Centre for Arbovirus cadde Discovery, Diagnostics, Genomics & Epidemiology

31 December 2020

First detection of the SARS-CoV-2 VOC (B.1.1.7) lineage in Brazil

Flavia Sales, Mariana Severo, Ingra Claro, Darlan Candido, Cristina Mendes de Oliveira, Luciano Scarpelli, Gustavo Campana, José Eduardo Levi, Jaqueline Goes de Jesus, Nuno Rodrigues Faria, Ester Cerdeira Sabino

Contact: Nuno Faria (nfaria@ic.ac.uk), Ester Sabino (sabinoec@usp.br) and José Eduardo Levi (jose.levi.ext@dasa.com.br)

Summary

We report the first two cases caused by the SARS-CoV-2 B.1.1.7 (VOC) lineage in Brazil. The findings come less than 36 hours upon sample collection. Samples were immediately analysed using a portable DNA sequencer as part of genomic surveillance activities from the Brazil-UK CADDE project. Sequencing and phylogenetic analysis confirm two separate introductions of the VOC lineage in Brazil, possibly from the UK. One case reported no travel outside of Brazil. Given the higher transmissibility of the VOC compared to non-VOC lineages, increased genomic surveillance is urgently needed to investigate the extent of VOC circulation in the country.

Background

Genomic sequencing of SARS-CoV-2 viruses has enabled the identification of over 800 distinct SARS-CoV-2 lineages since the beginning of the pandemic. Surveillance of SARS-CoV-2 mutations in the UK has recently revealed a growing number of infections and geographic spread associated with viruses belonging to a new phylogenetic cluster named B.1.1.7 lineage, also named as Variant of Concern 202012/01 (VOC) by Public Health England. This lineage originated in the late Summer to early Autumn 2020 in the southeast region of England, possibly from a chronically infected individual (1,2).

In relation to its closest known circulating lineage, VOC is defined by 8 mutations in the virus' spike protein (deletion 69-70, deletion 144, N501Y, A570D, D614G, P681H, T716I, S982A, D1118H), and several other mutations outside the spike protein, namely in the ORF1ab (T1001I, A1708D, I2230T, 3675-7 SGD deletion), ORF8 (Q27 stop, R52I, Y73C) and N (D3L, S235F). For a detailed description of the biological significance of each of these mutations we refer to the recent report from the COVID-19 Genomics Consortium UK (1).

Until 31 Dec 2020, VOC has been identified in 21 countries across Europe, Oceania, Asia, and North America (3). Importantly, epidemiological and phylogenetic studies indicate that the VOC lineage has a higher transmissibility compared to non-VOC lineages (2,4). This has been predicted to result in increases in incidence in 2021, with higher peaks in hospitalizations and deaths compared to 2020 (4).

Autochthonous transmission of VOC in Brazil

Between November and December 2020, around 400 samples were processed by Diagnosticos da America (DASA) laboratories (5) using the ThermoFisher TaqPath test (Thermo Fisher Scientific, Waltham, USA) for molecular detection of SARS-CoV-2, which includes the ORF1ab, S and N gene targets (6). As the spike deletions at positions 69 and 70 of the VOC lineage result in a false negative for the spike target of the ThermoFisher TaqPath commercial test (7), we screened suspected VOC samples based on negative S results and positive results for the ORF1ab and N targets. Samples were de-identified before receipt by the researchers. Ethical approval for this study was confirmed by the national ethical review board (Comissão Nacional de Ética em Pesquisa), protocol number CAAE 30127020.0.0000.0068.

On 30 December 2020, we received two cases that tested positive in Sao Paulo state, southeast Brazil, for the ORF1ab and N gene targets but negative for the S gene target (**Table 1**). A saliva sample was collected in Sao Paulo on 22 December from Patient 1, a female aged between 20 to 30 years old. Patient 1 reported no travel outside of Brazil. Symptoms initiated on 21 December and the test was conducted on the following day.

