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Viral dynamics and factors associated with duration of COVID-19 positivity: evidence from the first-three epidemiological waves in Cameroon

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Abstract

Background Coronavirus 2019 (COVID-19) disease progression evidence and viral clearance time remain limited in tropical settings. Understanding this is crucial for public health control measures at community-level. We evaluated the viral dynamics of SARS-CoV-2 infection and factors associated with positivity duration in COVID-19 cases in Cameroon.

Material and Methods We conducted a retrospective cohort-study of SARS-CoV-2 positive cases from the first to third wave (March 2020-October 2021) in Yaounde-Cameroon. RT-PCR was carried out on the participants using nasopharyngeal swabs after every 7 days. SARS-CoV-2 positivity duration was evaluated from the first to last positive PCR-test before a negative result. Epi-info V.7.0 was used for data analyses with $p < 0.05$ considered statistically significant.

Results A total of 282 participants were enrolled. The mean age was 41 ± 14 years, with male predominant (62.1%). We had 15.6% symptomatic participants of which 59% had cough. The overall median positivity duration was 15[IQR:

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9–23] days with 15[IQR: 13–22] in the first, 17[IQR: 12–26] in the second and 9[IQR: 6–12] in the third wave ($p < 0.0001$). Positivity duration was significantly higher in males (16 versus 14 days, $p = 0.03$) those aged [35–45] years (16 days) followed by those ≥ 46 years(15 days); $p = 0.008$). Positivity duration was not affected by presence or absence of symptoms ($p = 0.80$). No significant correlation was found with viral load ($r = 0.03$; $p = 0.61$). Considering baseline (24.7 ± 7.2Ct) and last viral load (29.3 ± 5.9 Ct), the ΔCt (4.6 ± 1.3) and positivity duration (15 days) revealed a kinetic in viral decay of 0.3 ± 0.087 Ct/day.

Conclusions A median positivity duration of 15 days is in accordance with viral clearance around 2 weeks for optimal confinement at community-level. Men and/or the elderly stand at higher risk of prolonged infection. Given the viral decay (0.3 Ct daily), we suggest personalized confinement periods. The variability of positivity duration according to waves could be function of strains which could be a factor influencing positivity duration.

Keywords SARS-CoV-2, Positivity duration, Determinants, Viral dynamics

Introduction

Coronavirus disease (COVID-19), caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), has rapidly spread worldwide since its emergence. As of March 2020, there were a total of 87 137 confirmed cases globally, with 2 977 (3.4%) deaths reported by the world health organization (WHO) [1]. By June 2023, there were 767 984 989 confirmed cases of COVID-19 with 6 943 390 deaths Worldwide, 9 536 174 with 175 381 deaths in Africa and 125 087 cumulative cases with 1 972 deaths in Cameroon [2], with countries still observing new rounds of lockdown.

