



The Brazilian Journal of INFECTIOUS DISEASES

www.elsevier.com/locate/bjid



Brief Communication

New Brazilian variant of the SARS-CoV-2 (P1/Gamma) of COVID-19 in Alagoas state

José Claudio da Silva ^{a,b,c,*}, Valtuir Barbosa Félix ^{a,d},
Sura Amélia Barbosa Felix Leão ^{e,f}, Euclides Maurício Trindade-Filho ^{a,b},
Fulvio Alexandre Scorza ^c

^a Centro Universitário CESMAC, Maceió, Alagoas, Brasil

^b Laboratório de Neurociência e comportamento, Núcleo de Ciências Biológicas, Universidade Estadual de Ciências da Saúde de Alagoas (NUCIB-UNCISAL), Maceió, AL, Brasil

^c Departamento de Neurologia e Neurocirurgia, Universidade Federal de São Paulo (EPM/UNIFESP), Escola Paulista de Medicina, São Paulo, SP, Brasil

^d Universidade Federal de Alagoas (HUPAA/UFAL/EBSERH), Divisão de apoio e diagnóstico terapêutico do Hospital Universitário, Maceió, AL, Brasil

^e Santa Casa de Maceió, Maceió, AL, Brasil

^f Universidade Federal de Alagoas (UFAL), Arapiraca, AL, Brasil

ARTICLE INFO

Article history:

Received 3 March 2021

Accepted 5 May 2021

Available online 19 May 2021

Keywords:

B.1.1.28.1

Coronavirus

SARS-CoV-2

COVID-19

ABSTRACT

Since the beginning of 2020, health authorities have been monitoring the cases of Coronavirus Disease 2019 (COVID-19), which has grown every day in Brazil and around the world, becoming pandemic. The new coronavirus, also called SARS-CoV-2 by scientists spreads rapidly, causing fear, deaths, and threats for the economy of several countries. This work aimed to describe the clinical characterization of the first cases of a new Brazilian variant of SARS-CoV-2 (P1) in the State of Alagoas, which occurred on February 16th, 2021. Two cases are described: first, a person infected in Amazonas State, where the new variant P1 was first described, who migrated to Alagoas State, and second, a case of probable community transmission within Alagoas, since the patient had no history of recent travel. In both confirmed cases the symptoms were mild. Further studies are necessary to better understand the clinical behavior of P1 SARS-CoV-2 variant and also the associated sequelae in the context of COVID-19.

© 2021 Sociedade Brasileira de Infectologia. Published by Elsevier España, S.L.U. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>)

The Coronavirus Disease 2019 (COVID-19) has shown to be a disease that may quickly evolve to severe conditions, including death, especially in older people, who are more

susceptible to SARS-CoV-2 infection.¹⁻⁵ The COVID-19 virus spreads quickly from person to person, starting clinically as a flu-like syndrome, which may progress to an acute viral pneumonia and severe acute respiratory syndrome, in which there is a need for artificial ventilatory support. On the other hand, autopsies of patients who died from COVID-19, and also

* Corresponding author at: Centro Universitário CESMAC, Maceió, Alagoas, Brasil.

E-mail address: jcsneuroc1@gmail.com (J.C. da Silva).

<https://doi.org/10.1016/j.bjid.2021.101588>

1413-8670/© 2021 Sociedade Brasileira de Infectologia. Published by Elsevier España, S.L.U. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>)

animal models, have shown serious histopathological injuries of the systems. In addition, people who survive from severe infectious have shown sequelae, as respiratory conditions, among others.^{5–11}

Studies suggest that expression of ACE2 cellular proteins and TMPRSS2 protease in the olfactory epithelium cells are involved in viral access to the human body and detection in oropharyngeal secretions.^{2,12} Since ACE2 proteins seem to be expressed in significantly higher levels in older people, this may explain the greater susceptibility of this age group to infection.

