



Commentary

SARS-CoV-2 Brazil variants in Latin America: More serious research urgently needed on public health and vaccine protection



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ABSTRACT

COVID-19 has not only created a pandemic but also affected both economically and socially in all countries. It has further created a socio-economic chaos throughout Latin America. Currently, some new SARS-CoV-2 variants are circulating in Latin America and one among the significant variant belongs to the P.1 lineage (B.1.1.28.1) that has 17 mutations. The essential modifications located in the spike glycoprotein RBD include E484K, K417T and N501Y. Along with the P.1 lineage, P.2 lineage (B.1.1.28.2) has also appeared recently. Details on all the variants are unknown, along with the Brazil variants at this time. Therefore, we call for intensive research to collect more data to understand the variants' virulence and the effects on vaccine efficacy.

The COVID-19 pandemic has created a critical crisis worldwide not only in death toll, but also economically and socially. The pandemic has impacted the Latin American and the Caribbean regions more seriously. In this region, the first case was reported in Brazil and it became the first Latin American country to declare the disease on Feb 25, 2020 [1]. Subsequently, the highest COVID-19 death rates were reported from the Latin American and Caribbean regions. A recent editorial in *Lancet* has reported that the COVID-19 pandemic has created a serious socio-economic crisis that evolved as a humanitarian disaster [2]. Another report analyzed how Latin American countries such as Peru, Brazil, Colombia, Argentina, Chile, and Mexico have addressed the pandemic with emergency health policies. In that report, Martinez-Valle observed a struggling phase for the Latin American countries to address the pandemic [3]. Another study noted that poverty might be a factor influencing the dispersal of COVID-19 in Latin America leading to higher mortality rates in the region [4]. Our preliminary analysis has also showed the infection rate and the death rate increase across the Latin American region (Fig. 1A–D). But, more focused efforts are needed by all Latin American countries to contain the pandemic from further impact.

Recently, a significant variant of COVID-19 was found in Brazil (Fig. 1E). We generally address this variant as lineage P.1 (B.1.1.28.1). There are 17 unique mutations are noted in SARS-CoV-2 and three are reported from these 17 mutations in the Brazil variant. The essential mutations in the spike include the glycoprotein RBD, E484K, K417T, and N501Y [5]. However, Faria et al. reported ten unique mutations accrued in the spike protein, which comprises of E484K and N501K [6,7]. Other than these three significant mutations, some other mutations are recorded in the P.1 lineage. These mutations are L18F, T20N, P26S, D138Y, R190S, D614G H655Y, T1027I, and V1176F [8]. On Jan 12, 2021, this variant was detected in Manaus city, Brazil [6] and it eventually created extensive infections in the city. The variant has also reached Japan through travelers. It has also been detected in the United States.

On the other hand, another new lineage has been detected in several parts of Brazil, including the Manaus city, entitled P.2 lineage

(B.1.1.28.2) [8]. This is a sub-lineage of B.1.128 and its separately accrued one significant spike glycoprotein mutation called E484K [9]. In this mutation, substitution has been noted at position 484 (Glutamate (E) to Lysine (K)) that causes E484K mutation in RBD. Other than the E484K mutation, some different mutations are noted in the P.2 lineage. These mutations are D614G and V1176F [8]. In Brazil, two people were re-infected by this SARS-CoV-2 variant [10]. On the other hand, the occurrence of the E484K mutation may neutralize convalescent sera. Greaney et al. noted that E484K mutation decrease neutralization in convalescent sera by polyclonal antibodies [11].

Another variant, 501Y.V1 of B.1.1.7 lineage, appeared in the United Kingdom, and the variant has spread to other parts of the world, including the United States [12,13]. One of the significant mutations in N501Y was noted in RBD. Other considerable modifications are A570D, D614G, P681H, 144Y deletion, and 69/70 deletion. It is a more virulent variant associated with an augmented risk of death when compared to other variants. However, it was observed that the mutations of different variants may influence vaccine efficacy [14]. It was also reported that the B.1.1.7 lineage has been circulating in Brazil [7].

