Heterogeneity of the Omicron variant in Senegal

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Dear Editor,

Since the first coronavirus disease 2019 (COVID-19) infection appeared in December 2019 in Wuhan, China [1], different variants of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) have been identified in the world. Thus, another variant of concern (VOC) was designated Omicron (B.1.1.529) on November 26, 2021 by the World Health Organization [2]. This highly mutated SARS-CoV-2 variant, first detected in samples collected on November 11, 2021 in Botswana and on November 14, 2021 in South Africa [3], has rapidly surged past other variants in many parts of the world [4].

However, based on these mutations, Omicron variant has recently been divided into several distinct lineages and has the highest transmissibility of previous SARS-CoV-2 variants.

In Senegal, the first Omicron strain was sequenced at IRESSEF on December 3, 2021 [5] and coincided with the sharp rise in new infections, heralding the onset of the fourth wave. This variant continues to exhibit high genetic variability, despite the decreased incidence of covid-19 in Senegal. In this study, we analyze the genomic evolution of omicron variant lineages detected in Senegal and their phylogenetic information.

One thousand and fifty (1050) nasopharyngeal swabs from patients positive for SARS-CoV-2 by RT-PCR were selected for sequencing from June 2020 to Avril 2022. Therefore, these samples were sequenced using nCoV-2019 ARTIC V3 protocol and GridION divise (Oxford Nanopore Technologies). The genome was assembled using the ARTIC pipeline bioinformatics workflow (https://artic.network/ncov-2019/ncov2019-bioinformatics-sop.html). Nexclade website (https://clades.nextstrain.org/) and Pangolin web platform (https://pangolin.cog-uk.io/) were used to determine the clade and the lineage of each genomic sequence respectively. Mutations analysis was done and confirmed using CoVsurver in GISAID (https://www.gisaid.org/epiflu-applications/covsurver-mutations-app/).

A total of 1050 samples were successfully sequenced. Thus, sequencing analysis showed that 337 samples belonged to the Omicron variant lineage, of whom 17.5% of BA.1 (184/1050), 1.9% of BA.1.1 (20/1050), 0.19% of BA.1.17 (2/1050), 11.6% of BA.2 (122/1050), 0.09% of BA.2.3 (1/1050), 0.57% of BA.3 (6/1050), 0.09% of XE (1/1050), 0.09% of XN (1/1050) and 713 belonged to other variants in majority Delta 20.28% (213/1050). Indeed, since its first detection, the Omicron variant has spread rapidly in Senegal and has surpassed other variants such as Delta (Fig. 1A). Focusing on the evolution of this variant over time, we found a high diversity of this variant despite the decrease in the incidence of Covid-19 in Senegal by the mid-January 2022 (Fig. 1B). Indeed, over the weeks new lineages of the Omicron variant were identified at IRESSEF.

Thus, BA.1 was the predominant lineage from December to early January 2022, causing the initial omicron surge and 4th wave in Senegal (Fig. 1A). Subsequently, the frequency of BA.2 increased steeply in January 2022 and replaced the BA.1 by mid-January 2022. This rapid increase in BA.2 led to a second peak during the 4th wave (Fig. 1B). However, the frequency of the BA.2 lineage continued to increase until February 2022, while the number of confirmed cases began to decline by the mid-January 2022 in Senegal (Fig. 1B). In addition, this lineage remains the predominant despite the emergence of new lineages of Omicron variant detected at IRESSEF such as BA.1.1, BA.3, BA.1.17 and BA.2.3 (Fig. 1B).

Recently, we identified a recombinant virus named XE and XN (recombinants lineages of BA.1 and BA.2). These new recombinants could be generated by the co-circulation of BA.1 and BA.2 lineages due to the high transmissibility of the omicron variant.

However, the pathogenicity of these lineages in humans and their capacity for transmission, particularly in a population

