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## SARS-CoV-2 emerging variants in Africa: view from Gabon

Since SARS-CoV-2 appeared in late 2019 in Wuhan, China, variants have emerged around the world. The general concern is that these variants appear to cause more severe disease, spread more easily between humans, and might change the effectiveness of current treatment and vaccines.<sup>1-5</sup> Travel-related dissemination of SARS-CoV-2 fuels the global pandemic and the spread of variants. Therefore, SARS-CoV-2 genomic surveillance would help trace the emergence and spread of variants to better understand and anticipate their impact on public health.

SARS-CoV-2 genomic surveillance in Africa has been portrayed as a challenge. Nevertheless, Gabon has taken up the challenge of setting up and implementing SARS-CoV-2 genomic surveillance. Gabon's strategy in the fight against COVID-19 includes SARS-CoV-2 PCR testing of volunteers and travellers (this applies to travel into and out of Gabon, as well as interprovincial travel within Gabon); contact tracing; and treatment. Here, we report the first data of the Gabonese genomic surveillance initiative.

A total of 120 samples from individuals diagnosed by PCR with SARS-CoV-2 infection between Jan 31, 2021, and March 4, 2021, were selected. 100 (83.3%) samples were from international travellers and 20 (16.7%) were from family clusters.

A total of 106 samples were successfully sequenced (by use of the Sanger method). Variants were found in 86 (81.1%) of 106 samples. The British variant (B.1.1.7) was found in 43 (40%) of 106 samples, variant B.1.525 was found in 34 (32%) of 86 samples, six (6%) of 106 samples had the South African variant (B.1.351), and three (3%) of 106 samples had the Indian variant. To the best of our knowledge, this is

the first report of the presence of the SARS-CoV-2 Indian variant in Africa.

Origins-based analysis (appendix) showed that the British variant of the B.1.1.7 lineage was found mainly in passengers from Burkina Faso (14), in family clusters (11), and in passengers from France (six). The B.1.525 variant was found mainly in passengers from Cameroon (13), followed by Nigeria (eight). The South African variant (B.1.351) was detected in passengers who came from Cameroon (two), France (two), Guinea (one), and Côte d'Ivoire (one). Our data clearly show that SARS-CoV-2 variants are spreading throughout Africa.

The B.1.525 variant was isolated from a patient arriving from Nigeria. This variant first emerged in Nigeria and the UK. The B.1.351 variant (South African variant) was supposedly introduced by two patients who arrived in Gabon from France. The detection of the B.1.1.7 variant in community samples after its first detection in December, 2020 (GenBank: MW650650.1) highlights the spread of this variant in Gabon.

Our findings highlight the introduction and circulation in Gabon of SARS-CoV-2 variants including British, South African, and Indian variants. Beyond Gabon, our data reveal the circulation of SARS-CoV-2 variants in many sub-Saharan African countries. These distributions should be interpreted with due consideration of surveillance limitations, including differences in sequencing capacities and prioritisation of samples for sequencing between countries.

In conclusion, variants with concerning mutations were found from our surveillance. Currently, additional sequencing is ongoing to better understand the origin, prevalence, and transmission characteristics of these SARS-CoV-2 variants.

We declare no competing interests. Financial support was provided by the Gabonese Government. The study was authorised by the national Comité de pilotage du Plan de veille et de Riposte sur L'épidémie à Coronavirus (COPI-L-CORONAVIRUS). We gratefully acknowledge Guy-Patrick Obiang

Ndong, Gabonese Ministry of Health, for his contribution to this project. We also acknowledge the Gabonese COVID-19 Scientific Committee. We thank the staff of Laboratoire Professeur Daniel Gahouma, CHU Mère-Enfant Fondation Jeanne Ebori, and CERMEC for their commitment to the fight against COVID-19.

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Published Online  
June 8, 2021  
[https://doi.org/10.1016/S2666-5247\(21\)00125-7](https://doi.org/10.1016/S2666-5247(21)00125-7)  
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