The three recent SARS-CoV-2 variants that are currently in circulation across Latin America include P.1 lineage, P.2 lineage and B.1.1.7 lineage. Therefore, to the world healthcare community must take the Brazil variants in Latin America more seriously. Also, all Latin American countries need to focus on the Brazil variants to handle the COVID-19 pandemic crisis efficiently. Nonetheless, some questions need to be urgently addressed: first, can the Brazil variants (P.1 lineage and P.2 lineage) of SARS-CoV-2 lineage create another wave of the pandemic? Second, can the Brazil variants change the vaccine efficacy and the ongoing vaccination programs worldwide? We know that there is a Center for Disease Control (CDC) for the African region. But, there is no CDC for the Latin American region. Therefore, the creation of a Latin American CDC is essential to generate more data on the Brazil variants of SARS-CoV-2. However, more research is needed about the P.1 lineage and the P.2 lineage, which can inform us about the properties like epidemiological characteristics (severity transmissibility and reinfection

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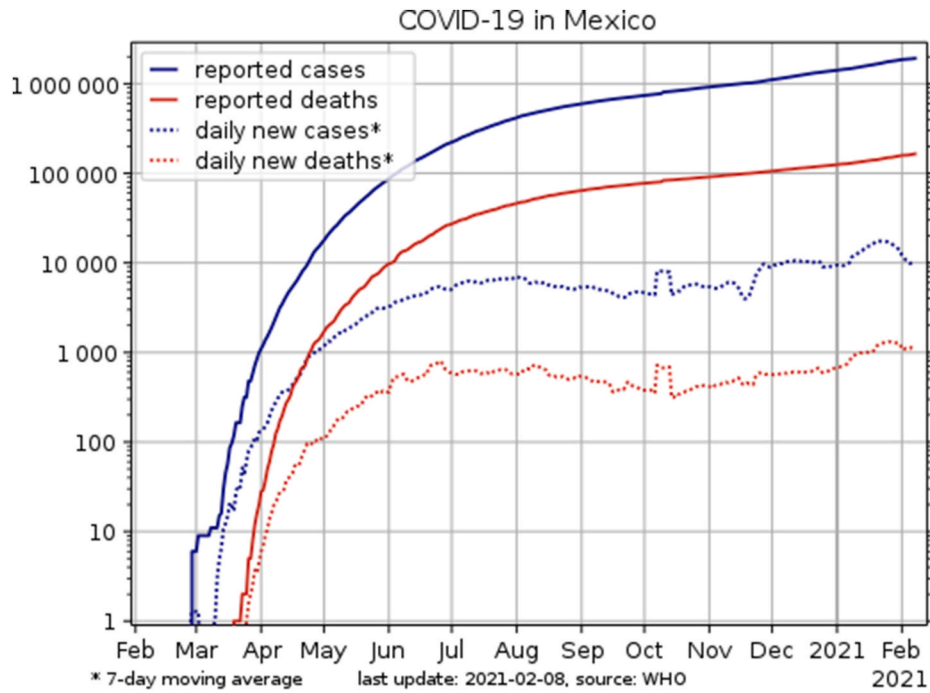
risk), impact immune escape, probable impact on disease severity, etc. This data will help to design future strategies and to end the pandemic.

Ethical approval

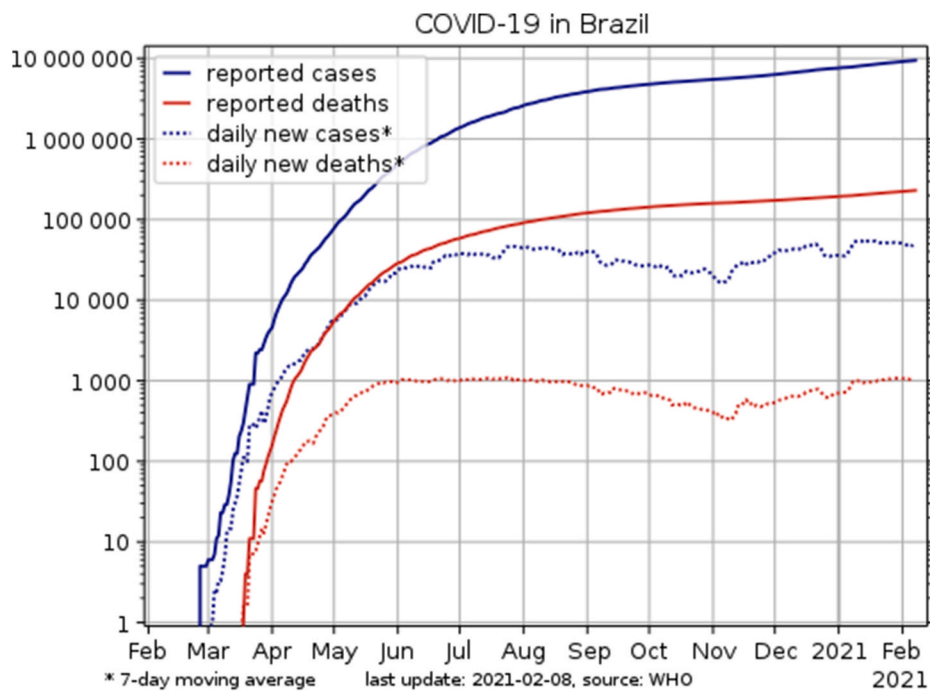
Not applicable.

