

Globally, to date, 141 countries and territories have detected cases of infection by one of the three variants of concern (VOC) currently recognized by WHO. Of this total, 32 countries and territories are in the Region of the Americas.

Introduction

At the global level, a constant change is observed in the proportion of predominant clades since the start of the pandemic to date. As of 5 July 2020, 49% of the samples available through GISAID were associated with the GR clade and by 22 August 2020 it had increased to 53%, whereas by 7 November 2020 the proportion had decreased to 37% and by 22 March 2021 it decreased further to 18% of the proportion of samples.

In contrast, there has been a relatively stable trend in proportion of the GH clade, contributing 35% to the total of samples available in GISAID sequenced as of 6 December 2020 and 30% as of 22 March 2021. Regarding the GRY clade, there has been an increase in proportion from 5% as of 6 December 2020 to 39% as of 22 March 2021 (**Figure 1**).

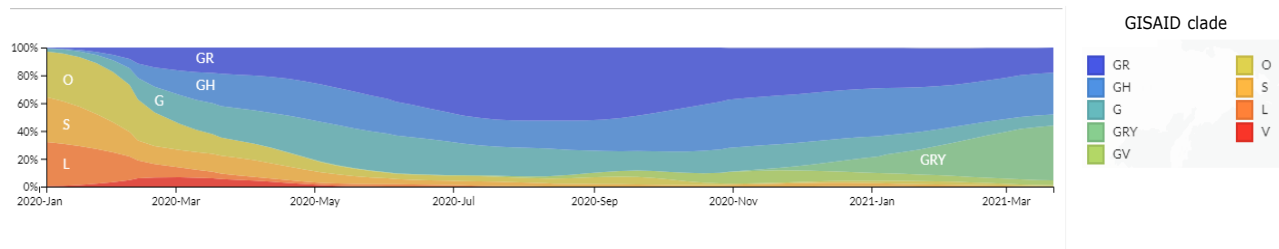
While data about the predominant clades at the global level is important, it should be interpreted with caution, due to the biased representation of the SARS-CoV-2 genomic sequencing data (GSD), with a greater contribution of high-income countries.¹ This bias must be considered when evaluating the presence or absence of a particular variant in a place and its relative frequency. Additionally, not all countries share their data through the GISAID platform.

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

In fact, some specific mutations define the viral genetic groups (also called lineages) that are currently circulating globally. Due to various microevolution processes and selection pressures, some additional mutations may appear, generating differences within each genetic group (called variants). It is important to mention that the name of the clade, lineage, variant, etc., are arbitrary and do not correspond to an official taxonomic hierarchy.

¹ WHO. SARS-CoV-2 genomic sequencing for public health goals: Interim guidance, 8 January 2021. WHO/2019-nCoV/genomic sequencing/2021.1. Available at: <https://bit.ly/38uIAr0>

Figure 1. Global distribution of GISAID clades by frequency percentage. January 2020 to March 2021.



Source: GISAID. Available at: <https://bit.ly/3qA9nXI> Accessed 22 March 2021.

Genomic characterization of SARS-CoV-2

Since the initial identification of SARS-CoV-2 until 22 March 2021, more than 845,000 complete genomic sequences have been shared globally through publicly accessible databases. The capacity to monitor the data in near real time has a direct impact on the public health response to the COVID-19 pandemic, allowing to identify changes in epidemiological patterns, in virulence, or in the decrease in therapeutic efficacy, among other changes.

SARS-CoV-2 Variants of Concern (VOC)

At a global level, to date, 3 variants of SARS-CoV-2 have been identified (B.1.1.7, B.1.351, and B.1.1.28.1) that have been classified by the WHO as variants of concern (VOC), in consultation with the WHO Working Group on the Evolution of SARS-CoV-2.

Among the factors that the WHO has considered for the operational definition for VOCs are:

- Increased transmissibility or detrimental change in COVID-19 the epidemiology;
- Increased in virulence or change in clinical presentation; or
- Decrease effectiveness of public health and social measures or available diagnostics, vaccines, and therapeutics.

