



Occurrence of variants of SARS-CoV-2 in the Americas. Preliminary information

11 January 2021

Through this document, the Pan American Health Organization / World Health Organization (PAHO/WHO) communicates to the Member States preliminary information on the detection in the Americas of two variants of interest of SARS-CoV-2 that have been associated with increased transmission in the United Kingdom and in the Republic of South Africa.

PAHO / WHO recommends that Member States continue with the sequencing of samples according to the guidelines of the regional genomic surveillance network and monitor sudden changes in the incidence of COVID-19, which occur in light of public health measures and of social distancing implemented and fulfilled by the population.

Introduction

The appearance of mutations is a natural and expected event within the evolution of the virus. Since the initial genomic characterization of SARS-CoV-2, the virus has been divided into different genetic groups or clades. In fact, some specific mutations define the viral genetic groups (also nominated lineages) that are currently circulating globally (**Table 1** and **Figure 1**). 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.

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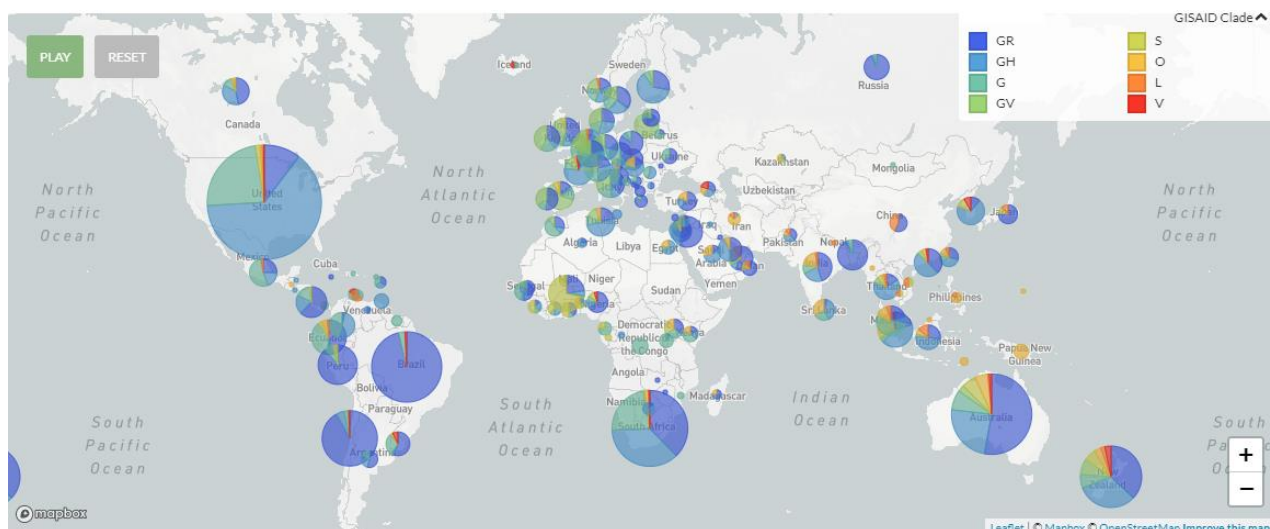
Table 1. Mutations that define the genetic variants of SARS-CoV-2

| Genetic Group | | Reference mutations for the genetic group | Mutations on the S protein |
|---------------|---------|--|---|
| S | A | C8782T, T28144C, NS8-L84S | |
| L | B | C241, C3037, A23403, C8782, G11083, G25563, G26144, T28144, G28882 | |
| V | B.2 | G11083T, G26144T, NSP6-L37F, NS3-G251V | |
| G | B.1 | C241T, C3037T, A23403G, S-D614G | E484Q E484G N501I A475S N439K G496C S494L A475V G446V S477I S477N F490L Q506K N487I F490V N501Y L455F N487D N437I Q493L T478K P499S |
| GH | B.1* | C241T, C3037T, A23403G, G25563T, S-D614G + NS3-Q57H | N501T E484Q K417N G504Y T478I N501Y E484K N439K T478K S494P G446V S477I S477N |
| GR | B.1.1.1 | C241T, C3037T, A23403G, G28882A, S-D614G + N-G204R | N501T Y505H V445I L455F N501Y E484K T478K A475V S494P F490S S477R F490L S477N S477I |
| GV | B.1.177 | C241T, C3037T, A23403G, C22227T, S-D614G + S-A222V | E484Q E484G N501I A475S N439K G496C S494L A475V G446V S477I S477N F490L Q506K N487I F490V N501Y L455F N487D N437I Q493L T478K P499S |

Source: GISAID. Available at: <https://platform.gisaid.org> Accessed on 11 January 2021.

With the information available to date, most of the changes in SARS-CoV-2 have had little or no impact on how it is transmitted or the severity of the disease it causes.