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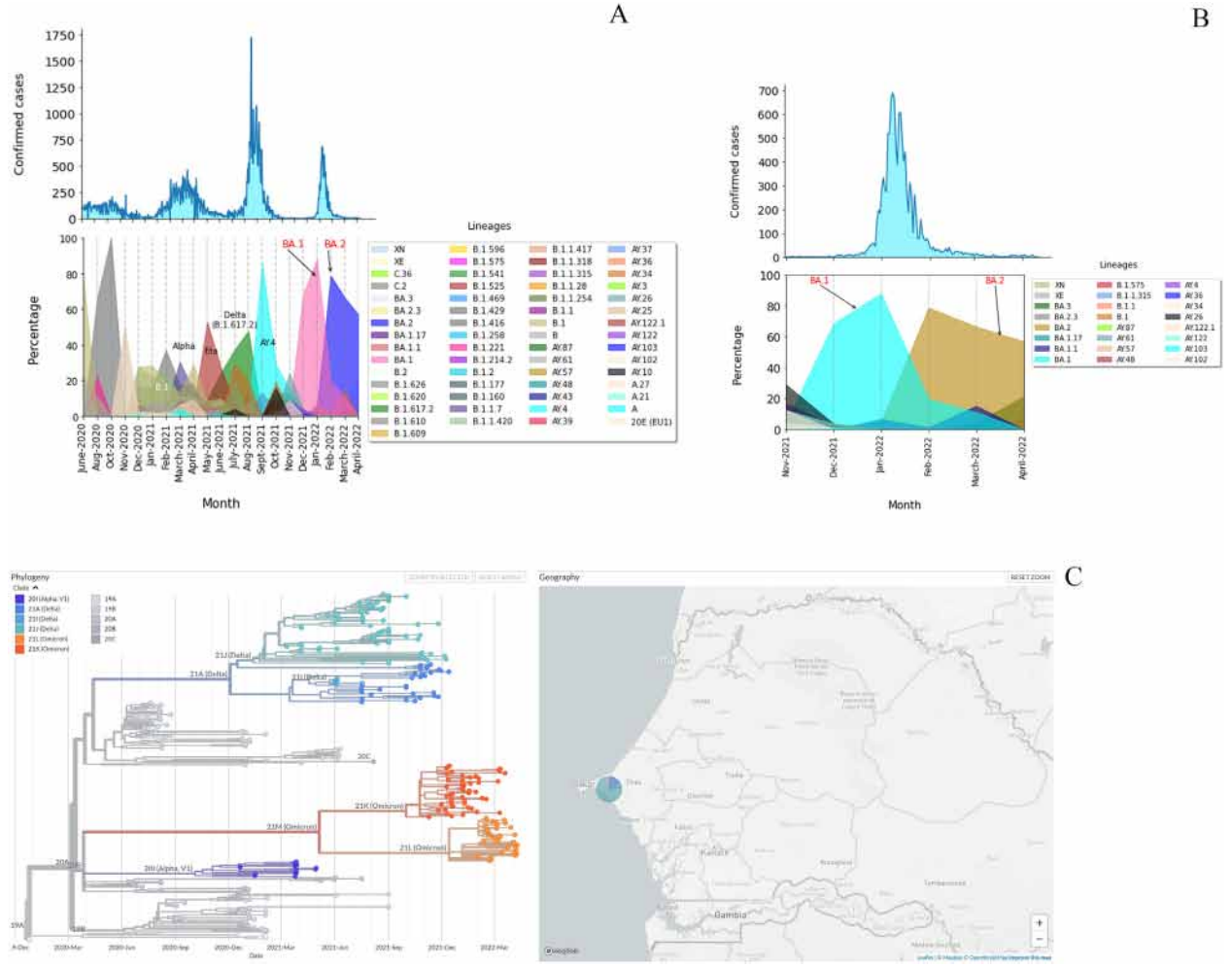

FIG. 1. A. Evolution of confirmed cases over time according to the WHO data and the different lineages of variant isolated at IRESSEF; **B.** Evolution of confirmed cases over time according to the WHO data and the different lineages of Omicron variant isolated at IRESSEF from the first detection of Omicron variant to last lineage of this variant and **C.** Phylogenetic information of the different lineage of different variants from Senegal isolated at IRESSEF (Phylogeny reconstruction was performed using the nextstrain/ncov tool (https://github.com/nextstrain/ncov) and then visualized with Auspice (https://docs.nextstrain.org/projects/auspice/en/stable/).

already exposed to natural infection or that has been vaccinated, are currently unknown. Further studies are therefore needed to determine more precisely the epidemiological characteristics and biological properties of these recombinant variants.

Importantly, the emergence of the BA.2 lineage at a time when the territories were experiencing the decline of the BA.1 wave underscores the need for high-quality surveillance.

Furthermore, phylogenetic analysis of the variants detected at IRESSEF showed that the Omicron variant did not evolve from the first VOC since its genome is so different from Alpha or Delta (Fig. 1C). In addition, the lineages of this variant appear to emerge at the same time suggesting that this variant had time to diversify before scientists discovered it.

In summary, despite a decrease in the incidence of covid-19 in Senegal, a significant variability of the omicron variant was observed. Due to the circulation of SARS-CoV-2 in the general population, which contributes to increased opportunities for recombination between genetically distinct variants, it is imperative to continue and to further strengthen genomic surveillance on a global scale and to rapidly assess the biological characteristics of potential emerging variants of concern that may be sources of new epidemic waves.

Conflict of interest

None declared.

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Ethical approval

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

Author contribution

CKD, AP, KG and SM conceived and designed the study. **SN, NL, SEN, NDD** and **CKD** performed the experiments. **CKD, AP, NL, SN, KG, NDD and YAD** recruited study participants and collected data. **CKD, AP and KG** analyzed and interpreted the data. **SM, PAD, MM, DW, NL, GL** contributed to reagents/materials/analysis tools. **CKD, AP, PAD, KG, AA, AS, AJN, GL, NL** participated to study design. **CKD, AP and SM**, participated to study coordination. **CKD, AP and KG** wrote/drafted the manuscript. **AM, MM, NL, GL, CL, DW, BC, CS, GL, PAD, MAC, AA, NCK and SM**, 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.

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