NATIONAL INSTITUTE FOR COMMUNICABLE DISEASES
Division of the National Health Laboratory Service

SARS-CoV-2 genomic surveillance update June 2021

Date of report 29 June 2021

Frequency of variants of concern in South Africa

The Network for Genomics Surveillance (NGS-SA)[1] has been performing genomic surveillance for SARS-CoV-2 since mid-2020. As of the 29th June, 10,200 SARS-CoV-2 genomes from South Africa have been generated and deposited into the GISAID database[2] (**Fig 1**). Given the progression of the third wave and a preliminary report of the dominance of the Delta variant in KwaZulu-Natal, we report updated data on the frequency of the Delta variant and other variants of concern, including Alpha, Beta and Eta which have begun to dominate in other parts of the world due to increased transmissibility and/or immune evasion.

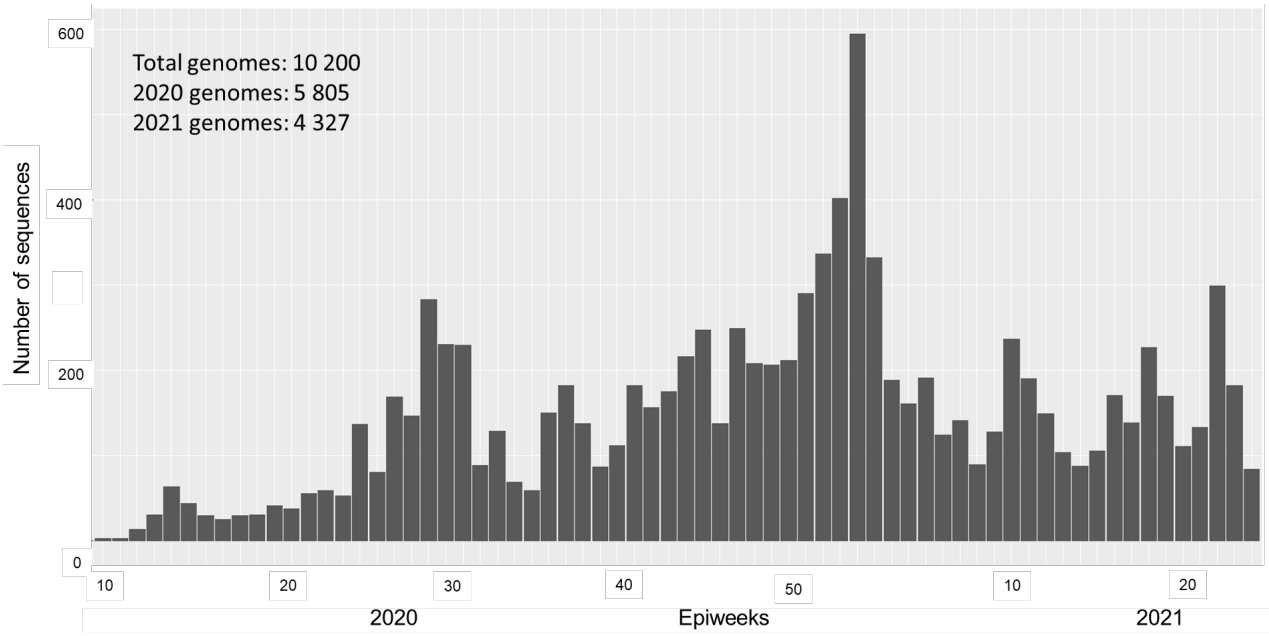

Figure 1. Number of SARS-CoV-2 genomes sequenced in each epidemiological week in 2020 and 2021 in South Africa (10,200 loaded on GISAID, downloaded 29 June 2021). All genomes apart from 32 were sequenced by the Network for Genomics Surveillance in South Africa (NGS-SA).

Genomic data for samples collected in May 2021 are available for 7 provinces and 70% of 680 genomes from this month were the Beta variant (**Fig 2**). The Alpha, Delta and Eta variants account for 6%, 13% and 1% of the May genomes. For June 2021, genomic data are available for 4 provinces, with 541 sequences available on GISAID. Genomes sequenced (n=541) from samples collected in June 2021 shows 39% Beta and 45% Delta variant frequency with the Alpha variant accounting for 7% (**Fig 2**).

