

## 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.

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.

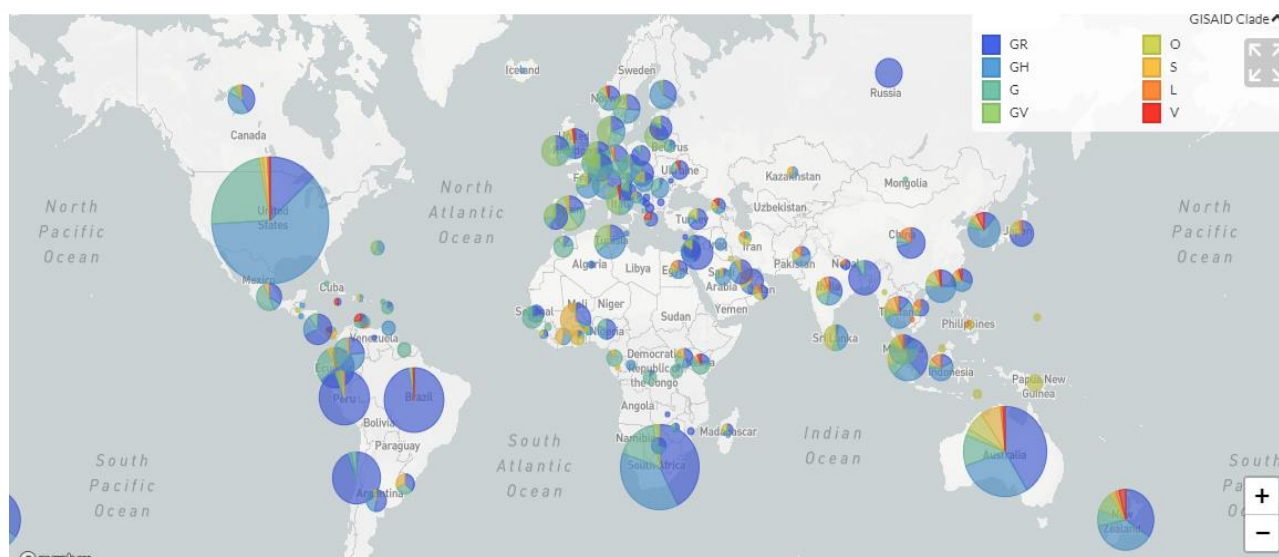
**Table 1.** Mutations that define the genetic variants of SARS-CoV-2

Genetic Group		Reference mutations for the genetic group	Mutations on the S protein
S	A	C8782T, T28144C, NS8-L84S	N439K N501T V503F S494P N501Y S477N
L	B	C241, C3037, A23403, C8782, G11083, G25563, G26144, T28144, G28882	N439K N501T V503F S494P N501Y S477N
V	B.2	G11083T, G26144T, NSP6-L37F, NS3-G251V	N439K N501T V503F S494P N501Y S477N
G	B.1	C241T, C3037T, A23403G, S-D614G	N501S N501H V503F T478I F490Y Y453F V445A A475S N439K A475V F490S G446V S477I S477N G476S T478R N501Y E484K N437S S477T S494P
GH	B.1*	C241T, C3037T, A23403G, G25563T, S-D614G + NS3-Q57H	N501T E484Q K417N V503F N501I N501Y E484A E484K N439K T478K G485R S494P A475V G446V Q493K S477N
GR	B.1.1.1	C241T, C3037T, A23403G, G28882A, S-D614G + N-G204R	K417N V503F Y453F S494L A475V G446V F490S S477R S477I F490L S477N G476S N501T V445I N501Y G447V E484K K458N T478K S494P
GV	B.1.177	C241T, C3037T, A23403G, C22227T, S-D614G + S-A222V	N501S N501H V503F T478I F490Y Y453F V445A A475S N439K A475V F490S G446V S477I S477N G476S T478R N501Y E484K N437S S477T S494P

**Source:** GISAID. Available at: <https://platform.gisaid.org>. Accessed on 19 January 2021.

**Suggested citation:** Pan American Health Organization / World Health Organization. Occurrence of variants of SARS-CoV-2 in the Americas. 20 January 2021, Washington, D.C.: PAHO/WHO; 2021

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



**Source:** GISAID. Available at: <https://bit.ly/3qA9nXI>. Accessed on 18 January 2021.

Since the initial identification of SARS-CoV-2 to date, more than 387,500 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.

