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Duration and determinants of SARS-CoV-2 RNA positivity in hospitalized patients in Guinea: a prospective cohort study

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Abstract

Background

This study aimed to determine the duration of SARS-CoV-2 RNA positivity and identify factors associated with delayed RNA clearance among hospitalized COVID-19 patients in Conakry, Guinea.

Methods

We conducted a prospective cohort study of patients with RT-qPCR-confirmed SARS-CoV-2 infection hospitalized in Conakry between January 2021 and January 2022. Patients were followed longitudinally until documented RNA clearance or censoring due to early outcome or loss to follow-up. Whole-genome sequencing was performed on eligible positive samples using the COVID-19Seq protocol, followed by mutation analysis with Nextclade. Factors associated with RNA clearance were assessed using multivariable generalized Gamma parametric survival regression within an accelerated failure time framework, with time ratios (Exp[β]) and two-sided P values < 0.05.

Results

Among 330 patients (median age, 39 years; IQR, 27–58; 56.7% male), 311 (94.2%) were followed to complete RNA clearance, whereas 19 (5.8%), primarily older ICU patients, had incomplete follow-up. Clinical presentations were mild (33.3%), moderate (30.6%), or asymptomatic (28.2%). Median RNA positivity duration was 9.0 days (IQR, 8.0–12.0; range, 3–91). Older age (≥ 60 years; Exp[β] = 1.16, P = 0.003), unemployment/farming/manual labor (Exp[β] = 1.14, P = 0.012), and ICU admission (Exp[β] = 1.32, P = 0.007) were independently associated with prolonged RNA positivity. Mild disease was associated with faster clearance than asymptomatic infection (Exp[β] = 0.83, P = 0.001). Among 14 sequenced samples, *Omicron* (35.7%), *Alpha* (28.6%), Eta (7.1%), and other lineages were identified.

Conclusion

Older age, occupational characteristics, and ICU admission were associated with prolonged SARS-CoV-2 RNA positivity, whereas mild disease was associated with faster RNA clearance. These findings support risk-stratified monitoring of hospitalized COVID-19 patients in resource-limited settings.

Introduction

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has caused one of the largest pandemics of the 21st century (1). It affects more than 500 million people worldwide, resulting in more than 6 million deaths (2). It is estimated that 15 to 20% of hospital mortality rates during the pandemic were attributable to this disease (3). Individuals aged over 65 years and those with comorbidities are at

the highest risk of elevated mortality from SARS-CoV-2 infection (4). The SARS-CoV-2 virus is initially transmitted to humans through animals and then rapidly spreads from humans to humans via several mechanisms, including aerosols (5). This virus causes COVID-19, which overwhelms global healthcare systems, posing enormous challenges to screening, epidemiological surveillance, and patient care, thereby necessitating urgent decisions that modify response strategies (6).

During the pandemic, Guinea developed a two-pronged strategy for monitoring and management: the first involved home follow-up of asymptomatic and uncomplicated patients by community health workers (7), whereas the second entailed management at an epidemiological treatment center (CTE-pi) for severe patients or those with comorbidities or who wished to isolate from family to avoid contaminating close contacts (8). The treatment of COVID-19, the duration of hospitalization or outpatient follow-up, and the period of transmission vary according to viral persistence in the patient, with therapeutic protocols adapted accordingly (9). Indeed, several studies on factors influencing the duration of viral RNA persistence have shown that it may vary according to age, disease severity, initial viral load, and comorbidities, although their respective effects remain debated (10–12).

The detection of SARS-CoV-2 viral RNA by real-time PCR (RT—PCR) constitutes the reference method for diagnosing infection and monitoring viral persistence (13,14). The virus may persist in various biological tissues, including the olfactory bulb, for several months after the initial infection, thereby increasing the risk of contamination (15,16). The objective of this study was to investigate the duration of SARS-CoV-2 positivity and associated factors in patients managed for COVID-19.

Methods

Study setting

This study was conducted at the epidemiological treatment center (CTEpi) in Gbessia, Conakry. It was the largest COVID-19 treatment facility established by the Ministry of Health for this purpose. It has a capacity of 438 beds, including 11 intensive care beds. This center is located in the Béhanzin neighborhood in the urban commune of Matoto (Fig. 1).

Study design and population

This was a cohort study involving all patients who tested positive and were managed at the CTEpi Gbessia for SARS-CoV-2 infection. All patients received standard treatment consisting of oral azithromycin, chloroquine, and vitamin C. Acetaminophen, administered orally or via infusion, was added as an antipyretic or analgesic depending on the patient’s clinical presentation. Patients in the intensive care unit received, in addition to standard medical treatment, oxygen therapy and treatment for comorbidities.

