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Short communication

Emergence and evolution of the Omicron SARS-CoV-2 variant in the island of Martinique



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ABSTRACT

Introduction: We aimed to describe the epidemiological situation during the Omicron variant circulation in light of genomic surveillance data in Martinique, a territory with low vaccination rates.

Patients and methods: We exploited COVID-19 national databases of virological tests, for the collection of hospital data and for the sequencing data from December 13, 2021 to July 11, 2022.

Results: Three prevailing sub-lineages of Omicron have been identified in Martinique (BA.1, BA.2, BA.5) during this period causing three distinct waves characterized by an increase in virological indicators compared to previous waves, with moderate severity in the first and last waves, caused by BA.1 and BA.5, respectively.

Conclusion: The SARS-CoV-2 outbreak is still progressing in Martinique. Genomic surveillance system in this overseas territory must be continued for rapid detection of emerging variants/sub-lineages.

1. Introduction

The Omicron variant (B.1.1.529) of SARS-CoV-2 was first identified in November 2021 in South Africa. It was classified as a variant of concern (VOC) by the World Health Organization (WHO) because of its high transmissibility and evasion from neutralizing antibodies induced by vaccination or natural infection with wild-type virus [1–3].

Like other countries worldwide, Martinique, a French Caribbean island with 361,225 people residing as of January 1, 2020, has had a circulation of SARS-CoV-2 viruses [4]. At the start of 2021, the seroprevalence rate of SARS-CoV-2 infections was estimated at 8.6% in Martinique [5]. On this island, the first case of Omicron variant was detected on December 15, 2021. The genomic surveillance system implemented by the EMERGEN Consortium has tracked and measured as accurately as possible the diffusion of this variant on the island. The current paper aims to describe the epidemiological

situation during the Omicron variant circulation in light of genomic surveillance data in Martinique, a territory with low vaccination rates.

2. Material and methods

We described the weekly incidence and positivity rates using COVID-19 national database of virological tests (PCR and antigen tests) named SI-DEP. We also described hospitalizations and deaths related to COVID-19 using the SI-VIC database for the collection of hospital data.

As in Metropolitan France, the monitoring of SARS-CoV-2 variants in Martinique relies on screening for mutations of interest and sequencing of the virus genome.

Reverse transcription followed by quantitative PCR (RT-qPCR) tests targeting SARS-CoV-2 S gene mutations at positions 417, 452, and 484 were performed on a subset of samples positive for SARS-CoV-2 RNA by the city and hospital laboratories of Martinique (EurobioPlex Sars-COV-2 Fast SVD, Eurobio, France). The results of the mutation screening recorded in SI-DEP were used to describe the evolution of the detection of these mutations. Sam-

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ples were considered as probable Omicron infection when displaying K417N mutation whether or not associated with L452R in the absence of E484K substitution [6].

In addition to screening, SARS-CoV-2 genome surveillance was implemented to monitor and detect both circulating and emerging variants. This surveillance has two components: a representative (Flash survey) and an interventional/targeted component (other sequencing indications). The National Reference Center for Respiratory Viruses performed sequencing of the samples from the Flash surveys, selected among the RT-PCR-positive tests from a specific day each week [7] and interventional/targeted sequencing were performed at the virology laboratory of University Hospital of Martinique.

The sequencing data from these analyses were uploaded to the EMERGEN database (EMERGEN-DB) that we exploited from December 13, 2021 to July 11, 2022 in this article.

3. Results

3.1. Epidemiological features

During the survey period, three distinct epidemic waves of SARS-CoV-2 were recorded in Martinique. Concomitant with the detection of the Omicron variant, the weekly test positivity rates increased from 2.4% in week 50–2021 (W50–2021) to 20.9% in.

W04–2022. Over the same period, an exponential rise in COVID-19 incidence was observed with the first peak recorded in W03–2022: 3,156 cases per 100,000 population, almost three-fold of the peak incidence rate during the Delta wave (Fig. 1).

The indicators started increasing in W09–2022, achieving their peak in W10–2022 with 29.3% for the weekly test positivity rate and 3,206 cases per 100,000 population for the incidence rate. In W17–2022, a new increase in epidemiological indicators was observed, with the peak of the weekly test positivity rate in W23–2022 (38.0%). Concomitantly, the highest incidence rate was observed in W23–2022 with 2,536 cases per 100,000 population.

