COVID-19 Genomic Surveillance Regional Network

Sequencing SARS-CoV-2 in the Americas

The COVID-19 Genomic Surveillance Regional Network was created in 2020 not only to strengthen the sequencing capacity in the participating laboratories, but also for them to establish a routine SARS-CoV-2 genomic sequencing, as a strategy to increase the amount of genetic sequence data available to the global community, which is critical to support the development of diagnostic protocols, the information for vaccine development and to better understand the evolution and molecular epidemiology of the SARS-CoV-2.

62,933 Virus sequences

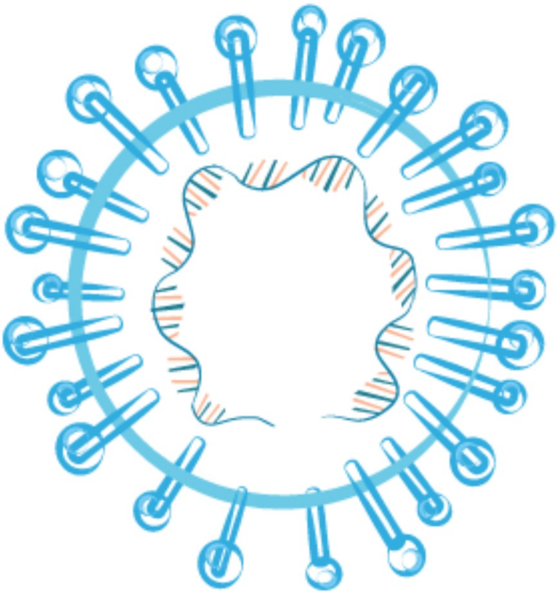
from Latin America and the Caribbean Member States of the Pan American Health Organization

Updated July 20, 2021

*Data Source from GISAID

The Network

The structure of the network includes a combination of in-country sequencing countries and those sending-out for external sequencing to either of the 2 Regional Sequencing Laboratories (Fundação Oswaldo Cruz/FIOCRUZ - Brazil and Instituto de Salud Publica/ISPCH-Chile), which provide external sequencing for the participating laboratories. Also, , regional and country-level trainings, and additional support actions to generate timely information of SARS-CoV-2 genomic sequencing data are available through the Network. PAHO encourages laboratories to sequence COVID-19 positive samples and timely share genetic information through the Global Initiative on Sharing All Influenza Data, GISAID platform.



COV|GEN

COVID -19 Genomic Surveillance Regional Network

The participation on the COVID-19 Genomic Surveillance Regional Network is open to all the countries of the Americas through the National Public Health Laboratories.

For more detailed information on partnering with us, please contact the PAHO Regional Office: leitejul@paho.org (mailto:leitejul@paho.org), ricoj@paho.org (mailto:ricoj@paho.org).

SARS-CoV-2 Genomic Sequencing Laboratories

Report production: Paho Health Emergencies Department (PHE): Influenza Surveillance Team/ Infectious Hazard Management (IHM) and Data Management, Analytics & Products/ Health Emergency Information & Risk Assessments (HIM).

The SARS-CoV-2 genome

Variants of SARS-CoV-2 in the Americas

Since the initial genomic characterization of SARS-CoV-2, the virus has been divided into different genetic groups. The occurrence of mutations is a natural and expected event within the evolution process of the virus.

- Mutation refers to any change in the virus genome.
- Some specific mutations define the viral genetic groups currently circulating globally.
- In general, a mutated virus is considered a variant of the original virus.
- There are different types of mutations. Variants can differ by one or more or those.
- Although most of the mutations have no impact, some may result in the virus being more transmissible, or facilitating the virus to escape immune response.
- In the community, the higher the transmission level, the higher is the likelihood of viral mutations to occur.

