SARS-CoV-2 Omicron Variant:

Epidemiology and implications for Public Health

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SARS-CoV-2 Genetic Characterization

General considerations:

- Mutations are expected natural events in the evolution of viruses and in their adaptation process.

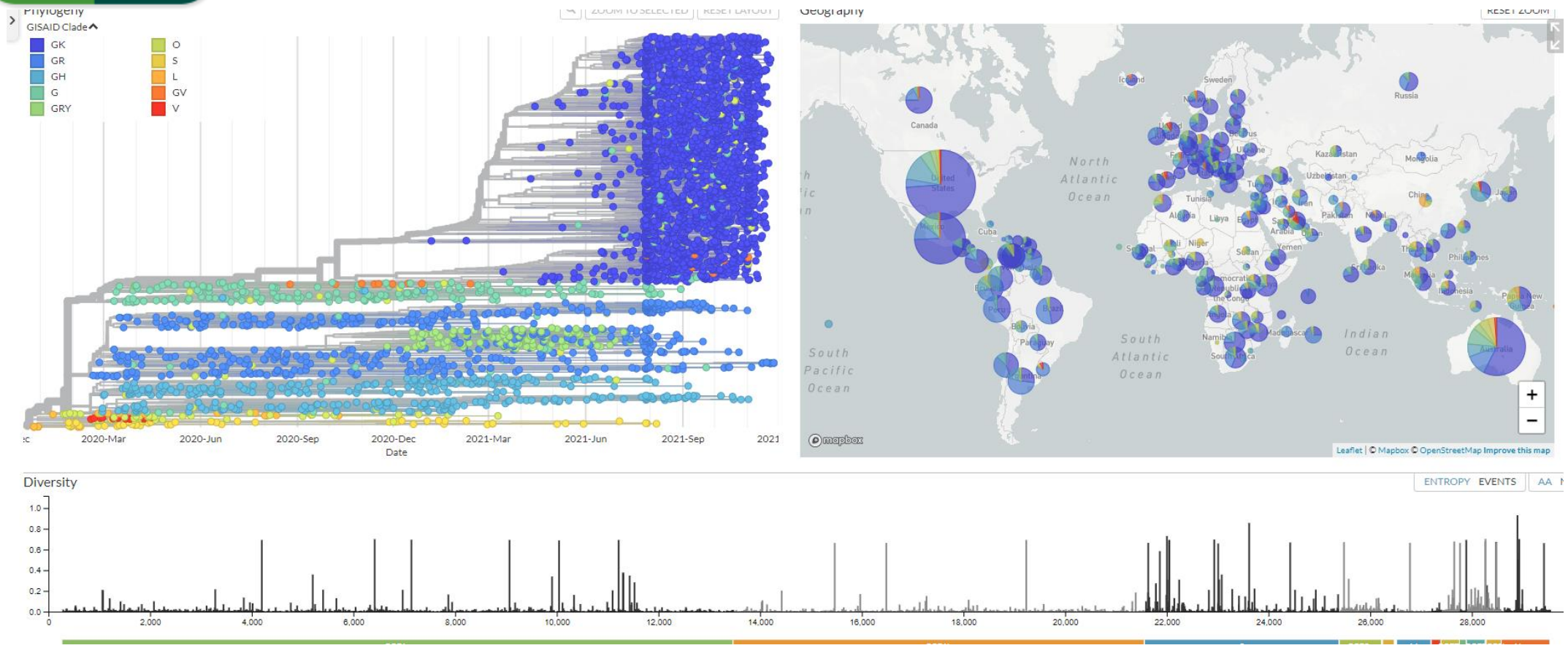
  Improve/increase transmission

  Escape immune response

- Usually, this type of virus (RNA) is more prone to generate mutations and, therefore, to generate genetic variations.