The impact of these three Omicron epidemic waves on the hospital system was heterogeneous and globally moderate compared to the previous waves (Fig. 2). The first wave led to an increase in new hospital and intensive care units (ICU) admissions, as well as in deaths. The impact of the second wave on the hospital system

was limited. An increase in hospital indicators was recorded during the last wave.

3.2. Virological finding

From W51–2021 to S25–2022, a total of 13,664 RT-qPCR-positive samples were screened for an average of 506 per week (Fig. 3A). An average of 33 positive RT-PCR samples was sequenced per week for a total of 891 samples sequenced during the study period. From W51–2021, a progressive decrease in the proportion of positive samples screened with the L452R mutation (mainly carried by the Delta variant) was observed. This mutation was detected at very low levels from W03–2022 to W17–2022. In contrast, an increase in samples carrying one of the mutations used as a proxy for the Omicron variant was observed as early as W52–2021, and quickly reached 50% from W03–2022. These screening results were confirmed by the detection of the Omicron variant by sequencing. First, the BA.1 lineage circulated from W51–2021 to W10–2022. The BA.2 lineage was introduced in W09–2022 and became dominant in W13–2022 (Fig. 3B). While the L452R mutation, previously used as a proxy for the Delta variant, had been detected at very low levels since W03–2022, it increased from 2.4% in W18–2022 to 12.2% in W20–2022. This increase in the detection of mutations at position L452 corresponded to the emergence of the BA.5 sub-lineage, revealed by sequencing from W18–2022. From W19–2022 BA.5 became dominant in Martinique (Fig. 3).

4. Discussion

Three successive increases in the weekly incidence and positivity rates were observed from W50–2021 to W25–2022 concurrent with the respective circulation of the sub-lineages BA.1, BA.2 and BA.5 of the Omicron variant. The circulation dynamics was similar to the Americas (North America, the Caribbean, Central America, and South America) where Omicron was introduced at the end of 2021 and rapidly replaced Delta and other lineages throughout the Region and globally [8]. The BA.1 sublineage circulated and was replaced by BA.2 between weeks 12 and 15 of 2022 which was replaced by BA.4 and BA.5 sublineages between weeks 25 and 34 [8].

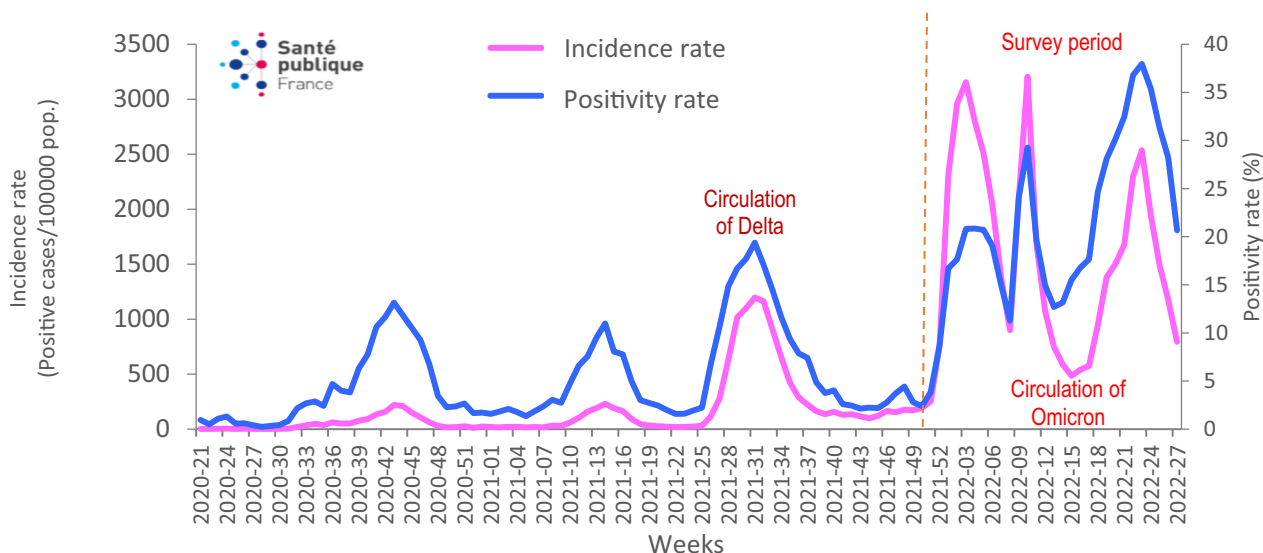


Fig. 1. Evolution of incidence and positivity rates per week from week 2020–21 (May 18–24, 2020) to week 2022–27 (August 04–10, 2022) in Martinique.