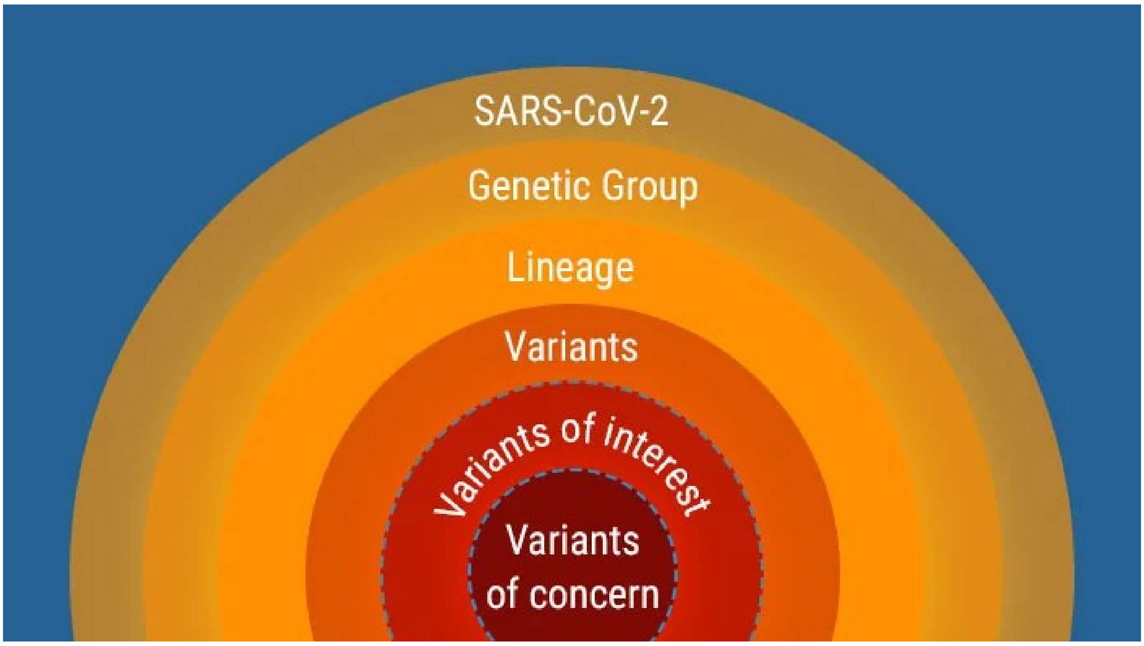
When these variants have a potential impact or risk for public health, they are considered variants of concern (VOC).

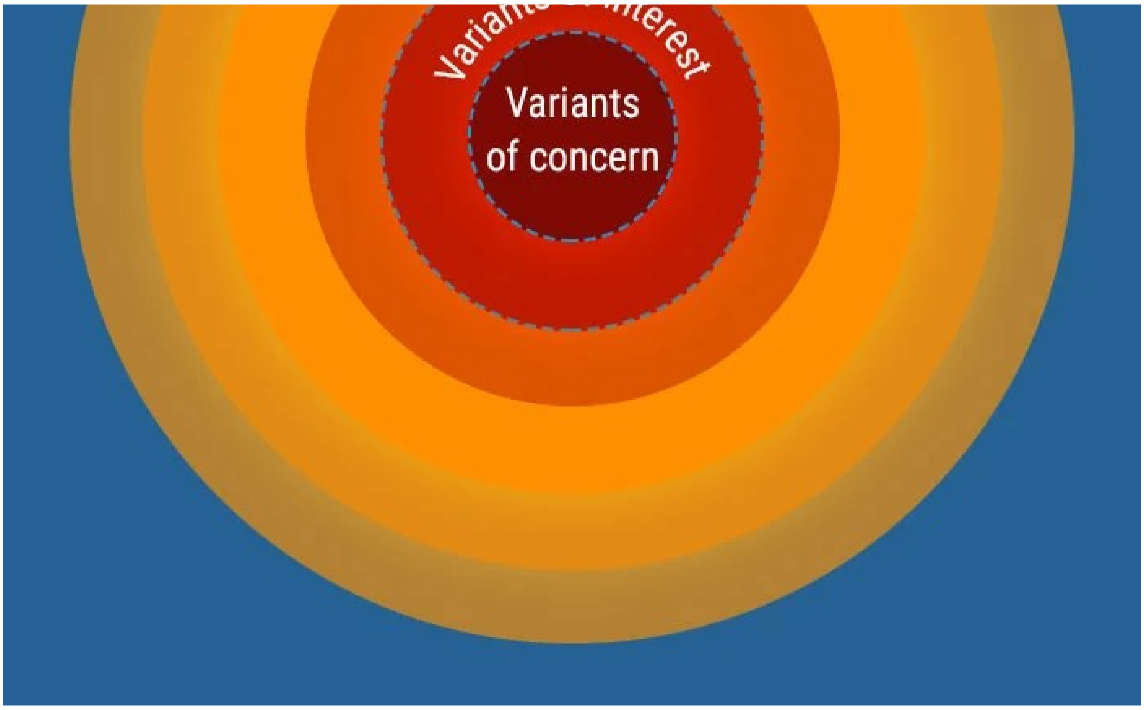
Variants classification[1]

SARS-CoV-2 Variant of Interest (VOI)

SARS-CoV-2 Variant of Concern (VOC)

[1] https://www.who.int/publications/m/item/covid-19-weekly-epidemiological-update (https://www.who.int/publications/m/item/covid-19-weekly-epidemiological-update)





GISAID - VARIANT TRACKER (HTTPS://WWW.GISAID.ORG/HCOV19-VARIANTS/)

Monitoring of SARS-CoV-2 variants

Virus mutations or variants are being monitored from the start of the COVID-19 pandemic through the Global Initiative on Sharing Avian Influenza Data (GISAID) sequencing database. WHO routinely assesses if variants of SARSCoV-2 have an impact on:

- Virus transmissibility;
- Disease severity;
- Efficacy of diagnostics, therapeutics and vaccines.