Data collection

Data were collected from medical records, the admissions register, and the laboratory database responsible for virological analyses. At admission, in addition to sociodemographic characteristics, the following clinical signs were recorded: mild (cough, fever, myalgia, headache, gastrointestinal symptoms, anosmia), moderate (dyspnea but oxygen saturation ≥ 94%), and severe/critical (respiratory rate > 30 breaths per minute, oxygen saturation ≤ 94%, respiratory failure, assisted ventilation).

Each patient was followed virologically throughout hospitalization. Thus, nasopharyngeal swabs were taken for PCR diagnosis. The first positive control swabs were collected systematically one week after the initial swab collection and regularly at four-day intervals until recovery. The samples were collected in tubes containing viral transport medium, kept cold in a cooler, and transported to the laboratory within four hours for analysis.

Laboratory analysis

RT-PCR tests were performed on all collected samples. RNA extraction and amplification were carried out via a COVID-19 kit (Hunan Runmei Gene Technology Co., Ltd., Changsha, China). This is a CDC China protocol approved by the World Health Organization (WHO) (17). The RNA extracts were stored at + 4°C prior to immediate amplification or at -80°C for long-term storage. All Ct values < 39 were considered positive regardless of the amplified gene. The N and ORF genes were targeted and amplified simultaneously.

All positive samples with a Ct value < 30 were considered for sequencing. Library preparation and sequence analysis were performed according to the procedures described in previous studies (18). The sequences were uploaded to the Nextclade for mutation analysis (19).

Statistical analysis

Statistical analyses were performed using R software, version 4.1.2. Categorical variables were summarized as frequencies and percentages. Following assessment of the normality of their distribution using the Shapiro–Wilk test, continuous variables were expressed as medians with interquartile ranges (IQRs).

Sociodemographic and clinical characteristics were compared according to positivity persistence using Pearson's chi-squared test or Fisher's exact test for categorical variables, as appropriate. For continuous variables, the non-parametric Wilcoxon–Mann–Whitney test was used. Statistical significance was defined as a two-sided p-value < 0.05.

The relationship between the mean cycle threshold (Ct) values for the N and ORF genes and the duration of positivity was explored visually using scatter plots. In addition, changes in the mean positivity rate within the cohort over time were illustrated using a trend plot.

The duration of viral persistence was estimated using survival analysis. Several parametric survival models were fitted to the data, including Weibull, log-normal, log-logistic, gamma, generalized gamma, and exponential models. The most parsimonious model with the best fit was selected based on the Akaike information criterion (AIC).

Finally, a multivariable analysis was performed using the generalized gamma parametric survival model, which provided the best fit, to identify factors independently associated with the duration of SARS-CoV-2 positivity. The results were reported as hazard ratios (HRs), interpreted here as exp(β), with corresponding 95% confidence intervals (95% CIs) and p-values derived from the Wald test%. Maps were generated via QGIS software (version 3.36.1).

Results

Sociodemographic and Clinical Characteristics

A total of 330 patients diagnosed with SARS-CoV-2 infection by RT-PCR at CTEpi Gbessia were enrolled in the study. Among them, 311 patients (94.2%) were successfully monitored longitudinally until complete viral clearance confirmed by a negative RT-PCR result. Nineteen patients (5.8%) experienced early censored outcomes or loss of follow-up (primarily elderly patients admitted to intensive care with severe clinical status) prior to documented viral clearance (Table 1).

The overall median age was 39 years (IQR: 27–58), and 56.7% were male. At initial clinical presentation, patients presented with mild (33.3%), moderate (30.6%), asymptomatic (28.2%), or severe (7.9%) disease (Table 1).

Table 1
Sociodemographic and clinical characteristics of patients managed for COVID-19 at CTEpi Gbessia, from January 2021 to January 2022.

Characteristic	Overall	Uncomplete Follow-up	Complete Follow-up	
	N = 330[1]	0, N = 19[1]	1, N = 311[1]	p value[2]
Sex				0.4
Female	143 (43.3%)	10 (7.0%)	133 (93.0%)	
Male	187 (56.7%)	9 (4.8%)	178 (95.2%)	
Age				< 0.001
Median (IQR)	39 (27,58)	68 (57, 81)	37 (27, 55)	
Age categories				< 0.001
Age < 60	255 (77.3%)	6 (2.4%)	249 (97.6%)	
Age ≥ 60	75 (22.7%)	13 (17.3%)	62 (82.7%)	
Occupation				0.032
Administrative staff	131 (39.7%)	3 (2.3%)	128 (97.7%)	
Trade workers	34 (10.3%)	4 (11.8%)	30 (88.2%)	
Healthcare workers	35 (10.6%)	3 (8.6%)	32 (91.4%)	
Student/pupil	48 (14.5%)	1 (2.1%)	47 (97.9%)	
Unemployed/farmers/laborers	82 (24.8%)	8 (9.8%)	74 (90.2%)	
Comorbidities				0.3
No	325 (98.5%)	18 (5.5%)	307 (94.5%)	
Yes	5 (1.5%)	1 (20.0%)	4 (80.0%)	
Hospitalization unit				< 0.001
General ward	307 (93.0%)	5 (1.6%)	302 (98.4%)	
Intensive care unit	23 (7.0%)	14 (60.9%)	9 (39.1%)	
Clinical status				< 0.001
Asymptomatic	93 (28.2%)	1 (1.1%)	92 (98.9%)	
Mild	110 (33.3%)	0 (0.0%)	110 (100.0%)	