The clinical course of the disease may vary among infected individuals, with most cases of infection usually asymptomatic [3]. Therefore, in addition to clinical monitoring, viral RNA (ribonucleic acid) monitoring is essential to monitor COVID-19 disease progression, and also as an indicator for the risk of SARS-CoV-2 transmissibility, which is higher at lower viral cycle threshold (CT) values [4, 5]. Evaluation of these CT values in routine care by polymerase chain reaction (PCR) will not only guide clinical management but may also influence hospital stay and confinement periods [6, 7]. Following successful viral replication in the host, the duration of viral shedding and PCR positivity may be influenced by several factors, such as biological characteristics of the virus, the host, symptomatology, vaccination status, or due to some pre-existing natural immunity [8–11]. Many studies so far, carried out mostly in developed countries, have shown an a mean viral clearance time (VCT) of around two weeks [12–14], although some cases of prolonged positivity have been reported, sometimes up till 83 days in the upper respiratory tract of some individuals [15]. Investigations into cases of persistence of covid-19 infection, remain pertinent to inform management guidelines. Despite widespread use of viral load testing in developed countries, challenges such as cost, complexity, infrastructure have limited its scale-up in low- and middle-income countries (LMIC) [16]. For this reason, data on viral dynamics remains scare in this region, necessitating further investigations [17]. It should be noted that several contextual differences exist in these regions as compared to other settings, which could greatly influence viral dynamics. These include socio-demographic, economic, cultural practices, availability/access of health services (such as vaccination or medication), comorbidities and co-infections (such as HIV/AIDS and malaria that are prevalent here). [18–20]. Indeed covid-19 severity appeared to be milder sub-Saharan Africa (SSA), with presence of pre-existing immunity of covid-19 in some sub-Saharan settings such as Cameroon, hypothesized as one of the factors, which would have contributed to the observed milder disease outcomes [10]. Also, the continuous viral evolution may influence viral dynamics in infected individuals. Between March 2020 and October 2021, three epidemiological waves of SARS-Cov-2 infection were observed in Cameroon [21].The first-wave from March-August 2020 was driven by the original SARS-CoV-2 lineage, the second wave from November 2020-June 2021 driven mainly by the Alpha and Beta variants, while the third wave from June to October 2021 driven mainly by the Delta variants [21]. For all these reasons mentioned above, an understanding of viral dynamics in covid-19 infection, in a resource limited setting like Cameroon where viral load monitoring using PCR may not be readily accessible for all infected individuals, is very crucial. This would be key in shaping management guidelines in and may also permit us ameliorate hospital stay durations and confinement periods. Currently, such data is lacking in Cameroon, reason why we sought therefore to describe COVID-19 positivity duration and viral dynamics within the first three epidemiological waves experienced in Cameroon, and identify potential factors that may influence positivity duration.

Materials and methods

Study design, enrolment procedure and eligibility criteria

We conducted a retrospective cohort-study among SARS-CoV-2-positive individuals, from March 2020 to October 2021 at the Chantal Biya International Reference Centre (CIRCB) in Yaoundé, Cameroon. This period comprised three epidemiological waves according with the first wave corresponding to the period between March- August 2020, the second wave from November 2020-June 2021 and the third from June to October 2021. The participants after the first positive test, were tested after every seven days until a negative PCR result was obtained, to evaluate viral dynamics and duration of PCR positivity.

Population description

Volunteers were those who came for a routine COVID-19 test, contact cases were those exposed to COVID-19 positive patients and suspected cases were those having at least one of the COVID-19 related symptoms. Participant ages were categorised as follows: children and adolescents were classified as such in accordance with world health organisation data [22], the stratification in the adult category was done to explore any difference which may occur between early-aged (defined here as 19–35 years), middle-aged (35–45 years) or older-aged adults (defined here as ≥46 years).

Method

A standard questionnaire was administered to participants by interviewers trained on the study protocol. It covered clinical and socio-demographic characteristics. Participants were enrolled consecutively based on the following inclusion criteria: (1) All participants coming for COVID-19 testing in the different sampling sites between March 2020 and October 2021, (2) all persons who had given their consent to participate in the study. Excluded were: (1) all SARS-CoV-2 negative persons; (2) SARS-CoV-2-positive persons who provided incomplete information, (3) all invalid RT-PCR sample tests, (4) lost to follow-up participants.

Determination of positivity duration and viral decay

The SARS-CoV-2 positivity duration was estimated by considering the number of days between the first and last positive test before the negative result. Viral decay was calculated as recommended by the world health organisation (WHO) using the formular (a-b)/c, where 'a' is the median CT value at baseline, 'b' the median CT value at the end of follow-up and 'c' the median duration of positivity.

N/B: Baseline CT is the CT of the first positive test of each participant and last viremia the viral load of the last positive test.

Clinical and laboratory procedures

Nasopharyngeal swab test collection was done using Ottawa Public health recommendations (https://www.ottawapublichealth.ca/en/professionals-and-partners/how-to-collect-a-nasopharyngeal--np--swab.aspx). The obtained samples were analysed by real-time PCR (RT-PCR) either using *Abbott m2000 sp* according to manufacturer instructions (https://www.molecular.abbott/int/en/products/infectious-disease/RealTime-SARS-CoV-2-Assay), targeting the RNA-dependent RNA polymerase (*RdRp)* and Nucleocapsid (*N)* gene or *DA aN Gene* systems (https://en.daangene.com) which targets the Open Reading Frame (*ORF1ab)* and Nucleocapsid *(N)* gene of the SARS-CoV-2. Cycle threshold (CT) was used as a proxy of Viral load (VL).

