

Insights into SARS-CoV-2 in Angola during the COVID-19 Peak: Molecular Epidemiology and Genome Surveillance

NGIAMBUDULU M. FRANCISCO¹, Stephanie Van Wyk², Monika Moir², James San², Cruz Sebastiao³, Houriiyah Tegally⁴, Joicymara Xavier², Akhil Maharaj², Zoraima Neto⁵, Pedro Afonso³, Domingos Jandondo³, Joana Paixão⁶, Julio Miranda³, Kumbelembe David³, Luzia Inglês³, Amilton Pereira³, Agostinho Paulo⁷, Ralisa Carralero³, Helga Freitas⁸, Franco Mufinda⁵, Silvia Lutucuta⁹, Mahan Ghafari¹⁰, Marta Giovanetti¹¹, Jennifer Giandhari⁴, Sureshnee Pillay⁴, Yeshnee Naidoo², Lavanya Singh¹², Derek Tshiabuila¹², Darren Martin¹³, Lucious Chabuka¹², Wonderful Choga¹², Dorcas Wanjohi¹⁴, Sarah Mwangi¹⁴, Yusasha Pillay¹², Yenew Kebede¹⁴, Edwin Shumba¹⁵, Pascale Ondoa¹⁵, Cheryl Baxter¹², Eduan Wilkinson¹⁶, Sofonias Tessema¹⁴, Aris Katzourakis¹⁷, Richard Lessells¹⁰, Tulio de Oliveira¹⁰, and Joana Morais⁶

¹Instituto Nacional de Investigação em Saúde

²CERI, Stellenbosch University

³INIS, Angola

⁴University of KwaZulu-Natal Nelson R Mandela School of Medicine

⁵MINSa, Angola

⁶INIS, Luanda

⁷INIS, ANGOLA

⁸DNSP, Angola

⁹MINSa

¹⁰KRISP, UKZN

¹¹Oswaldo Cruz Foundation, Rio de Janeiro, Brazil

¹²Stellenbosch University Faculty of Medicine and Health Sciences

¹³University of Cape Town Faculty of Health Sciences

¹⁴Africa CDC

¹⁵ASLM

¹⁶Stellenbosch University

¹⁷Oxford University

June 21, 2023

Abstract

Background: In Angola, COVID-19 cases have been reported in all provinces, resulting in >105,000 cases and >1,900 deaths. However, no detailed genomic surveillance into the introduction and spread of the SARS-CoV-2 virus has been conducted in Angola. We aimed to investigate the emergence, and epidemic progression during the peak of the COVID-19 pandemic in Angola. Methods: We generated 1,210 whole-genome SARS-CoV-2 sequences, contributing West African data to the global context, that were phylogenetically compared against global strains. Viral movement events were inferred using ancestral state reconstruction. Results: The epidemic in Angola was marked by four distinct waves of infection, dominated by 12 viral lineages,

including VOCs, VOIs, and the VUM C.16, which was unique to Southwestern Africa and circulated for an extended period within the region. Viral exchanges occurred between Angola and its neighboring countries, and strong links with Brazil and Portugal reflected the historical and cultural ties shared between these countries. The first case likely originated from southern Africa. Conclusion: A lack of a robust genome surveillance network and strong dependence on out-of-country sequencing limit real-time data generation to achieve timely disease outbreak responses, which remains of the utmost importance to mitigate future disease outbreaks in Angola.

Hosted file

Francisco_and_van_Wyk_et_al_19.06.2023.docx available at <https://authorea.com/users/631188/articles/650652-insights-into-sars-cov-2-in-angola-during-the-covid-19-peak-molecular-epidemiology-and-genome-surveillance>







