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

*Up to Feb 10/2022

https://www.gisaid.org/phyldynamics/global/nextstrain/
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.
SARS-CoV-2 Variants Global Circulation

Prevalence of Variants of Concern in Last 60 Days and Historic Detections

Situation as of November 30, 2021

**Alpha**

**Beta**

**Gamma**

**Delta**

Proportion of VOC among total sequences*

- 0.501 - 1.000
- 0.101 - 0.500
- 0.011 - 0.100
- >0.000 - 0.010

VOC detected, too few sequences to estimate proportion

No new VOC sequences, VOC previously reported**

No presence of VOC reported to WHO

*Prevalence calculated as a proportion of VOC sequences among total sequences uploaded to GISAID with a sample collection date within the past 60 days prior to the latest date of collection, including 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 unreported reports of VOC detections.

The designations employed and the presentation of the material in this publication do not imply the expression of any opinion whatsoever on the part of WHO concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted and dashed lines on maps represent approximate border lines for which there may not yet be full agreement.

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

Not applicable

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

thomasppeacock opened this issue 8 days ago · 15 comments

thomasppeacock commented 8 days ago · edited by chrisrui

New proposed lineage
By Tom Peacock

**Description**

Sub lineage: B.1.1

Earliest Sequence: 2021-11-11

Latest Sequence: 2021-11-31

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

**Description:**


Conserved non-Spike mutations - NSP3 - K38R, V106I, Δ1265/Δ1266, A1892T, NSP4 - T482I, NSP5 - P123H, NSP6 - Δ105-107, A189V; NSP12 - P323L; NSP14 - Δ42V; E - T96I, M - D39, 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/JSL_6590608 (partial RBD Sanger sequencing from Hong Kong)
EPI/JSL_6640996
EPI/JSL_6640919
EPI/JSL_6640915
Variant B.1.1.529

Mutational profile

- 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
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 Africa
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
### Variants Circulation at PAHO Region

(Accumulated)

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

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Delta = 54

Omicron = 48

Detection, Verification and Risk Assessment (DVA) Team, PAHO
Variants Circulation at PAHO Region

Distribution of SARS-CoV-2 variants by subregion, Region of the Americas, 27 June, 2021 to 30 January, 2022

https://ais.paho.org/phip/viz/SARS_CoV2_variants_regional.asp
Dashboard developed by PAHO-IMST
Variants Circulation at PAHO Region

Delta vs Omicron

Prevalence of SARS-CoV-2 variants by subregion, Region of the Americas, Dec 2021 - Jan 2022

Source: GISAID

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)
    o Increased risk of both re-infections and breakthrough infection

  • Vaccine Efficacy against infection and asymptomatic infection
    o Significant reduction in neutralization after 2 doses when compared to Delta
    o High efficacy after a booster (limited evidence regarding duration)

  • Efficacy of vaccines for hospitalization:
    o Noticeable reduction in individuals with complete scheme
    o Decrease close to 90% in individuals with booster
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