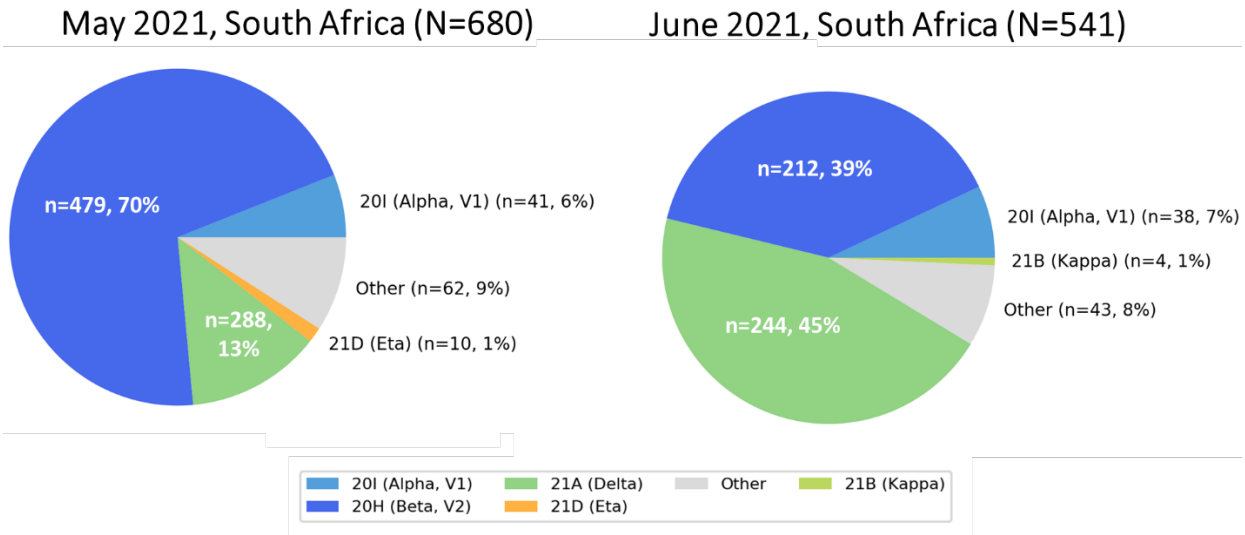

Figure 2. Percentage of SARS-CoV-2 clades sequenced in May and June 2021 in South Africa. Variants of concern, namely Alpha, Beta, Delta. Kappa and Eta are shaded in different colours, while non-variants of concern are shaded in grey.

Frequency of variants of concern in Gauteng

Gauteng is currently the epicenter of the third wave in South Africa, accounting for 65% of daily new cases on the 27th June. Of the 244 genomes sequenced from May 2021 (epidemiological weeks 17-22), 15% of Gauteng genomes belonged to the Beta variant, while 13%, 15% and 0.8% were Alpha, Delta and Beta variants observed (**Fig 3**). However, in June 2021 (epidemiological weeks 22-24), where 341 genomes were sequenced, the frequency of the Delta variant has increased to 53% (**Fig 3**). In June, 37% of genomes in Gauteng were Beta variant (**Fig 3**).

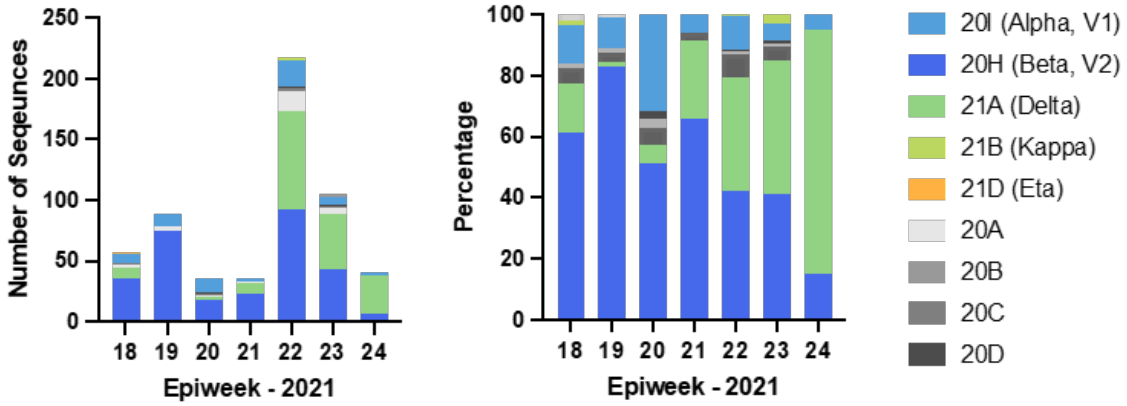

Figure 3. Percentage of SARS-CoV-2 clades sequenced in May (epi week 20-21) and June (epi week 22-24) 2021 in Gauteng province. Variants of concern, namely Alpha, Beta, Delta and Kappa are shaded in different colours, while non-variants of concern are shaded in grey.

