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


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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.

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