[2] Pearson's Chi-squared test; Wilcoxon rank sum test; Fisher's exact test

Characteristic	Overall	Uncomplete Follow-up	Complete Follow-up	
	N = 330[1]	0, N = 19[1]	1, N = 311[1]	p value[2]
Moderate	101 (30.6%)	3 (3.0%)	98 (97.0%)	
Severe	26 (7.9%)	15 (57.7%)	11 (42.3%)	
Duration of positivity				0.085
Median (IQR)	9.0 (7.0,12.8)	7.0 (6.0, 14.0)	9.0 (8.0, 12.0)	
[1] n (%)				
[2] Pearson's Chi-squared test; Wilcoxon rank sum test; Fisher's exact test				

Estimation of the Viral Persistence Duration

The Ct values for the N and ORF1ab genes increased over time, while the SARS-CoV-2 positivity rate steadily declined following initial diagnosis during follow-up (Fig. 2-I-J). Analysis of viral clearance dynamics (Fig. 2-K) indicated that the majority of patients cleared the virus within 10 days, whereas a minority maintained viral RNA positivity beyond three weeks. Among patients with complete longitudinal follow-up (N = 311), the median duration of viral positivity was 9.0 days (IQR: 8.0–12.0; overall cohort median: 9.0 days, IQR: 7.0–12.8).

Factors associated with positivity duration

Multivariate survival analysis using the generalized Gamma model (Table 2) evaluated factors independently associated with the duration of viral positivity, where exponentiated coefficients Exp (β) represent Time Ratios (TR) under an Accelerated Failure Time (AFT) framework.

Older age (≥ 60 years) was independently associated with a significantly longer duration of viral positivity compared to younger individuals (Exp (β) = 1.16; 95% CI: 1.05–1.29; p = 0.003). Similarly, working in manual or informal occupations (Unemployed/Farmer/Laborer) was associated with prolonged positivity duration relative to administrative staff (Exp (β) = 1.14; 95% CI: 1.03–1.27; p = 0.012). Within CTEpi Gbessia, admission to the intensive care unit (ICU) was independently associated with extended viral persistence compared to standard general ward admission (Exp (β) = 1.32; 95% CI: 1.08–1.62; p = 0.007).

Conversely, patients presenting with a mild clinical status displayed a significantly shorter duration of viral positivity (faster viral clearance) compared to asymptomatic individuals (Exp (β) = 0.83; 95% CI: 0.75–0.93; p = 0.001).

Table 2
Analysis of factors associated with the duration of SARS-CoV-2 positivity in COVID-19 patients at CTEpi Gbessia, from January 2, 2021, to January 25, 2022

Covariates	Exp (β) value (95% CI)	P value (Wald test)	AIC value for model
Age			1754.02
Age category < 60 (ref)	------		
Age category > = 60	1.16 (1.05–1.29)	0.003	
Profession			1760.79
Administrative staff (ref)	------	------	
Trade workers	1.07 (0.93–1.24)	0.357	
Healthcare workers	1.09 (0.94–1.25)	0.246	
Student/pupil	0.99 (0.88–1.12)	0.889	
Unemployed/farmers/laborers	1.14 (1.03–1.27)	0.012	
Comorbidities			1761.89
No (ref)	------	------	
Yes	1.14 (0.81–1.61)	0.457	
Hospitalization unit			1755.42
General ward (ref)	------	------	
Intensive care unit	1.32 (1.08–1.62)	0.007	
Clinical status			1740.08
Asymptomatic (ref)	------	------	
Mild	0.83 (0.75–0.93)	0.001	
Moderate	1.05 (0.95–1.17)	0.35	
Severe	1.15 (0.95–1.40)	0.148	
Sex			1762.38
Female (ref)	------	------	
Male	0.99 (0.91–1.08)	0.882	

SARS-CoV-2 Variants

Among the tested samples, 14 were eligible for genomic sequencing (Table 3). Sequence analysis revealed a diversity of SARS-CoV-2 variants circulating during the study period, ranging from early

lineages (R.1) to later variants of concern (*Alpha*, Eta, and *Omicron*). The *Omicron* variant was the most frequently identified lineage among the sequenced samples (5/14; 35.7%, patients 10–14), comprising sub-lineages BA.1, BA.1.1, and BA.1.15.1. The *Alpha* variant (B.1.1.7) was detected in 4 of 14 patients (28.6%, patients 2, 3, 4, and 8), followed by the Eta variant (B.1.525; 1/14, 7.1%, patient 7) and other lineages (R.1, B.1.629, and B.1.318; 4/14, 28.6%).

