JIDC | THE JOURNAL OF INFECTION IN DEVELOPING COUNTRIES

Coronavirus Pandemic

Epidemiological profile of SARS-CoV-2 in Mauritania

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Abstract

Introduction: This study was conducted with a profound sense of urgency and has provided significant results that will complement previous studies carried out in Mauritania—a country with unique socio-economic and healthcare characteristics—to monitor the epidemiological situation of coronavirus disease 2019 (COVID-19). The study aimed to comprehensively and rigorously investigate the epidemiological profile of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) strains circulating in Mauritanian patients.

Methodology: This descriptive study was carried out on 84 patients at the Cheikh Mohamed Ben Zayed Hospital and the National Institute of Hepato-Virology in Nouakchott. The samples were sequenced by next-generation sequencing (NGS) of the Illumina NextSeq 2000 type. The data were analyzed by the EPI Info 7 and SPSS 21 software.

Results: The average age of the patients was 51 years, and the distribution of cases by age showed that the virus did not select a specific age group. The results indicated that the most frequent variant was Delta (33.33%). The death rate was very high (34.52%) compared to the national death rate, with a peak in the 58–69 years age group.

Conclusions: This study provides an overview of the epidemiological characteristics of COVID-19 in Mauritania. These findings not only help identify what policies or strategies should be designed to combat the COVID-19 pandemic, but also pave the way for a more effective response to similar pandemics in the future.

Key words: epidemiology; SARS-CoV-2; Delta variant; Mauritania.

J Infect Dev Ctries 2025; 19(11):1592-1597. doi:10.3855/jidc.20677

(Received 03 August 2024 – Accepted 16 May 2025)

Introduction

The emergence of the novel coronavirus, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), and its associated disease, coronavirus disease 2019 (COVID-19), in December 2019, in the city of Wuhan, China, has had profound global implications, affecting populations across continents with varying degrees of severity and impact [1].

SARS-CoV-2 is classified taxonomically within the order Nidovirales, specifically in the subfamily Orthocoronavirinae, and is categorized into 4 genera: Alphacoronavirus (α), Betacoronavirus (β), Gammacoronavirus (γ), and Deltacoronavirus (δ) [2,3]. It is an enveloped virus that contains a single positive-strand RNA genome of approximately 30 kb, which encodes 14 non-structural proteins and 4 structural proteins [4]. The receptor for SARS-CoV-2 is the angiotensin-converting enzyme 2 [5].

According to the World Health Organization (WHO), the number of confirmed infections among the reported cases was more than 778 million, with a death toll of 7,094,447, globally, until 13 April 2025. In Africa, the number of confirmed cases was more than 9.6 million, resulting in a death toll of 175,534 [6]. In Mauritania, the first case of COVID-19 was reported on 13 March 2020, in a 40-year-old man from Australia, who returned from Spain, and tested positive for SARS-CoV-2 [7,8]. To date, 63,972 cases have been confirmed, and 997 deaths have been registered in the country [6].

The majority of COVID-19 patients present mild to moderate symptoms; however, approximately 14% of cases progress to the severe stage, and at least 5% develop critical illness, of which nearly half result in mortality [9,10]. Mortality rates ranging from 1.46% to 4.3% have been reported across various regions or hospitals [11,12]. Mortalities were more frequent among the elderly patients, particularly those with chronic and multiple underlying health conditions, including hypertension, diabetes, cardiovascular diseases, or respiratory illness [13].

The rapid spread of SARS-CoV-2 in various countries raises the intriguing question of whether variations in the viral genome sequences contribute to variations in infection and mortality rates [14]. However, there are still limited data on the genomic sequence of SARS-CoV-2 variants circulating in African countries, notably Mauritania [15]. Moreover, very few studies have been published in Mauritania [8,16]. These studies have only been based on severe cases and deaths, so they require further investigation. This study aimed to comprehensively investigate the epidemiological profile of SARS-CoV-2 strains circulating in Mauritanian patients.