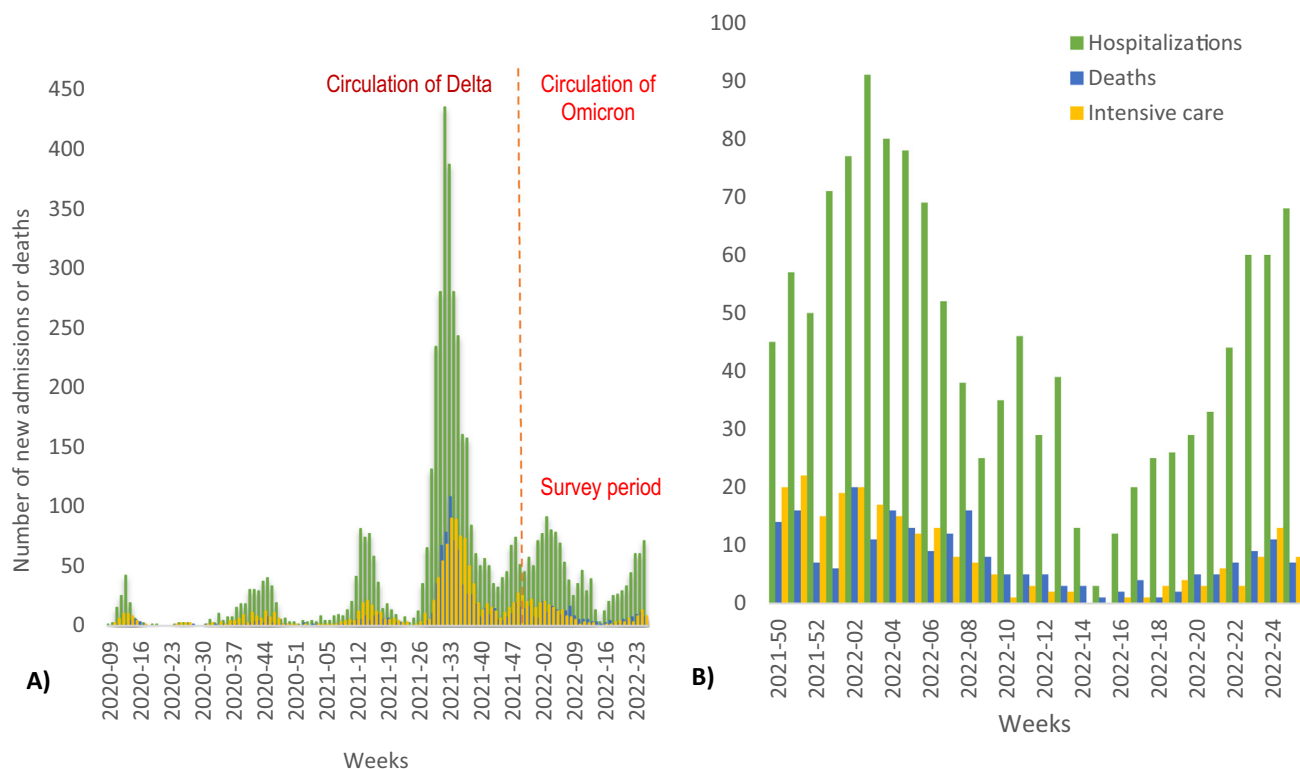


Fig. 2. Number of new hospital admissions (green bars), intensive care unit admissions (orange bars), new deaths (blue bars) per week from the emergence of SARS-CoV-2 in Martinique (week 2020–20; February 24–March 01, 2020) to week 2022–25 (June 20–26, 2022) (A) with a focus on the study period (B).

During these periods, very high incidence rates (almost triple that of the Delta wave peak) were reached. The increased transmissibility of the Omicron variant compared with all previous SARS-CoV-2 variants and additional increases of transmissibility between the successive sublineages played a role in these important waves [9,10]. Indeed, a study found that the effective reproduction number of Omicron BA.1 and BA.2 were 1.99 (95% CI 1.98–2.02) and 2.51 (95% CI 2.48– 2.55) times higher than the effective reproduction number of Delta, respectively [9]. Similarly, a study showed that Omicron BA.5 had a growth advantage of 12% per day compared to BA.2 [11].

