

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

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**Key considerations.** While mutations of the SARS-CoV-2 (the etiological agent of COVID-19) have been reported in the literature and media, they remain within the expected patterns for a coronavirus. Evidence indicates that the SARS-CoV-2 variants identified to date have a much lesser influence, if any at all, on the transmissibility and severity of COVID-19 than other risk factors, such as age or underlying conditions.

Genetic characterization of viral pathogens is the basis for the development of diagnostic protocols, vaccines, and antiviral treatments. This strategy is also a useful tool in public health for response to outbreaks and for disease control through molecular epidemiology studies. Among respiratory viruses, the genetic characterization of influenza viruses is a classic example of how the approach has provided information, among others, for vaccine composition, molecular diagnosis, antiviral resistance monitoring, and surveillance of circulating viruses and thus has contributed disease mitigation [1-5].

Likewise, genomic sequencing of SARS-CoV-2 and timely release of the information has not only allowed the characterization of the etiological agent involved in the initial outbreak, but also the timely development of diagnostic protocols and further monitoring of the evolution of the evolving COVID-19 pandemic. Thus, genomic sequencing has also been an essential tool to generate virological data on SARS-CoV-2, to support the laboratory response and to better understand the dispersal and evolutionary patterns [6-7].

## Genomic characterization of SARS-CoV-2

### Genetic variants of SARS-CoV-2 in the Americas

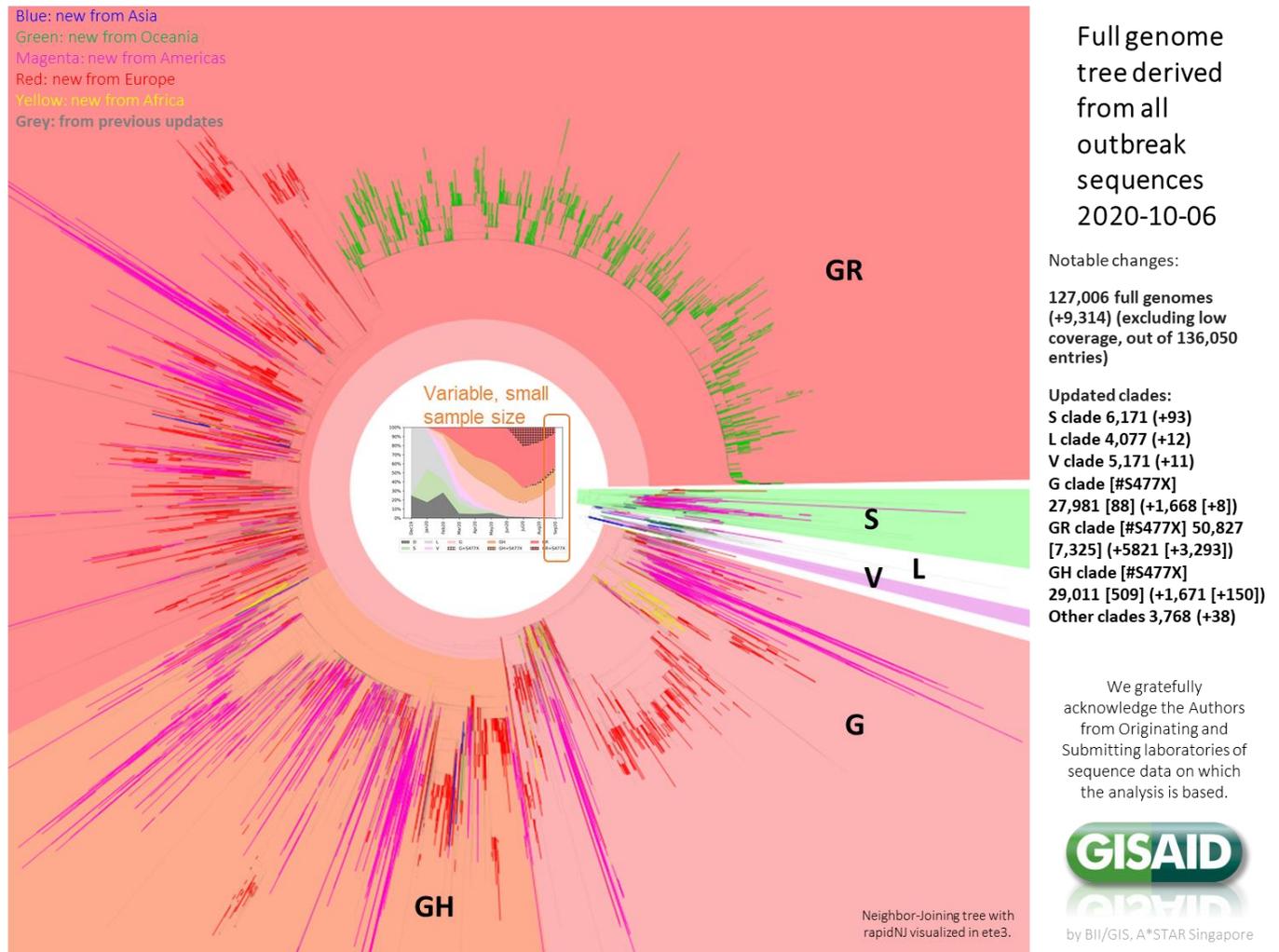
Since the initial genomic characterization of SARS-CoV-2, the virus has been divided into different genetic groups or *clades* (6). **The occurrence of mutations is a natural and expected event within the evolution process of the virus.** In fact, some specific mutations define the viral genetic groups currently circulating globally (Table 1). The mutations identified to date remain within the expected patterns for a coronavirus.

