

Contribution of point-of-care laboratories in the molecular diagnosis and monitoring of COVID-19 in Niakhar, Dielmo and Ndiop rural areas in Senegal

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Dear Editor

Since December 2019, the world has been fighting the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), originating from Wuhan in China. Senegal is one of the countries most impacted by COVID-19 in West Africa, with 88,900 confirmed cases and 1,968 deaths as of 29/12/2022. In addition to the ancestral virus, several variants have been reported since the detection of the first case, including the variant of concern (VOC), B.1.1.7 (according to the Pangolin classification) [1]. In November 2011 in Dielmo (13°43'N, 16°24'W) and in September 2015 in Niakhar (14°28'N, 16°24'W), point-of-care (POC) laboratories were set up for the molecular diagnosis of infectious diseases in rural settings. Real-time RT-PCR assays have been implemented in these laboratories to locally identify SARS-CoV-2 and its variants and provide information about their circulation in rural areas in Senegal.

From April 2020 to February 2022, nasal swabs were collected from febrile patients (temperature $\geq 37.5^{\circ}\text{C}$) with respiratory symptoms (cough, expectoration, dyspnoea, sore throat and/or rhinitis) consulting at several health posts and analyzed by molecular biology. Primers and probes developed by Corman et al. were used to detect the ancestral virus [2]. In-house qPCR systems targeting variant-specific regions were used to detect other SARS-CoV-2 variants and their mutations namely: the spike N501Y substitution present in B.1.1.7 [20I (V1)], B.1.351 (a.k.a. Beta, 20H (V2)), B.1.1.28.1 [a.k.a. P.1, Gamma, 20J (V3)], and B.1.1.529 (a.k.a. Omicron, 21K, 21L) variants; the spike L452R and P681R substitutions present in the B.1.617.2 (a.k.a. Delta, 21I, 21J) or 21A) variant [3]; the spike G21848C (E96Q) mutation that is common to B.1.640.1 (a.k.a. Congo-Breton) and B.1.640.2 (a.k.a. IHU) variants and the spike P681H and GGG2888AAC substitutions present in B.1.1.529 (a.k.a. Omicron, 21K, 21L) variants.

The project was approved by the National Ethics Committee for Health Research of Senegal (NECHR), authorization number No. 00087 MSAS/ DGS/ DS/ CNERS.

Statistical analyses were performed using Epi Info software, version 7.0.8.0 (Centers for Disease Control and Prevention,

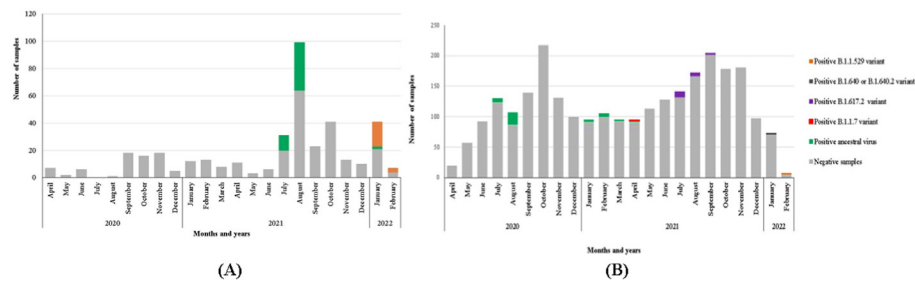


FIG. 1. Number of collected samples and SARS-CoV-2 variants diagnosed by month in the Dielmo, Ndiop (A) and Niakhar (B) areas.

Atlanta, GA, USA). Data were compared using the Pearson chi² or Fisher exact tests when applicable and the statistical significance threshold was set at $p \leq 0.05$.

A total of 3,064 samples were analyzed, including 2,673 from the Niakhar area and 391 from Dielmo and Ndiop (a neighboring village). The overall prevalence of SARS-CoV-2 infection in the Niakhar area was 2.2% (58/2,673), while that in Dielmo and Ndiop villages was significantly higher, reaching 18.4% (72/391) ($p = 0.0000001$).

In Niakhar, the ancestral virus was predominant, accounting for 62.1% (36/58) of positive samples, and was detected from July 2020 to April 2021. The B.1.617.2 variant ranked second (24.1%, 14/58) and was detected from July to September 2021 (Fig. 1). One suspected case of B.1.1.7 (1.7%) was diagnosed in April 2021. Two cases of B.1.640.1/2 variants were diagnosed in January 2022 (3.5%) and one case of the B.1.1.529 variant was diagnosed in February 2022 (1.7%).

In Dielmo and Ndiop villages, the ancestral virus accounted for 48 of 72 positive samples (67.0%) and was detected in July and August 2021 and January 2022 (Fig. 1). The B.1.1.529 variant was detected in 21 samples (29.2%) in January and February 2022.

The overall prevalence of COVID-19 was higher in Dielmo and Ndiop, which may have been the result of easier access to the POC laboratory in these villages, whereas the POC of Niakhar covers a much larger geographical area. A lower diversity of SARS-CoV-2 variants was observed in Dielmo and Ndiop.

We noted that the onset of SARS-CoV-2 infection in Niakhar, Dielmo, and Ndiop coincided with the Tabaski (Aïd el-Kebir) in July or with the end of the year, when much of the population visit their relatives. This likely contributed to the spread of SARS-CoV-2 and its variants in these areas. Herein, we complete the knowledge of the circulation of the virus and its variants in rural Senegalese areas, for which no data are available to the best of our knowledge. The results suggest that the persistence of the pandemic was due to the high mutation potential of the virus and the constant appearance of VOC. Thus, as observed throughout the world, the successive waves

that have been recorded in Senegal were each due to the emergence and spread of variants [4].

Availability of data and material

Data are available upon request from the corresponding author and will be transmitted in a format that allows the protection of the participants' personal information.

Declaration of competing interest

I declare that the authors have no competing financial, professional, or personal interests as defined by the journal that might be perceived to influence the results and/or discussion reported in this article.

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