Experiments using machine learning models based on algebraic topology, evaluated the possible changes in the relation between COVID-19 virus and angiotensin 2-converting enzyme receptor host, after confirmation of virus mutations.¹⁰ In this way, studies indicate a higher ability of the mutated virus to infect humans, who will have greater difficulty to control its replication.^{13–15} Researchers have shown that three among six SARS-CoV-2 subtypes have become slightly more infectious, while the other three subtypes have significantly strengthened their infectiousness, bringing greater risks of illness to the general population.^{10,13,16,17}

This is a descriptive cross-sectional study using public informatics data from the Center for Strategic Information and Response in Health Surveillance, of the Health Department of the State of Alagoas (CIEVS/SESAU/AL). This project was initially approved by the research ethics committee of the Federal University of São Paulo (UNIFESP) under the CAAE 37172620.0.0000.5505. For public data collection, updated epidemiological reports were daily accessed through the CIEVS/SESAU/AL website. Patient samples were confirmed by RT-PCR according to the Central Public Health Laboratory - LACEN and associated to the virus genetic sequencing at Oswaldo Cruz Foundation (FIOCRUZ). Data were available in the Informative Note SUVISA No. 07/2021, of February 17th, 2021.

The diagnosis of the first two cases of the new SARS-CoV-2 variant in Alagoas State occurred on February 16th, 2021. The first case was of a person infected in the Amazonas State who migrated to Alagoas State. The second case is characterized by community transmission within Alagoas. The confirmation of the new variant was carried out by the reference national laboratory (Laboratory of Respiratory Viruses and Measles, from FIOCRUZ-RJ), which, upon receiving positive samples confirmed by LACEN's RT-PCR, performed the virus genetic sequencing. After confirmation, state authorities where the virus had emerged, were immediately informed for virus variant monitoring procedures in that region. Patients G#1 and G#2, respectively with and without travel history to the Amazon, were diagnosed with the P1 variant of the new coronavirus either in the prodromal state period of COVID-19 or immediately after. G#1 was a 36-year-old female, with history of three days exposure to family members in the Amazon region. The woman gradually evolved to a flu-like condition associated with dyspnea and cough symptoms and was instructed to do family isolation after positive test for SARS-CoV-2 (Table 1). A patient sample was sent to Oswaldo Cruz Foundation (FIOCRUZ) for virus sequencing. After being informed about the new variant, the Brazilian Ministry of Health recommended virus genetic sequencing of individuals suspected of COVID-19 contamination and history of travel to Amazon. Government officials also instructed the submission

Table 1 – Characteristics of patients with confirmed infection with SARS-CoV-2 P1 variant.

Sex	G#1 Female	G#2 Female
Age	36	64
Travel to Manaus (last month)	Yes	No
Positive RT-PCR	Yes	Yes
Allochthonous cases	Yes	Yes
Countryside	Yes	Yes
Genetic sequencing	Yes	Yes
Cough	Yes	Yes
Coryza	No	Yes
Myalgia	No	Yes
Softness	No	Yes
Dyspnea	Yes	No

of randomly and systematically positive samples of SARS-CoV-2 to carry out genetic sequencing and possible virus monitoring.

The second case was a 64-year-old female, living in Alagoas State and with no history of recent travel or contact with persons from any other State, when the presence of the new circulating variant had been already confirmed in Amazonas. In this woman, P1 variant infection was also confirmed by genetic sequencing exam. The symptomatic picture of this patient was characterized as mild, as in G#1 patient; however, symptoms as recurrent cough, slight coryza, myalgia and physical asthenia were also observed (Table 1). Onset of symptoms began on January 19th, 2021 with test confirmation on next 25th, probably on the post-prodromal period. P1 virus seems to be more transmissible, is associated with higher viral loads, and possible reinfections.^{18,19} Epidemiological investigation indicates that these cases (G#1 and G#2 patients) were characterized as allochthonous cases, meaning that the virus was imported from another state.

The P1 SARS-CoV-2 variant found in Alagoas, which might be probably circulating in the state nowadays, is derived from the B.1.1.28 lineage, present in Brazil. This new strain contains a unique composition of mutations in the spike protein, responsible for the entry of the virus into human cells. Studies indicate that this new variant has greater transmission capacity, even though it is not associated with more severe clinical conditions in relation to the original strain.

The new coronavirus has caused deaths and losses to the Alagoas State economy and also to the country and world, as well. On the other hand, low population adherence to social distance associated with poor health care and no proper prevention measures during the pandemic have contributed to an increasing incidence of the new variant. In the same way, the beginning of the seasonal period of respiratory diseases associated to the presence of both the ancestral SARS-CoV-2 and the P1 variant may increase the risk of respiratory infections, death or even aggravate the situation of collapsing hospital care.

Funding

This research did not receive any specific grant from funding agencies in the public, private or non-for-profit sectors.