The growing understanding of how genomic sequencing data (GSD) can contribute to improving public health, supports and encourages expanding sequencing capacity; however, challenges for widespread implementation persist (e.g., having sufficient trained personnel, availability of equipment, reagents and bioinformatics infrastructure, data quality assurance, and capacities for its interpretation and use). Currently, sequencing capacity and data are not uniformly distributed globally, with a skewed representation of the SARS-CoV-2 GSD from high-income countries.<sup>1</sup> 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

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 (U.K.) and Northern Ireland and 501Y.V2, lineage B.1.351, in South Africa.

### VOC 202012/01 variant, B.1.1.7 lineage

On 14 December 2020, the U.K. 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 United Kingdom at the time it was detected. It is unclear how and where it originated.

<sup>1</sup> 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>

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 SARS-CoV-2 lineages circulating in the U.K. Although no higher severity is observed among cases, the increase in transmissibility is of concern; the increase in cases in a limited time-period is associated with a significant public health impact.<sup>2</sup>

As of 19 January 2021, 60 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<sup>3</sup>(**Figure 2**); this represents 20 additional countries and territories since the publication of the "Occurrence of variants of SARS-CoV-2 in the Americas, Preliminary Information as of 11 January 2021."<sup>4</sup>

### **Variant 501.V2, 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 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 necessary.

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.<sup>5</sup> 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 pressure.<sup>6</sup>

As of 19 January 2021, 23 countries outside of South Africa in four of the six WHO Regions have reported cases of 501Y.V2 (**Figure 2**); this represents 17 additional countries and territories since the publication of the "Occurrence of variants of SARS-CoV-2 in the Americas, Preliminary Information as of 11 January 2021."<sup>4</sup> However, no increase in circulation or sustained increase in the spread of this variant has been reported in these countries or territories.

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<sup>2</sup> WHO. SARS-CoV-2 Variants. Disease Outbreak News. 31 December 2020. Available at: <https://bit.ly/2Nifli6>

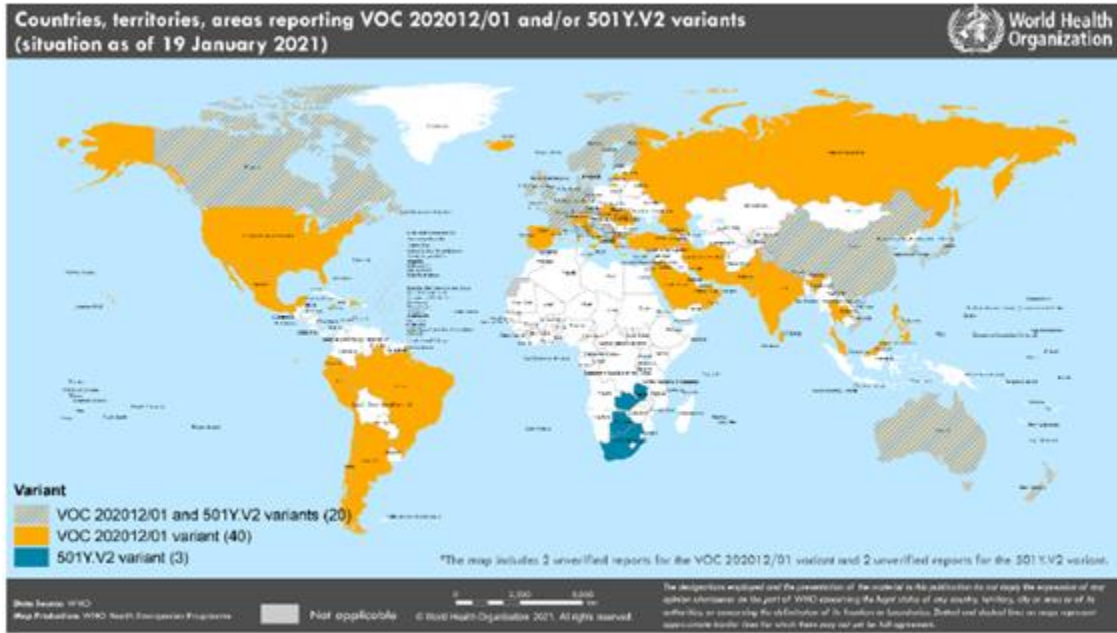
<sup>3</sup> WHO. Weekly epidemiological update. Published on 19 January 2021. Available at: <https://bit.ly/2LE5Kl5>