Provenance and peer review

Not commissioned, externally peer reviewed.



A



B

Fig. 1. COVID-19 death toll in Latin America, Caribbean region and significant mutations in SARS-CoV-2 Brazil variants (A) COVID-19 death toll in Mexico, (B) COVID-19 death toll in Brazil, (C) COVID-19 death toll in Argentina, (D) COVID-19 death toll in Columbia.(Data source: Fig. 1. A, B, C, D, https://commons.wikimedia.org/wiki/User:Hbf878#COVID-19_Charts). (E) Significant mutations in P.1 and P.2 lineage of Brazil variants.

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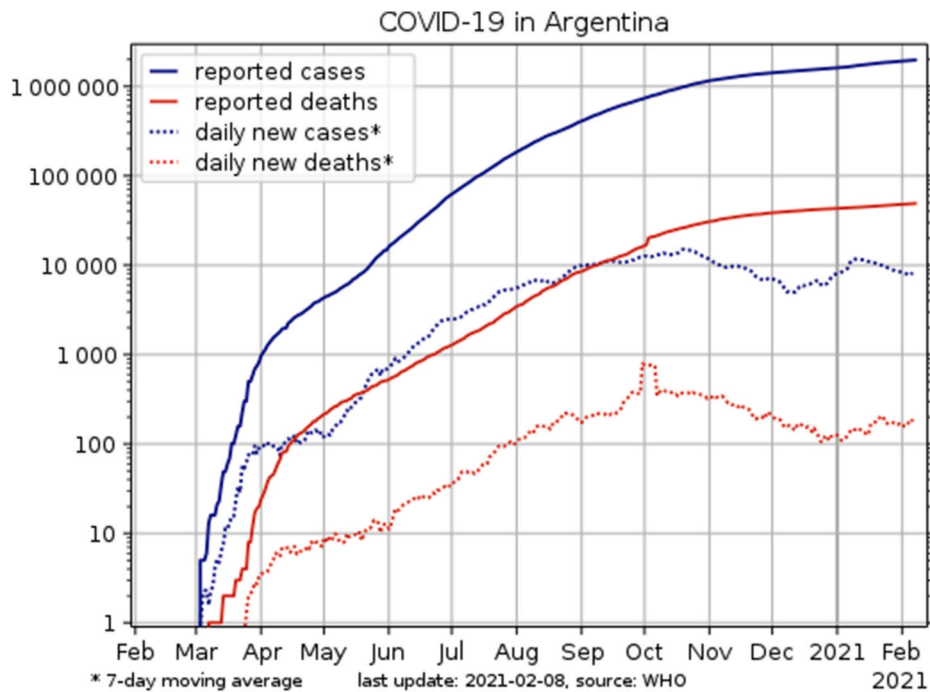
Not applicable.

Registration of research studies

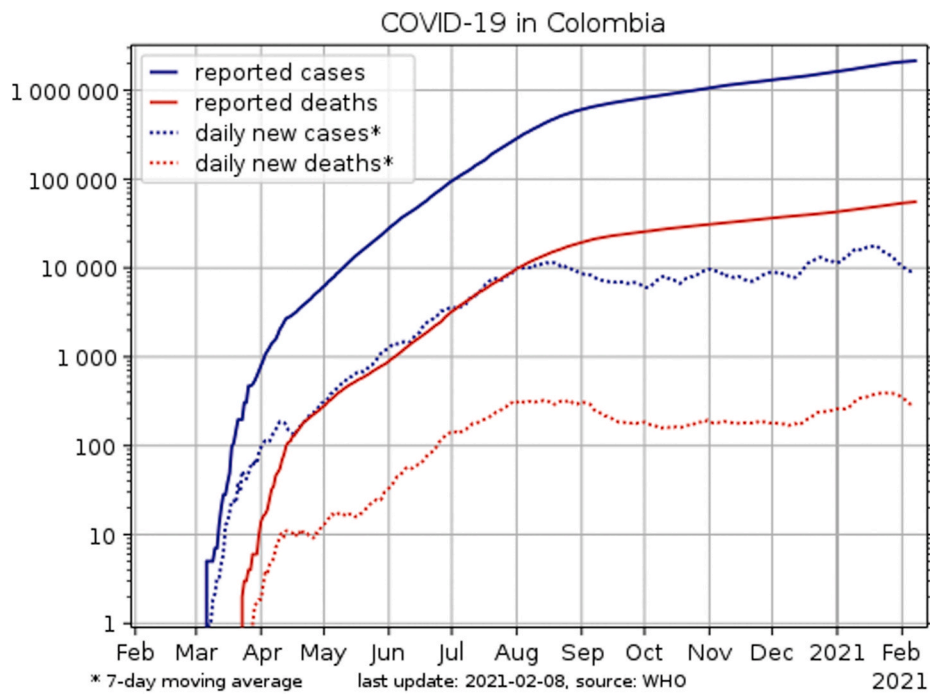
Name of the registry: Not applicable.