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

Genetic Group	Mutations
S	C8782T, T28144C, NS8-L84S
L	C241, C3037, A23403, C8782, G11083, G25563, G26144, T28144, G28882
V	G11083T, G26144T, NSP6-L37F, NS3-G251V
G	C241T, C3037T, A23403G, <b>S-D614G</b>

GH C241T, C3037T, A23403G, G25563T, **S-D614G** + NS3-Q57H  
 GR C241T,C3037T, A23403G, G28882A, **S-D614G** + N-G204R

Figure 1 shows the phylogenetic tree of the SARS-CoV-2.<sup>1</sup> Viruses classified in the genetic group G, that includes the subgroups GH and GR, are the most frequent globally. All viruses in this group share the D614G mutation.



**Figure 1.** Phylogenetic tree with globally circulating SARS-CoV-2 genomic data, showing the prevalence of genetic group G and its subgroups GH and GR. Source: GISAID (<https://platform.gisaid.org>), 06-Oct-2020.

## Mutations and variants virulence

Although some researchers have associated the mutations defying the genetic variants of group G (particularly the D614G) to increased virulence [8-9], no sufficient evidence currently exists to conclude that any circulating SARS-CoV-2 virus has increased virulence or infectivity.

<sup>1</sup> The phylogenetic tree originates from the global genetic data platform GISAID, <https://platform.gisaid.org>.

In fact, current evidence suggests that the mutation **D614G**, which defines the variants of genetic group G, is **much less important, if at all of any importance, for COVID-19 transmissibility and severity than other risk factors, such as age or comorbidities** [9]. Likewise, additional epidemiological factors must be considered in the process of viral dispersal and evolution.

## SARS-CoV-2 Genomic Surveillance

Genetic sequencing data on circulating SARS-CoV-2 has been generated by the countries laboratories. This genetic information on circulating viruses in the Region is needed to establish dispersal and evolution patterns, develop diagnostic protocols, vaccines and antiviral drugs. Sequencing platforms are used for the genetic characterization of SARS-CoV-2 in laboratories that have sequencing capacity, either by the Sanger method or by applying Next Generation Sequencing (NGS) techniques [10].

PAHO encourages laboratories to timely sequence COVID-19 positive samples and share genetic information through the global platform GISAID. In addition, PAHO is working to strengthen a COVID-19 genomic sequencing network in the Region of the Americas, so that genomic data is available in a timely manner through GISAID. The **COVID-19 Genomic Surveillance Regional Network** is open to all the countries of the Americas through the National Public Health Laboratories. This network also includes two Regional Sequencing Laboratories (Fiocruz-Brazil and the Institute of Public Health-Chile), which provide external sequencing for the participating laboratories without such capacity [11]. For additional information, the PAHO Regional Office can be contacted at the email addresses [leitejul@paho.org](mailto:leitejul@paho.org), [ricoj@paho.org](mailto:ricoj@paho.org).

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