- There are different types of mutations, some more important than others

SARS-CoV-2 Genetic Characterization



> 8,087,443 sequences reported to GISAID

https://www.gisaid.org/phylodynamics/global/nextstrain/

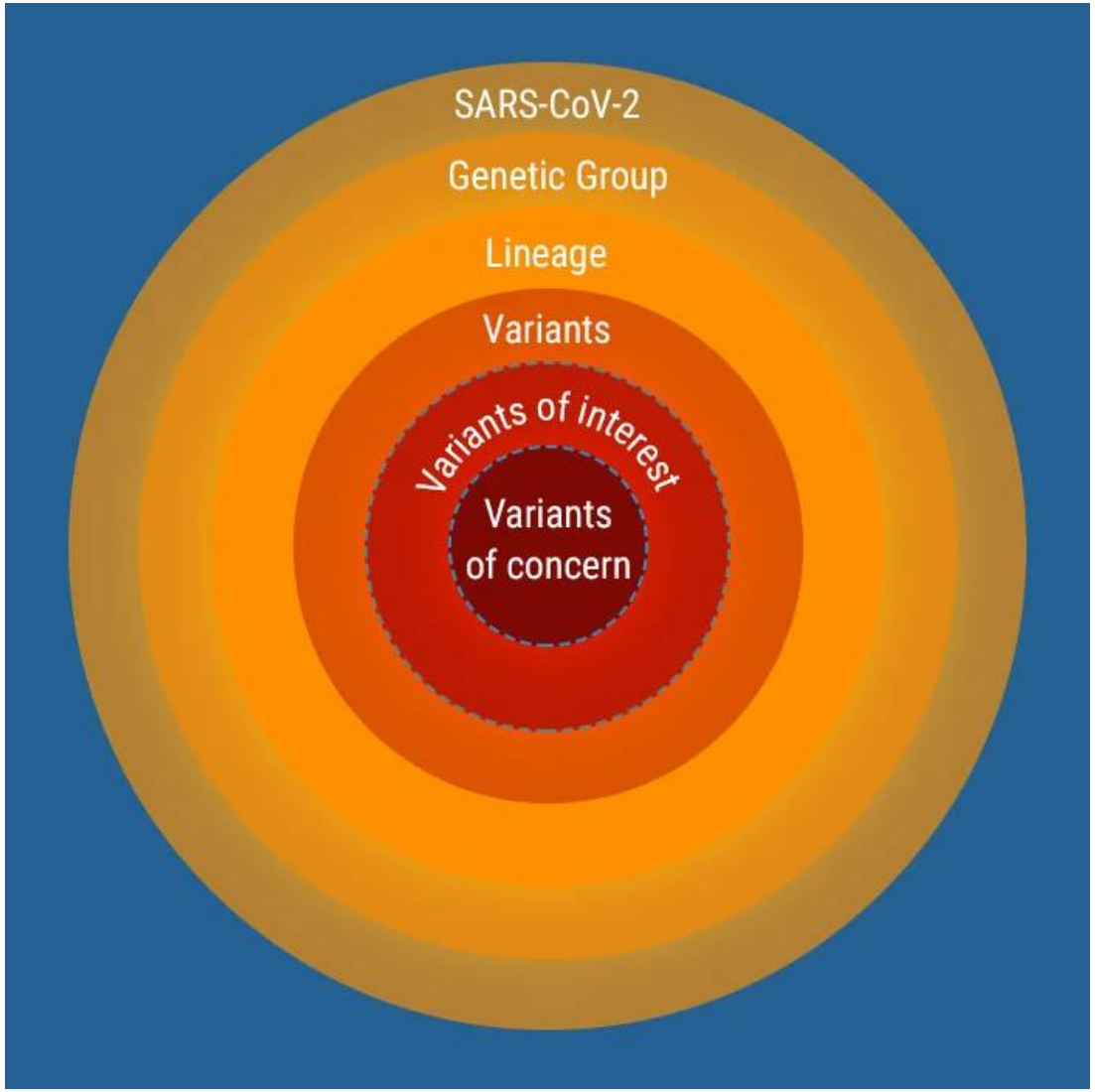
*Up to Feb 10/2022

Pan American Health Organization

World Health Organization
Regional Office for the Americas

SARS-CoV-2 Genetic Characterization

It is important to mention that the denominations as *clade*, *lineage*, *variant*, etc., are relatively arbitrary and do not correspond to an official taxonomic hierarchy.

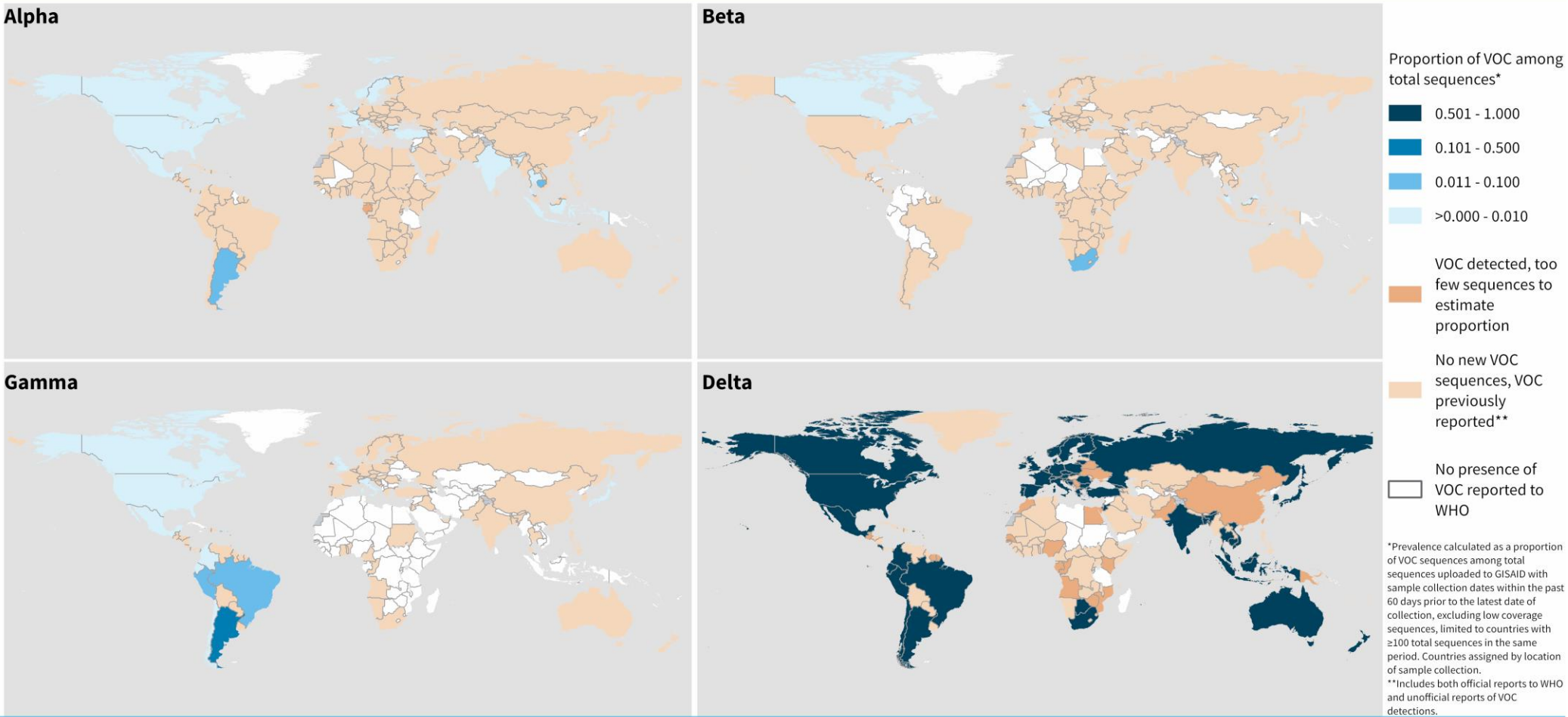


Laboratory Response Team
https://www.paho.org/es/temas/influenza/red-regional-vigilancia-genomica-covid-19

SARS-CoV-2 Variants Global Circulation

Prevalence of Variants of Concern in last 60 days and historic detections

(situation as of November 30, 2021)



Data Source: World Health Organization, GISAID
Map Production: WHO Health Emergencies Programme

Not applicable

World Health Organization

B.1.1 decendant associated with Southern Africa with high number of Spike mutations #343

New issue

Closed thomasppeacock opened this issue 8 days ago · 15 comments

thomasppeacock commented 8 days ago • edited by chrisruis

New proposed lineage
By Tom Peacock

Description
Sub-lineage of: B.1.1
Earliest Sequence: 2021-11-11
Latest Sequence: 2021-11-13

Countries circulating: Botswana (3 genomes), Hong Kong ex S. Africa (1 genome, partial)

Description:
Conserved Spike mutations - A67V, Δ69-70, T95I, G142D/Δ143-145, Δ211/L212I, ins214EPE, G339D, S371L, S373P, S375F, K417N, N440K, G446S, S477N, T478K, E484A, Q493R, G496S, Q498R, N501Y, Y505H, T547K, D614G, H655Y, N679K, P681H, N764K, D796Y, N856K, Q954H, N969K, L981F

Conserved non-Spike mutations - NSP3 – K38R, V1069I, Δ1265/L1266I, A1892T; NSP4 – T492I; NSP5 – P132H; NSP6 – Δ105-107, A189V; NSP12 – P323L; NSP14 – I42V; E – T9I; M – D3G, Q19E, A63T; N – P13L, Δ31-33, R203K, G204R

