

Attention and/or concern variants for COVID-19 genomic sequencing in Brazil

Variantes de atenção e/ou preocupação por sequenciamento genômico do COVID-19 no Brasil

Variantes de atención y / o preocupación para la secuenciación genómica de COVID-19 no Brasil

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In the city of Wuhan, Hubei province in the People's Republic of China, an event classified as an outbreak was registered by the local authorities, which allowed the diagnosis of pneumonia (PNM) to be carried out.^{1,2} This important phenomenon was dated to the month of December of the year 2019, being identified a strain of coronavirus unknown until that time, and which spread rapidly, showing its high potential for transmissibility in twenty-four (24) other countries.¹⁻³

In this context, this fact was notified on January 7, 2020, as a new strain belonging to the coronavirus, which was not recognized in humans to date.³⁻⁵ As of January 30, 2020, the Organization World Health Organization (WHO), defended that this outbreak was constituted as a noisy public health problem, constituting also as a true Public Health Emergency of International Importance (PHEII).⁴⁻⁵

On February 11, 2020, it was given the designation of SARS-CoV-2, as it was responsible for causing the disease that became known as COVID-19.^{4,5,6} On February 26, 2020, the first notification of a confirmed case in Brazil by the Ministry of Health (MH) of COVID-19 and, on March 11 of the same year, the WHO characterized COVID-19 as a pandemic, communicating to all nations updated information on its complexity and magnitude of this new phenomenon.^{6,7,8}

According to the MS, the most identified classes of coronaviruses to date are the “alpha coronavirus HCoV-229E”, the “alpha coronavirus HCoV-NL63”, the “beta coronavirus HCoV-OC43”, the “beta coronavirus HCoV-HKU1”, “SARS-CoV”, which has been identified as the cause of severe acute respiratory syndrome (SARS), “MERS-CoV”, which has been identified as the cause of Middle East respiratory syndrome (MERS) and also SARSCoV-2.⁹ Regarding the different types of classification of the aforementioned variants of COVID-19, the WHO took the initiative of bringing together an association of experts, which instituted the nomenclatures to be used to designate what is understood as “Variants of Interest” (VOI) and the “Variants of Concern” (VOC), using letters of the Greek alphabet for this action, such as alpha (α), beta (β), delta (Δ or δ), gamma (Γ or γ) and omicron (O or \omicron).^{10,11}

With regard to SARS-CoV-2 VOCs, they receive this designation, as they have the possibility of increased frequency in their virulence, changes in their clinical presentation, increased transmissibility or harmful alteration of COVID-19, or even in the reduction of its effectiveness in social and diagnostic measures, public health or accessible therapies.^{10,11} The VOI, on the other hand, have this designation because it caused community transmission of multiple cases of COVID-19, and also, of its genome having undergone mutations that changed its viral phenotype, in addition to needing to be detected in several nations.^{10,11}

Another important issue that characterizes VOI is that it can be classified by carrying out an assessment by the Working Group on the Evolution of the SARS-CoV-2 Virus or otherwise by the WHO.^{10,11} In table 1, COVID-19's VOCs of concern are presented in relation to the labels instituted by WHO, strains, GISAID clade/strain, first documented samples and respective designation dates.

Table 1 – COVID-19 variants of concern (VOC), strains, GISAID clade/strain, place of identification of first documented samples and date designations: *, **, ***

WHO Label	Lineage	GISAID Clado/lineage	First document samples	Designation date
Alpha	B.1.1.7	GRY(antigamente GR/501Y.V1)	Reino Unido, september/ 2020	18/12/2020
Beta	B.1.351	GH/501Y.V2	África do Sul, may/2020	18/12/2020
Gamma	P.1	GR/501Y.V3	Brasil, november/2020	11/01/2021
Delta	B.1.617.2	G/452R.V3	Índia, october/2020	VOI: 04/04/2021 VOC:11/05/2021

Source: Adapted from WHO, 2021.

* The data presented here were updated on 12/01/2021.

** Due to the potential complexity of COVID-19 and its variants, the aforementioned data is updated daily.

*** The authors are faithful to the sources consulted..

In Table 1, the frequencies of confirmed and notified cases of the variants, federative units (UF) in Brazil, between epidemiological weeks (EW) 2 to 47, up to November 2021, are presented, totaling a universe of 44,334 cases with mean and standard deviation (1.642± 2.916,3).