The operational definitions will be periodically reviewed and updated, as necessary.²

Since the first notification of each of the three VOCs in December 2020 until 23 March 2021, an increasing number of countries and territories have reported the detection of one or more VOCs (**Table 1**).

² WHO. Weekly epidemiological update. Published on 25 February 2021. Available at: <https://bit.ly/2O173vt>

Table 1. Summary of countries and territories reporting cases of VOC as of 23 March 2021.

Summary	Name of the variant *		
	Variant B.1.1.7	Variant B.1.351	Variant B.1.1.28.1
Number of countries/territories reporting cases globally	125	75	41
Number of countries/territories reporting cases in the Americas	28	9	15

Note: *PANGO name of lineage

Some countries and territories have reported the detection of more than one of the VOC.

Source: WHO. Weekly epidemiological update. Published on 23 March 2021. Available at: <https://bit.ly/3v6e0Mi>

Regarding the situation in the Americas, as of 23 March 2021, 32 countries and territories have reported the detection of VOC cases, since the 11 March 2021 Epidemiological Update on Coronavirus disease (COVID-19)³ one additional territory has reported the detection of VOC.

All three VOC have been reported in Aruba, Canada, Martinique, Saint Martin, and the United States of America (**Table 2**).

³ PAHO/WHO. Epidemiological Update: Coronavirus disease (COVID-19). 11 March 2021, Washington, D.C.: PAHO/WHO; 2021. Available at: <http://bit.ly/3t8BEWQ>

Table 2. Countries and territories in the Americas reporting the detection of VOC, as of 23 January 2021.

Country	Variant B.1.1.7	Variant B.1.351	Variant B.1.1.28.1
Argentina	Yes	No	Yes
Aruba	Yes	Yes	Yes
Barbados	Yes	No	No
Belize	Yes	No	No
Brazil	Yes	No	Yes
Bonaire	Yes	No	No
Canada	Yes	Yes	Yes
Cayman Islands	Yes	No	No
Chile	Yes	No	Yes
Colombia	No	No	Yes
Costa Rica	Yes	Yes	No
Cuba	No	Yes	No
Curacao	Yes	No	No
Dominican Republic	Yes	No	No
Ecuador	Yes	No	No
French Guiana	Yes	No	Yes
Guadeloupe	Yes	Yes	Yes
Jamaica	Yes	No	No
Martinique	Yes	Yes	Yes
Mexico	Yes	No	Yes
Panama	No	Yes	No
Peru	Yes	No	Yes
Puerto Rico	Yes	No	No
Saint Barthélemy	Yes	No	No
Saint Martin	Yes	Yes	Yes
Saint Lucia	Yes	No	No
Sint Maarten	Yes	No	No
Trinidad and Tobago	Yes	No	No
Turks and Caicos	Yes	No	No
United States of America	Yes	Yes	Yes
Uruguay	Yes	No	Yes
Venezuela	No	No	Yes

Source: Information shared by the International Health Regulations (IHR) National Focal Points (NFPs) or published on the websites of the Ministries of Health, Health Agencies or similar and reproduced by PAHO/WHO.

SARS-CoV-2 Variants of Interest (VOI)

In addition to the SARS-CoV-2 VOC, WHO has provided a working definition² for other variants, called variant of interest (VOI) if the SARS-CoV-2 isolate is:

- phenotypically changed compared to a reference isolate or has a genome with mutations that lead to amino acid changes associated with established or suspected phenotypic implications⁴;

AND

- has been identified to cause community transmission /multiple COVID-19 cases/clusters, or has been detected in multiple countries;