Currently only 4 sequences so would recommend monitoring for now. Export to Asia implies this might be more widespread than sequences alone would imply. Also the extremely long branch length and incredibly high amount of spike mutations suggest this could be of real concern (predicted escape from most known monoclonal antibodies)

Genomes:
EPI_ISL_6590608 (partial RBD Sanger sequencing from Hong Kong)
EPI_ISL_6640916
EPI_ISL_6640919
EPI_ISL_6640917

Assignees
No one assigned

Labels
designated

Projects
None yet

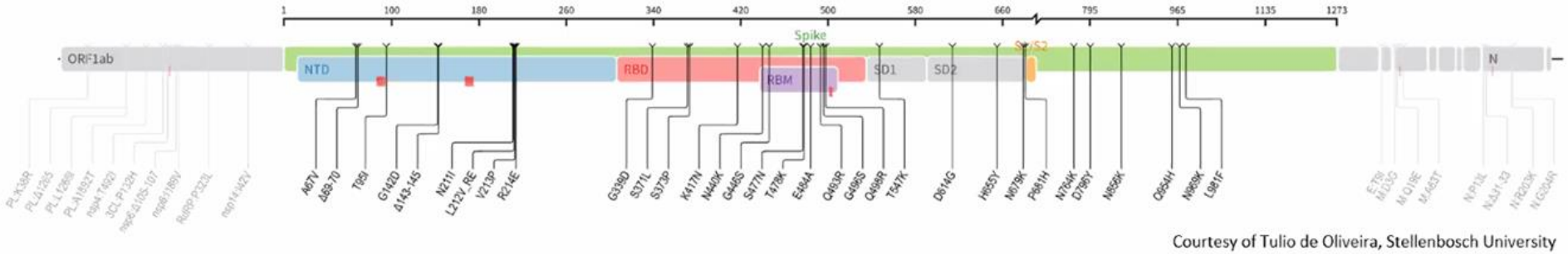
Milestone
B.1.1.529

Linked pull requests
Successfully merging a pull request may close this issue.
None yet

10 participants

Variant B.1.1.529

Mutational profile

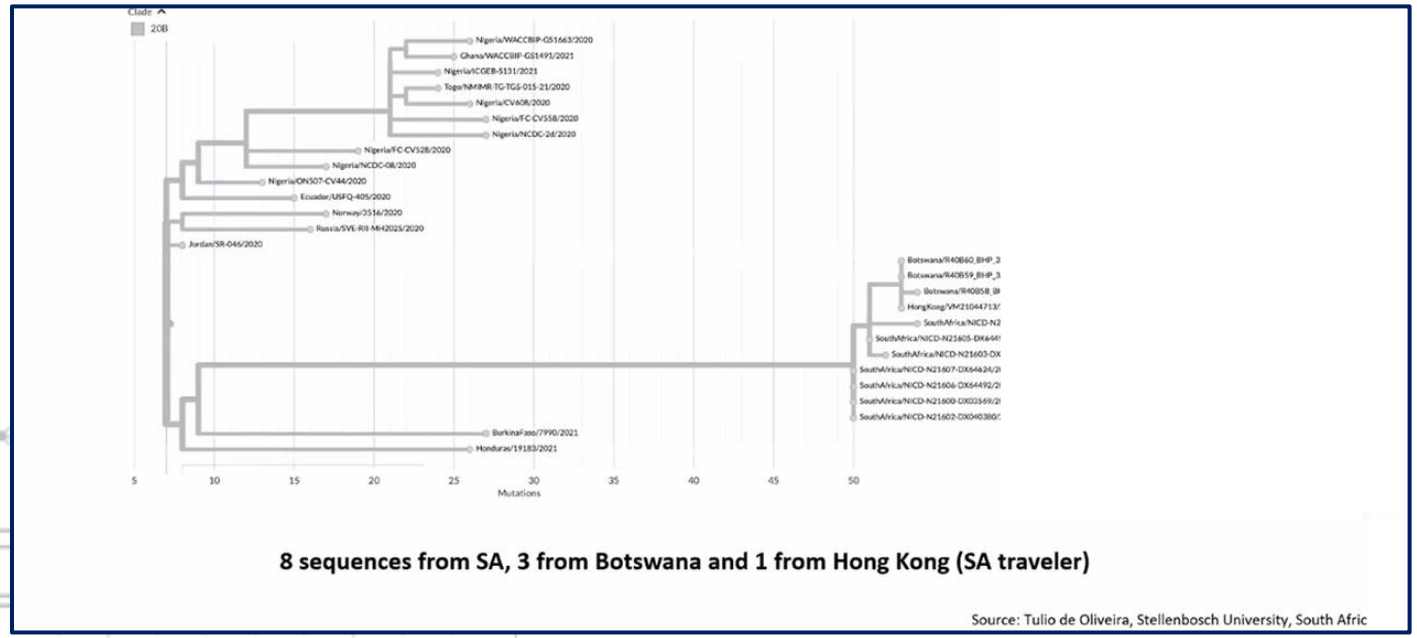


Courtesy of Tulio de Oliveira, Stellenbosch University

- 45-52 amino acid changes (including deletions) across the whole genome; 26-32 changes in Spike
- Overlapping mutations with Alpha, Beta, Gamma & Delta associated with:
  (Δ69-70; T95I; G142D/Δ143-145; K417N; T478K; N501Y; N655Y; N679K; P681H)
  - impact one particular PCR test by S-gene target failure
  - increase transmissibility
  - improve binding affinity - make it easier for virus to attach to cells
  - enable the virus to partially escape antibodies

