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Letter to the Editor

First identification of SARS-CoV-2 lambda (C.37) variant in Southern Brazil

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To the Editor—Since the emergence of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in December 2019, new lineages of this virus have been described. The recent emergence of SARS-CoV-2 variants of interest (VOIs) and variants of concern (VOCs) with potentially increased transmissibility and reduced sensitivity to antibody neutralization may affect the efficacy of strategies to control the coronavirus 2019 (COVID-19) pandemic.[1] A novel VOI within the B.1.1.1 lineage (termed C.37), which was designated by the World Health Organization (WHO) as "the lambda variant" in June 15, 2021, was detected in Peru in August 2020. It has been identified in 26 countries in America, Europe, and Oceania, drawing international attention for its rapid spread.[2–5] Despite the global dissemination of the lambda variant, in Brazil this lineage was reported only in São Paulo state in February 2021.[5] Here, we describe the first report of the SARS-CoV-2 lambda variant in Southern Brazil. This study was approved by the Ethics Committees from Hospital de Clínicas de Porto Alegre (CAAE: 30767420.2.0000.5327).

A young male who had been in Argentina initiated respiratory symptoms compatible with viral infection while returning to his town, which borders Argentina, in Rio Grande do Sul, the southernmost Brazilian state. On day 4 after the beginning of the symptoms, he tested positive for SARS-CoV-2 by a point-of-care test. On the following day, he was admitted to a local hospital. Due to the worsening of symptoms, he was transferred to the intensive care unit of Hospital de Clínicas de Porto Alegre, a tertiary-care, COVID-19 referral hospital in the state, 2 days after hospital admission. Oro/nasopharyngeal swabs were collected, and real-time reverse transcription-PCR testing for 2 genes of the nucleocapsid protein (N1 and N2) for SARS-CoV-2 was performed,[6] confirming the SARS-CoV-2 infection. The specimen (203_LABRESIS) was submitted for whole-genome sequencing (WGS) as part of an epidemiological study. Sequencing libraries were prepared using the CleanPlex SARS-CoV-2 panel protocol (Paragon Genomics, Hayward, CA) for target enrichment and library preparation, following the manufacturer's instructions (https://www.paragongenomics.com/wp-content/uploads/2020/03/UG4001-01_-CleanPlex-SARS-CoV-2-Panel-User-Guide.pdf). The resulting libraries were sequenced using MiSeq (Illumina, San Diego, CA). Consensus sequences were generated by the QIASeq SARS-CoV-2 pipeline (QIAGEN CLC Genomics Workbench 21, Germantown, PA) with high-quality whole-genome sequence (average coverage 3,142; <2% Ns; 29,873 Kb). The specimen 203_LABRESIS was classified as the C.37 variant using the Phylogenetic Assignment of Named Global Outbreak Lineages (Pangolin) software tool (version 3.0.2),[3] and the sequence was deposited in the GISAID database (no. EPI_ISL_2617911).[5]

The lambda variant (C.37) is defined by a deletion in the ORF1a gene (Δ3675–3677), which is also present in the alpha (B.1.1.7, United Kingdom), beta (B.1.351, South African), and gamma (P.1, Brazil) VOCs. In addition, the lambda variant displays a novel deletion and multiple nonsynonymous mutations in the spike gene (Δ246-252, G75V, T76I, L452Q, F490S, D614G, and T859N).[2,4] The mutations L452Q and F490S are mapped in the receptor-binding domain (RBD) region and the F490S has been associated with reduced susceptibility to antibody neutralization.[1] The isolate 203_LABRESIS presented all 8 of the C.37-defining lineage mutations described above in addition to other 19 mutations that have already been described in members of this lineage (Supplementary Material online).[2,4,7] The 203_LABRESIS sequence was aligned with high quality and coverage-complete genome sequences from Brazil (n = 1), Argentina (n = 16), Chile (n = 24), and Peru (n = 26) that were available in the EpiCoV database in GISAID. We used them to perform a comparative phylogenetic tree. The 203_LABRESIS sequence clustered together with another C.37 variant sequence from Argentina that was also identified in February 2021 (Supplementary Material online).

The high prevalence of the lambda variant has been described particularly in South American countries such as Chile, Peru,

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Ecuador, and Argentina, where this new VOI is associated with substantial rates of community transmission.[2] The critical healthcare system situation and recent reports of increased deaths in these countries are thought to be associated with the increasing prevalence of the lambda variant.[8–10]

Notably, on June 15, 2021, the lambda variant was deemed a VOI by the World Health Organization.[2] Whether the lambda variant is more transmissible or more pathogenic than other variants or whether it is able to evade the effects of available vaccines remains unknown. The novel S: Δ246-252 deletion and additional mutations in the spike protein should be considered to understand their effects on viral fitness and host interaction. This first report of the SARS-CoV-2 lambda variant in Southern Brazil raises concern regarding a possible dissemination of this lineage in the region. Moreover, considering that this VOI has rapidly spread in Peru, Ecuador, Chile, and Argentina, we believe that this lambda variant has considerable potential to become a VOC.

Supplementary material. To view supplementary material for this article, please visit https://doi.org/10.1017/ice.2021.390

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