Results were interpreted as follow:

Positive to SARS-CoV-2: Internal control <33 Ct-value (or negative); *N* and *ORF1ab* gene <37 Ct-value (for *DA an gene*) and when the *RdRp* and *N* gene were <37 CN (for *Abbott*);
Negative to SARS-CoV-2: Internal control <33 Ct-value, *N* and *ORF1ab* gene ≥ 37 Ct-value (for *DA an gene*) and when the *RdRp* and *N* gene were ≥37 CN (for *Abbott*);
Indeterminate results: Internal control <33 Ct-value, and when one of the two genes (*ORF1ab* or *N*) is <37 Ct-value and the other ≥37 Ct-value (for *DA an gene*). Such samples were reprocessed and classified positive if the result was reproducible.
Invalid results: For DA an gene (internal control ≥ 33 Ct-value; *N* and *ORF1ab* genes negative); for *Abbott* protocol (analysis failure). Such samples were reprocessed and resampled if the result was reproducible.

Correspondence between Abbott and DA an gene

The correspondence between the CN values obtained on Abbot and CT values obtained with DA an gene was previously described in a previous publication from our team (https://doi.org/10.4081/jphia.2022.2163) [23]. For the N gene, the correspondence used is Y = 0,9568*X + 7,427 and Y = 0,9055*X + 10,27 for the ORF gene; where Y= CT value correspondence for DA an gene and X the CN value obtained on Abbott.

Stratification of CT Values

PCR cycle threshold (CT) values were categorised as low (CT ≤20), moderate (CT value: Between 21 and 30), or high(between 31 and 36) [24]. CT values of 37 or more were considered negative according to national guidelines [25, 26].

N/B: Baseline viremia is the viral load of the first positive test of each participant and last viremia the viral load of the last positive test.

Statistical analysis

Data were entered in an excel spread sheet and double-checked for any errors during data cleaning. The updated dataset was then analysed using the software Graph Pad prism version 8 (GraphPad Software, Inc; https://graphpad-prism.software.informer.com/6.0/) and Epi info version 7.0 (trademark of Centre for Disease Control Atlanta; (https://epi-info.freedownloadscenter.com/windows/). Normality was evaluated by visual inspection for normality curves and using the Kolmogorov–Smirnov test. Correlations were used to assess the relationships between quantitative variables, with provision of correlation coefficients (r) and *p* values. The independent Chi squared test was used to compare proportions between groups and Mann–Whitney U tests for comparison between medians. Survival analysis was used to describe PCR positivity duration/time to viral clearance in participants. The threshold of significant was set at 0.05. Multiple linear regression, (including all factors with $p<0.2$ on bivariate analysis), was used to identify independent factors associated to prolonged SARS-Cov-2 positivity.

Ethical considerations

This study was conducted in conformity with the core principles of the World Medical Association (WMA) declaration of Helsinki version D-1964–01–2013 [27]. An administrative authorization was obtained from the CIRCB; ethical clearance was obtained from the Institutional Ethics Committee for Research on Human Health of ESS-UCAC (ref N° 2021/020431/CEIRSH/ESS/MBC) and from the Cameroon national committee for human health research (N°2020/05/1227/CNERSH/SP). Written informed consent/assent were obtained from all the participants; data were processed using unique identifiers to ensure confidentiality; laboratory results were returned to participants. All positive patients were referred to the take-care centres.

Results

Characteristics of study population

We enrolled a total of 282 participants from 2 collection sites (*"Ecole de Police"* and *"Palais Polyvalent des Sports")*. From the 282 participants, 231 were volunteers, 18 contact cases and 43 suspected cases. Most individuals (84.4%) were asymptomatic. Overall, the mean age ± SD was 41 ± 14 years, and the male to female ratio was 1.64. Considering the periods corresponding to the epidemiological waves, 16.7% (47/282) of participants were from the first wave, 68.4% (193/282) from the second wave and 14.9% (42/282) from the third wave. The sex distribution was similar across all three waves with male predominance, while the mean age appeared higher (42 ± 15 years) in the first wave as compared to the second (36 ± 9 years) and third waves (36 ± 15 years), $p = 0.0019$. Table 1 summarizes baseline characteristics of the study population.