<sup>4</sup> PAHO/WHO. Occurrence of variants of SARS-CoV-2 in the Americas. Preliminary Information as of 11 January 2021, Washington, D.C.: PAHO/WHO; 2021. Available at: <https://bit.ly/2KrYFmO>

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

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

**Figure 2.** Geographic distribution of SARS-CoV-2 genetic variants: VOC 202012/01 and 501Y.V2. 19 January 2021.



**Source:** WHO. Weekly epidemiological update. Published on 19 January 2021. Available at: <https://bit.ly/2LE5K15>

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.

**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<sup>5</sup>

**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%).<sup>7</sup>

**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.

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

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.<sup>5</sup>

On 12 January 2021, researchers in **Brazil**<sup>8</sup> reported on the detection of a variant of the B.1.1.28 lineage that, like the P.1 variant, has the E484K mutation, which has probably evolved independently of the variant detected among the travelers reported by Japan. The detection was carried out in the state of Amazonas.

Additionally, other researchers from Brazil reported 148 sequences of the complete SARS-CoV-2 genome from the state of Amazonas, in which 69 (47%) B.1.1.28 sequences were identified among the samples from different municipalities between 13 April and 13 November 2020, making this variant the most prevalent variant in that Brazilian state.<sup>9,10,11</sup>

### **Variant L452R**

In the **United States**, the California Department of Public Health (CDPH), in coordination with Santa Clara County and the University of California, San Francisco (UCSF), announced on 17 January 2021 that the SARS-CoV-2 variant, L452R, is detected more frequently, by genomic sequencing of the virus in several counties of the state of California. Research on this variant and its impact on public health is ongoing<sup>12</sup>.

### **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-19<sup>13,14</sup> which 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.<sup>15</sup>

As of 19 January 2021, countries and territories of the Americas have published 87,851 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

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<sup>8</sup>Faria N, Morales I, Candido D, et al. Genomic characterization of an emergent SARS-CoV-2 lineage in Manaus: preliminary findings. Available at: <https://bit.ly/3ax9aEU>

<sup>9</sup> Ministry of Health of Brazil. Oswaldo Cruz Foundation Genomic Network (Fiocruz). Technical Note 2021/01. Available at: <https://bit.ly/3sBdYLe>

<sup>10</sup> Naveca F, Nascimento V, Souza V. et al. Phylogenetic relationship of SARS-CoV-2 sequences from Amazonas with emerging Brazilian variants harboring mutations E484K and N501Y in the Spike protein. Available at: <https://bit.ly/3sC2Tji>

<sup>11</sup> Information available at: <https://bit.ly/38VU3yH>

<sup>12</sup> California Department of Public Health. Press release. COVID-19 Variant First Found in Other Countries and States Now Seen More Frequently in California. Available at: <https://bit.ly/3bu0qez>

<sup>13</sup> Regional Network for Genomic Surveillance of COVID-19. Available at: <https://bit.ly/3bu0qez>

<sup>14</sup> 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."

<sup>15</sup> 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>



and the Grenadines, Suriname, Trinidad and Tobago, United States of America, Uruguay, and Venezuela.

Regarding the situation in the Region of the Americas, as of 18 January 2021, 10 countries (2 additional countries since the 11 January 2021 publication<sup>3</sup>) have reported the detection of the VOC 202012/01 variant (**Table 2**), one country reported the detection of the 501Y.V2 variant, and two countries 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, and other mutations of interest to public health in the Region of the Americas, as of 18 January 2021.

Country	Variant SARS-CoV-2 VOC 202012/01	Variant 501Y.V2	Other mutations of potential interest to public health
Argentina	Yes	No	No
Brazil	Yes	No	Yes (E484K)
Canada	Yes	Yes	No
Chile	Yes	No	No
Dominican Republic	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	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.

As of 19 January 2021, the **United States** is the country in the Region of the Americas that has reported the highest number of cases in which the variant SARS-CoV-2 VOC 202012/01 has been detected (122 cases<sup>16</sup>), distributed among 20 states;<sup>17</sup> California and Florida States concentrate 70% of the reported cases.

As of 15 January 2021, Canada<sup>18</sup> and Chile<sup>19</sup> have reported 23 cases and 20 cases of the variant SARS-CoV-2 VOC 202012/01, respectively.

