

Epidemiological update: Variants of SARS-CoV-2 in the Americas

26 January 2021

Highlights

- It has recently been documented that people infected with the **VOC 202012/01 variant** have a higher risk of death than people infected with other variants.²
- Preliminary studies suggest that the **501Y.V2 variant** is associated with a higher viral load, which could suggest a potential for greater transmissibility.⁴
- An increase in the proportion of cases associated to the P.1 variant lineage B.1.1.28 has been documented in Manaus (Amazonas State, Brazil). This proportion represented 52.2% (n = 35/67) of the genotyped samples of SARS-CoV-2 in December 2020, and increased to 85.4% (n = 41/48) in January 2021.⁸

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 called 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.

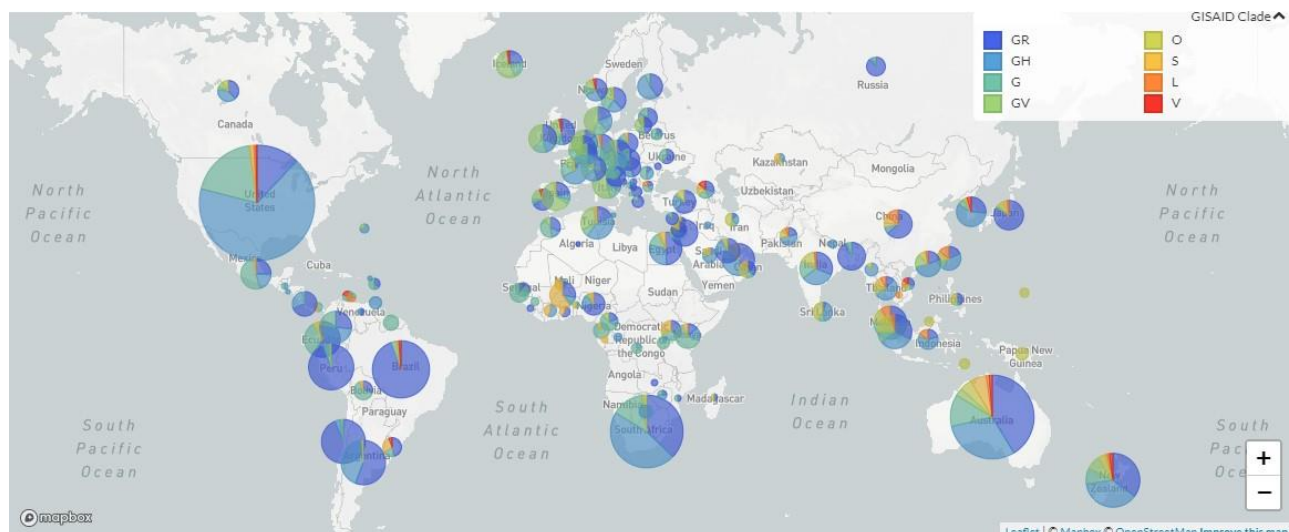
Suggested citation: Pan American Health Organization / World Health Organization. Occurrence of variants of SARS-CoV-2 in the Americas. 26 January 2021, Washington, D.C.: PAHO/WHO; 2021

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	E484K K417N N501Y S477N
L	B	C241, C3037, A23403, C8782, G11083, G25563, G26144, T28144, G28882	E484K K417N N501Y S477N
V	B.2	G11083T, G26144T, NSP6-L37F, NS3-G251V	E484K K417N N501Y S477N
G	B.1	C241T, C3037T, A23403G, S-D614G	N501S E484Q T478I S477G N439K A475V F456L F490S S477R S477I S477N S494A N501Y V445I E484K T478K S494P
GH	B.1*	C241T, C3037T, A23403G, G25563T, S-D614G + NS3-Q57H	N501T K417N Y453F N501Y E484K E484D N439K S494P S477R G446V S477N
GR	B.1.1.1	C241T, C3037T, A23403G, G28882A, S-D614G + N-G204R	Q493R F490Y Y453F S477G A475V F490S G446V S477R S477I S477N G502V K417T N501Y G446S G447V E484K K458N T478K S494P
GV	B.1.177	C241T, C3037T, A23403G, C22227T, S-D614G + S-A222V	N501S E484Q T478I S477G N439K A475V F456L F490S S477R S477I S477N S494A N501Y V445I E484K T478K S494P

Source: GISAID. Available at: <https://platform.gisaid.org>. Updated January 22, 2021. Changes in glycoprotein S (spike) for 14,399 new complete genomes). Accessed 25 January 2021.