Key points about Delta variant

- While Beta was 25% more transmissible compared to original lineage, the Delta is 97% more transmissible than the original lineage[3].
- Vaccines are still highly effective in preventing severe illness, with the Pfizer-BioNTech vaccine displaying 96% effectiveness against hospitalization with delta variant[4] after two doses[4].
- Reinfection with Delta is possible following a Beta infection, because the individual's antibody levels may have waned.
- Current PCR tests are able to detect Delta variant.
- Limited data are currently available on whether different symptoms result following Delta infection.
- Preliminary data from the UK suggests that the Delta variant may cause more severe illness[5].

Summary and implications

While the Delta variant is becoming more dominant in South Africa, sequencing data from specimens collected 3 weeks ago in Gauteng shows a mixture of variants, including a large proportion of Beta variant genomes. Delta variant is more transmissible than Beta variant, emphasizing the need for all individuals in South Africa to limit their movements to essential activities only. However, vaccines still show high levels of protection from severe disease caused by this variant.

Acknowledgements

These data are presented on behalf of the Network for Genomics Surveillance in South Africa (NGS-SA), with particular thanks to:

- our colleagues at both private and public testing laboratories, who submit samples for sequencing despite numerous challenges.
- the sequencing teams at the KwaZulu-Natal Research Innovation and Sequencing Platform (KRISP) at the University of KwaZulu-Natal (UKZN); the Division of Medical Virology at NHLS Tygerberg Hospital, Stellenbosch University (SU); the Division of Medical Virology at NHLS Groote Schuur Hospital, University of Cape Town (UCT); the Division of Virology at NHLS Universitas Academic Laboratories, University of the Free State (UFS) The Division of Virology at NHLS Inkosi Albert Luthuli Central Hospital (IALCH), University of KwaZuluNatal (UKZN), the Zoonotic Arbo and Respiratory Virus Program at the University of Pretoria (UP) and the Department of Virology at NHLS, University of the Witwatersrand (WITS).

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At the NICD, we would like to acknowledge the Centre for Respiratory Diseases and Meningitis, Sequencing Core Facility and Centre for HIV and STIs. In addition, we thank Hyarax Biosciences, Bridge-the-Gap and the Cape Town Immunology Laboratory for rapid and efficient assistance.

Sequencing activities at the NICD were supported by: a conditional grant from the South African National Department of Health as part of the emergency COVID-19 response, a cooperative agreement between the National Institute for Communicable Diseases of the National Health Laboratory Service and the United States Centers for Disease Control and Prevention (grant number 5 U01IP001048-05-00); the African Society of Laboratory Medicine (ASLM) and Africa Centers for Disease Control and Prevention through a sub-award from the Bill and Melinda Gates Foundation grant number INV-018978; the UK Foreign, Commonwealth and Development Office and Wellcome (Grant no 221003/Z/20/Z); the South African Medical Research Council (Reference number SHIPNCD 76756); the Department of Health and Social Care and managed by the Fleming Fund and performed under the auspices of the SEQAFRICA project. [The Fleming Fund is a £265 million UK aid programme supporting up to 24 low- and middle-income countries (LMICs) generate, share and use data on antimicrobial resistance (AMR) and works in partnership with Mott MacDonald, the Management Agent for the Country and Regional Grants and Fellowship Programme.]

References and Links

1. Global Initiative on Sharing All Influenza Data (GISAID, https://www.gisaid.org/)

2. Network for Genomics Surveillance in South Africa (http://www.krisp.org.za/ngs-sa/ngs-sa_network_for_genomic_surveillance_south_africa/)

3. https://www.eurosurveillance.org/content/10.2807/1560-7917.ES.2021.26.24.2100509#html_fulltext

4. https://khub.net/web/phe-national/public-library/-/document_library/v2WsRK3ZlEig/view_file/479607329?_com_liferay_document_library_web_portlet_DLPortlet_INSTANCE_v2WsRK3ZlEig_redirect=https%3A%2F%2Fkhub.net%3A443%2Fweb%2Fphe-national%2Fpublic-library%2F-%2Fdocument_library%2Fv2WsRK3ZlEig%2Fview%2F479607266

5. Sheikh A, McMenamin J, Taylor B, Robertson C. SARS-CoV-2 Delta VOC in Scotland: demographics, risk of hospital admission, and vaccine effectiveness. Lancet 2021; published online June 14. http://dx.doi.org/10.1016/S0140-6736(21)01358-1.