



Genomic Surveillance Tracks the First Community Outbreak of the SARS-CoV-2 Delta (B.1.617.2) Variant in Brazil

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As 2021 comes to a close, the advances in vaccination against COVID-19 allow the world to glimpse an end to the pandemic. In Brazil, the disease has cost more than 600,000 lives and affected more than 21 million people. When the second wave of COVID-19 hit in early 2021, the country saw more than 3,500 daily deaths. As Brazil started to recover from this number, the first reports of infection by the Delta (B.1.617.2) variant of concern (VoC) in the country were emerging. The first confirmed case of this variant occurred on 26 April 2021, with five states registering infections by it in the following 3 months. At the time, these cases were considered isolated or contained imported events. Here, we describe the early phase of the first large-scale community transmission of the Delta variant in Brazil and the associated interstate dispersal.

Through biweekly sequencing of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) randomized sampling, the Corona-ômica-RJ Network (<http://www.corona-omica.rj.incc.br>) has been tracking lineage dynamics of the pandemic in the state of Rio de Janeiro, Brazil (1). We first detected the Delta VoC in two samples collected on 16 and 17 June 2021, which represented 0.57% ($n = 2/353$) of genomes sequenced at the time. Both originated from citizens without prior contact or history of travel in the 14 days preceding symptom onset. By tracking direct contacts with both cases, three more active infections with the variant were promptly identified. No hospital admission was necessary for any of these cases. As monitoring of contacts progressed, we conducted the next randomized sequencing round of positive COVID-19 samples from the state. We identified 60 additional samples carrying the Delta lineage, an astounding increase to 16% of samples ($n = 60/377$) in 15 days. Because of this fast growth, we consider Delta to have already jumped from individual to community transmission in Rio de Janeiro in June 2021.

The evolutionary relationship between all SARS-CoV-2 sequences from Brazil available in mid-July 2021 indicates that the spread of Delta in the country can be described by at least six introductory events (Fig. 1A). The first reported cases, from the MV Shandong Da Zhi carrier ship in the state of Maranhão (2), are possibly related to the origin of the variant in the state of Goiás, more than 1,600 km away. Two transmission clusters in the state of Paraná have different origins, and one isolated case was found in the states of Minas Gerais and São Paulo. The outbreak in Rio de Janeiro

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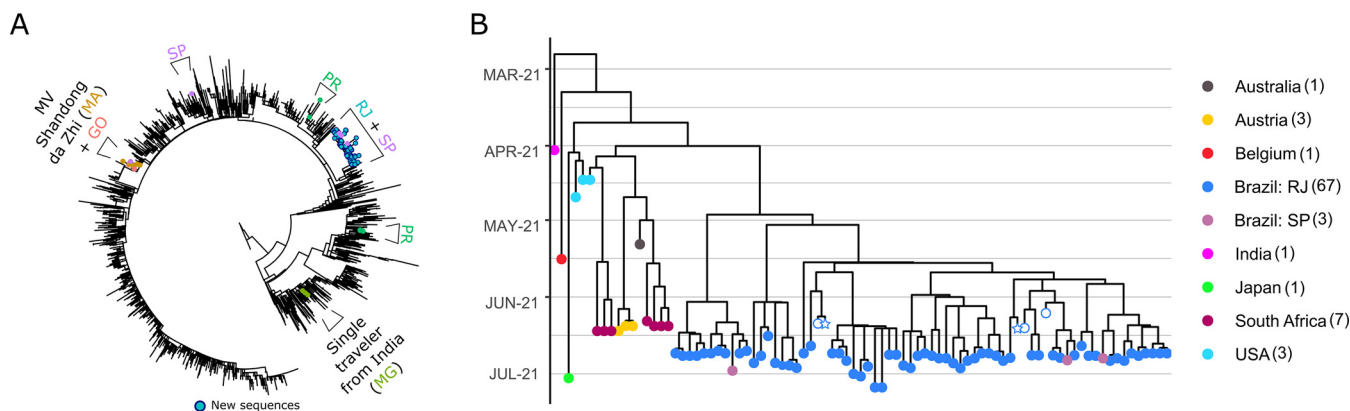


FIG 1 Evolutionary relationship between samples of Delta variant collected in Brazil. (A) Maximum likelihood tree including 1,409 SARS-CoV-2 genomes shows that at least six independent introductions of the variant occurred in Brazil. Colored points indicate samples from different Brazilian states (MG, Minas Gerais; MA, Maranhão; GO, Goiás; PR, Paraná; RJ, Rio de Janeiro; SP, São Paulo). All samples from Rio de Janeiro were sequenced by the Corona-ômica-RJ Network. (B) Bayesian time tree of the outbreak in Rio de Janeiro. Color of points corresponds to sampling locality. Empty stars represent the first two cases detected in Rio de Janeiro, and empty circles represent their primary contacts.

originated with a single entrance, though it has spread to the state of São Paulo independently at least three times (Fig. 1B). We estimate the introduction in Rio de Janeiro to have happened in the last days of April or the beginning of May 2021, and most of the spread has occurred around mid-June. The Rio de Janeiro clade has four mutations in ORF1ab pervasive to all samples sequenced as follows: I1091V, T4087I, syn5373A→G and syn12951T→C. Indeed, all independent introductions have characteristic mutations when compared to one another, which can be a helpful resource to rapidly assign new cases to each of these events (see Table S1 in the supplemental material).

Recent studies have demonstrated that Delta has higher transmissibility (3) and suggest that it can evade the immune response induced by previous infections or incomplete vaccination (4–6). Even though the variant has now become dominant in Brazil, a new surge of COVID-19 cases in the country was not observed. We attribute the current success in subduing the pandemic to the advances in vaccination coverage: as of 19 October 2021, at least 70% of the population had taken the first vaccine dose and 49.7% have completed the immunization chronogram. We warn that prematurely relaxing nonpharmacological interventions, such as social distancing and use of masks, can threaten the current trend of decline in cases. This work provides a first view of how Delta has repeatedly entered Brazil. Still, we note the possibility of other importing events passing undetected in genomic surveillance programs across the country. Enhancing comprehensive genomic surveillance programs in all Brazilian states can help track and monitor the introduction and spread of lineages across the country. The proper financing of these genomic surveys is of paramount importance to Brazil.

Data availability. Next-generation sequencing (NGS) data generated in our study are publicly available in SRA-NCBI under BioProject accession no. [PRJNA774631](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA774631). Genome sequences were also deposited in GISAID (<https://www.gisaid.org/>) and are fully accessible for registered users within the “browse” option of the EpiCoV database (see Table S1 in the supplemental material).

SUPPLEMENTAL MATERIAL

Supplemental material is available online only.

SUPPLEMENTAL FILE 1, XLSX file, 0.02 MB.

SUPPLEMENTAL FILE 2, PDF file, 0.2 MB.

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