Spike protein mutation analysis demonstrated substantial variability in mutational burden across lineages: 14 to 29 Spike mutations in *Omicron* sub-lineages (BA.1, BA.1.1, BA.1.15.1), 7 mutations in *Alpha* (B.1.1.7), 6 mutations in Eta (B.1.525), and 4 to 8 mutations in other lineages (R.1, B.1.318, B.1.629). Variation in hospitalization duration was observed across lineages, ranging from 6 to 19 days depending on patient clinical status and underlying variant type.

Table 3
Diversity of SARS-CoV-2 in COVID-19 patients at CTEpi Gbessia, from January 2, 2021, to January 25, 2022

PATIENT	LINEAGE	VARIANT TYPE	LENGTH OF HOSPITALIZATION (PER DAY)	SPIKE PROTEIN MUTATIONS
1	R.1	Other	19	S:W152L; S:E484K; S:D614G; S:G769V
2	B.1.1.7	*Alpha*	9	S:N501Y; S:A570D; S:D614G; S:P681H; S:T716I; S:S982A; S:D1118H
3	B.1.1.7	*Alpha*	14	S:N501Y; S:A570D; S:D614G; S:P681H; S:T716I; S:S982A; S:D1118H
4	B.1.1.7	*Alpha*	14	S:N501Y; S:A570D; S:D614G; S:P681H; S:T716I; S:S982A; S:D1118H
5	B.1.629	Other	15	S:G142D; S:K182R; S:L452R; S:T478K; S:D614G; S:P681H; S:D796Y; S:C1235F
6	B.1.629	Other	9	S:G142D; S:K182R; S:L452R; S:T478K; S:D614G; S:P681H; S:D796Y; S:C1235F
7	B.1.525	*Eta*	6	S:Q52R; S:A67V; S:E484K; S:D614G; S:Q677H; S:F888L
8	B.1.1.7	*Alpha*	7	S:N501Y; S:A570D; S:D614G; S:P681H; S:T716I; S:S982A; S:D1118H
9	B.1.1.318	Other	10	S:E484K; S:D614G; S:P681H; S:D796H
10	BA.1.15.1	*Omicron*	8	S:A67V; S:T95I; S:G339D; S:S371L; S:S373P; S:S375F; S:K417N; S:N440K; S:G446S; S:S477N; S:T478K; S:E484A; S:Q493R; S:G496S; S:Q498R; S:N501Y; S:Y505H; S:T547K; S:D614G; S:H655Y; S:N679K; S:P681H; S:N764K; S:D796Y; S:N856K; S:Q954H; S:N969K; S:L981F; S:I1081V
11	BA.1.1	*Omicron*	9	S:A67V; S:T95I ; S:Y145D; S:N211R ; S:G339D ; S:R346K; S:S371L; S:S373P; S:N440K; S:G446S; S:S477N; S:T478K; S:E484A; S:Q493R; S:G496S; S:Q498R; S:N501Y; S:Y505H; S:T547K; S:D614G; S:H655Y; S:N679K; S:P681H ; S:N764K; S:D796Y; S:N856K; S:Q954H; S:N969K;S:L981F

PATIENT	LINEAGE	VARIANT TYPE	LENGTH OF HOSPITALIZATION (PER DAY)	SPIKE PROTEIN MUTATIONS
12	BA.1	*Omicron*	6	S:A67V ; S:T95I ; S:G339D ; S:S477N ; S:T478K ; S:E484A ; S:Q493R; S:G496S; S:Q498R; S:N501Y; S:Y505H; S:T547K ; S:D614G; S:H655Y; S:N679K ; S:P681H ; S:N764K ; S:D796Y ; S:N856K ; S:Q954H ; S:N969K ; S:L981Z
13	BA.1.15.1	*Omicron*	6	S:A67V ; S:T95I ; S:T547K ; S:D614G ; S:H655Y ; S:N679K ; S:P681H; S:N764K; S:D796Y ; S:N856K ; S:Q954H ; S:N969K ; S:L981F ; S:I1081V
14	BA.1.15.1	*Omicron*	19	S:A67V ; S:T95I ; S:G339D ; S:S371L ; S:S373P ; S:S375F : S:K417N ; S:N440K; S:Y505H: S:T547K; S:D614G; S:H655Y; S:N679K; S:P681H ; S:N764K ; S:D796Y ; S:N856K ; S:Q954H; S:N969K; S:L981F; S:I1081V

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12. EPI_ISL_14578556
13. EPI_ISL_14578567
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Discussion

In the context of public health support aimed at better understanding the dynamics of viral infections, this study was conducted to evaluate the duration of persistence of viral RNA positivity in patients with

COVID-19.