Sample 2 was collected in Sao Paulo on 21 December from a male patient aged between 30 to 40 years old. No additional information was available for this patient. Sequencing was conducted in duplicate using the ARTIC protocol for SARS-CoV-2 nanopore sequencing protocols (8), as previously described (9,10,11). Library negative controls had undetectable DNA. Diagnostic and sequencing statistics can be shown in **Table 1**. For the two new sequences, a B.1.1.7 lineage identification (assignment probability. 1.0) was obtained using the pangolin COVID-19 lineage Assigner (https://pangolin.cog-uk.io/).

Table 1. Diagnostic and sequencing statistics of the two confirmed VOC lineage patients. Reference used Wuhan-Hu-1 (GenBank Accession number MN908947.3).

Sample (GISAID ID)	Cycle threshold values	No. mapped reads	No. bases covered >25x	Reference covered
Patient 1 (EPI_ISL_754236)	S: Undetected ORF1ab: 28.1 N: 27.29	56,565	28,023	92.4%
Patient 2 (EPI_ISL_754237)	S: Undetected ORF1ab: 25.8 N: 24.5	51,761	26,339	87.1%

Exploratory phylogenetic analysis and interpretation

To contextualize our findings, we estimated a preliminary maximum likelihood (ML) phylogenetic tree including the two novel Brazilian VOC genomes and 127 available VOC genomes from around the world available on GISAID (12) until the 31st December 2020. Patient 1 genome groups within a well-supported cluster (bootstrap 85%) of 10 sequences (60% from the UK). Moreover, the closest available sequence to Patient 2 sequence was collected in the UK on 27 Nov 2020.

An international import of the VOC lineage from the UK to Brazil is consistent with the travel history of an asymptomatic family member who was in close contact with Patient 1. Indeed, Patient 1 was in contact with a contact that arrived in Sao Paulo from the UK and Italy on the 17 December. One of Patient 1's contact who reported travelling to the UK and Italy tested positive by a rapid test on 23 December. The travel history of Patient 2 remains unknown at the time of writing. Yet, our phylogenetic analysis indicates that (i) Patient 2 infection represents an independent introduction possibly also from the UK, where this lineage was first detected on 20 September 2020, and (2) that is unlikely that Patient 2 is epidemiologically related to Patient 1.

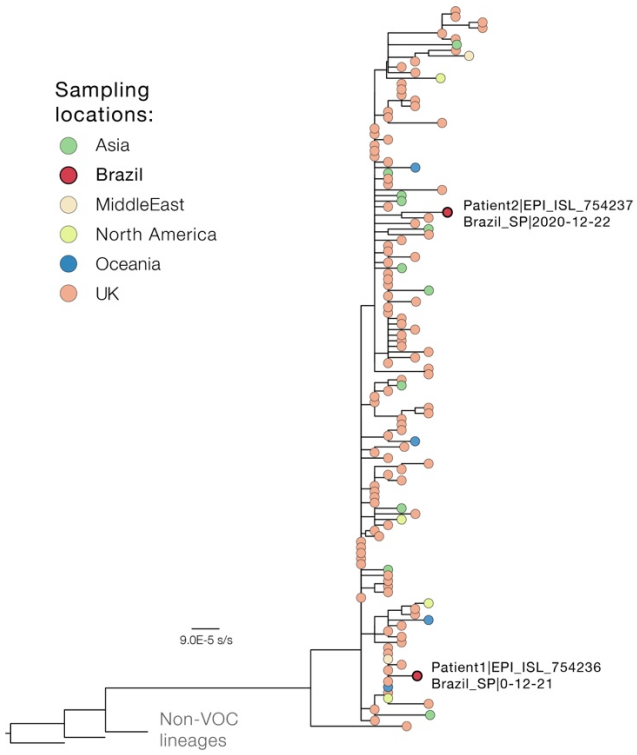

Figure 1. Phylogenetic context of the two novel VOC genomes from Brazil. SARS-CoV-2 VOC sequences (*n*=4,693, 31 December 2020) were down sampled by selecting 1 sequence per country per day. As outgroups, we included two B.1.1 UK sequences closely related to the lineage of interest and sequence WH04 from Wuhan. Details on multiple alignment and phylogenetic tree reconstruction have been reported elsewhere (11).