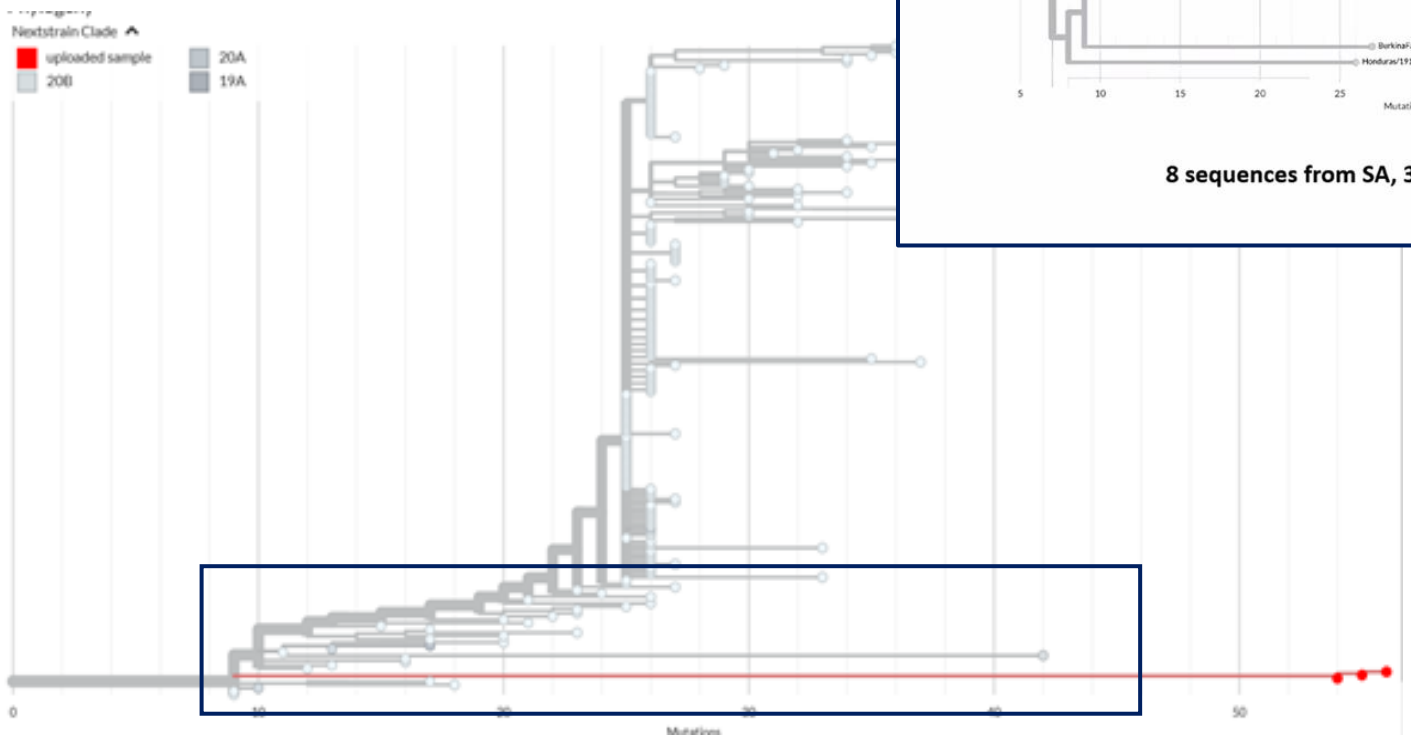
World Health Organization

Variant B.1.1.529

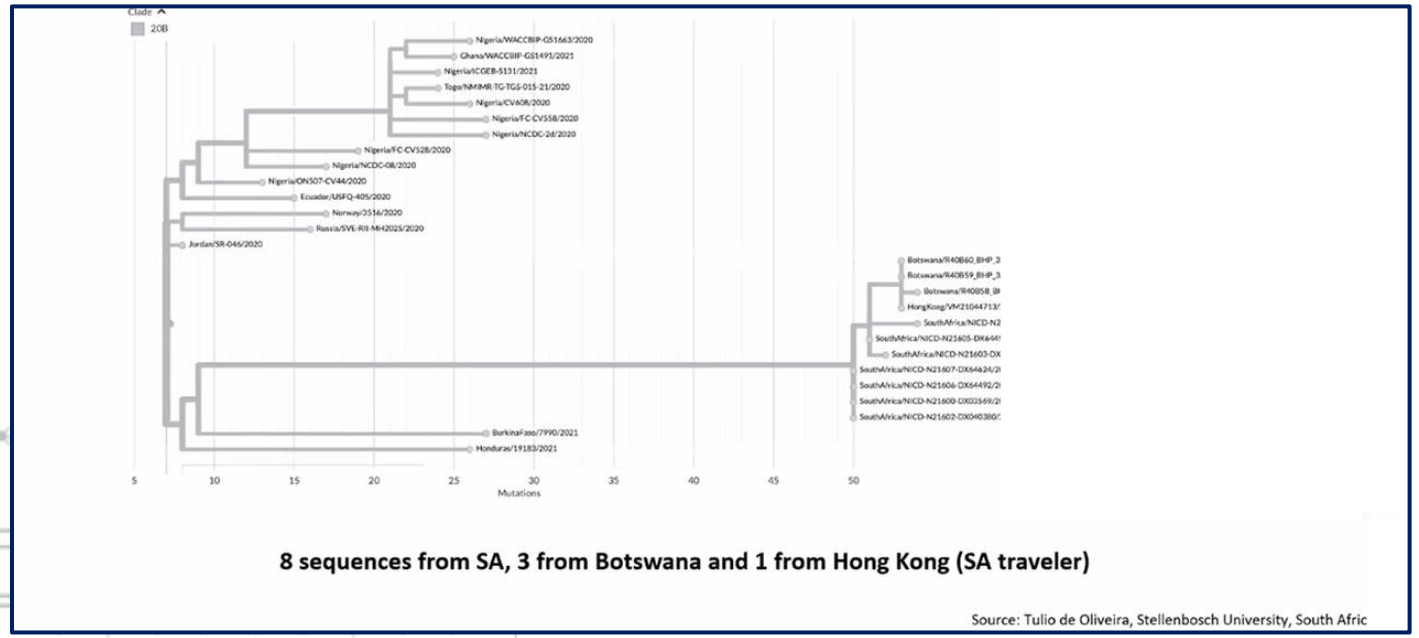


8 sequences from SA, 3 from Botswana and 1 from Hong Kong (SA traveler)