Figure 1. Geographic distribution of the genetic variants of SARS-CoV-2



Source: GISAID. Available at: <https://www.gisaid.org/phylogenetics/global/nextstrain/>

Since the initial identification of SARS-CoV-2 to date, more than 280,000 complete genomic sequences have been shared globally through publicly accessible databases. Having the ability to monitor the data in near real time has a direct impact on the public health response to the COVID-19 pandemic.

The growing understanding of how genomic sequencing data (GSD) can contribute to improving public health justifies and urges expanding sequencing capacity; however, challenges for widespread implementation persist (sufficient trained personnel, availability of equipment, reagents, and bioinformatics infrastructure, assurance of data quality, and capacities for its interpretation and use). Currently, sequencing capacity and data are not uniformly distributed worldwide, with a skewed representation of the SARS-CoV-2 GSD from 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.

Genomic characterization of SARS-CoV-2

Genetic variants of SARS-CoV-2 in the Americas

The Region of the Americas has contributed to the generation of genomic sequencing data through the Regional Network for Genomic Surveillance of COVID-19²³, which is open to all countries in the region, through their National Public Health Laboratories, or equivalent public institutions. This Network includes two Regional Sequencing Laboratories (Fiocruz-Brazil and the Institute of Public Health-Chile), which provide external sequencing for participating laboratories in the network that do not have the capacity to sequence.⁴

Until 11 January 2021, countries and territories in the Americas have published 79,144 SARS-CoV-2 genomes on the GISAID platform, collected between February and December 2020. The countries and territories that have contributed are: Antigua and Barbuda, Argentina, Aruba, Belize, Bermuda, Brazil, Canada, Chile, Colombia, Costa Rica, Cuba, Curacao, the Dominican Republic, Ecuador, El Salvador, Guadeloupe, Guatemala, Jamaica, Mexico, Panama, Peru, Saint Barthelemy, Sint Eustatius, Saint Kitts and Nevis, Saint Martin, Saint Vincent and Grenadines, Suriname, Trinidad and Tobago, Uruguay, United States of America, and Venezuela.

Recent reports of different variants of SARS-CoV-2 have reawakened interest and concern about the impact of viral changes. In recent months, two different variants of SARS-CoV-2 have been reported to WHO as unusual public health events: VOC 202012/01, lineage B.1.1.7 in the United Kingdom and Northern Ireland and 501Y.V2, lineage B.1.35, in the Republic of South Africa.

Findings and preliminary data, as much epidemiological, modeling, phylogenetic and clinical, suggest that SARS-CoV-2 VOC 202012/01 has higher transmissibility. However, preliminary analysis currently available suggest that there are no changes in the severity of the disease (measured by the duration of hospitalization and the 28-day case fatality rate), or the occurrence of reinfection among cases positive for this variant compared to cases by other

¹ WHO. SARS-CoV-2 genomic sequencing for public health purposes. Provisional guide, 8 January 2021. Available at: <https://bit.ly/38ulAr0>

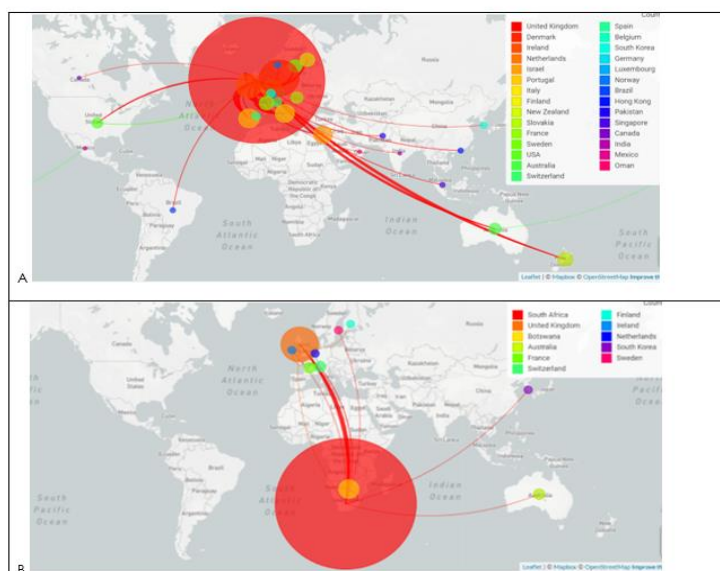
² Regional Network for Genomic Surveillance of COVID-19. Available at: <https://bit.ly/3bu0qez>

³ According to Resolution CD58.R9 - The COVID-19 pandemic in the Region of the Americas, "The 58th Directing Council resolves to request the Director to: maintain the regional network for the surveillance of influenza and other respiratory viruses, and expand it by creating a regional genomic surveillance network.

