlovu Research
Hugo Tempelman
CJ Umunnakwe

Lancet
Allison J. Glass

Ampath
Terry Marshall
Cindy van Deventer
Eddie Silberbauer

Pathcare Vermaak
Andries Dreyer
Howard Newman
Riaan Writes
Marianne Wolfaardt
Warren Lowman

Bridge-the-Gap
Raymond Rott

Cytespace Africa Laboratories
Christa Viljoen

ARC-OVI
Lia Rotherham

CAPRISA
Salim Abdool Karim
Nigel Garret

UKZN - Big Data
Francesco Pettruccione
Ilya Sinayskiy

University of Oxford
José Lourenço

FioCruz, Brazil
Vagner Fonseca
Marta Giovanetti
Luiz Carlos Junior Alcantara

Africa CDC
John Nkengasong
Sofonias Tessema

Netcare:
Richard Friedland
Craig Murphy
Caroline Maslo
Liza Sitharam

DSI
Glaudina Loots

SA MRC
Glenda Gray
Multiple labs from NGS-SA are contributing to the sequencing effort. Sequencing efforts have increased with the third wave.
# 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>
<thead>
<tr>
<th>WHO label</th>
<th>Pango* lineages</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.
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.)