Source: Tulio de Oliveira, Stellenbosch University, South Afric



Omicron VOC



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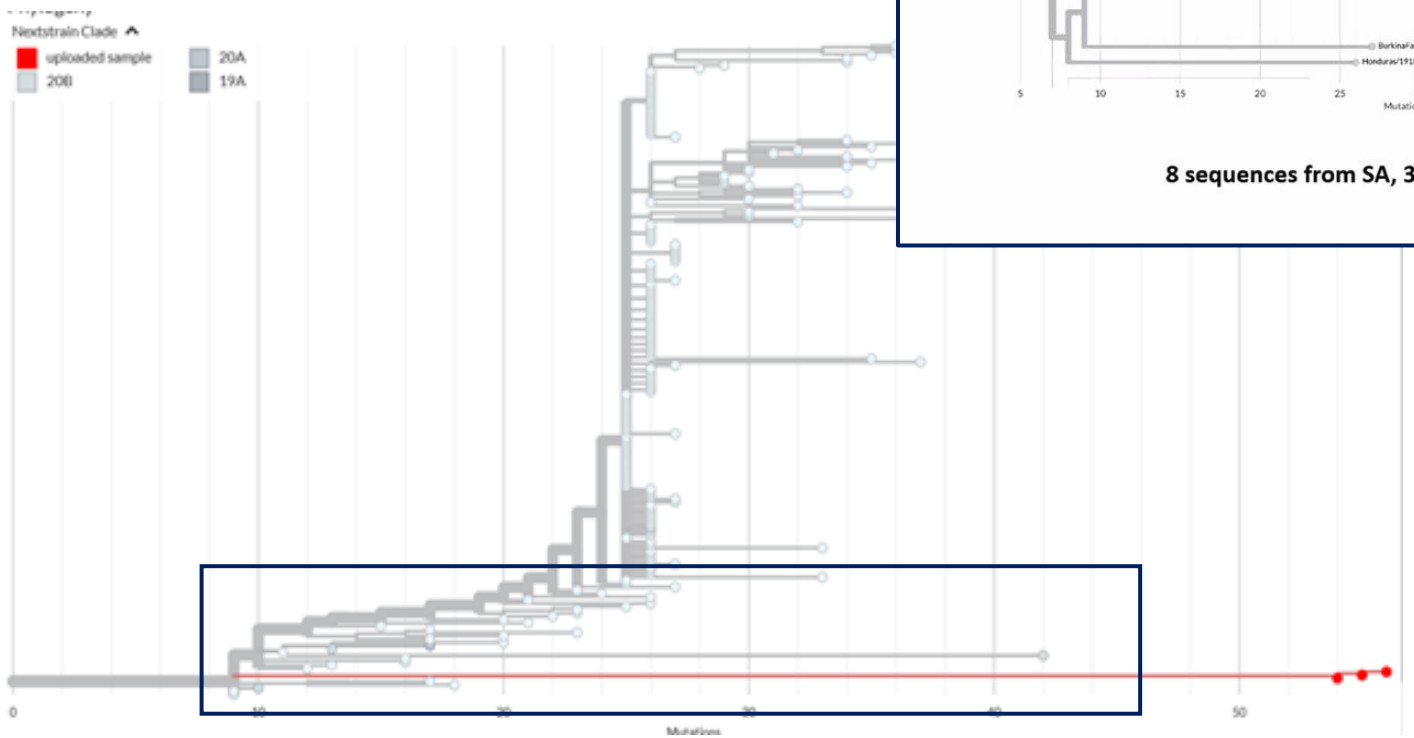
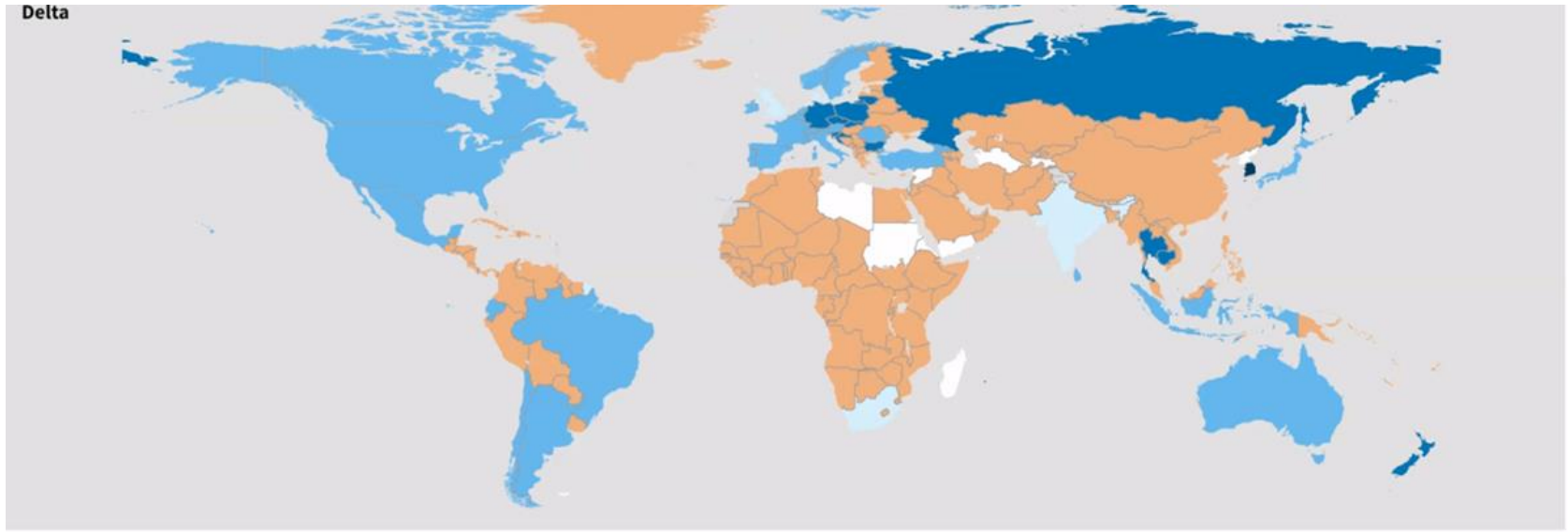
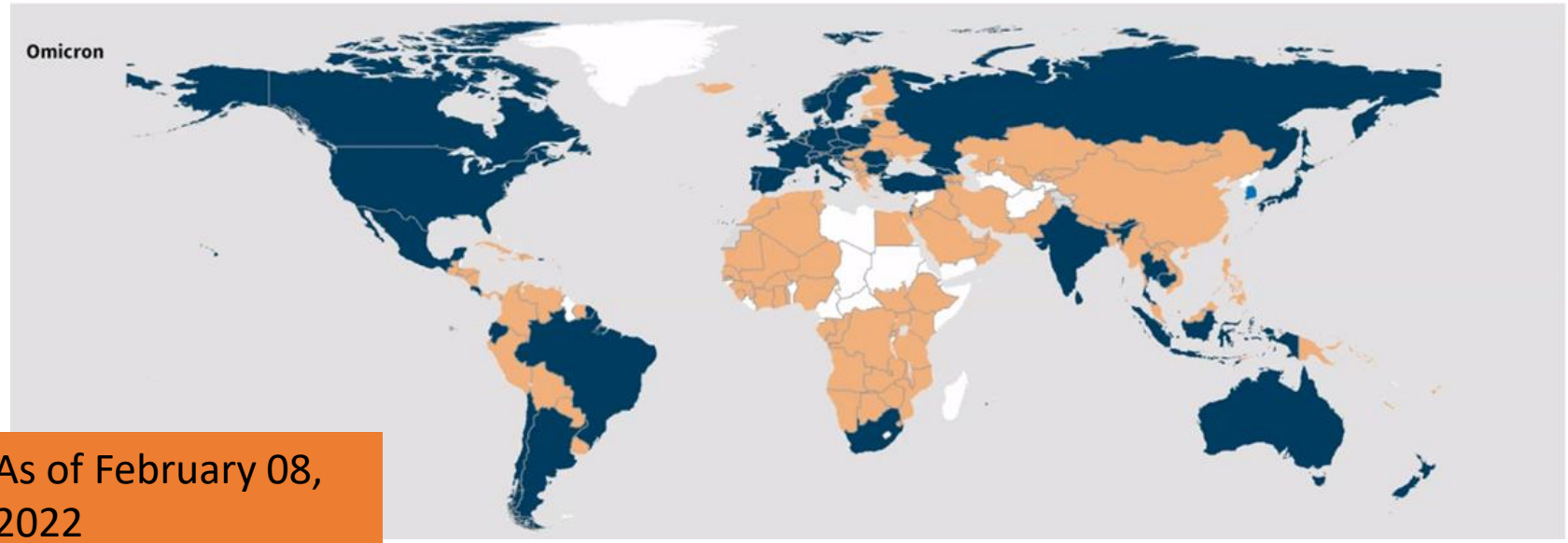