Methodology

Ethical considerations

Each patient was informed of the study's purpose and gave explicit and free consent before any sample was collected. A questionnaire was specifically developed to collect patient data. The ad hoc ethics committee at the University of Nouakchott, Mauritania, approved this questionnaire. Strict confidentiality was ensured by only considering the code from each patient's clinical record, demonstrating utmost respect for the patients' privacy.

Study design

This descriptive study targeted 84 patients with COVID-19 (Ct < 30). All confirmed positive cases during the given period were included, after excluding cases where the information necessary for the study was missing. Data collection began in late 2022. The number of patients was low (84). The number of hospitals was limited to only two: the Sheikh Mohamed Ben Zayed Hospital, where conscious patients were recruited, and the National Institute of Hepato-Virology/National Institute of Veterinary Surgeons (INHV). The collected samples were stored at – 80 °C at the INHV and the National Public Health Research Institute (INRSP).

The samples were collected from two facilities: 15 samples from the Cheikh Mohamed Ben Zayed Hospital and 69 samples from the National Institute of Hepato-Virology. The samples were sent to the INHV by various health facilities as follows: 7 health facilities in Nouakchott (National Institute of Hepato-Virology (36), Hospital Cheikh Mohamed Ben Zayed (15), National Hospital Center (19), Hospital of Friendship (4), Military Hospital (2), National Heart Center (1), and National Oncology Center (1)); and 3 health facilities were located in the south-eastern region of Mauritania (Aleg (1), Kiffa (1), and Kaédi (4)).

The 84 samples with Ct < 30 were stored at – 80 °C and sequenced by the Institute Pasteur Casablanca using Illumina NextSeq 2000 (California, USA) next-generation sequencing (NGS). The steps followed for NGS were:

RNA extraction

Viral RNA was extracted from nasopharyngeal samples using a nucleic acid purification kit (MagaBio DNA/RNA Purification Kit, BioFlux, New Hampshire, USA). A laboratory automation system, Bioer (NPA-32P; Hangzhou, China), was used to make the process more efficient and reproducible.

Library preparation and sequencing

Libraries were prepared following the Illumina COVIDSeq Assay (RUO) protocol (Illumina Inc., California, USA). After first-strand cDNA synthesis, the cDNA was amplified by multiplex polymerase chain reaction (PCR) using the ARTIC-V4 (Coralville, USA) primer pool, producing 98 amplicons across the SARS-CoV-2 genome. The libraries were sequenced on the Nextseq 2000 platform (California, USA). using the Nextseq 1000/2000 P2 kit (300 cycles) with 2 × 150 bp paired-end indexed duplicate reads.

Data analysis

The demultiplexing raw sequencing data in Illumina's cloud-based BaseSpace Sequence Hub was used to generate FASTQ files for each sample by using the Binary Base Call Convert (BCL convert) application. Both the forward and reverse FASTQ files for each sample were then analyzed using the BaseSpace DRAGEN COVID Lineage App (RUO) to generate the consensus sequence for each sample in FASTA format, identify SARS-CoV-2 variants, and annotate mutations in accordance with international virology standards.

Five parameters were studied: age, gender, reason for analysis, sampling structure, and variant type. Epi_Info version 7.2.4.0 [17] and the IBM Statistical Package for the Social Sciences (SPSS) version 21 [18] softwares were used for data analysis. Descriptive statistics was used to calculate the mode, median, mean, variance, standard deviation, number, and percentage. Tests of associations between two parameters, one qualitative and the other quantitative, was based on the t-test. A p value < 0.005, was considered statistically significant.

Results

A total of 84 COVID-19 patients were included in the study, 40 of whom were men (47.62%) and 44

Table 1. Epidemiological characteristics of patients.

Characteristics	n	%	C.I.
Age (years)			
Mean	51.49		
Minimum	7		
Maximum	90		
Gender			
Ratio females/males	1:1		
Males	40	47.6	
Females	44	52.4	
Reason for analysis			
Deaths	29	34.2	90–95
Severe symptoms	13	15.49	90–95
Mild symptoms	37	44.04	90–95
Travel	5	5.95	90–95
Total	**84**	**100**	**90–95**

C.I.:Confidence Interval.

women (52.38%). The mean age was 51.49 years, and the range was 7–90 years (Table 1). The gender ratio (female/male) was 1.1. The targeted patients were sampled in different health facilities, with a percentage ranging from 7.14% to 42.86% (Table 2).