Distribution according to COVID-19 related symptoms

Overall, 15.6% (44/282) of the study population presented symptoms, with decreasing percentage of symptomatic

Table 1 Characteristics of study population

Variables	N (%)	Wave 1 (*N* = 47)	Wave 2 (*N* = 193)	Wave 3 (*N* = 42)
Gender				
Male	175 (62.1)	27 (57.4%)	131(67.9%)	17(40.5%)
Female	107 (37.9)	20(42.6%)	62(32.1%)	25(59.5%)
Age				
[0–19]	22 (7.9)	1 (2.2%)	15 (7.8%)	6 (15.0%)
[19–35]	83 (29.7)	25 (54.3%)	43 (22.3%)	15 (37.5%)
[35–45]	71 (25.4)	10 (21.7%)	51 (26.4%)	10 (25.0%)
≥ 46	103 (36.9)	10 (21.7%)	84 (43.5%)	9 (22.5%)
Symptomatology				
Symptomatic	44 (15.6)	18 (38.3%)	22 (11.4%)	4 (9.5%)
Asymptomatic	238 (84.4)	29 (61.7%)	171 (88.6%)	38 (90.5%)

This table presents the distribution of demographic and clinical characteristics across three waves of data collection (Wave 1, Wave 2, and Wave 3). Calculation of percentages among variables was column-based

individuals from the first (38.3%) through the second (11.4%) and third waves (9.5%), p< 0.00001. The predominant symptom was cough 59.09% (26/44) which was present significantly across all three epidemiological waves. Symptoms such as vomiting and loss of smell were present only in the first and second waves, while rhinorrhoea was present only in the third wave. Figure 1 shows the prevalence of all symptoms across the epidemiological waves.

SARS-CoV-2 baseline viral load (CT-value)

Overall, the duration of PCR positivity ranged from a minimum of 3 days to a maximum of 89 days and was similar between the first (3 to 89 days) and second waves (3 to 86 days) but different from the third wave (3–29 days). The mean baseline CT was 24.8 ±7.1 with similar distribution between males and females; mean of 25.47 ±6.9 for female and 24.4 ±7.2 for male, $p=$ 0.3. After classifying viral load value as high (≤ 20 Ct), moderate (21–30 Ct) and low (31–36 Ct), we found a similar distribution (p = 0.31) between both genders, (Table 2). Concerning base line viral load according to age, the mean Ct values were similar across all age categories (Infant and adolescents (0–19 years): 24.7 ±6.7 Ct; young adults (20–35 years): 25.1 ±7.7 Ct; adults (36–45 years): 25.2 ±6.8 Ct, and old adults (> 45 years): 24.3 ±7.1 Ct, $p=$ 0.87. Concerning baseline viral load distribution with disease waves, it was similar with a mean of 23.1 ±8.1 Ct in the

