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CASE REPORT

# SARS-CoV-2 variant VUI 202012/01 (B.1.1.7) in a pediatric patient: first case report in Ecuador

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## Abstract

**Introduction:** RNA viruses are known to have a high genetic variability. To date, SARS-CoV-2 has produced several variants that can change the clinical presentation of COVID-19. The first clinical case of variant B.1.1.7 with a critical clinical status in a pediatric patient is presented. It indicates that surveillance of new variants and their relationship to critical cases in pediatric patients are required.

**Clinical case:** A pediatric patient with a history of infantile cerebral palsy, complete severe subcortical atrophy, Lennox–Gastaut syndrome, and recurrent pneumonia. She had a slow evolution requiring intensive therapy for acute respiratory distress syndrome (ARDS) that was related to SARS-CoV-2 variant B 1.1.7.

**Evolution:** Initially, she was treated at a private hospital because she required intensive care due to ARDS, and she was then transferred to a public hospital. She was discharged after 35 days due to a favorable evolution of her infectious etiology.

**Conclusions:** New SARS-CoV-2 variants may show new clinical behaviors. Despite this patient's history, a clinical course towards severe symptoms had not been previously observed in pediatric patients with COVID-19. The severe symptoms could be related to the SARS-CoV-2 variant B.1.1.7 infection in this patient.

**Keywords:** Pulmonary edema; Coronavirus infections; SARS-CoV-2 variant B.1.1.7, child, critical care, Case report.

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## Introduction

Mutation is an expected event in viruses, and SARS-CoV-2 is no exception [1, 2]. In November 2020, the rapid increase in COVID-19 cases in the UK was associated with the emergence of a new variant that was identified by genomic sequencing and reported to the World Health Organization (WHO) on December 14, 2020 [1-3]. Called the SARS-CoV-2 VUI 202012/01 (B.1.1.7), this variant is defined by multiple mutations, approximately 17 of which have been detected in peak proteins such as deletion 69–70, deletion 144, N501Y, A570D, D614G, P681H, T716I, S982A, and D1118H [2, 4-6]. One of the most important mutations is within the receptor-binding domain (N501Y) that the virus uses to bind to the human angiotensin-converting enzyme (ACE)2 receptor [4, 6, 7].

The objective is to present the first case report of the new variant SARS-CoV-19 VUI 202012/01 (B.1.17) in a pediatric patient from Ecuador who presented in critical condition.

## Case report

The patient was a 12-year-old girl who was born and resided in Quito, Ecuador. She had a history of infantile cerebral palsy, complete severe subcortical atrophy, and Lennox–Gastaut syndrome that was diagnosed at 7 months of age. The patient was receiving treatment with the following antiepileptic drugs: clobazam (1 mg/kg/day), lacosamide (10 mg/kg/day), and valproic acid (15 mg/kg/day). She also had a history of recurrent pneumonia (an average of one hospitalization per year) up to 2 years before admission. She underwent surgery for strabismus when she was 1 year and 8 months old, gastrostomy surgery at 2 years old, and surgery for gastroesophageal reflux at 5 years old.

Since January 1, 2021, her father, mother, and sister had a fever and cough. Seven days later, the patient also developed a fever, cough, dyspnea, tachypnea, and subcostal retractions, and the family was tested at a public entity where real-time polymerase chain reaction (RT-PCR) tests for SARS-CoV-2 were performed with a positive result for all family members.

Initially, the patient was managed at home with oxygen through a nasal catheter. However, she developed peripheral desaturation of up to 77% by pulse oximetry, for which she was admitted to a private hospital in Quito 4 days after the diagnosis. There, a pulmonary computed tomography scan was performed, which revealed consolidation foci in both lung fields, perihilar bronchiectasis, which was predominantly alveolar, and mixed infiltrate. Acetaminophen was started at 10 mg/kg/dose and methylprednisolone at 2 mg/kg loading dose followed by maintenance with 2 mg/kg/day. The patient was admitted to the hospital.

On day 4 of hospitalization, she showed increased respiratory distress and persistent fever. Induced sputum culture on admission revealed Enterobacter cloacae and Streptococcus pneumoniae, so intravenous cefepime (50 mg/kg/dose) every 8 h was started. After 5 days of hospitalization, the patient developed acute respiratory distress syndrome (ARDS), which required invasive mechanical ventilation. Due to the lack of physical space in the intensive care unit, she was transferred to a public hospital, where she continued to undergo invasive mechanical ventilation.

### Diagnostic workshop

Based on the clinical evolution and critical condition of the patient, the viral genome was sequenced, and the SARS-CoV-2 variant B.1.1.7 was identified. This sequence was reported to the GISAID gene bank with the accession number EPI_ISL_877562, and it included the following mutations: Spike A570D, Spike D614G, Spike D1118H, Spike N501Y, Spike P681H, Spike Q52K, Spike S982A, Spike T716I, N D3L, N G204R, N R203K, N S235F, NS8 K68stop, NS8 R27I52, NSP, A738C, NSP NSP3 T183I, NSP12 P323L, and NSP14 L493F (Fig. 1).