There are several limitations to our analysis. As there is limited VOC available information from other locations outside of the UK, our interpretations based on phylogenetic data are biased by the heterogeneous capacity in generating and sharing genomic data around the world. Moreover, the samples were selected from a small subset of RT-PCR confirmed cases in Sao Paulo, Brazil. Thus, it is likely that the number of current cases caused by the VOC lineage in Sao Paulo and other locations in Brazil is higher than the number reported here.

In conclusion, we report the first two SARS-CoV-2 COV cases in Brazil and in Latin America. Phylogenetic analysis suggests that both cases are consistent with travel history from the UK. As of 25 December 2020, Brazil has temporarily suspended flights from the UK. However, one of the confirmed cases reported no travel history outside Brazil, indicating local transmission of the new lineage in the country. Additional genomic surveillance throughout Brazil is urgently needed to investigate community transmission of VOC and non-VOC lineages.

Acknowledgments

We thank all colleagues and authors who deposited genome data on GISAID. GISAID acknowledgment tables for all sequences used in this report can be found as Tables S1, S2, S3 and S4.

Funding

This project was supported by a Medical Research Council-São Paulo Research Foundation (FAPESP) CADDE partnership award (MR/S0195/1 and FAPESP 18/14389-0) (http://caddecentre.org/). FAPESP further supports I.M.C. (2018/17176-8 and 2019/12000-1), J.G.J. (2018/17176-8 and 2019/12000-1, 18/14389-0), F.C.S.S. (2018/25468-9). N.R.F. is supported by a Wellcome Trust and Royal Society Sir Henry Dale Fellowship (204311/Z/16/Z). D.S.C. is supported by the Clarendon Fund and by the Department of Zoology, University of Oxford.

References

1. Preliminary genomic characterisation of an emergent SARS-CoV-2 lineage in the UK defined by a novel set of spike mutations. Available at https://virological.org/t/563 (2020).
2. Volz, Mishra, Chand, Barrett, Johnson et al. Transmission of SARS-CoV-2 Lineage B1.1.7 in England: Insights from linking epidemiological and genetic data – Imperial College Report 42. Available at https://www.imperial.ac.uk/mrc-global-infectious-disease-analysis/covid-19/report-42-sars-cov-2-variant/
3. O'Toole et al. New variant report 2020-12-31, Available at https://cov-lineages.org/global_report.html

4. Davies, Barnard et al. Estimated transmissibility and severity of novel SARS-CoV-2 Variant of Concern 202012/01 in England, CMMID Repository, Available at https://cmmid.github.io/topics/covid19/uk-novel-variant.html
5. DASA Laboratories https://dasa.com.br/
6. TaqPath COVID-19 Multiplex Diagnostic Solution, Available at https://www.thermofisher.com/uk/en/home/clinical/clinical-genomics/pathogen-detection-solutions/covid-19-sars-cov-2/multiplex.html
7. Bal, Destras, Gaymard et al. Screening of the H69 and V70 deletions in the SARS-CoV-2 spike protein with a RT-PCR diagnosis assay reveals low prevalence in Lyon, France, medRxiv preprint doi: https://doi.org/10.1101/2020.11.10.20228528;
8. SARS-CoV-2 Artic Network, Available at https://artic.network/ncov-2019
9. Faria et al. First cases of COVID-19 in Brazil, South America, Available at https://virological.org/t/first-cases-of-coronavirus-disease-covid-19-in-brazil-south-america-2-genomes-3rd-march-2020/409
10. de Jesus et al. Importation and early local transmission of COVID-19 in Brazil, 2020, Rev Inst Med Trop S Paulo 62, 11 May 2020, Available at https://www.scielo.br/scielo.php?pid=S0036-46652020000100218&script=sci_arttext
11. Candido, Claro, Jesus, Souza et al. Evolution and epidemic spread of SARS-CoV-2 in Brazil, Science 2020, 369:6508, Available here: https://science.sciencemag.org/content/369/6508/1255
12. Shu and McCauley, GISAID: global initiative on sharing all influenza data – from vision to reality, Available at https://www.eurosurveillance.org/content/10.2807/1560-7917.ES.2017.22.13.30494

Contacts

Nuno Faria (nfaria@ic.ac.uk)
Ester Sabino (sabinoec@usp.br)
José Eduardo Levi (jose.levi.ext@dasa.com.br)