Rapidly rising cases with Omicron in Senegal

A. Padane^{1,2}, M. Mbow^{1,3}, A. Mboup¹, C. K. Diedhiou¹,
K. Gueye¹, C. I. Lo², S. Ndiour¹, N. Leye¹, A. S. Ndoye¹,
A. J. Selbé Ndiaye¹, N. D. Diagne¹, S. Ndiaye¹, M. Beye²,
M. Sarr², G. Lo¹, D. Wade¹, A. Ahouidi¹, P. A. Diaw¹,
M. Camara¹, N. C. Touré Kane¹ and S. Mboup¹
I) Institut de Recherche en Santé, de Surveillance Épidémiologique et de Formation (IRESSEF), Dakar, Senegal, 2) IHU Méditerranée Infection,
Marseille, France and 3) Service d'Immunologie FMPO, Université Cheikh Anta Diop de Dakar, Dakar, Senegal

Original Submission: 9 January 2022; Revised Submission: 11 January 2022; Accepted: 14 January 2022 Article published online: 21 January 2022

Corresponding author: A. Padane, Institut de Recherche en Santé, de Surveillance Épidémiologique et de Formation (IRESSEF), Dakar, Senegal. Tel.: +221 775080727; fax: +221 338502017. E-mail: abdou.padane@iressef.org

Dear Editor,

Since the first confirmed case in Wuhan, China, in December 2019 [1], Senegal has experienced several waves of COVID-19 pandemic. The British variant was dominant during the second pandemic wave [2]. Its presence in Senegal was revealed by the laboratory of the Institut de Recherche en Santé, d'Epidémiologie et de Formation (IRESSEF), which performs daily phylodynamic monitoring of SARS-CoV-2 (A). Since the start of the pandemic, the World Health Organization (WHO) designated five variants as Variant of Concern (VOC). The Omicron variant is the fifth VOC after Alpha (B.I.I.7), Beta (B.I.351), Gamma (P.I), and Delta (B.1.617.2) [3]. This Omicron (B.1.1.529) variant detected for the first time in South Africa in November 24, 2021 [4]. Thus several countries such as Brazil, United Kingdom, USA, Israel, Canada, Saudi Arabia, and Singapore have established a restriction on flights from southern African countries such as Botswana, Lesotho, Namibia, Malawi, Mozambique, and South Africa [5]. In this report, we describe the first case of Omicron variant detected in Senegal and its evolution over the weeks (Fig. 1).

To track the spread of the Omicron variant in Senegal, IRESSEF's Genomic laboratory has collected many samples in collaboration, with health authorities. Samples were collected in the regions of Dakar and Thiès, areas where the variant was first detected. Samples were also collected from contacts of patients for sequencing using Oxford nanopore platform and ARTIC protocol. FASTQ files were analyzed using ARTIC bioinformatic pipeline. Pangolin (version) was used to determine the lineage for each sample. Mutations analysis was done and confirmed using CoVsurver in GISAID. All consensus genomes were deposited in GISAID.

IRESSEF detected the first positive case of the Omicron variant on Friday, December 3, 2021, in an outgoing traveler. The RT-PCR test using nasopharyngeal swab was positive for the SARS-COV-2 virus with a cycle threshold (CT) of 27. The patient was a 58-year-old male French visiting Senegal. He arrived on Monday, November 22, 2021 by a flight from a country in the sub-region. He received his first vaccination dose on April 13, 2021 with AstraZeneca and the second one on June 25th with Pfizer. He stayed in Dakar in a local hotel and participated in an event attended by nearly three hundred people of different nationalities. The event took place from November 24 to 25, 2021. He was quarantined and followed in a local health center. As of December 4, 2021, the infected patient was still asymptomatic.

On December 3, 2021, out of 24 sequenced samples, we characterized 21 new variants of concern, including 20 Delta B.1.617.2 and I Omicron B.1.1.529. The case was notified to the Directorate General of Health on Friday, December 3, 2021. The surveillance division of the Direction of Prevention proceeded with the investigation of the case on Saturday, December 4, 2021. The second notification was done on December 19, 2021 when 16 new variants of concern were detected, of which 11 samples were positive for the Omicron variant and 5 for the Delta variant. The third notification on December 25, 2021, out of 24 samples sequenced we obtained 22 variants of concern including: 20 Omicron variants and 2 Delta variants.