Risk assessment for variants of concern to determine if there will be public health implications are routinely performed.

Main actions by a Member State, if a VOI or VOC is identified:

- Immediately report to PAHO/WHO initial cases/clusters associated with VOI or VOC infection through the IHR mechanism.
- Submit complete genome sequences and associated metadata to a publicly available database, such as GISAID.
- Where capacity exists and in coordination with the international

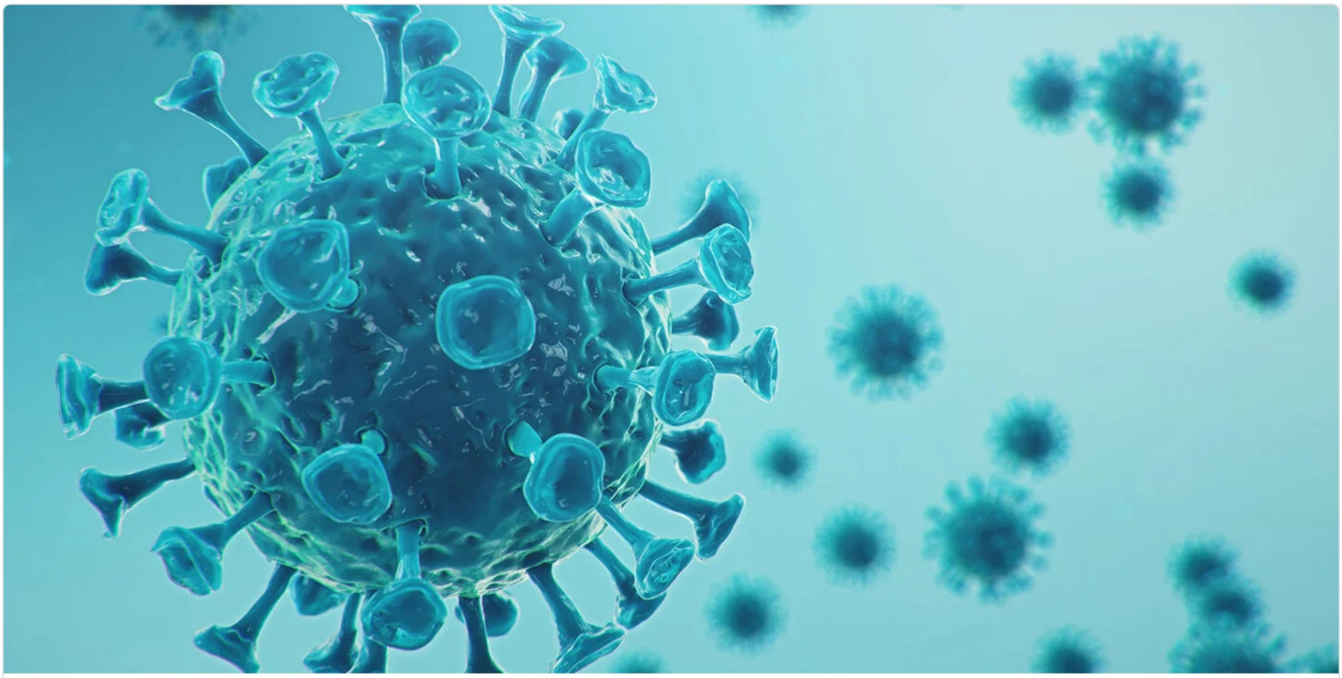
community, perform field investigations to improve understanding of the potential impacts of the VOI or VOC on COVID-19 epidemiology, severity, effectiveness of public health and social measures, or other relevant characteristics.
- Perform laboratory assessments or contact WHO for support to conduct laboratory assessments on the impact of the VOI or VOC on diagnostic methods, immune responses, antibody neutralization or other relevant characteristics.

SARS-CoV-2 Phylodynamics

Phylodynamics of pandemic coronavirus in Latin America and the Caribbean.

