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Rapid Communication

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First Report of SARS-CoV-2 B.1.1.251 lineage in Brazil

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Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is a novel single-stranded RNA virus that belongs to the β coronavirus family and is defined as the causal agent of coronavirus disease 2019 (COVID-19). The spike (S) protein of the SARS-CoV-2 plays a pivotal role in the infection because it mediates the virus entry into human host-cells, through interactions between the SARS-CoV-2 S receptor-binding domain (RBD) and the angiotensin-converting enzyme 2 (ACE2) receptor.[1] For some patients, the binding of SARS-CoV-2 S protein to the ACE2 leads to a dysregulated immune response with increased release of cytokines especially IL-6 implicated in multi-organ damage and risk of death.

New coronavirus lineages have been identified worldwide but the impact of mutations in SARS-CoV-2 genomes on the nature and severity of COVID-19 and on the effectiveness of available vaccines is still uncertain. Recently, new lineages defined by multiple S protein mutations associated with increased transmissibility of SARS-CoV-2 have been identified in the UK (B.1.1.7 lineage) and South Africa (B.1.351 lineage). In Brazil, two new variants from the B.1.1.28 lineage, namely P.1 and P.2, which present an E484K mutation in the S protein RBD, have been associated with increase in transmissibility, changes in antigenic profile and reinfection.[2]

On 29 January 2021, we identified a new circulating lineage of SARS-CoV-2 in Brazil, located in Sergipe state, Northeast region. The B.1.1.251 lineage was identified in a 32-old-man with headache, sore throat and coryza, and no history of recent travel. SARS-CoV-2 infection was confirmed by using real-time reverse transcription polymerase chain reaction after nasal swab specimen collection. The whole-genome sequences of SARS-CoV-2 were recovered using nanopore sequencing protocol previously established and used by Genomic Coronavirus Fiocruz Network to recover high-quality genomes.[3,4]

B.1.1.251 lineage has been found especially in the USA (69.0%), the UK (20.0%), Sweden (2.0%), Peru (2.0%) and Colombia (1.0%), but there are no reports of this lineage in Brazil (https://cov-lineages.org/lineages/lineage_B.1.1.html). At least 40 different lineages of SARS-CoV-2 have been identified in the country since March 2020, with a higher prevalence of B.1.1.28 and B.1.1.33. The first case of COVID-19 in Sergipe was confirmed on 14 March 2020 in a female patient with recent travel to Spain infected with SARS-CoV-2 lineage B.1, which is the predominant known global lineage and is subdivided into >70 variants. Until 29 January 2021, other six SARS-CoV-2 lineages have been reported in Sergipe including B.1.1.28 and B.1.1.33, as well as B.1.1.119, B.1.212, P.2 and the emergent B.1.1.251 lineage.

Even without a report of international or domestic travel, the untraced entry of this SARS-CoV-2 lineage in Sergipe cannot be ruled out. Travel restriction measures have varied from country

to country and cases of imported lineages have been confirmed since the early phase of COVID-19 pandemic.[5,6] Despite SARS-CoV-2 genetic diversity across states seems to be geographically compartmentalized,[7] the relaxing distancing control measures and the increasing intercity population mobility have contributed to the spread of multiple lineages across different geographical regions in the country.

Since this is the first reported case of an individual infected with the B.1.1.251 lineage in Brazil, additional genome sequencing in this region is critically needed to investigate the prevalence of this lineage over time. Moreover, genomic surveillance of SARS-CoV-2 lineages is essential to understand whether mutations in the S protein can mediate escape from host antibodies and compromise vaccine effectiveness.[8] Further studies are needed to evaluate the transmissibility and virulence of this emergent coronavirus lineage in Brazil.

Authors' Contributions

All authors contributed equally to the manuscript.

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