OR

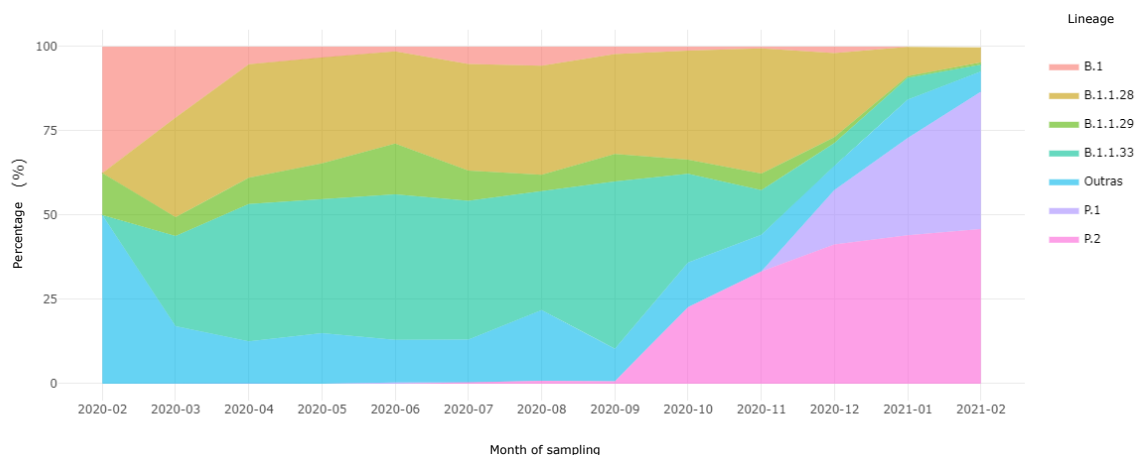
- is otherwise assessed to be a VOI by WHO in consultation with the WHO SARS-CoV-2 Virus Evolution Working Group.

As of 23 March 2021, WHO has classified as variants of interest (VOI), the following: B.1.525, B.1.427/B.1.429, and B.1.1.28.2, alias P.2⁵.

Some of the countries in the Americas that have reported VOIs are Brazil and the United States of America. A brief update of those variants is presented below.

In **Brazil**, variant P.2 has been reported, which is characterized due to the increase observed in the proportion of this variant in the country between September 2020 (0.7%) and February 2021 (45%) (**Figure 2**). This variant has also been reported in the Americas in Argentina, Chile, Mexico, Sint Maarten, the United States, Uruguay, and Venezuela.

Figure 2. Percentage distribution of the major SARS-CoV-2 lineages by month of sampling. Brazil, February 2020 to January 2021.



Source: Fiocruz genomic network. Available at: <https://bit.ly/2YmCSjH> Accessed on 22 March 2021.

⁴ Phenotypic changes include changes in the epidemiology, antigenicity, or virulence or changes that have or potentially have a negative impact on available diagnostics, vaccines, therapeutics or public health and social measures. WHO will provide guidance on amino acid changes with established or suspected phenotypic implications, and may be informed by a database on key amino acid changes, or as reported in the scientific literature.

⁵ WHO. Weekly epidemiological update. Published on 23 March 2021. Available at: <https://bit.ly/3v6e0Mi>

In the **United States**, VOIs have been reported, two of which were first detected in New York B.1.526 and B.1.525 and two were first detected in California, B.1.427 and B.1.429⁶. Of note, the variants first detected in California, B.1.427 and B.1.429 are classified nationally as Variants of Concern (VOC) by the United States Centers for Disease Control and Prevention (CDC), but globally and by the WHO, as of 23 March 2021 they remain classified as variants of interest (VOI).

The variants detected in New York are characterized by a potential reduction in neutralization by monoclonal antibody treatments and a potential reduction in neutralization by convalescent and post-vaccination sera.

In the variants detected in California, some attributes similar to those of New York have been observed, such as the moderate reduction in neutralization using convalescence and post-vaccination sera. At the same time, they present other attributes that are more concerning, such as approximately 20% more transmissibility and a significant impact on the neutralization of some therapies used in the country.

In the Americas, to date, the detection of the following variants has been reported in Aruba variants B.1.526 and B.1.427/B.1.429; in Chile, variants B.1.525 y B.1.427/B.1.429; in Costa Rica, variants B.1.427/B.1.429 and B.1.525; in México, variant B.1.427/B.1.429; in Saint Martin, variants B.1.427/B.1.429 and B.1.526, and in Sint Maarten variants B.1.427/B.1.429 and B.1.526.