On 26 November 2021, the World Health Organization (WHO) designated the SARS-CoV-2 virus lineage B.1.1.529 as a variant of public health concern (VOC), and assigned the name according to the Greek

Delta was rapidly replaced by omicron





Proportion of VOC among total sequences (countries with ≥100 sequences in last 30 days)*

- 0.501 - 1.000
- 0.101 - 0.500
- 0.011 - 0.100
- >0.000 - 0.010
- VOC detected, proportion not estimated**
- No presence of VOC reported

Situation as of February 8, 2022

*Prevalence calculated as a proportion of VOC sequences among total sequences uploaded to GISAID with sample collection dates within the past 30 days prior to the latest date of collection, excluding low coverage sequences, limited to countries with ≥100 total sequences in the same period. Countries assigned by location of sample collection.
**Includes both official reports to WHO and unofficial reports of VOC detections.

Data Source: World Health Organization, GISAID
Map Production: WHO Health Emergencies Programme

World Health Organization

As of February 08, 2022

Country/Territory	Alpha	Beta	Gamma	Delta	Omicro
Anguilla	Yes	No	No	Yes	Yes
Antigua and Barbuda	Yes	Yes	Yes	Yes	Yes
Argentina	Yes	Yes	Yes	Yes	Yes
Aruba	Yes	Yes	Yes	Yes	Yes
Bahamas	Yes	No	Yes	Yes	No
Barbados	Yes	No	Yes	Yes	Yes
Belize	Yes	No	Yes	Yes	No
Bermuda	Yes	Yes	No	Yes	Yes
Bolivia	Yes	No	Yes	Yes	Yes
Bonaire	Yes	No	Yes	Yes	Yes
British Virgin Islands	Yes	No	Yes	Yes	Yes
Brazil	Yes	Yes	Yes	Yes	Yes
Canada	Yes	Yes	Yes	Yes	Yes
Cayman Islands	Yes	Yes	Yes	Yes	Yes
Chile	Yes	Yes	Yes	Yes	Yes
Colombia	Yes	No	Yes	Yes	Yes
Costa Rica	Yes	Yes	Yes	Yes	Yes
Cuba	Yes	Yes	No	Yes	Yes
Curacao	Yes	Yes	Yes	Yes	Yes
Dominica	Yes	No	No	Yes	No
Dominican Republic	Yes	No	Yes	Yes	Yes
Ecuador	Yes	No	Yes	Yes	Yes
El Salvador	Yes	No	Yes	Yes	No
Falkland Islands	Yes	Yes	No	No	No
French Guiana	Yes	Yes	Yes	Yes	Yes
Grenada	Yes	No	Yes	Yes	Yes
Guadeloupe	Yes	Yes	Yes	Yes	Yes
Guatemala	Yes	Yes	Yes	Yes	Yes
Guyana	No	No	Yes	Yes	No
Haiti	Yes	No	Yes	Yes	No
Honduras	Yes	No	Yes	Yes	Yes
Jamaica	Yes	No	No	Yes	Yes
Martinique	Yes	Yes	Yes	Yes	Yes
Mexico	Yes	Yes	Yes	Yes	Yes
Montserrat	Yes	No	Yes	Yes	No
Nicaragua	Yes	Yes	Yes	Yes	No
Panama	Yes	Yes	Yes	Yes	Yes
Paraguay	Yes	No	Yes	Yes	Yes
Peru	Yes	No	Yes	Yes	Yes
Puerto Rico	Yes	Yes	Yes	Yes	Yes
Saba	No	No	No	Yes	No
Saint Barthélemy	Yes	No	No	Yes	Yes
Saint Kitts and Nevis	No	No	No	Yes	Yes
Saint Lucia	Yes	No	No	Yes	No
Saint Martin	Yes	Yes	No	Yes	Yes
St Vincent and the Grenadines	No	No	Yes	Yes	Yes
Saint Pierre et Miquelon	No	No	No	Yes	No
Sint Maarten	Yes	Yes	Yes	Yes	Yes
Suriname	Yes	Yes	Yes	Yes	Yes
Trinidad and Tobago	Yes	No	Yes	Yes	Yes
Turks and Caicos	Yes	No	Yes	Yes	No
United States of America	Yes	Yes	Yes	Yes	Yes
Uruguay	Yes	Yes	Yes	Yes	Yes
Venezuela	Yes	No	Yes	Yes	Yes
Virgin Islands (US)	Yes	Yes	Yes	Yes	No

Variants Circulation at PAHO Region

(Accumulated)

