

SARS-CoV-2 genomic surveillance update

June 2021

Date of report 29 June 2021

Frequency of Variants of Concern (VOC) in South Africa

The Network for Genomics Surveillance (NGS-SA – list of all contributors listed in acknowledgments)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 database² (**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 VOCs in Gauteng and South Africa, including Alpha and Beta, and Eta (a Variant of Interest [VOI]), which have begun to dominate in other parts of the world due to increased transmissibility and/or immune evasion.

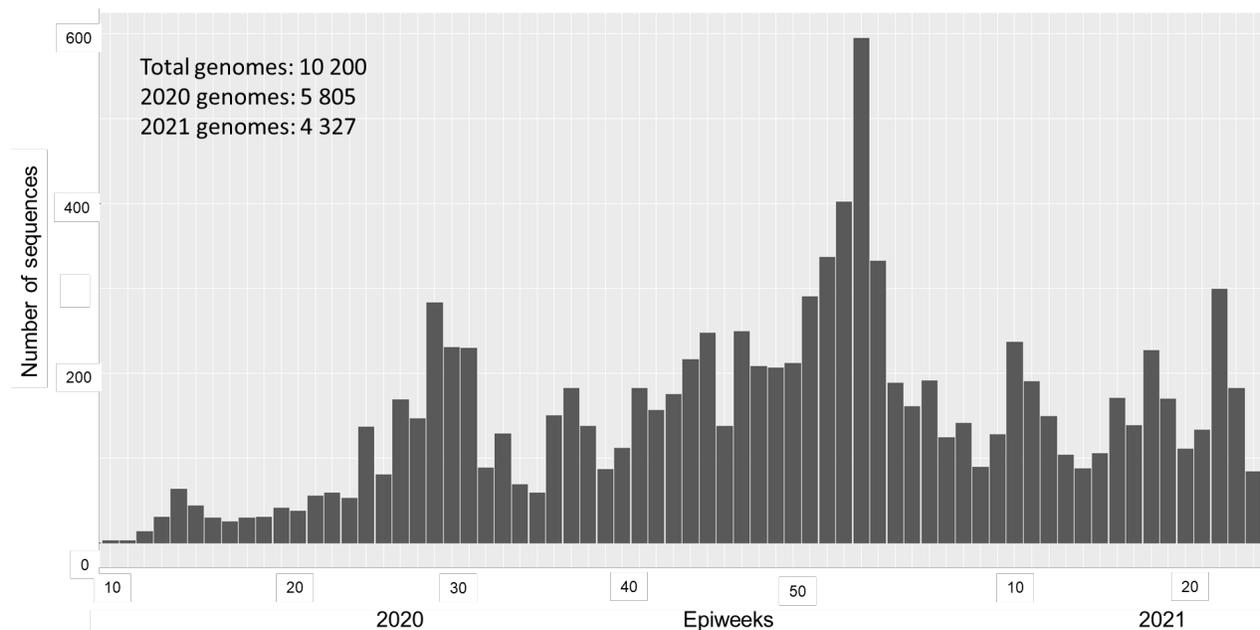


Figure 1. Number of SARS-CoV-2 genomes sequenced in each epidemiological week in 2020 and 2021, in South Africa (10,200 loaded on GISAID, downloaded 29 June 2021). All genomes apart from 32 were sequenced by the Network for Genomics Surveillance in South Africa (NGS-SA).

Genomic data for samples collected in May 2021 are available for 7 provinces, and 70% of 680 genomes from May 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**).

May 2021, South Africa (N=680)

June 2021, South Africa (N=541)