Among the study sample, there were 34.52% deaths, 15.49% had severe symptoms such as dyspnea or asthenia, 40.04% had mild symptoms such as fever or cough, and 5.95% were travelers (Table 1). The distribution of cases according to age showed that the virus did not select a specific age group, as there were positive cases among all age groups. These results are significant because the curve is chimeric (Figure 1) and the *p* value was *0.001281*. The distribution of the variants according to the severity of the disease showed that the dominant variant was AY.34.1 (Delta), which was found in 28 patients (33.33%). The least abundant variants were B1.177, B1.416, and BA.521 (Omicron) (Figure 2). Comparison of the age of the patients showed that the mean age was almost identical for both genders, at around 55 years ($p = 0.357$; Figure 3).

Figure 2. Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) variant lineage by reason for analysis.

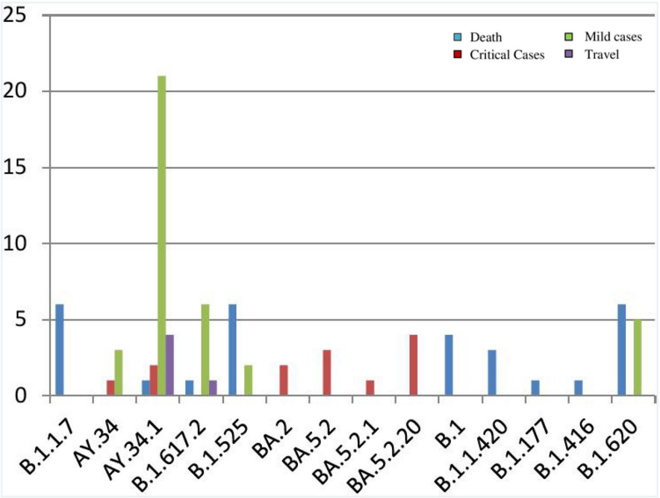
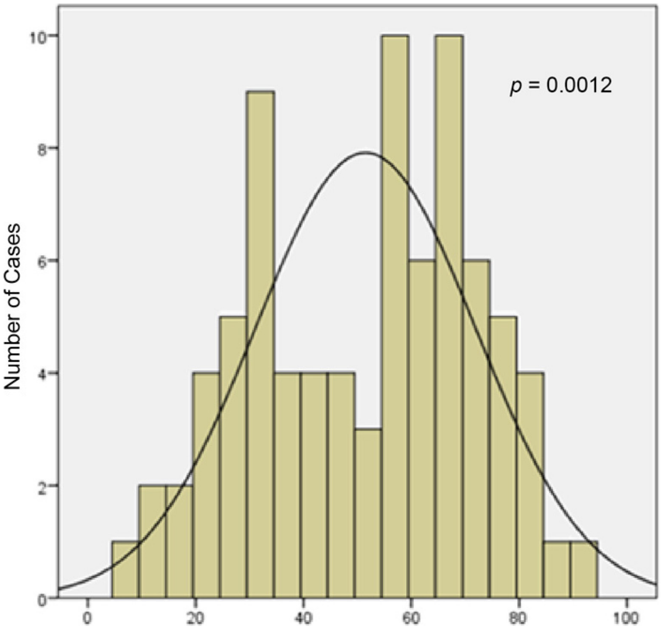


Table 2. Distribution of cases by health facility.