The median positivity duration was nine days from the date of the diagnostic infection swab. However, variability was observed among certain patients. The longest viral persistence was observed in an elderly patient who was HIV positive, admitted with severe COVID-19, and presented a high initial viral load. Another study reported the case of a 50-year-old immunocompromised patient hospitalized for severe COVID-19 who remained positive for viral RNA for 71 days, which aligns with our observations (20). Other researchers reported durations of 58, 81, and 137 days of SARS-CoV-2 RNA positivity persistence in patients without immunosuppression or severe COVID-19, suggesting the need to explore factors related to this persistence as well as the potential risk of viral transmission (21). The variability in viral positivity durations, observed around medians or at extremes, may be explained by differences related to viral variants, vaccination status, and host characteristics, particularly age, comorbidities, and sex (22,23). Furthermore, certain studies have reported mean viral excretion durations of 17.0–17.2 days in various biological fluids for SARS-CoV-2, with extremes reaching 83 days in the respiratory tract, with the peak of viral excretion generally occurring during the first week (24). In comparison, MERS-CoV and SARS-CoV-1 exhibit similar excretion profiles, with overall longer viral loads than their observed peaks after symptom onset between the 7th and 10th days (24).

Consistent with the clinical profiles observed in this study and in previous studies conducted in Africa and other continents, the global response to COVID-19 highlighted prolonged RNA viral persistence in humans, sometimes well beyond the acute phase, not necessarily reflecting active infectivity (25). A median duration of viral excretion of 20 days, approximately twice that reported in this study, was reported in patients with COVID-19, including a 34-year-old patient who remained positive for viral RNA for 45 days (25). Similarly, other studies reported a median duration of viral persistence identical to that reported in this study in COVID-19 patients, with rapid recovery within the first two weeks of follow-up; other patients with prolonged positivity in the absence of symptoms were released from confinement in accordance with guidelines from the World Health Organization (WHO) and the European Centre for Disease Prevention and Control (ECDC) (26). The variability of SARS-CoV-2 infection persistence across different patient cohorts and sample types, as well as sociodemographic and clinical characteristics, has been demonstrated (27,28). Consistent with the described variability, researchers have indicated that the duration of mean SARS-CoV-2 positivity ranges from approximately 7 days in blood to over 22 days in stools, with upper respiratory tract samples showing a mean duration of approximately 18 days (27). Additionally, persistent infections exceeding 30 days have been documented in patients with high initial viral loads (28). Similarly, certain elderly, smoking, alcoholic, or obese COVID-19 patients presented a maximum mean viral persistence of 38 days, whereas those with severe forms or anosmia/ageusia presented approximately 52 days of viral positivity (29). In Zhejiang Province, China, a multicenter retrospective study in children from families with SARS-CoV-2-infected members revealed fecal viral RNA detection in 91.4% of cases (32/35), with some children showing positivity exceeding 70 days (30). In immunocompromised patients, another study revealed that prolonged viral persistence was linked to new infection episodes, reporting 20 cases among 116 COVID-19 patients, including 7 (35%) with reinfections, 8 with prolonged excretions, and 6 with relapses (31). Finally, the viability of SARS-CoV-2

persistence varies by biological sex, with longer durations in women in certain hospital cohorts linked to the immunomodulatory effects of oestrogens and progesterone (32), whereas pre- or peripandemic psychological distress is associated with an increased risk of prolonged post-COVID-19 symptoms (fatigue, cognitive disorders, anxiety) (33).

In our multivariate AFT model, presenting with mild symptoms was independently associated with a shorter duration of viral RNA positivity compared to asymptomatic carriers, indicating faster viral clearance in mild cases. While some literature reports extended shedding in mild outpatients attributed to lower systemic immune engagement (12), our results indicate that symptomatic mild cases mount an effective, targeted immune response that accelerates viral clearance relative to asymptomatic carriers who may experience prolonged low-level viral shedding. According to Friedman et al., the duration of prolonged SARS-CoV-2 positivity is comparable between people living with HIV and the general population (34). Similarly, a South African study reported similar viral persistence in HIV-positive and nonimmunocompromised subjects, although viral loads remained higher in the former (35).