Epidemiological analysis involving the patient's relatives suggested that the father contracted COVID-19 from a friend during a work meeting in the province of Zamora, in southern Ecuador. All of the family members recovered from the disease.

### Evolution

The patient's disease evolution was good with respect to her infectious symptoms, and she was discharged after 38 days of hospitalization. She was not on supplemental oxygen, but she underwent respiratory therapy and physical therapy.

## Discussion

The new SARS-CoV-2 variant B.1.1.7 is estimated to be 70–71% more transmissible than the previously circulating form of the virus [8–10]. In London in September 2020, this variant accounted for only one in four new COVID-19 diagnoses, and it increased to almost two-thirds of new cases by mid-December 2020 [1, 8].

In infected patients, it has been shown that this new variant presents with worse clinical disease severity [1], and there is a greater risk of hospital admission and mortality [4, 8, 9].

Currently, vaccines are less likely to be effective against the variant.. Although the new variant has mutations in the peak protein that is targeted by the three major vaccines (Pfizer, Moderna & AstraZeneca), they produce antibodies against various regions of the peak protein. However, over time, as more mutations emerge, the vaccines may need to be modified [11]. There is currently evidence that this variant is covered by vaccines that are currently produced by VaxzevriaTM (AstraZeneca), ModernaTM (Moderna TX, Inc) and Pfizer-BioNTechTM (Pfizer Inc & BioNTech) [4, 11, 12].

This case draws attention due to its slow evolution that led to the patient requiring intensive therapy for ARDS, which is an unusual evolution in children. The molecular sequencing study confirmed that this was the first case with this variant in a pediatric patient in Ecuador. Because there was no history of international travel by her family, this means that the SARS-CoV-2 variant B.1.1.7 is already circulating in the community.

There is current evidence of greater virulence for the variant B.1.1.7. A matched pair study study showed a mortality risk of 1.64 (95% confidence interval [CI] 1.32 to 2.04) compared to the original SARS-CoV-2 strain [1], and the slow evolution of this patient's symptoms may have been caused by her multiple comorbidities. However, in the authors' experience, this patient's respiratory evolution is unusual, and observing it in a pediatric patient with COVID-19 despite the existence of comorbidities suggests that a contributing factor is the new variant that was detected [1].

New variants of SARS-CoV-2 can show new clinical behaviors and even be more lethal, according to Challen et al. [1]. In the present case, it is advisable to strengthen surveillance systems using molecular epidemiology in Ecuador and the region to identify many similar cases that may not otherwise be identified or reported [13].

## Conclusions

COVID-19 in this pediatric patient, whose condition deteriorated so that she required mechanical ventilation due to the presence of ARDS, was related to infection with the SARS-CoV-2 variant B.1.1.7. Because there was no history of international travel by her family, it was epidemiologically established that the SARS-CoV-2 variant B.1.1.7 is already circulating in the community.

### Abbreviations

ARDS: acute respiratory distress syndrome.
COVID-19: a viral disorder usually characterized by high fever; cough; dyspnea chills; persistent tremor; Muscle pain; headache; throat pain; a new loss of taste and / or smell and other symptoms of viral pneumonia.
RT-PCR: Reverse transcriptase polymerase chain reaction.
SARS-CoV-2: A species of BETACORONAVIRUS that causes atypical respiratory disease (COVID-19) in humans. The organism was first identified in 2019 in Wuhan, China. The natural host is the Chinese intermediate horseshoe bat, RHINOLOPHUS affinis.

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### Authors' contributions

All authors contributed equally to this scientific article.
All authors read and approved the final version of the manuscript.

### Financing

The authors financed the expenses incurred in the production of this clinical case.

### Availability of data and materials

The data sets generated and / or analyzed during the current study are not publicly available due to the confidentiality of the participants, but are available through the corresponding author upon reasonable academic request.