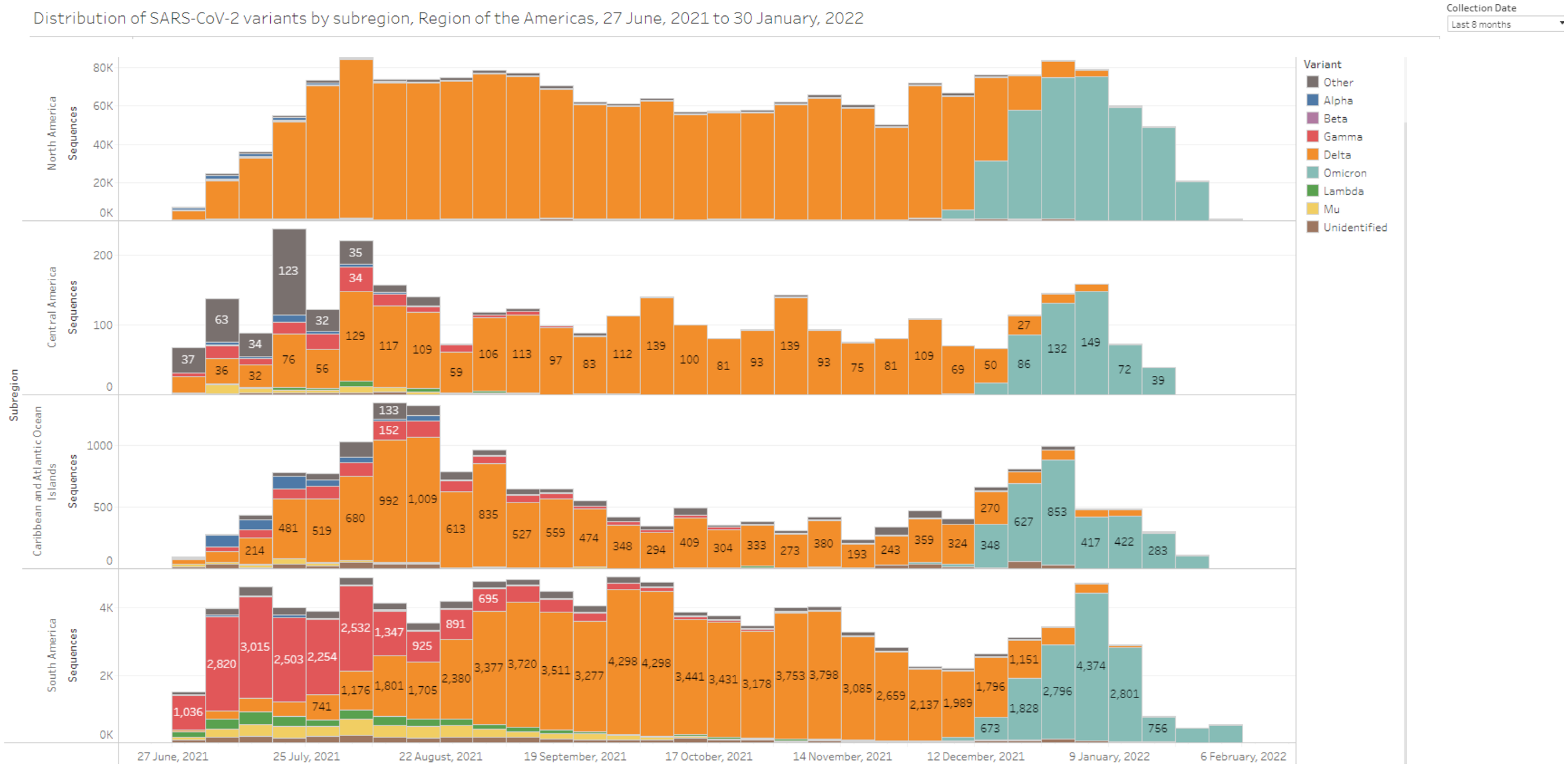
55 Countries/Territories have detected at least 1 VOC (As of February 08)