Other factors that were most likely involved in the initiation of these waves are the progressive removal of protection measures after almost two years of restriction and several large meeting and festive events (Caribbean carnival, Easter's day, etc.), which attracted several thousands of people, held on the island.

Despite high incidence, a moderate hospital impact was observed during the circulation of the Omicron sublineages compared with the previous wave, dominated by the Delta variant. In spite of the lower vaccination coverage, the impact of the Omicron wave on hospitalizations was similar in Martinique compared to Metropolitan France. Indeed, based on the first cases of the Omicron variant described, anosmia (loss of smell) and ageusia (loss of taste) were less frequent and severe forms were more scarce [6]. Similarly, fewer hospitalizations and deaths were recorded during the Omicron wave in South Africa. Indeed, a South African study described that the fourth wave due to the Omicron variant was responsible for 11.2%, 3.9%, and 3.3% of all hospitalizations, recorded deaths, and additional deaths due to COVID-19, respectively. As a comparison, the third wave, in which the Delta variant was dominant, contributed 43.6%, 49.3%, and 52.7% [3]. Also, a rapid investigation of the first cases of BA.4 and BA.5 in France (including three overseas territories: Martinique, Guadeloupe, and Reunion Island) showed no severe clinical presentation [12]. A

Canadian study also demonstrated the lower risk of severe outcomes in Omicron-infected individuals compared with the Delta variant [13]. Part of the lower severity of the Omicron variant is explained by pre-existing immunity in the population that was induced by previous natural infection and vaccination [3].

While at the peak of the Delta wave, 437 new hospitalizations and 108 new deaths were recorded in W32-2021 and W33-2021 respectively [14], the BA.1 wave generated a maximum of 91 new hospitalizations in W03-2022 and 20 deaths in W02-2022 during its peak. While the wave related to the BA.5 lineage is still in progress, a trend of its hospital impact identical to BA.1 has been observed. The hospital impact related to BA.2 was lower. A study from South Africa also described similar risks of hospitalization or death between wave BA.1 and wave BA.4/BA.5 [15].

The SARS-CoV-2 outbreak is still in progress in Martinique, with the circulation of three sublineages of the highly transmissible Omicron variant since December 2021. Weekly incidence and positivity rates never achieved in the previous waves were observed during this period. However, the hospital impact related to the circulation of this variant is moderate, similar to other countries. Vaccination efforts, especially with booster doses, must continue to mitigate the impact of the disease. The implementation of a genomic surveillance system in this overseas territory has allowed, in addition to PCR screening, to identify circulating variants. Consolidation of this surveillance system must be continued to detect new emerging variants in order to quickly assess the potential impact of these new variants and the need for additional control measures.

Ethical statement

The authors declare that this report does not contain any personal information that could lead to the identification of the patient(s) and/or volunteers. All analyses were conducted on pseu-