During the first two weeks of patient follow-up, viral RNA was strongly detected in nasopharyngeal samples for both the N and ORF genes. Furthermore, in a COVID-19 study targeting these same SARS-CoV-2 viral genes, the N gene was more sensitive and was predominantly detected in nasopharyngeal samples (36). This strong detection of SARS-CoV-2 in nasopharyngeal samples confirms its marked tropism for nasopharyngeal epithelial cells, the gold standard site where the viral load is maximal, particularly early in infection (37). Nasopharyngeal swabs exhibit greater sensitivity and viral load detection than other sampling methods do, which is essential for accurate diagnosis and surveillance (38). At the origin of this predominance, the N gene (located at the 3' end of the genome) is present in all subgenomic mRNAs produced during viral replication, explaining its massive detection compared with other genes (39,40). The ORF1ab gene, detected in parallel, reflects the presence of complete genomic RNA, indicating active assembly of infectious virions (41). During the acute infection phase, simultaneous massive codetection of N and ORF1ab characterizes the peak viral load and maximum transmission risk (42).

We observed a predominance of mild COVID-19 cases among patients at admission to the CTEpi compared with more severe cases. These results are similar to those of a meta-analysis of 4,499 COVID-19 patients in Africa, which reported the most frequent symptoms as fever (42.8%), cough (33.3%), respiratory disorders (16.8%), and headaches (11.3%) (43). In the Democratic Republic of Congo, a study of hospitalized SARS-CoV-2-positive patients revealed that 57%, 12%, and 31% of the patients were mild, moderate, and severe, respectively (44). Furthermore, in Gabon, among 837 patients hospitalized for COVID-19, 62.6% were asymptomatic, followed by 33.7% with mild cases and 3.7% with severe cases in intensive care, with elderly patients having high CRP levels (45). Outside Africa, particularly in China, Guan et al. reported 84.3% mild forms, characterized by cough (67.8%) and fever (43.8%), with pneumonia as the main complication (46).

Our study revealed that age, occupation, hospitalization unit, and clinical status were determinants of the duration of viral persistence. Advanced age, working-class occupations, and intensive care admission were independently associated with prolonged viral shedding. Other studies have identified comorbidities associated with this persistence, notably diabetes, hypertension, chronic respiratory diseases, cardiovascular diseases, cancers, and HIV (47).

The significant influence of the hospitalization unit within CTEpi Gbessia, where intensive care admission was associated with a 32% increase in viral positivity duration (Exp (β) = 1.32) relative to standard general wards, is directly explained by clinical disease severity and intra-host viral kinetics. Patients admitted to intensive care typically present with significantly higher initial viral loads, widespread tissue involvement, and impaired host immune clearance mechanisms (48). Furthermore, critical illness and associated systemic complications in ICU settings frequently delay viral clearance despite supportive care measures (49). A study evaluating viral RNA persistence in COVID-19 patients reported prolonged excretion associated with renal abnormalities, notably elevated urea in 2.8% of patients and creatinine-related imbalances in 29.2% of patients with mild forms (50). However, other studies have identified factors that favour prolonged viral RNA detection, such as male sex (51),

Genomic analysis demonstrated a diversity of circulating lineages, with *Omicron* (5/14; 35.7%) and *Alpha* (4/14; 28.6%) representing the primary variants detected in our sequenced subset. Over the course of the study period (January 2021 to January 2022), early lineages and the *Alpha* variant were progressively supplanted by later lineages, culminating in the emergence of *Omicron* (52,53). The higher mutational burden observed in the Spike coding region of *Omicron* sub-lineages (up to 29 mutations) is consistent with the genomic diversity and evolution of SARS-CoV-2 variants described in Guinea (52,53).

Despite its inherent limitations, notably its limited patient sample size and absence of data on self-medication and vaccination status, this study contributes to characterizing SARS-CoV-2 persistence in sub-Saharan Africa, particularly in Guinea. This method has the advantages of longitudinal follow-up and the collection of high-quality data.

Conclusion

This study evaluated viral persistence duration in COVID-19 patients managed at CTEpi Gbessia and revealed SARS-CoV-2 RNA excretion in upper respiratory tract samples for up to 91 days, with an overall decrease in viral load over follow-up. Rapid viral clearance was observed in the majority of patients within the first two weeks (median positivity duration of 9.0 days, IQR: 8.0–12.0). Advanced age (≥ 60 years), working-class occupation, and admission to the intensive care unit were independently associated with prolonged viral persistence. Conversely, presenting with a mild clinical status was associated with a shorter duration of viral shedding compared to asymptomatic cases. Genomic characterization identified multiple circulating SARS-CoV-2 lineages, with *Omicron* and *Alpha* representing the main variants detected among sequenced cases. A small subset of severely ill and elderly ICU patients experienced early censored outcomes prior to clearance, highlighting the critical

disease burden in high-risk groups. These findings illustrate the utility of molecular testing for understanding viral infection dynamics and advocate for adapting patient management and isolation protocols based on clinical severity and age-related risk profiles within epidemic treatment facilities.