REFERENCES

- Bi Q, Wu Y, Mei S, Ye C, Zou X, Zhang Z, Liu X, Wei L, Truelove SA, Zhang T, Gao W, Cheng C, Tang X, Wu X, Wu Y, Sun B, Huang S, Sun Y, Zhang J, Ma T, Lessler J, Feng T. Epidemiology and transmission of COVID-19 in 391 cases and 1286 of their close contacts in Shenzhen, China: a retrospective cohort study. *The Lancet Infectious Diseases*. 2020;20(8):911–9. [https://doi.org/10.1016/S1473-3099\(20\)30287-5](https://doi.org/10.1016/S1473-3099(20)30287-5).
- Butowt R, von Bartheld CS. Anosmia in COVID-19: underlying mechanisms and assessment of an olfactory route to brain infection. *Neuroscientist*. 2020;00(0):1–22. <https://doi.org/10.1177/1073858420956905>. Sep 11:1073858420956905. doi: Epub ahead of print. PMID: 32914699; PMCID: PMC7488171.
- Bilinska K, Jakubowska P, Bartheld CSV, Butowt R. Expression of the SARS-CoV-2 Entry Proteins, ACE2 and TMPRSS2, in cells of the olfactory epithelium: identification of cell types and trends with age. *ACS Chem Neurosci*. 2020: 1–20. <https://doi.org/10.1021/acchemneuro.0c00210>.
- Song J, Deng YK, Wang H, Wang ZC, Liao B, Ma J, He C, Pan L, Liu Y, Alobid I, Wang DY, Zeng M, Mullol J, Liu Z. Self-reported taste and smell disorders in patients with COVID-19: distinct features in China. *Curr Med Sci*. 2021;41(1):14–23. <https://doi.org/10.1007/s11596-021-2312-7>. Epub 2021 Feb 13. PMID: 33582900; PMCID: PMC7881907.
- Zeng M, Wang DY, Mullol J, Liu Z. Chemosensory dysfunction in patients with COVID-19: what do we learn from the global outbreak? *Curr Allergy Asthma Rep*. 2021;21(2):6. <https://doi.org/10.1007/s11882-020-00987-5>. PMID: 33537862; PMCID: PMC7857344.
- Chan JF, Yuan S, Kok KH, To KK, Chu H, Yang J, Xing F, Liu J, Yip CC, Poon RW, Tsoi HW, Lo SK, Chan KH, Poon VK, Chan WM, Ip JD, Cai JP, Cheng VC, Chen H, Hui CK, Yuen KY. A familial cluster of pneumonia associated with the 2019 novel coronavirus indicating person-to-person transmission: a study of a family cluster. *Lancet*. 2020;395:514–23. [https://doi.org/10.1016/S0140-6736\(20\)30154-9](https://doi.org/10.1016/S0140-6736(20)30154-9). PMID: 31986261; PMCID: PMC7159286.
- Mitrani RD, Dabas N, Goldberger JJ. COVID-19 cardiac injury: implications for long-term surveillance and outcomes in survivors. *Heart Rhythm*. 2020;17(11):1984–90. <https://doi.org/10.1016/j.hrthm.2020.06.026>. Epub 2020 Jun 26. PMID: 32599178; PMCID: PMC7319645.
- Chan JF, Zhang AJ, Yuan S, Poon VK, Chan CC, Lee AC, Chan WM, Fan Z, Tsoi HW, Wen L, Liang R, Cao J, Chen Y, Tang K, Luo C, Cai JP, Kok KH, Chu H, Chan KH, Sridhar S, Chen Z, Chen H, To KK, Yuen KY. Simulation of the clinical and pathological manifestations of coronavirus disease 2019 (COVID-19) in golden syrian hamster model: implications for disease pathogenesis and transmissibility. *Clin Infect Dis*. 2020 Dec 3;71(9):2428–46. <https://doi.org/10.1093/cid/ciaa325>.
- Zappulli V, Ferro S, Bonsembiante F, Brocca G, Calore A, Cavicchioli L, Centelleghè C, Corazzola G, De Vreese S, Gelain ME, Mazzariol S, Moccia V, Rensi N, Sammarco A, Torrigiani F, Verin R, Castagnaro M. Pathology of coronavirus infections: a review of lesions in animals in the one-health perspective. *Animals (Basel)*. 2020 Dec 11;10(12):2377. <https://doi.org/10.3390/ani10122377>. PMID: 33322366; PMCID: PMC7764021.