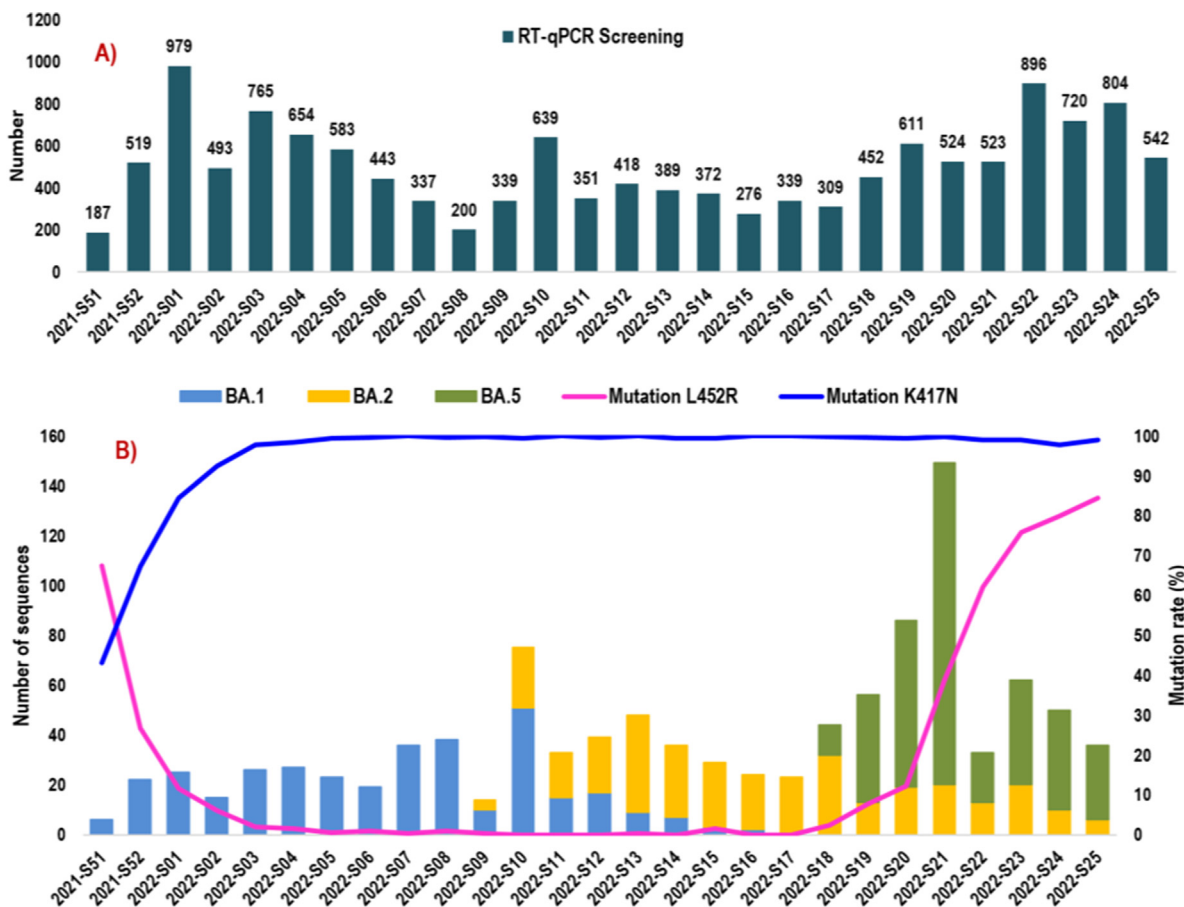


Fig. 3. Number of sequences for Omicron sublineages (bars) detected in Martinique per sampling week, from week 2021–51 (December 20–26, 2021) to week 2022–25 (June 20–26, 2022). The lines indicate the proportion of RT-qPCR screening results (blue line, detection of one of the Spike protein mutations K417N in absence of E484K and light purple line, detection of the L452R mutation).

donymized or anonymized data, in accordance with the legislative and regulatory prerogatives granted to *Santé publique France* to fulfil its public interest mission and in compliance with the provisions of the GDPR. In this context, the opinion of an ethics committee was not required.

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Data availability statement

All inquiries of data can be directed to the author Jacques Rosine (Jacques.ROSINE@santepubliquefrance.fr), the Head of the Regional Unit of French National Public Health Agency in the French West Indies.

CRediT authorship contribution statement

G.N. Gbaguidi: Conceptualization, Methodology, Formal analysis, Writing – original draft, Writing – review & editing. **L. Aubert:** Conceptualization, Methodology, Formal analysis, Writing – original draft, Writing – review & editing. **J. Schaeffer:** Writing – review & editing. **L. Fagour:** Writing – review & editing. **A. Dubremetz:** Writing – review & editing. **Vincent Enouf:** Writing – review & editing. **M.-H. Glaudon-Louveau de la Guigneraye:** Writing – review & editing. **F. Nestour:** Writing – review & editing. **J. Rosine:** Writing – review & editing. **G. Dos Santos:** Conceptualization, Methodology, Formal analysis, Writing – original draft, Writing – review & editing.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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References