Declarations

Ethics approval and consent to participate

The study received approval from the Guinea National Ethics Committee for Health Research (CNERS) under No. 114/CNERS/20. The protection of confidentiality was ensured for all participants in accordance with the ethical standards outlined in the Declaration of Helsinki. Each participant provided informed consent to participate in the study.

Consent for publication

This manuscript does not contain data from any individual person.

Competing interests

We have no competing interests.

Availability of sequencing data

Sequencing data including in this study are available on GISAID (https://gisaid.org/).

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Author Contribution

A.K.S. wrote the first draft of the manuscript, which was circulated to all co-authors for review. N.V., E.G., A.A., E.D., M.P., A.T. and Alpha Kabinet KEITA provided critical comments and suggestions, which were taken into account in the final revision of the manuscript. H.D., Alpha Kabiné KEITA, A.C., A.K., T.A.C.G., C.G.H., L.K., A.M., J.B.K. and K.J.J.O.K. reviewed the manuscript. All authors read and approved the final version of the manuscript.

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Data Availability

Sequencing data including in this study are available on GISAID (https://gisaid.org/).

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Figures

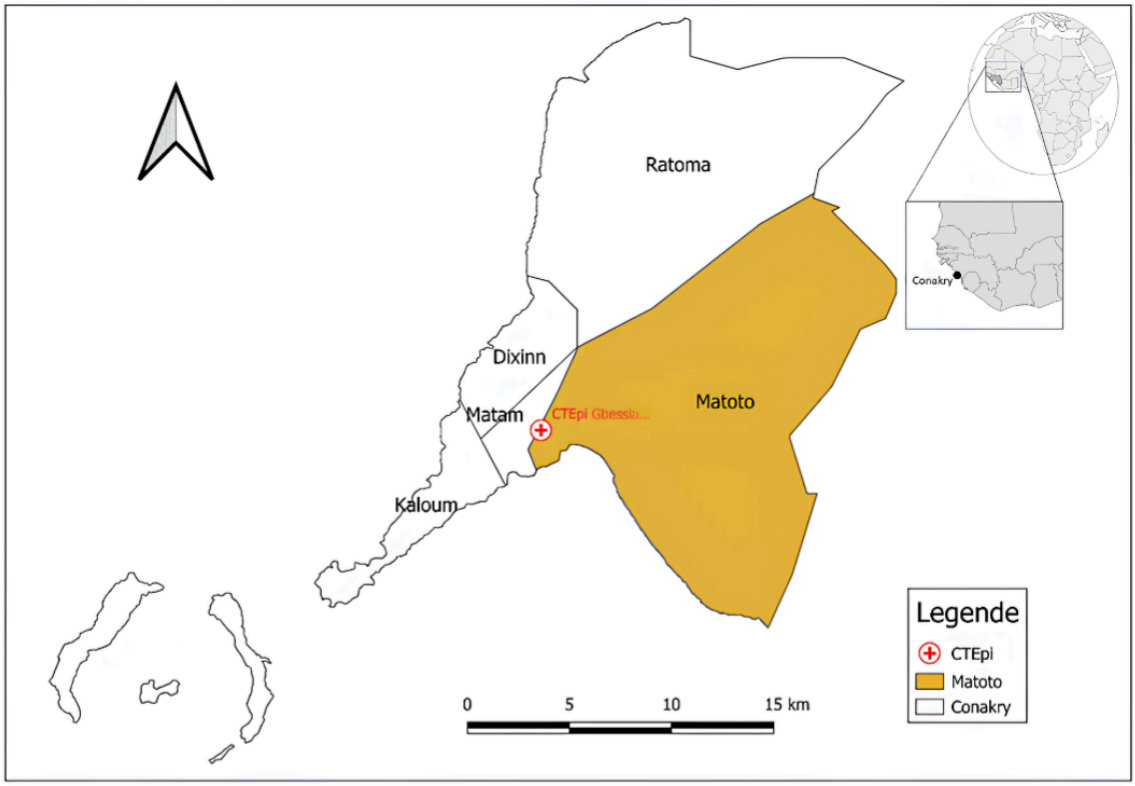


Figure 1

Location of the study site in Conakry, Guinea.

Map of the five communes of Conakry (Kaloum, Dixinn, Matam, Ratoma and Matoto). Matoto commune (yellow) hosts the Gbessia Epidemic Treatment Center (CTEpi, red cross). Inset: location of Conakry in West Africa and on the African continent.