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



Source: GISAID. Available at: <https://bit.ly/3qA9nXI>. Accessed on 25 January 2021.

Since the initial identification of SARS-CoV-2 to date, more than 414,575 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.

There is a growing understanding of how genomic sequencing data (GSD) can contribute to improving public health actions, therefore the importance of expanding sequencing capacity in the Region. Currently, sequencing capacity and data are not uniformly distributed globally, 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.

The following is a summary of the SARS-CoV-2 variants that have or could have an impact on public health.

Genomic characterization of SARS-CoV-2

VOC 202012/01 variant, lineage B.1.1.7

On 14 December 2020, the United Kingdom authorities notified WHO of a variant named by the U.K. as SARS-CoV-2 VOC 202012/01. This variant contains 23 nucleotide substitutions and is not phylogenetically related to the SARS-CoV-2 virus circulating in the U.K. at the time it was detected. It is unclear how and where it originated.

Recent findings and preliminary data, published by the U.K. government indicate:

- The variant VOC 202012/01, B.1.1.7 appears to have substantially increased transmissibility compared to other variants and has grown quickly to become the dominant variant in much of the U.K.
- According to the initial assessment by Public Health England (PHE) on the severity of the disease through a matched case-control study reported no significant difference in the risk of hospitalization or death in people infected with confirmed B.1.1.7 infection versus infection with other variants.
- Based on different analysis of deaths in persons who were positive for variant B.1.1.7 versus those infected with other variants, there is a real possibility that the first group of people (those infected with variant B. 1.1.7), have an increased risk of death compared to infection with non-VOC viruses.²

As of 25 January 2021, 62 countries and territories outside of the U.K. in all six WHO Regions have reported either imported cases or community transmission of VOC 202012/01 ; this represents 2 additional countries and territories since the publication of the 20 January 2021 Epidemiological Update on Occurrence of variants of SARS-CoV-2 in the Americas by PAHO."³

501.V2, variant lineage B.1.351

On 18 December 2020, South African national authorities announced the detection of a new variant of SARS-CoV-2 that is spreading rapidly in three South African provinces. South Africa has named this variant 501Y.V2, due to a N501Y mutation. While the VOC 202012/01 variant also

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>

² United Kingdom Government. NERVTAG paper on COVID-19 variant of concern B.1.1.7. Published 22 January 2021. Available at: <https://bit.ly/39ft5hd>

³ PAHO/WHO. Occurrence of variants of SARS-CoV-2 in the Americas. 20 January 2021, Washington, D.C.: PAHO/WHO; 2021. Available at: <http://bit.ly/2KCKUly>

has the N501Y mutation, phylogenetic analysis has shown that the 501Y.V2 detected in South Africa is a different variant.

Genomic data highlighted that the 501.V2 variant rapidly displaced other lineages circulating in South Africa. Preliminary studies suggest that this variant is associated with a higher viral load, which could suggest a potential for greater transmissibility. However, further investigation of this and other factors that influence transmissibility is necessary⁴.

Also, at this stage of ongoing research, there is no clear evidence that the new variant is associated with more severe disease or worse outcome. More research is needed to understand the impact on transmission, clinical severity of infection, laboratory diagnostics, therapeutics, vaccines, or public health preventive measures.⁵ Although this new variant does not appear to cause more serious disease, the rapid increase in the number of cases has put health systems under pressure⁶.

As of 25 January 2021, 30 countries outside of South Africa in five of the six WHO Regions have reported cases of 501Y.V2; this represents 7 additional countries and territories since the publication of the 20 January 2021 Epidemiological Update on Occurrence of variants of SARS-CoV-2 in the Americas by PAHO.³ However, no increase in circulation or sustained increase in the spread of this variant has been reported in these countries or territories.

Further epidemiological and virological research is underway 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.