Guidance for national authorities

The Pan American Health Organization / World Health Organization (PAHO/WHO) encourages Member States to coordinate genomic surveillance in their national territory, ensure the timely publication of sequences on the GISAID platform, and to immediately notify the first detection of cases of infection by SARS-CoV-2 VOC in accordance with the WHO guidance on genomic sequencing of SARS-CoV-2 available at: <https://bit.ly/3sd4Psb>

Understanding that the detection of SARS-CoV-2 variants is dependent on the capacity that each country has to implement genomic surveillance, since March 2020, PAHO/WHO is supporting countries to strengthen said surveillance within the framework of the Regional Network for Genomic Surveillance of COVID-19. PAHO/WHO invites Member States to participate in this Network and to carry out sequencing, in accordance with the recommended samples and technical approaches of the Network. The Network is aligned with the calls of the WHO to develop sequencing coverage on a global level to ensure that genomic surveillance is capable of detecting and monitoring virus evolution globally and fueling evidence-based decision-making processes.

Additionally, PAHO/WHO reiterates the recommendations published through COVID-19 Epidemiological Alerts and Updates issued to date and available at: <https://bit.ly/2MMQnGW>

The following are links to a series of guides, scientific reports, and other resources published by PAHO/WHO and WHO.

⁶ All of names according to Pango lineage

<p align="center">Surveillance, rapid response teams, and case investigation</p> <p align="center"></p>	<p align="center">Clinical management</p> <p align="center"></p>
<p>WHO resources, available at: https://bit.ly/30zjmCj</p> <p>PAHO/WHO resources available at: https://bit.ly/36DJi3B</p>	<p>WHO resources, available at: https://bit.ly/3li6wQB</p> <p>PAHO/WHO resources available at: https://bit.ly/3sadTxQ</p>
<p align="center">Laboratory</p> <p align="center"></p>	<p align="center">Infection prevention and control</p> <p align="center"></p>
<p>WHO resources, available at: https://bit.ly/3d3TJ1g</p> <p>PAHO/WHO resources available at: https://bit.ly/3oD2Qen</p>	<p>WHO resources, available at: https://bit.ly/3d2ckuV</p> <p>PAHO/WHO resources available at: https://bit.ly/3nwyOaN</p>
<p align="center">Critical preparedness, readiness, and response actions</p> <p align="center"></p>	<p align="center">Travel, Points of entry and border health</p> <p align="center"></p>
<p>WHO resources, available at: https://bit.ly/3ljWHBT</p> <p>PAHO/WHO resources available at: https://bit.ly/36DJi3B</p>	<p>WHO resources, available at: https://bit.ly/3ivDivW</p> <p>PAHO/WHO resources available at: https://bit.ly/36DJi3B</p>
<p align="center">Schools, workplaces, & institutions</p> <p align="center"></p>	<p align="center">Other resources</p>
<p>WHO resources, available at: https://bit.ly/3d66iJO</p> <p>PAHO/WHO resources available at: https://bit.ly/36DJi3B</p>	<p>WHO resources, available at: https://bit.ly/33zXqRQ</p> <p>PAHO/WHO resources available at: https://bit.ly/36DJi3B</p>

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3. WHO. Diagnostic tests for SARS-CoV-2. Interim Guidance, 11 September 2020. Available at: <https://bit.ly/3iKfF4D>
4. WHO. Weekly epidemiological update. Published on 23 March 2021. Available at: <https://bit.ly/3v6e0Mi>
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9. Report by the **Costa Rica** International Health Regulations (IHR) National Focal Point (NFP), received by PAHO/WHO via email
10. Report by the **Mexico** International Health Regulations (IHR) National Focal Point (NFP), received by PAHO/WHO via email
11. Report by the **Netherlands** International Health Regulations (IHR) National Focal Point (NFP), received by PAHO/WHO via email
12. **United States** Centers for Disease Control and Prevention. SARS-CoV-2 Variant Classifications and Definitions. Available at: <https://bit.ly/2QxgdRj>
13. **Uruguay** Interinstitutional Working Group on SARS-CoV-2 Surveillance. Available in Spanish at: <https://bit.ly/31diymC>
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