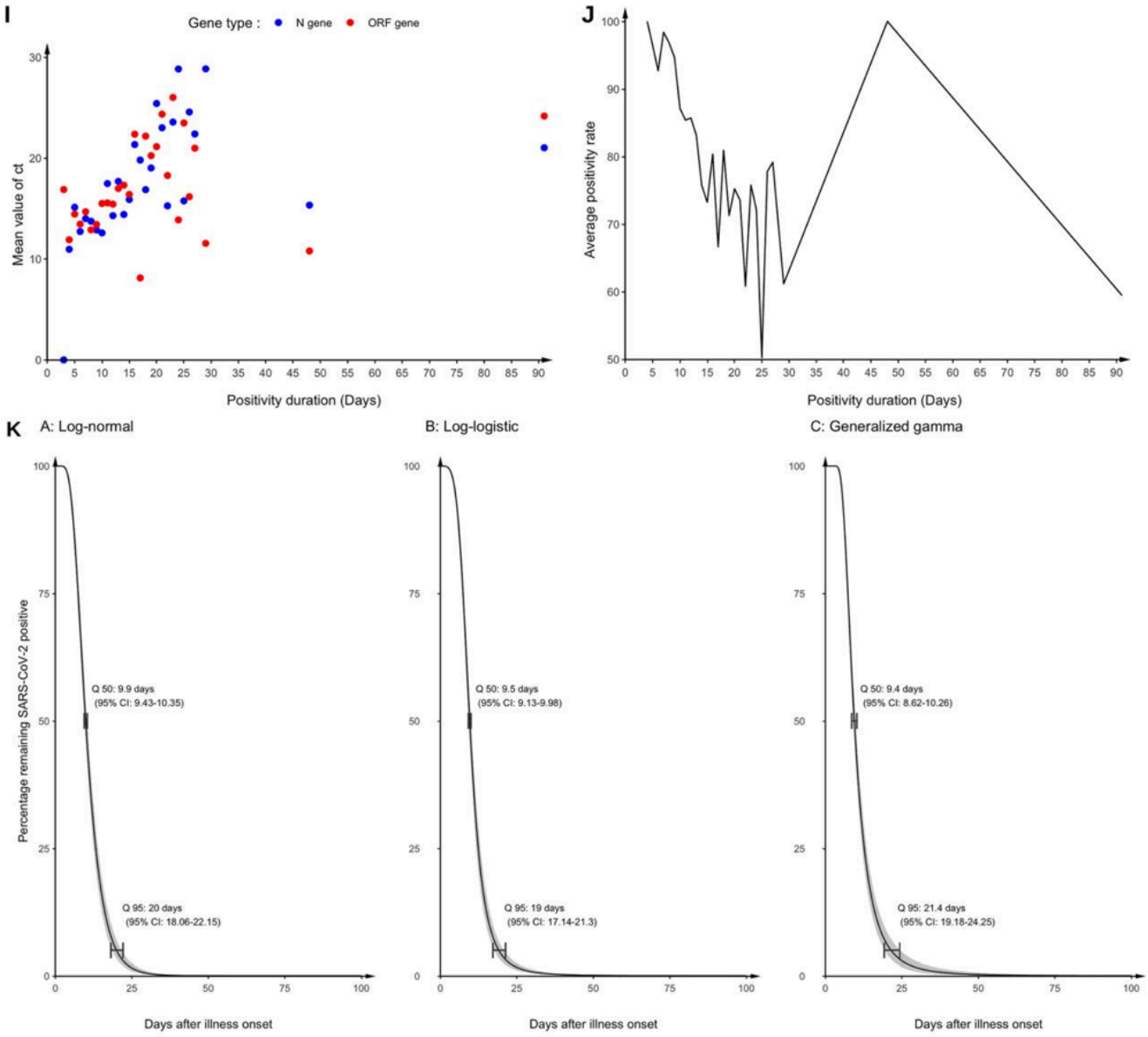


Figure 2

Evolution of SARS-CoV-2 positivity persistence among hospitalized COVID-19 patients at CTEpi Gbessia, Guinea, from January 2, 2021, to January 25, 2022.

(I) Scatter plot of the mean cycle threshold (Ct) values for the N gene (blue) and ORF1ab gene (red) according to the duration of positivity (days). **(J)**Average SARS-CoV-2 positivity rate according to the duration of positivity (days). **(K)** Estimated viral clearance curves, showing the percentage of patients remaining SARS-CoV-2 positive as a function of days after illness onset, using three parametric survival

models: (A) log-normal, (B) log-logistic and (C) generalized gamma. Shaded areas represent the 95% confidence intervals. Q50 and Q95 indicate the time (in days) by which 50% and 95% of patients, respectively, had cleared the virus. Q50 (95% CI): 9.9 (9.43–10.35), 9.5 (9.13–9.98) and 9.4 (8.62–10.26) days; Q95 (95% CI): 20.0 (18.06–22.15), 19.0 (17.14–21.30) and 21.4 (19.18–24.25) days for the log-normal, log-logistic and generalized gamma models, respectively.

Supplementary Files

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