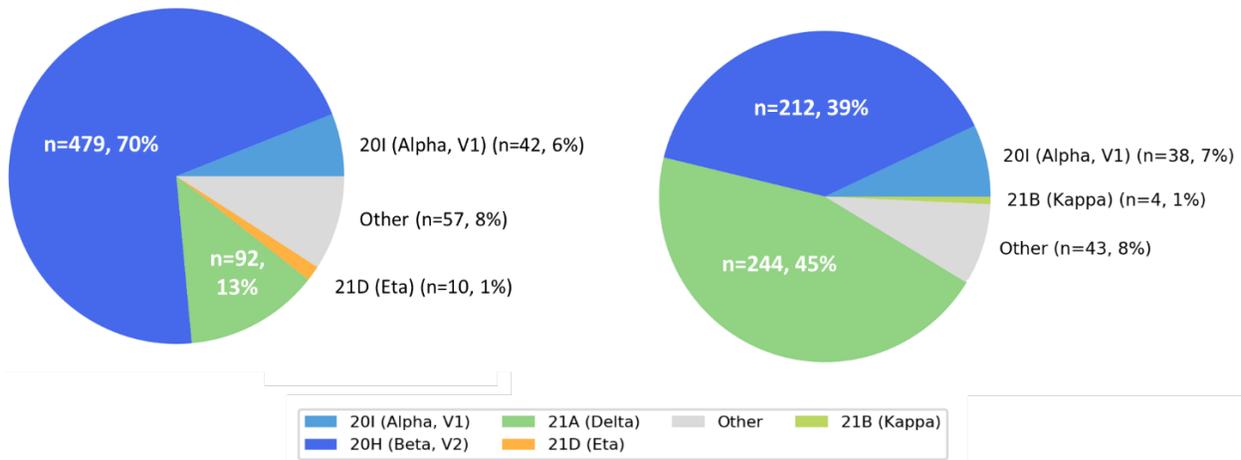


Figure 2. Percentage of SARS-CoV-2 clades sequenced in May and June 2021 in South Africa. Variants of Concern (VOC) and Interest (VOI), namely Alpha, Beta, Delta, Kappa and Eta are shaded in different colours, while other lineages are shaded in grey.

Frequency of Variants of Concern (VOC) 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%. In June, 37% of genomes in Gauteng were Beta variant (**Fig 3**).

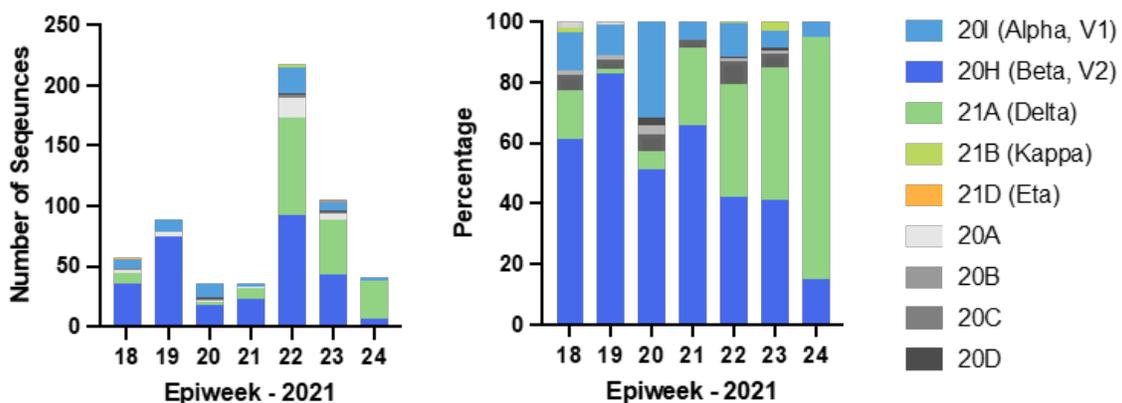


Figure 3. Percentage of SARS-CoV-2 clades sequenced in May (epi week 20-21) and June (epi week 22-24) 2021 in Gauteng Province. Variants of Concern (VOC) and Interest (VOI), namely Alpha, Beta, Delta, Kappa and Eta are shaded in different colours, while other lineages are shaded in grey.

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, emphasising 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

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- 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 KwaZulu-Natal (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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References and useful links

1. Global Initiative on Sharing All Influenza Data (GISAIID, <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/v2WsRK3ZIEig/view_file/479607329?com.liferay.document_library_web_portlet_DLPortlet_INSTANCE_v2WsRK3ZIEig_redirect=https%3A%2F%2Fkhub.net%3A443%2Fweb%2Fphe-national%2Fpublic-library%2F-%2Fdocument_library%2Fv2WsRK3ZIEig%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](http://dx.doi.org/10.1016/S0140-6736(21)01358-1).
6. <https://www.who.int/publications/m/item/weekly-epidemiological-update-on-covid-19---22-june-2021>