- Chen J, Wang R, Wang M, Wei GW. Mutations strengthened SARS-CoV-2 infectivity. *J Mol Biol*. 2020 Sep 4;432(19):5212–26. <https://doi.org/10.1016/j.jmb.2020.07.009>. Epub 2020 Jul 23. PMID: 32710986; PMCID: PMC7375973.
- Kunnumakkara AB, Rana V, Parama D, Banik K, Girisa S, Sahu H, Thakur KK, Dutta U, Garodia P, Gupta SC, Aggarwal BB. COVID-19, cytokines, inflammation, and spices: how are they related? *Life Sci*. 2021;1-135:119201. <https://doi.org/10.1016/j.lfs.2021.119201>.
- Vaz SN, Santana DSD, Netto EM, Wang W-K, Brites C. Validation of the GeneXpert Xpress SARS-CoV-2 PCR assay using saliva as biological specimen. *Braz J Infect Dis*. 2021;24:1–4. <https://doi.org/10.1016/j.bjid.2021.101543>.
- Fontenele RS, Kraberger S, Hadfield J, Driver EM, Bowes D, Holland LA, Faleye TOC, Adhikari S, Kumar R, Inchausti R, Holmes WK, Deitrick S, Brown P, Duty D, Smith T, Bhatnagar A, Yeager RA, Holm RH, Hoogesteijn von Reitzenstein N, Wheeler E, Dixon K, Constantine T, Wilson MA, Lim ES, Jiang X, Halden RU, Scotch M, Varsani A. High-throughput sequencing of SARS-CoV-2 in wastewater provides insights into circulating variants. medRxiv [Preprint]. 2021;25. <https://doi.org/10.1101/2021.01.22.21250320>. Jan 25:2021.01.22.21250320. PMID: 33501452; PMCID: PMC7836124.
- Lamback EB, Oliveira MAD, Haddad AF, Vieira AFM, Neto ALF, Maia TDS, Chrisman JDR, Spinetti PDDM, Mattos MAD, Costa E. Hydroxychloroquine with azithromycin in patients hospitalized for mild and moderate COVID-19. *Braz J Infect Dis*. 2021;25(2):479–584. <https://doi.org/10.1016/j.bjid.2021.101549>.
- Wong Carlos KH, Wan Eric YF, Luo Sihui, Ding Yu, Lau Eric HY, Ling Ping, Hu Xiaowen, Lau Edward CH, Wong Jerry, Zheng Xueying, Cowling Benjamin J, Weng Jianping, Leung Gabriel M. Clinical outcomes of different therapeutic options for COVID-19 in two Chinese case cohorts: a propensity-score analysis. *E Clin Med*. 2021;32:1–10. <https://doi.org/10.1016/j.eclinm.2021.100743>.
- Pachetti M, Marini B, Benedetti F, Giudici F, Mauro E, Storici P, Masciovecchio C, Angeletti S, Ciccozzi M, Gallo RC, Zella D, Ippodrino R. Emerging SARS-CoV-2 mutation hot spots include a novel RNA-dependent-RNA polymerase variant. *J Transl Med*. 2020;18:179. <https://doi.org/10.1186/s12967-020-02344-6>. Published online 2020 Apr 22. doi: PMCID: PMC7174922.
- Muñoz M, Patiño LH, Ballesteros N, Paniz-Mondolfi A, Ramírez JD. Characterizing SARS-CoV-2 genome diversity circulating in South American countries: signatures of potentially emergent lineages? *Int J Infect Dis*. 2021;105:329–32. <https://doi.org/10.1016/j.ijid.2021.02.073>. S1201-9712(21)00159-4. doi: Epub ahead of print. PMID: 33618008; PMCID: PMC7895695.
- Sabino EC, Buss LF, Carvalho MPS, Prete CA, Crispim MAE, Fraiji NA, et al. Resurgence of COVID-19 in Manaus, Brazil, despite high seroprevalence. *Lancet*. 2021 Feb 6;397(10273). [https://doi.org/10.1016/S0140-6736\(21\)00183-5](https://doi.org/10.1016/S0140-6736(21)00183-5).
- Singh J, Samal J, Kumar V, Sharma J, Agrawal U, Ehtesham NZ, Sundar D, Rahman SA, Hira S, Hasnain SE. Structure-function analyses of new SARS-CoV-2 variants B.1.1.7, B.1.351 and B.1.1.28.1: clinical, diagnostic, therapeutic and public health implications. *Viruses*. 2021;13(3):439. <https://doi.org/10.3390/v13030439>.