GO TO GISAID DATA
(HTTPS://PHYLODYNAMICS.PANDEMICPREPARDNESS.ORG
/DIST/START.HTML?ID=TGF0AW4LMJBBBWVYAWNH&S=1&H=0)

News

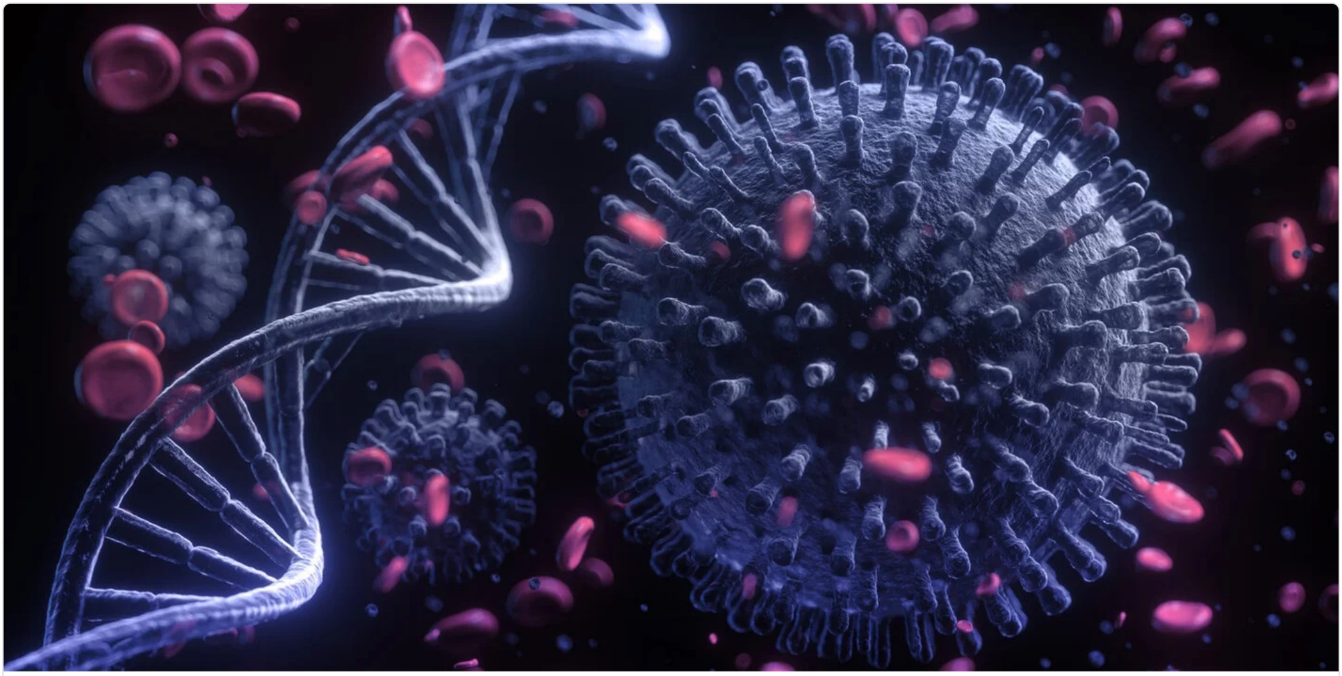


PAHO: COVID-19 cases in the Americas rose 14% since Jan. 15, but increase is lower than previous period

(https://www.paho.org/en/news/11-2-2021-paho-covid-19-cases-americas-rose-14-jan-15-increase-lower-previous-period)

PAHO Director says COVID-19 vaccines for the Americas still recommended despite new variants

(https://www.paho.org/en/news/10-2-2021-paho-director-says-covid-19-vaccines-americas-still-recommended-despite-new-variants)



Three variants of the COVID-19 virus found in 14 countries in the Americas, PAHO reports

(https://www.paho.org/en/news/28-1-2021-three-variants-covid-19-virus-found-14-countries-americas-paho-reports)

Documents

Technical Note: SARS-CoV-2 genomic characterization and circulating variants in the Region of the Americas

(https://www.paho.org/en/documents/technical-note-sars-cov-2-genomic-characterization-and-circulating-variants-region)

Guidance for SARS-CoV-2 samples selection for genomic characterization and surveillance

(https://www.paho.org/en/documents/guidance-sars-cov-2-samples-selection-genomic-characterization-and-surveillance)

Epidemiological Update:

Occurrence of variants of SARS-CoV-2 in the Americas (26 January 2021)

(https://iris.paho.org/handle/10665.2/53239)

Epidemiological Update: Occurrence of variants of SARS-CoV-2 in the Americas (20 January 2021)

(https://iris.paho.org/handle/10665.2/53219)

Occurrence of variants of SARS-CoV-2 in the Americas (11 January 2021)

(https://iris.paho.org/handle/10665.2/53217)

More information

(WHO) - Genomic sequencing of SARS-CoV-2: a guide to implementation for maximum impact on public health (https://www.who.int/publications/i/item/9789240018440)

COVID-19 Weekly Epidemiological Update - 25 February 2021 - Special edition: Proposed working definitions of SARS-CoV-2... (https://www.who.int/publications/m/item/covid-19-weekly-epidemiological-update)

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Regional Office for the Americas of the World Health Organization