⁴ WHO. SARS-CoV-2 Variants. Available at: <https://bit.ly/39hRvXT>

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

⁶ WHO. Weekly epidemiological update. Published on 12 January 2021. Available at: <https://bit.ly/2YeXlas>

Other variants of potential public health interest

In addition to the variants already mentioned, Brazil, Japan, and the United States of America, have reported the detection of variants. The extent and public health significance of these new variants require further epidemiological and laboratory investigation.⁵

Lineage B.1.1.28

The lineage was described for the first time in Brazil on 5 March 2020 by the Adolfo Lutz Institute in a 22-year-old patient. This lineage has been circulating in the U.K (3.0%, in Australia (1.0%), in the United States (1.0%), and in Portugal (1.0%).⁷

Variant P.1, lineage B.1.1.28

On 9 January 2021, **Japan** notified WHO about a new variant of SARS-CoV-2, B.1.1.28 (initially reported as B.1.1.248), detected in four travelers from Brazil. This variant is not closely related to the SARS-CoV-2 VOC 202012/01 variant or to the 501Y.V2 variant, and it was identified in Manaus, Amazonas State, Brazil in December 2020⁸ (**Figures 2, 3**)

This variant has 12 mutations to the spike protein, including three mutations of concern in common with 501Y.V2, i.e.: K417N/T, E484K, and N501Y, which may impact transmissibility and host immune response.⁶

According to a group of researchers from Brazil, a recent increase in the proportion of P.1 cases has been observed in Manaus, Amazonas. P.1 was not detected in Manaus between March and November 2020, however, 52.2% (n = 35/67) of the genotyped samples of SARS-CoV-2 from December were caused by P.1 and in January 2021, the proportion increased to 85.4% (n = 41/48). They also detected an increase in the proportion of cases of the P.2 variant in December 2020 to 25.4% (n = 17/67), but a decrease to 6% in January 2021. The proportion of other lineages decreased from 96.3% between March and November 2020 to 8.3% in January 2021.

The new analysis suggests that the most recent cases in Manaus are being caused by local transmission of P.1, although P.2⁹ and other lineages may still be circulating. These results should be considered preliminary at this stage. Larger representative datasets are required to investigate in more detail changes in the frequency of this lineage in Manaus and elsewhere.¹⁰

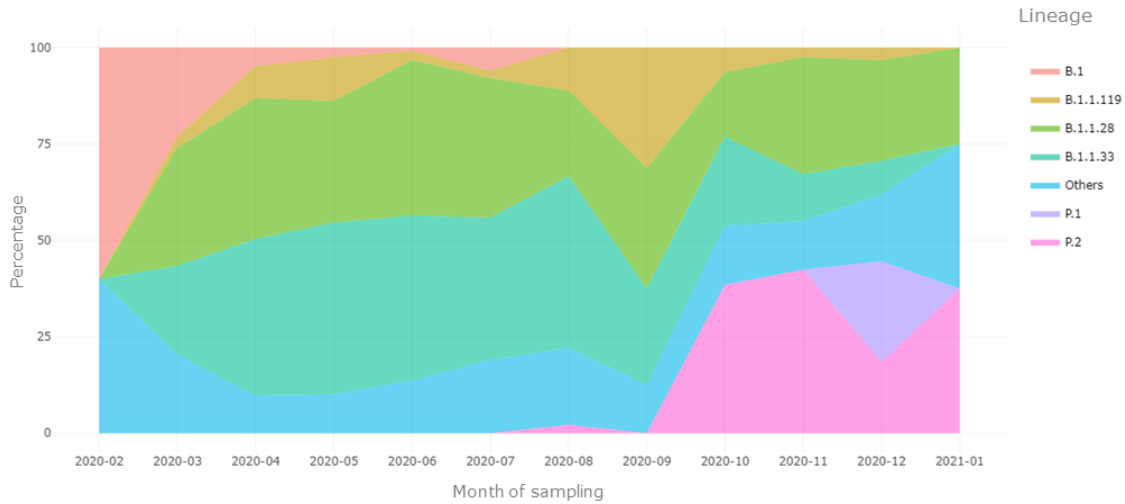
⁷ GISAID. Available at: <https://www.gisaid.org/>

⁸ Faria N, Morales I, Candido D. Genomic characterization of an emergent SARS-CoV-2 lineage in Manaus: preliminary findings. Disponible en: <https://bit.ly/3a4n22X>

⁹ Voloch C, Da Silva F Jr R, de Almeida L, et al. Genomic characterization of a novel SARS-CoV-2 lineage from Rio de Janeiro, Brazil. Available at: <https://bit.ly/2KQEn6T>