Health facility	n	%	C.I.
National Institute of Hepato-Virology	36	42.86	90–95
National Hospital Center	19	22.62	
Cheikh Mohamed ben Zayed Hospital	15	17.86	90–95
Other health facilities in Nouakchott	8	9.52	
South-eastern Mauritania health structures	6	7.14	90–95
Total	84	100	

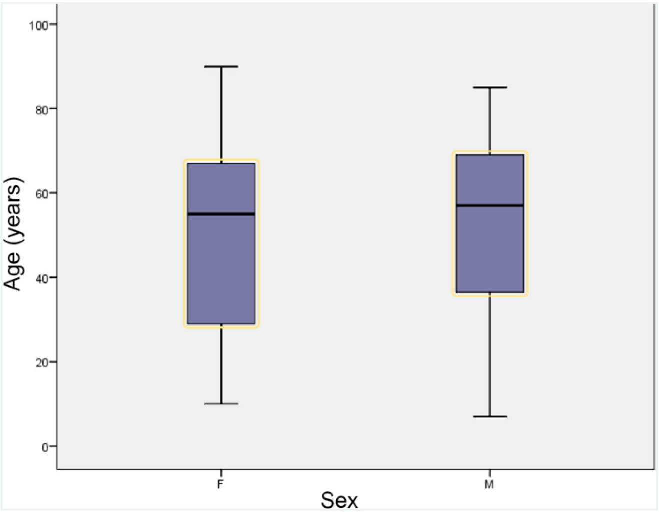
Other health facilities: Hospital of Friendship, Military Hospital, National Heart Center and National Oncology Center. South-eastern Mauritania: Aleg, Kiffa and Kaédi. C.I.:Confidence Interval.

Figure 1. Distribution of coronavirus disease 2019 (COVID-19) cases by age.



*Among the 84 cases, there are 3 whose age could not be determined. Mean = 51.49; SD = 20.41.

Figure 3. Relationship between patient age and gender.



Thus, the difference between genders was not significant. Analysis of the age at death showed that the highest number of variants were found in the 58 to 69 years age group (Figure 4).

Discussion

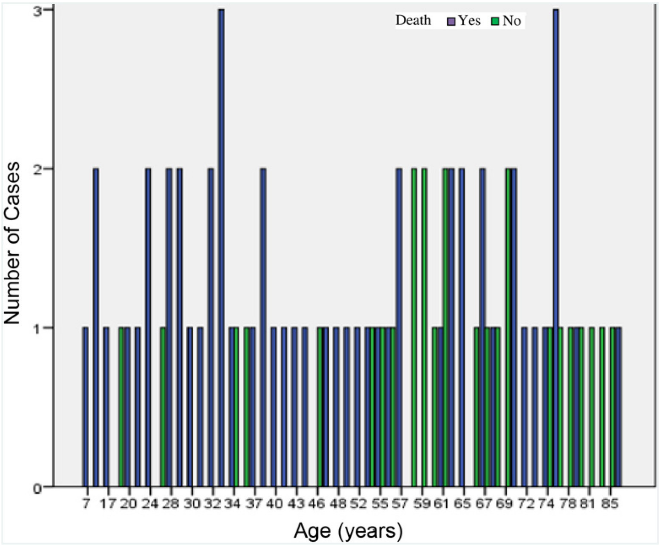
A total of 84 patients with COVID-19 from several healthcare facilities were included in the study of the epidemiological profile of SARS-CoV-2 in the Mauritanian population, half of whom had severe symptoms and the remainder had mild symptoms or were asymptomatic. The mean age of the study sample was 51.49 years. This is in line with data obtained from Senegal where the mean age was 49 years [19], and in Morocco where the mean age was 48 years [20]; however, the age was higher in Tunisia (64.9 years) [21] and lower in Mali (37 years) [22].

In this study, the age distribution showed that all age groups were exposed to the risk of contracting SARS-CoV-2. These results are significant because the curve is chimeric, aligning with the observations in literature [23,24].

There was a predominance of females (52.4%), but the difference was not statistically significant ($p = 0.357$). This predominance was also observed in Morocco, where females represented 57.2% of the cases [13], and the difference was significant ($p < 0.001$). This predominance of females may be because women represent 51.4% of the general population, according to the National Office of Statistics of Mauritania [25], while in Tunisia and Mali, there is a predominance of males in the population, with men accounting for 58.7% [22] and 57% [22] respectively.