Table 1 – Frequency of confirmed and notified cases of attention and/or concern (VOC) variants by genomic sequencing, by FUs, in Brazil, between SE 2 to 47, in the year 2021 (n=44.334):*,**,***

	Total	VOC Gama	VOC Delta	VOC Alfa	VOC Beta	VOC Ômicron
UF	f (%)	f (%)	f (%)	f (%)	f (%)	f (%)
SP	14.113 (31,8)	2.915 (12,7)	11.138 (53,4)	54 (12)	3 (60)	3 (100)
RJ	6.403 (14,4)	3.522 (15,3)	2.825 (13,5)	56 (12,4)	-	-
MG	5.057 (11,4)	3.019 (13,1)	1.831 (8,8)	207 (46)	-	-
GO	2.889 (6,5)	2.199 (9,6)	652 (3,1)	37 (8,2)	1 (20)	-
DF	2.147 (4,8)	1.026 (4,5)	1.113 (5,3)	8 (1,8)	-	-
AM	1.930 (4,4)	1.687 (7,3)	242 (1,2)	1 (0,2)	-	-
PE	1.683 (3,8)	1.304 (5,7)	376 (1,8)	3 (0,7)	-	-
CE	1.552 (3,5)	1.132 (4,9)	419 (2)	1 (0,2)	-	-
ES	1.131 (2,6)	429 (1,9)	684 (3,3)	18 (4)	-	-
SC	1.107 (2,5)	715 (3,1)	386 (1,8)	6 (1,3)	-	-
BA	933 (2,1)	566 (2,5)	326 (1,6)	40 (8,9)	1 (20)	-
RO	925 (2,1)	883 (3,8)	42 (0,2)	-	-	-
PR	917 (2,1)	618 (2,7)	288 (1,4)	11 (2,4)	-	-
RS	495 (1,1)	427 (1,9)	66 (0,3)	2 (0,4)	-	-
MS	480 (1,1)	379 (1,6)	101 (0,5)	-	-	-
PB	385 (0,9)	257 (1,1)	127 (0,6)	1 (0,2)	-	-
AL	361(0,8)	348 (1,5)	12 (0,1)	1 (0,2)	-	-
SE	324 (0,7)	294 (1,3)	29 (0,1)	1 (0,2)	-	-
PA	308 (0,7)	239 (1)	69 (0,3)	-	-	-
AC	250 (0,6)	231(1)	19 (0,1)	-	-	-
RR	236 (0,5)	234 (1)	2 (0,0)	-	-	-
MA	227 (0,5)	174 (0,8)	53 (0,3)	-	-	-
TO	163 (0,4)	137 (0,6)	26 (0,1)	-	-	-
RN	109 (0,2)	75 (0,3)	33 (0,2)	1 (0,2)	-	-
PI	103 (0,2)	103 (0,4)	-	-	-	-
MT	90 (0,2)	84 (0,4)	4 (0,0)	2 (0,4)	-	-
AP	16 (0,0)	11 (0,0)	5 (0,0)	-	-	-
Total	44.334 (100)	23.008 (100)	20.868 (100)	450 (100)	5 (100)	3 (100)

Source: Adapted from the State Departments of Health (SDH) and MS, 2021.

* The data presented here were last updated on the day 01/12/2021.

** Due to the potential complexity of COVID-19 and its variants, the aforementioned data is updated daily.

*** The authors are faithful to the sources consulted.

Among the SE 2 to 47 of the year 2021, it was found that the VOC Gamma registered the greatest preponderance with 51.9% (n=23,008), followed by VOC Delta with 47.1% (n= 20,868), VOC Alpha with 1% (n=450), VOC Beta with 5% (n=0.01) and VOC Ômicron 0.01% (n=03).¹² The state of São Paulo (SP) registered the greatest preponderance among the FUs analyzed, adding 31.8% (n=14,113) and Amapá (AP) the smallest with 0.04% (n=16).¹²

What is noteworthy in this table is the presence of three (03) cases of VOC Ômicron identified in the state of SP in November 2021.

According to WHO, the first known Ômicron VOC infection (B.1.1.529) was from a sample collected on 9 November 2021, which was first reported to WHO South Africa on 24 November from 2021.¹³⁻¹⁵

Thus, and according to some researchers, Ômicron VOC (B.1.1.529) comprises a high number of developed mutations, some of which are possibly classified as worrisome.¹³⁻¹⁵ The complexity and magnitude of Ômicron VOC (B.1.1.529) is such that preliminary evidence suggests the presence of an increased risk of reinfection in people affected by it, when compared to other types of VOCs in COVID-19.¹³⁻¹⁵

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