- [1] Classification of Omicron (B.1.1.529): SARS-CoV-2 Variant of Concern [Internet]. [cited 2022 Jul 11]. Available from: [https://www.who.int/news/item/26-11-2021-classification-of-omicron-\(b.1.1.529\)-sars-cov-2-variant-of-concern](https://www.who.int/news/item/26-11-2021-classification-of-omicron-(b.1.1.529)-sars-cov-2-variant-of-concern).
- [2] GISAIID – Initiative [Internet]. [cited 2022 Jul 11]. Available from: <https://www.gisaid.org/>.
- [3] Madhi SA, Kwatra G, Myers JE, Jassat W, Dhar N, Mukendi CK, et al. Population Immunity and Covid-19 Severity with Omicron Variant in South Africa. *N Engl J Med* 2022. [NEJMoa2119658](https://doi.org/10.1056/NEJMoa2119658).
- [4] Insee. 361 225 habitants au 1er janvier 2020 en Martinique [Internet]. [cited 2023 Jan 17]. Available from: <https://www.insee.fr/fr/statistiques/6681780>.
- [5] Santé publique France. COVID-19 : une étude pour connaître la part de la population infectée par le coronavirus en France [Internet]. [cited 2023 Jan 18]. Available from: <https://www.santepubliquefrance.fr/maladies-et-traumatismes/maladies-et-infections-respiratoires/infection-a-coronavirus/articles/covid-19-une-etude-pour-connaître-la-part-de-la-population-infectee-par-le-coronavirus-en-france>.
- [6] Maisa A, Spaccaperri G, Fournier L, Schaeffer J, Deniau J, Rolland P, et al. First cases of Omicron in France are exhibiting mild symptoms, November 2021-January 2022. *Infect Dis Now* 2022;52(3):160–4.
- [7] Consortium EMERGEN [Internet]. [cited 2022 Jul 12]. Available from: <https://www.santepubliquefrance.fr/dossiers/coronavirus-covid-19/consortium-emergen>.
- [8] Pan American Health Organization. Update on the emergence of SARS-CoV-2 Omicron sublineages and recombination events [Internet]. [cited 2023 Jan 18]. Available from: <https://www.paho.org/en/documents/update-emergence-sars-cov-2-omicron-sublineages-and-recombination-events>.
- [9] Ito K, Piantham C, Nishiura H. Estimating relative generation times and relative reproduction numbers of Omicron BA.1 and BA.2 with respect to Delta in Denmark. *medRxiv*. 2022 [preprint];2022.03.02.22271767. doi: <https://doi.org/10.1101/2022.03.02.22271767>.
- [10] Lyngse FP, Kirkeby CT, Denwood M, Christiansen LE, Mølbak K, Møller CH, et al. Transmission of SARS-CoV-2 Omicron VOC subvariants BA.1 and BA.2: Evidence from Danish Households. *medRxiv*. 2022 [preprint];2022.01.28.22270044. doi: <https://doi.org/10.1101/2022.01.28.22270044>.
- [11] Tegally H, Moir M, Everatt J, Giovanetti M, Scheepers C, Wilkinson E, et al. Continued Emergence and Evolution of Omicron in South Africa: New BA.4 and BA.5 lineages. *Nat Med* 2022;28(1785–1790). <https://doi.org/10.1038/s41591-022-01911-2>.
- [12] Kouamen AC, Da Cruz H, Hamidouche M, Lamy A, Lloyd A, Castro Alvarez J, et al. Rapid investigation of BA.4/BA.5 cases in France. *Frontiers in Public Health* [Internet]. 2022 [cited 2023 Jan 18];10. Available from: <https://www.frontiersin.org/articles/10.3389/fpubh.2022.1006631>.
- [13] Harrigan SP, Wilton J, Chong M, Abdia Y, Garcia HV, Rose C, et al. Clinical severity of Omicron SARS-CoV-2 variant relative to Delta in British Columbia, Canada: A retrospective analysis of whole genome sequenced cases. *Clin Infect Dis* 2022:ciac705.
- [14] Santé publique France. Bulletin de santé publique COVID-19 en Martinique, décembre 2021 [Internet]. [cited 2022 Jul 30]. Available from: <https://www.santepubliquefrance.fr/regions/antilles/documents/bulletin-regional/2021/bulletin-de-sante-publique-covid-19-en-martinique-decembre-2021>.
- [15] Davies MA, Kassanje R, Rosseau P, Morden E, Johnson L, Solomon W, et al. Outcomes of laboratory-confirmed SARS-CoV-2 infection in the Omicron-driven fourth wave compared with previous waves in the Western Cape Province, South Africa. *medRxiv*. 2022 [preprint];2022.01.12.22269148. doi: [10.1101/2022.01.12.22269148](https://doi.org/10.1101/2022.01.12.22269148).