We aimed to sequence any positive sample collected and ensure real time surveillance of the coronavirus strains circulating in Senegal (**B**). With real-time sequencing, we were able to detect the first patient infected with the new coronavirus variant Omicron present with 32 mutations in the spike protein, 15 in the Receptor Binding Domain (RBD) 23 alone (residues 319-541) [4]. This new variant of interest was first reported to the WHO from South Africa on November 9th 2021 and spread around the world. The number of cases has increased rapidly in South Africa reaching proportions of 80% (Ingrid Torjesen). In Senegal, according to the latest data we have from Iressef, the contamination rate is over 75%. As part of the response to the Covid-19 pandemic, Senegal has strengthened its surveillance system following the notification by the WHO of the Omicron variant. Our results show clearly



FIG. 1. A. Daily Phylodynamic evolution of SARS-CoV-2 in Senegal; B. Phylogenetic position of Omicron isolated in IRESSEF (Phylogeny reconstruction was performed using the nextstrain/ncov tool (https://github.com/nextstrain/ncov) then visualised with Auspice (https://docs.nextstrain.org/ projects/auspice/en/stable/). The genome of the original Wuhan-Hu-1 coronavirus isolate (GenBank accession no. NC_045512.2) was added as outgroup. Major (most prevalent) variants are labeled) and **C**. Evolution Omicron variant over time in Senegal.

shows rapid progression of the Omicron variant and this new variant has become clearly predominant in new infections of SARS-CoV-2 (**C**).

In this very particular context of the emergence of SARS-CoV-2 variants, daily surveillance is carried out to prevent the risk of the virus spreading in an African context where vaccination coverage is not optimal to protect the population. Close collaboration exists between the authorities in charge of health and the Institut de Recherche en Santé, de Surveillance Epidémiologique et de Formations for phylodynamic surveillance (**A**), to prevent the spread of new variants which is a source of concern and panic for countries as well as the world.

Conflict of interest

The authors have declared that no competing interests exist.

Funding source

This study was funded by the "European and Developing Countries Clinical Trials Partnership" (EDCTP) (Grant Nr: RIA2020EF-2961), the "West African Task Force for the Control of Emerging and Re-

© 2022 The Author(s). Published by Elsevier Ltd, NMNI, 45, 100959

This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/).

emerging Infectious Diseases" (WATER), and "Innovation in Laboratory Engineered Accelerated Diagnosis" (iLEAD) (Grant Nr. OPP1214434/INV-009631). The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript. The views expressed are those of the authors, and the funders are not responsible for any use that may be made of the information contained herein.

Ethical approval

This study was approved by the National Ethics Committee for Health Research of Senegal under the following number: 000159/MSAS/CNERS/Sec, on August 21st, 2020. Free and informed consent is provided by each adult individual who participated in this study.

Author contributions

AP, KG, SM conceived and designed the study. SN, NL, SEN, DD and CD performed the experiments. AP, NL, CD, SN, KG, and DD recruited study participants and collected data. AP and KG analyzed and interpreted the data. SM, PAD, MM, DW, NL, GL contributed to reagents/materials/ analysis tools. AP, PAD, KG, CD, AA, AS, GL, NL participated to study design. AP, SM, participated to study coordination. AP, KG, SN, and CL wrote/drafted the manuscript. AM, DW, NL, GL, CL, MM, PAD, NCK, SM, AA, GL, PAD, MAC, MS and MB reviewed critically the manuscript for important intellectual content. SM, NCK and MAC approved the final version to be published. All authors approved the final version of the manuscript.

Acknowledgements

We gratefully thank the individuals that participated in this study and the IRESSEF's personnel involved in the SARS-CoV-2 testing and sequencing.

References

- Huang C, Wang Y, Li X, Ren L, Zhao J, Hu Y, et al. Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China. Lancet Févr 2020;395(10223):497–506.
- [2] Padane A, Kanteh A, Leye N, Mboup A, Manneh J, Mbow M, et al. First detection of SARS-CoV-2 variant B.1.1.7 in Senegal. New Microb New Infect Mai 2021;41:100877.
- [3] Tracking SARS-CoV-2 variants [cité 30 déc 2021]. Disponible sur, https://www.who.int/emergencies/what-we-do/tracking-SARS-CoV-2variants.
- [4] Sahoo JP, Samal KC. World on alert: WHO designated South African new COVID strain (Omicron/B.1.1.529) as a variant of concern. Biot Res Today 29 Nov 2021;3(11):1086–8.
- [5] Gao S-J, Guo H, Luo G. Omicron variant (B.1.1.529) of SARS-CoV-2, a global urgent public health alert! J Med Virol [Internet]. [cité 30 déc 2021];n/a(n/a). Disponible sur: https://onlinelibrary.wiley.com/doi/abs/ 10.1002/jmv.27491.