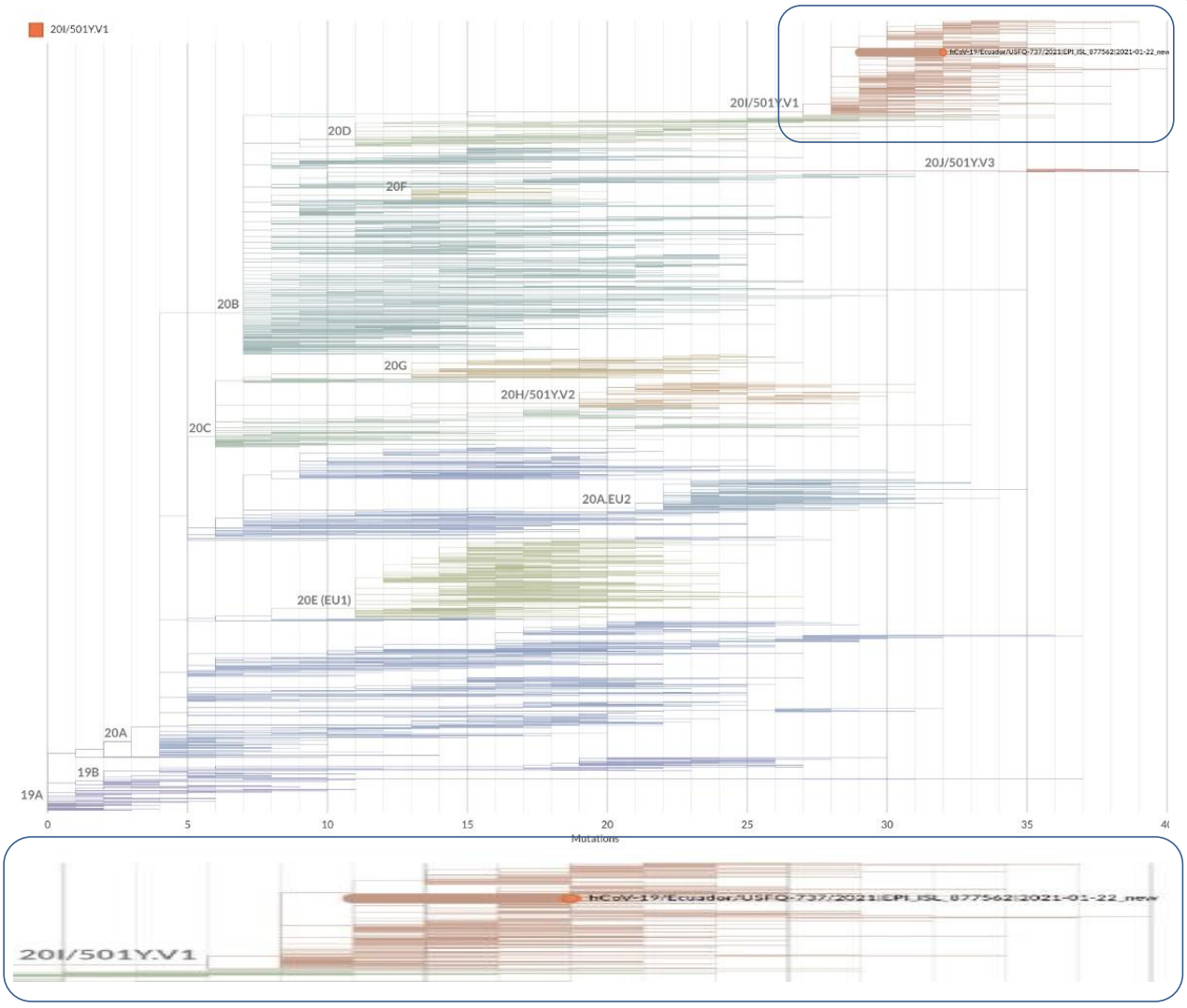
### Ethical statements

#### Protection of people

The authors declare that the procedures followed were in accordance with the ethical standards of the responsible human experimentation committee and in accordance with the World Medical Association and the Singapore Declaration.

### Data confidentiality

The authors declare that they have followed the protocols of their work center on the publication of patient data without identification.




| Virus detail | |
|---|---|
| **Virus name:** | hCoV-19/Ecuador/USFQ-737/2021 |
| **Accession ID:** | EPI_ISL_877562 |
| **Type:** | betacoronavirus |
| **Clade** | GRY |
| **Pango Lineage** | B.1.1.7 (version: 2021-03-16) |
| **AA Substitutions** | Spike A570D, Spike D614G, Spike D1118H, Spike N501Y, Spike P681H, Spike Q52K, Spike S982A, Spike T716I, N D3L, N G204R, N R203K, N S235F, NS8 K68stop, NS8 Q27stop, NS8 R52I, NS8 Y73C, NSP3 A890D, NSP3 I1412T, NSP3 T183I, NSP12 P323L, NSP14 L493F |
| **Variant** | VUI202012/01 GRY (B.1.1.7) |
| **Passage details/history:** | Original |

**Fig. 1** Phylogenetics of the sample. Phylogenetic location of sample USFQ-737 in the Nexstrain.org classification and mutation listing based on information from gisaid.org.

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**Publication consent**

Written informed consent was obtained from the patient's legal guardian for the publication of this case report and accompanying images. A copy of the written consent is available for review by the Editor-in-Chief of this journal

**Conflicts of interest**

The authors declare not to have any interest conflicts.

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