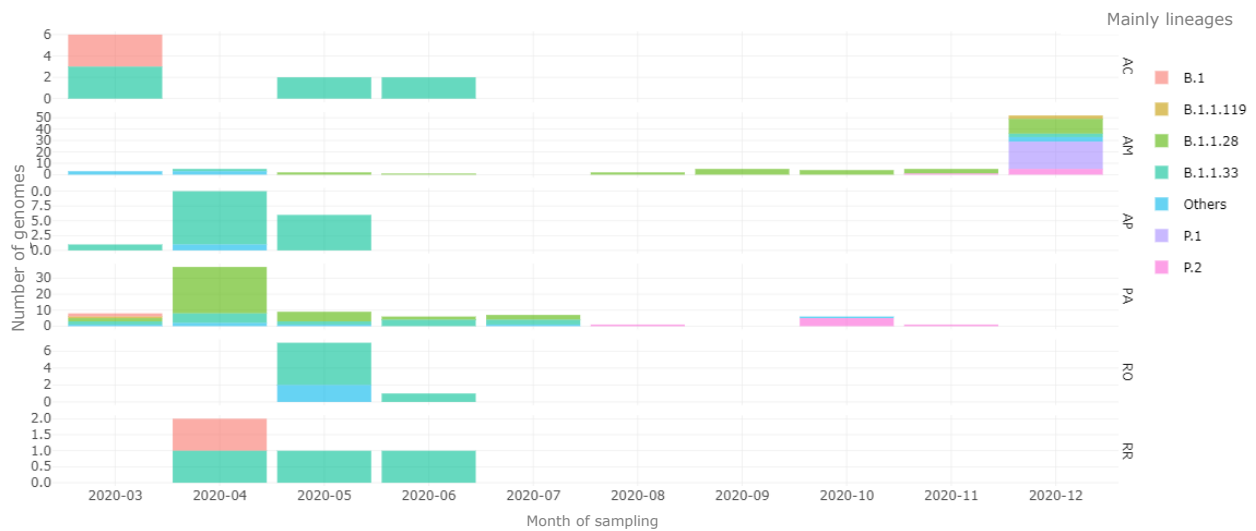
¹⁰ Faria Nuno, Sabino Ester. Increasing frequency of the P.1 lineage in Manaus. Available at: <https://bit.ly/3ccOaiO>

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



Source: Fiocruz genomic network. Available at: <https://bit.ly/2YmCSjH> Accessed on 26 January 2021.

Figure 3. Distribution of the main SARS-CoV-2 lineages by sampling month and States in the North Region in Brazil. March 2020 to January 2021.



Note:

States, North Region, Brazil

AC = Acre

AM = Amazonas

AP = Amapá

PA = Pará

RO = Rondônia

RR = Roraima

Source: Fiocruz genomic network. Available at: <https://bit.ly/2YmCSjH> Accessed on 26 January 2021.

As of 25 January 2021, 7 countries in three all the six WHO Regions have reported cases of P.1 lineage B.1.1.28 variant.

Genetic variants of SARS-CoV-2 in the Americas

In the Region of the Americas the Regional Network for Genomic Surveillance of COVID-19^{11,12} has contributed to the generation of genomic sequencing data. This network is open to all countries in the region, through the 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.¹³

As of 25 January 2021, 32 countries and territories of the Americas have published 94,183 SARS-CoV-2 genomes on the GISAID platform, collected between February 2020 and January 2021. The countries and territories that have contributed are Antigua and Barbuda, Argentina, Aruba, Belize, Bermuda, Bolivia, Brazil, Canada, Chile, Colombia, Costa Rica, Cuba, Curaçao, the Dominican Republic, Ecuador, El Salvador, Guadeloupe, Guatemala, Jamaica, Mexico, Panama, Peru, Saint Barthelemy, Saint Eustatius, Saint Kitts and Nevis, Saint Martin, Saint Vincent and the Grenadines, Suriname, Trinidad and Tobago, United States of America, Uruguay, and Venezuela.

As of 25 January 2021, 14 countries (4 additional countries since the 20 January 2021 publication³) have reported the detection of the VOC 202012/01 variant, 501Y.V2, and P.1 variant. Additionally, two countries have reported the detection of mutations of potential interest to public health (**Table 2**).

Table 2. Detection of the SARS-CoV-2 VOC 202012/01 variant, the 501Y.V2 variant, the P.1 variant, and other mutations of interest to public health in the Region of the Americas, as of 25 January 2021.

¹¹ Regional Network for Genomic Surveillance of COVID-19. Available at: <https://bit.ly/3bu0qez>

¹² 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."