Delta = 54

Omicron = 48

Detection, Verification and Risk Assessment (**DVA**) Team, PAHO

Variants Circulation at PAHO Region

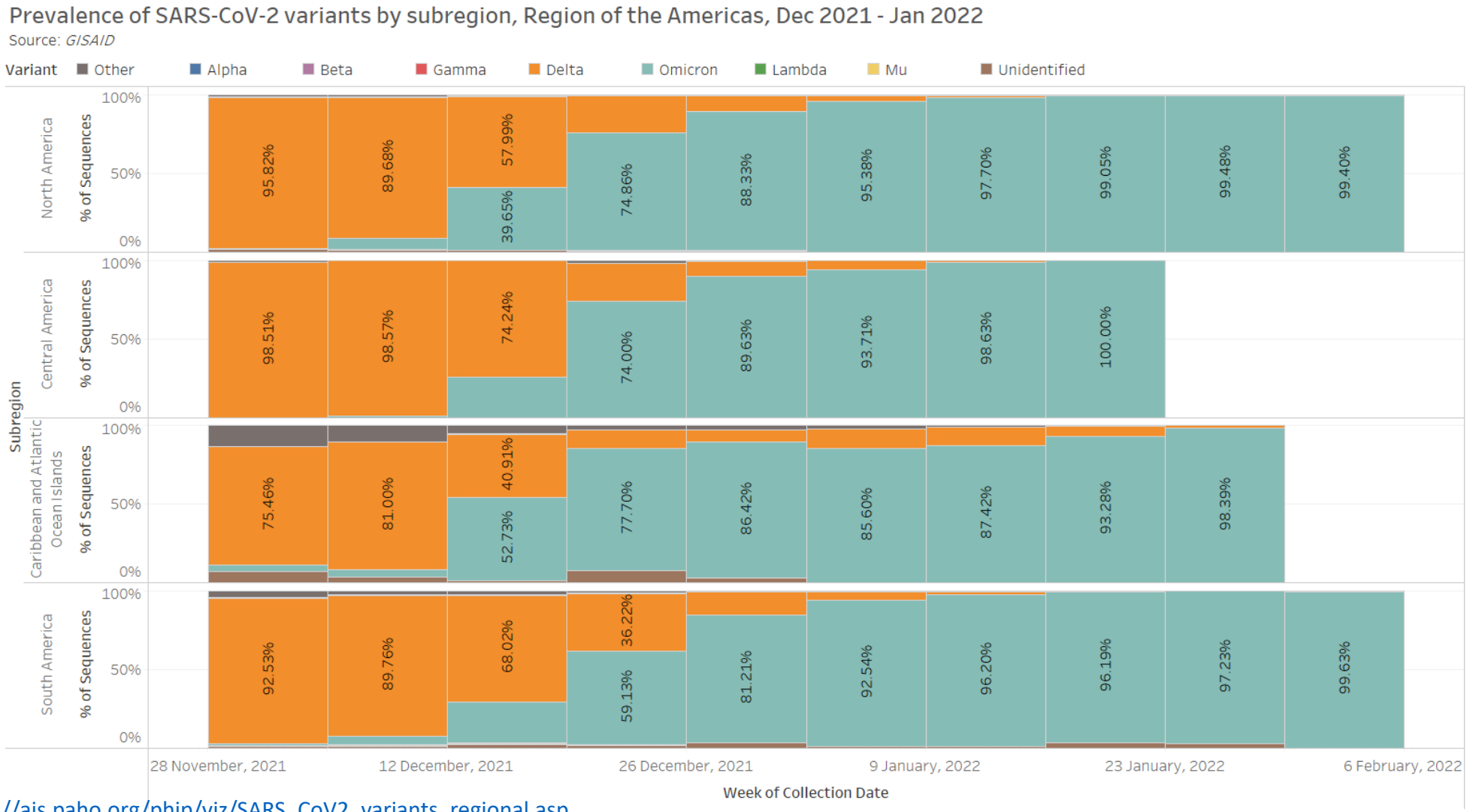


https://ais.paho.org/phip/viz/SARS_CoV2_variants_regional.asp

Dashboard developed by PAHO-IMST

Variants Circulation at PAHO Region

Delta vs Omicron



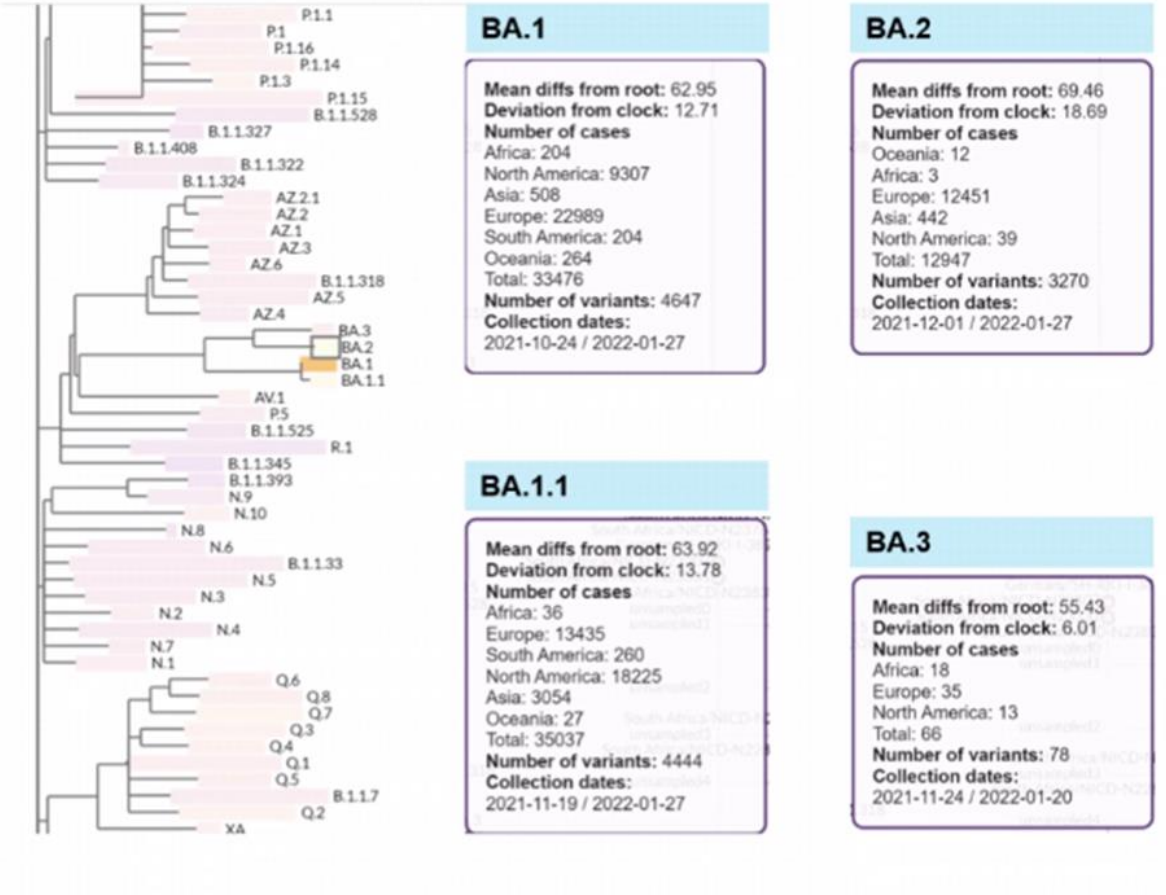
https://ais.paho.org/phip/viz/SARS_CoV2_variants_regional.asp

Dashboard developed by PAHO-IMST

What do we know about omicron?

- Genetics

  - 4 different sublineages of Omicron have been described: BA.1, BA.1.1, BA.2, and BA.3.
  - Globally, BA.1 is the predominant sublineage.
  - Currently, the BA.1 and BA.1.1 sublineages have been identified in more than 98% of samples from North America and more than 97% of samples from South America and the Caribbean.
  - The BA.2 sublineage has been identified mainly in Africa (27%) In Asia (19%) and Europe (14%).
  - In the Americas, BA.2 has been officially reported in USA, Mexico, Argentina and Brazil; represents less than 0.5% of samples reported to GISAID.



So far, no solid evidence of any critical change in terms of transmissibility, clinical presentation, severity, or immune evasion, beyond those already described for the VOC Omicron.

What do we know about omicron?

- Transmissibility
  - Increased tropism to infect upper respiratory tract (compared to Delta and other VOC)
  - Highly transmissible
  - High growth rate
    - Infection rate up to 3.5 times higher than delta
    - Shorter incubation period (~2.2 days vs ~3.2 days for delta)
  - It is unclear whether it has a higher intrinsic transmission capacity, or the increased transmission is due to evasion of the immune response (or a combination of the two factors)
  - Secondary attack rate up to 42% (compared to 25 for delta)*

    *https://www.medrxiv.org/content/10.1101/2022.01.28.22270044v1.full.pdf

- Severity
  - Current data clearly indicate a decrease in hospitalization, ICU admissions, and case fatality rates for Omicron when compared to Delta
    - Hospitalization risk: reduction between 50-70%
  - In addition to an intrinsic lower capacity of the virus to generate severe disease, the **natural immune response** (previous infection) and the **vaccine response** are critical

What do we know about omicron?

- Impact on diagnosis (molecular or antigen detection):
  - The reference protocol for molecular detection (Charité, Germany) recommended by PAHO for universal surveillance of SARS-CoV-2 is not affected
  - The WHO-CC influenza and SARS-CoV-2 multiplex protocol for influenza, CDC-USA implemented for sentinel surveillance is not affected
  - In-house or commercial protocols aimed at detecting other genes (N, RdRP, Orf1, etc.) have not been affected so far.
  - Omicron mutations are mainly concentrated in the S gene, while AgRDT detect protein N
  - There is no evidence (so far) to infer that the sensitivity and specificity of rapid the AgRDT have changed.

What do we know about omicron?

- Immune response and vaccination
  - Increasing evidence of immune evasion (both natural or vaccine induced)
    - Increased risk of both re-infections and breakthrough infection
  - Vaccine Efficacy against infection and asymptomatic infection
    - Significant reduction in neutralization after 2 doses when compared to Delta
    - High efficacy after a booster (limited evidence regarding duration)
  - Efficacy of vaccines for hospitalization:
    - Noticeable reduction in individuals with complete scheme
    - Decrease close to 90% in individuals with booster

Final comments

- Mutations and the emergency of variants is a normal biological and evolutionary process that normally leads to greater transmission, but less lethality
- The more the virus is transmitted, the more likely mutations will occur: More variants are expected (including more escape variants…)
- **Stopping transmission** is the only way to prevent variants from occurring.
- **Maintain all public health measures and strengthen surveillance** (genomic and epidemiological), independent of any variant in circulation…
- **Vaccination is critical** and has been shown to be useful in reducing severity, hospitalization and death

Thank you !!

PAHO/WHO

IMST Laboratory Response Team

Pan American Health Organization

World Health Organization
REGIONAL OFFICE FOR THE Americas