In this study, the death rate was very high (34.52%), compared to previous studies on the epidemiology of SARS-CoV-2 in Mauritania, which revealed a rate of 2.4% [22]. This is because the majority of patients were recruited at the National Institute of Hepato-Virology (42.86% or 69 samples, including 29 deaths) were collected at the INHV, to which the different healthcare centers send the samples of the dead to determine if their death was linked to COVID-19.

Figure 4. Distribution of deaths by age.



In addition, analysis of the age of death showed that the highest number of deaths was in the 58–69 years age group, in concordance with the observations from Senegal [26]. This association between advanced age and mortality was also reported in the USA [27]. This may be explained by the fact that the elderly are more at risk due to the physiological changes accompanying ageing, a weakened immune system, and potential health problems [23].

The rate of severe cases was 15.49%, which is about the same as in Tunisia, where the rate during the second COVID-19 wave was 16.8% [21], and slightly higher than in Morocco, where the rate was 11% [28]. This study also showed that patients with mild symptoms accounted for 40.04%, which is in line with the study in Morocco [28].

The distribution of patients by healthcare facility showed that the percentage varied from 7.14% in the Wilayas of south-eastern Mauritania to 92.86% of cases in Nouakchott which is Mauritania's capital, where the vast majority of the population is concentrated, with high inter-urban mobility, according to a report by the National Office of Statistics of Mauritania [25]. In most countries, the capital is generally the epicenter of the epidemic [29].

This study showed that the dominant variant was Delta, in line with the observations in Tunisia [30]. This is explained by the fact that the Delta variant is 100% more contagious than the original virus [31]. In addition, according to a Chinese study pre-published on 12 July 2021, on the medRx website, the Delta variant has a shorter incubation period of 4 days instead of 6 days for the original strain. Li *et al.* reported that the viral load of the Delta variant is 1000 times higher than that of the original strain, suggesting the potentially faster rate of viral replication and greater contagiousness of the Delta variant at an early stage of infection [32]. In addition to being more contagious, the Delta variant could be more virulent, causing many more severe cases in unvaccinated individuals [33].

Study limitations

This study encountered difficulties accessing samples at the National Institute for Public Health

Research (INRSP), which receives samples from different healthcare facilities. As a result, the sample size was limited and the study was conducted at only two healthcare facilities which received a limited number of patients.

Conclusions

Despite some limitations, this study provides an overview of the epidemiological characteristics of COVID-19 in Mauritania. It underscores the predominance of the Delta variant, which is more contagious than the original virus. The results of this study indicate that all age groups are at risk of contracting SARS-CoV-2, with a mean age of 51.49 years. In this study, 92.86% of patients were from Nouakchott, the capital of Mauritania, indicating unequal access to testing.

In terms of disease severity, the death rate was very high (34.52%) compared with the national death rate, and the highest number of deaths were found in the 58–69 years age group, emphasizing the need for targeted, proactive measures for this high-risk population.

Expansion of the rapid diagnostic testing and implementation of mobile testing to reach underserved communities is recommended to mitigate future outbreaks. In addition, scaling up genomic surveillance to monitor emerging variants, and establishing partnerships with regional and international sequencing centers, is recommended. All previous studies on COVID-19 in Mauritania should be considered to identify what policies or strategies should be designed according to the characteristics of the population to possibly flatten a COVID-19 curve or a similar pandemic in the future.

Acknowledgements

Authors would like to thank the team at the Institut National d'Hepato-Virology and the Hôpital Cheikh Mohamed Ben Zayed for all the work done, especially the sampling and the friendship shared. We want to thank all the workers in the virology laboratory at the Institut Pasteur du Maroc for helping us find the sequencing results, in particular Pr Abdelhamid Barakat, Dr Adil El Hamouchi, Dr Abdelmajid El Walid, and Dr Nourlile Jalal. We would also like to thank Dr Brahim Abade for his help in transporting the samples.

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Conflict of interest

No conflict of interest is declared.

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