Consent

Not applicable.



C



D

Fig. 1. . (continued).

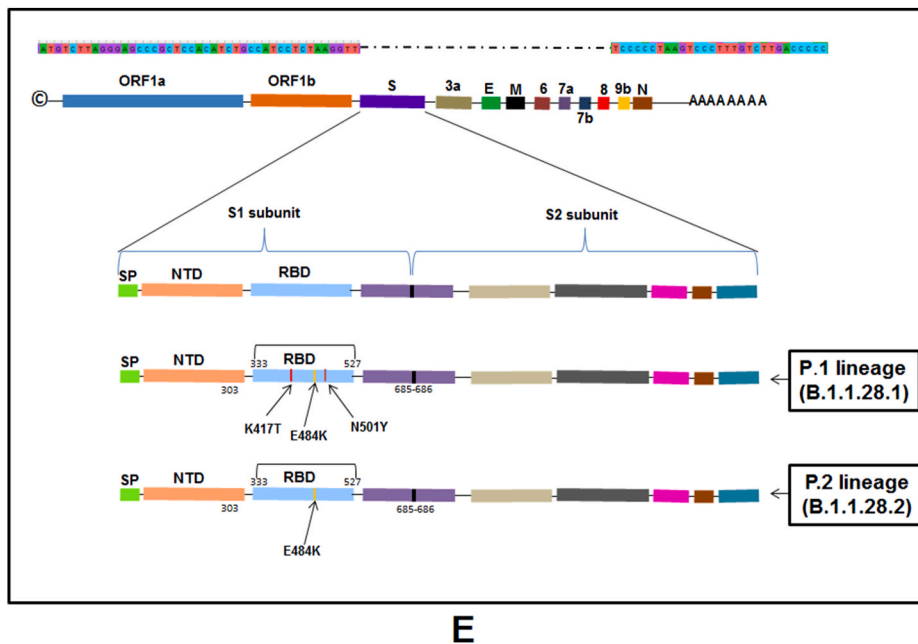


Fig. 1. . (continued).

Declaration of competing interest

All authors declare no conflicts of interest.

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Ethical approval

Research studies not involving any patients.

Consent

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Author contribution

Study concept and design, data collection, data analysis and writing main draft by C. Chakraborty. Writing-review and editing by M. Bhat-tacharya and A. R. Sharma. Review-editing and overall supervision by S. S. Lee and G. Agoramoorthy. All authors approved the final draft of the manuscript.

Registration of research studies

Not required.

Guarantor

Prof. Chiranjib Chakraborty, Department of Biotechnology, School of Life Science and Biotechnology, Adamas University, Barasat-Barrackpore Rd, Jagannathpur, Kolkata, West Bengal 700126, India. E-mail: drchiranjib@yahoo.com Tel: +91-9871608125.

Prof. Govindasamy Agoramoorthy, College of Pharmacy and Health Care, Tajen University, Yanpu, Pingtung 907, Taiwan, Email: agora_m@tajen.edu.tw Tel: +886-7-5253623.

Declaration of competing interest

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Chiranjib Chakraborty^{a,*}, Manojit Bhattacharya^b, Ashish Ranjan Sharma^c, Sang-Soo Lee^c, Govindasamy Agoramoorthy^{d,**}

^a Department of Biotechnology, School of Life Science and Biotechnology, Adamas University, Barasat-Barrackpore Rd, Kolkata, West Bengal, 700126, India

^b Department of Zoology, Fakir Mohan University, Vyasa Vihar, Balasore, 756020, Odisha, India

^c Institute for Skeletal Aging & Orthopedic Surgery, Hallym University-Chuncheon Sacred Heart Hospital, Chuncheon-si, 24252, Gangwon-do, Republic of Korea

^d College of Pharmacy and Health Care, Tajen University, Yanpu, Pingtung, Taiwan

* Corresponding author. Department of Biotechnology, School of Life Science and Biotechnology, Adamas University, Barasat-Barrackpore Rd, Jagannathpur, Kolkata, West Bengal, 700126, India.

** Corresponding author. College of Pharmacy and Health Care, Tajen University, Yanpu, Pingtung, 907, Taiwan.
E-mail addresses: drchiranjib@yahoo.com, chiranjib.chakravartty@adamasuniversity.ac.in (C. Chakraborty), agoram@tajen.edu.tw (G. Agoramoorthy).