¹³ PAHO/WHO. Technical Note: Genomic characterization of SARS-CoV-2 and circulating variants in the Region of the Americas. Available at: <https://bit.ly/3i4klf>

Country	VOC 202012/01	501Y.V2	P.1	Other mutations of potential interest to public health
Argentina	Yes	No	No	No
Brazil	Yes	No	Yes	Yes (E484K, K417N)
Canada	Yes	Yes	No	No
Chile	Yes	No	No	No
Cuba	No	Yes	No	No
Dominican Republic	Yes	No	No	No
Ecuador	Yes	No	No	No
Jamaica	Yes	No	No	No
Mexico	Yes	No	No	No
Panama	No	Yes	No	No
Peru	Yes	No	No	No
Saint Lucia	Yes	No	No	No
Trinidad and Tobago	Yes	No	No	No
United States of America	Yes	No	Yes	Yes (L452R)

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 guidance for national authorities

National and local authorities should continue to strengthen existing disease control activities, including monitoring COVID-19 closely through ongoing epidemiological surveillance and strategic testing; conducting outbreak investigation and contact tracing; and where appropriate, adjusting public health and social measures to reduce transmission of SARS-CoV-2.

The data and information available indicate that both variants of concern (VOC 202012/01 and 501Y.V2) have been identified in the Americas. The frequency of detection of these variants is still very limited to date. Nonetheless, it is expected 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 supported 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 variant, 501Y.V2 variant, P.1 variant and all other variants that may have a public health impact, at the first admin-level based on minimum data in accordance with the WHO document, available at: <https://bit.ly/3sd4Psb>

Further, 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 with compliance by the population. Use of the date of onset of symptoms for the calculation and monitoring of the incidence (compared to the date of report) should contribute to improving the monitoring timeliness.

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 meeting¹⁴, 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 are encouraged to implement coordinated, time-limited, risk-based, and evidence-based approaches for health measures in relation to international travel.

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

¹⁴ WHO. Statement on the sixth meeting of the International Health Regulations (2005) Emergency Committee regarding the coronavirus disease (COVID-19) pandemic. 15 January 2021. Available at: <https://bit.ly/39iAyQY>

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

<p>Surveillance, rapid response teams, and case investigation</p> 	<p>Clinical management</p> 
<p>WHO resources, available at: https://bit.ly/30zjmCi</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>Laboratory</p> 	<p>Infection prevention and control</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/3nwyQaN</p>
<p>Critical preparedness, readiness, and response actions</p> 	<p>Travel, Points of entry and border health</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>Schools, workplaces, & institutions</p> 	<p>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/33zXgRQ</p> <p>PAHO/WHO resources available at: https://bit.ly/36Dji3B</p>

References

1. WHO. SARS-CoV-2 genomic sequencing for public health goals. Interim guidance, 8 January 2021. Available at: <https://bit.ly/38ulAr0>
2. WHO. SARS-CoV-2 Genomic Sequencing of SARS-CoV-2: A Guide to Implementation for Maximum Impact on Public Health. 8 January 2021. Available at: <https://bit.ly/3sd4Psb>
3. WHO. Diagnostic tests for SARS-CoV-2. Interim Guidance, 11 September 2020. Available at: <https://bit.ly/3iKfF4D>
4. PAHO/WHO. COVID-19 Genomic Surveillance Regional Network. Available at: <https://bit.ly/38WD8fs>
5. Ministry of Health of **Cuba**. Available in Spanish at: <https://bit.ly/3aEajwq>
6. Ministry of Health of **Panama**. Available in Spanish at: <https://bit.ly/3aPTyfj>
7. Ministry of Health and Wellness of **Saint Lucia**. Available at: <https://bit.ly/39fDEpa>
8. Report by the **Trinidad and Tobago** International Health Regulations (IHR) National Focal Point (NFP), received by PAHO/WHO via email
9. **United States** Centers for Disease Control and Prevention. U.S. COVID-19 cases Caused by Variants. Available at: <https://bit.ly/2XvvaCC>
10. Minnesota (**United States**) Department of Health. Available at: <https://bit.ly/3pmXVyD>
11. WHO. Considerations for implementing a risk-based approach to international travel in the context of COVID-19: interim guidance, 16 December 2020. Available at: <https://bit.ly/3aBbmUv>
12. WHO. Risk assessment tool to inform mitigation measures for international travel in the context of COVID-19. Available at: <https://bit.ly/3iuxYKR>
13. WHO. COVID-19 diagnostic testing in the context of international travel. Scientific brief. 16 December 2021. Available at: <https://bit.ly/39l6dAp>