Additionally, as of 15 January 2021 in the Region of the Americas, only in Canada has the 501.V2 variant, lineage B.1.35, been detected (2 cases).

<sup>16</sup> The number of cases is based on a sampling of SARS-CoV-2-positive specimens and do not represent the total number of B.1.1.7 lineage cases that may be circulating in the United States and may not match numbers reported by states, territories, tribes, and local officials. Centers for Disease Control and Prevention. Available at: <https://bit.ly/39K33pV>

<sup>17</sup> Centers for Disease Control and Prevention. Available at: <https://bit.ly/39K33pV>

<sup>18</sup> Public Health Agency of Canada. Statement from the Chief Public Health Officer of Canada on January 16, 2021 Available at: <https://bit.ly/39K4F2X>

<sup>19</sup> Ministry of Health of Chile. Report of the circulation of SARS-CoV-2 VOC 202012/01 in Chile. Available at: <https://bit.ly/2KuWS0s>

## Conclusions and guidance for national authorities

National and local authorities should continue to strengthen existing disease control activities, including monitoring their epidemics 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 interest (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, 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 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 and 501Y.V2 variants 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 meeting<sup>20</sup>, 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.

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<sup>20</sup> 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://www.who.int/news/item/15-01-2021-statement-on-the-sixth-meeting-of-the-international-health-regulations-\(2005\)-emergency-committee-regarding-the-coronavirus-disease-\(covid-19\)-pandemic](https://www.who.int/news/item/15-01-2021-statement-on-the-sixth-meeting-of-the-international-health-regulations-(2005)-emergency-committee-regarding-the-coronavirus-disease-(covid-19)-pandemic)

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>

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

<p><b>Surveillance, rapid response teams, and case investigation</b></p> 	<p><b>Clinical management</b></p> 
<p>WHO resources, available at: <a href="https://bit.ly/30zjmCj">https://bit.ly/30zjmCj</a></p> <p>PAHO/WHO resources available at: <a href="https://bit.ly/36Dji3B">https://bit.ly/36Dji3B</a></p>	<p>WHO resources, available at: <a href="https://bit.ly/3li6wQB">https://bit.ly/3li6wQB</a></p> <p>PAHO/WHO resources available at: <a href="https://bit.ly/3sadTxQ">https://bit.ly/3sadTxQ</a></p>
<p><b>Laboratory</b></p> 	<p><b>Infection prevention and control</b></p> 
<p>WHO resources, available at: <a href="https://bit.ly/3d3TJ1g">https://bit.ly/3d3TJ1g</a></p> <p>PAHO/WHO resources available at: <a href="https://bit.ly/3oD2Qen">https://bit.ly/3oD2Qen</a></p>	<p>WHO resources, available at: <a href="https://bit.ly/3d2ckuV">https://bit.ly/3d2ckuV</a></p> <p>PAHO/WHO resources available at: <a href="https://bit.ly/3nwyOaN">https://bit.ly/3nwyOaN</a></p>
<p><b>Critical preparedness, readiness, and response actions</b></p> 	<p><b>Travel, Points of entry and border health</b></p> 
<p>WHO resources, available at: <a href="https://bit.ly/3ljWHBT">https://bit.ly/3ljWHBT</a></p> <p>PAHO/WHO resources available at: <a href="https://bit.ly/36Dji3B">https://bit.ly/36Dji3B</a></p>	<p>WHO resources, available at: <a href="https://bit.ly/3ivDivW">https://bit.ly/3ivDivW</a></p> <p>PAHO/WHO resources available at: <a href="https://bit.ly/36Dji3B">https://bit.ly/36Dji3B</a></p>
<p><b>Schools, workplaces, &amp; institutions</b></p> 	<p><b>Other resources</b></p>
<p>WHO resources, available at: <a href="https://bit.ly/3d66iJO">https://bit.ly/3d66iJO</a></p> <p>PAHO/WHO resources available at: <a href="https://bit.ly/36Dji3B">https://bit.ly/36Dji3B</a></p>	<p>WHO resources, available at: <a href="https://bit.ly/33zXgRQ">https://bit.ly/33zXgRQ</a></p> <p>PAHO/WHO resources available at: <a href="https://bit.ly/36Dji3B">https://bit.ly/36Dji3B</a></p>



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