⁴ PAHO/WHO. Technical Note: Genomic characterization of SARS-CoV-2 and circulating variants in the Region of the Americas. Available at: <https://bit.ly/3i4klIf>

SARS-CoV-2 lineages circulating in the United Kingdom. To date, outside the UK, 40 countries in five of the six WHO regions have reported VOC 202012/01 cases, while outside of South Africa, six countries, in two of the six WHO regions, have reported cases of the 501Y.V2 variant.⁵ (**Figure 2**)

Figure 2. Geographic distribution of the new genetic variants of SARS-CoV-2: VOC 202012/01 (A) and 501Y.V2 (B). 11 January 2021.



Source: GISAID. Available at: <https://platform.gisaid.org> Accessed on 11 January 2021

Countries continue to conduct further epidemiological and virological research to further assess the transmissibility, severity, risk of reinfection, and antibody response to these new variants, as well as the potential impact on public health measures, including diagnosis, treatment, and vaccines.

Regarding the situation in the **Americas**, until 11 January 2021, 8 countries have reported the detection of the VOC 202012/01 variant (**Table 2**), one country reported the detection of the 501Y.V2 variant, and one country reported the detection of mutations of potential interest to public health (**Table 2**).

⁵ WHO. COVID-19 weekly epidemiological update. Published on 5 January 2021. Available at: <https://bit.ly/3oGtAeg>

Table 2. Detection of the SARS-CoV-2 VOC 202012/01 variant, the 501Y.V2 variant, and other mutations of interest to public health in the Region of the Americas, as of 11 January 2021.

| Country | Variant SARS-CoV-2 VOC 202012/01 | Variant 501Y.V2 | Other mutations of potential interest to public health |
|--------------------------|----------------------------------|-----------------|--|
| Brazil | Yes | Yes | Si (Mutaciones del SARS-CoV-2 (E484K)) |
| Canada | Yes | Yes | No |
| Chile | Yes | No | No |
| Ecuador | Yes | No | No |
| Jamaica | Yes | No | No |
| Mexico | Yes | No | No |
| Peru | Yes | No | No |
| United States of America | Yes | No | No |

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.

Conclusions and preliminary guidance for national authorities

Preliminary data and information suggest that both variants of interest (202012/01 and 501Y.V2) have been identified in the Americas. However, the frequency of detection of these variants is still very limited to date. Nonetheless, there is a possibility that the detection of these variants will gradually increase in the coming weeks and months.

In addition to global circulation patterns, detection of SARS-CoV-2 variants in a specific country and location also depends on each country's capacity to conduct genomic surveillance.

PAHO / WHO has been strengthening the capacity of each country to carry out genomic surveillance since March 2020 within the framework of the Regional Network for Genomic Surveillance of COVID-19 and urges Member States to participate in this Network and carry out sequencing, in accordance with the recommended samples and the technical approaches of this Network.

In addition to recommending the timely publication of the sequences on the GISAID platform, PAHO / WHO requests that the countries immediately notify the first detection of the VOC 202012/01 and 501Y.V2 variants at the first subnational level based on minimum data from according to the WHO document, available at: <https://bit.ly/3sd4Psb>

Moreover, it is recommended to constantly monitor sudden and significant changes in incidence (for example, 50% in a period of 2–4 weeks) that occur despite implemented public health and social distancing measures, complied by the population. The calculation and

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monitoring of the incidence based on the date of onset of symptoms (compared to the date of notification) should contribute to improve the timing of monitoring.

PAHO/WHO recommends that in the event of symptoms suggesting acute respiratory illness during or after travel, travelers are advised to seek medical attention and share their travel history with their healthcare provider. Health authorities should work with the transport and tourism sectors to provide travelers with information to reduce the risk of infection.

In line with the advice provided by the Emergency Committee on COVID-19 at its most recent meeting, WHO recommends that States Parties should regularly re-consider measures applied to international travel in compliance with Article 43 of the International Health Regulations (2005) and continue to provide information and rationale to WHO on measures that significantly interfere with international traffic. Countries should also ensure that measures affecting international traffic are risk-based, evidence-based, coherent, proportionate and time limited.

In all circumstances, essential travel (e.g., emergency responders; providers of public health technical support; critical personnel in transport and security sector such as seafarers; repatriations; and cargo transport for essential supplies such as food, medicines and fuel) identified by countries should always be prioritized and facilitated.

Additionally, PAHO/WHO maintains 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.

| | |
|---|---|
| Surveillance, rapid response teams, and case investigation  | Clinical management  |
| <p>WHO resources, available at: https://bit.ly/30zmCj</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> |
| Laboratory  | Infection prevention and control  |
| <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/3nwyQaN</p> |
| Critical preparedness, readiness, and response actions  | Travel, Points of entry and border health  |
| <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> |
| Schools, workplaces, & institutions  | Other resources |
| <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/33zXgRQ</p> <p>PAHO/WHO resources available at: https://bit.ly/36DJi3B</p> |

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