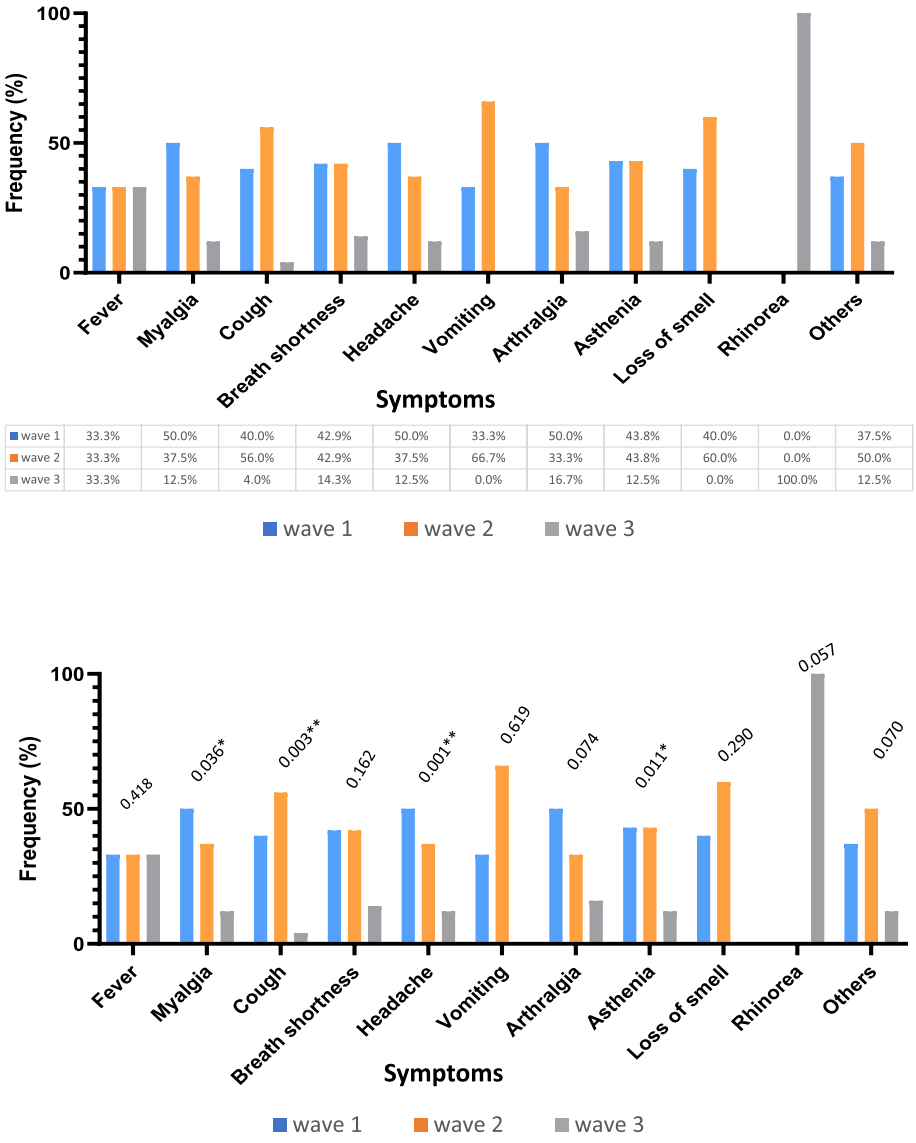

Fig. 1 Symptoms distribution of participants in respect to waves

Table 2 Baseline CT value according to gender, age and symptomatology

	CT value ranges			
	≤ 20	21–30	31–36	Total
Gender				
Female	17 (23.9%)	29 (40.8%)	25 (35.2%)	71
Male	30 (21.3%)	73 (51.8%)	38 (27.0%)	141
Age				
[0–19]	4 (26.7%)	8 (53.3%)	3 (20.0%)	15
[19–35]	15 (25.9%)	25 (43.1%)	18 (31.0%)	58
[35–45]	9 (18.0%)	24 (48.0%)	17 (34.0%)	50
≥ 46	19 (22.1%)	46 (53.5%)	21 (24.4%)	86
Symptomatology				
Symptomatic	13(27.7%)	14(13.3%)	6(10.5%)	33
Asymptomatic	34(72.3%)	91(86.7%)	51(89.5%)	176

This table presents the distribution of baseline CT ranges according to clinical characteristics. Calculation of percentages among variables was column-based

first, 25.3 ± 7.0 Ct in the second and 24.2 ± 6.3 Ct in the third wave, $p = 0.24$ (Table 2). Regarding baseline viral load distribution with symptoms, viral load was significantly associated with the presence of symptoms with a mean Ct value of 21.5 ± 7.7 in symptomatic participants vs. 25.3 ± 6.8 in asymptomatic, ($p = 0.009$). When stratifying symptomatology according to waves, we found a significant difference despite that both symptomatic and asymptomatic participants where mostly in the second wave, $p = 0.0034$ (Table 2).

SARS-CoV-2 positivity duration and potential determinants

Overall, the median positivity duration was 15 [IQR: 9–23] days. This duration was statistically different between disease waves, 15 [IQR: 13–22] days in the first, 17 [IQR: 12–26] days in the second and 9 [IQR: 6–12] days in the third wave, $p = 0.007$. Most participants 55.6% (157/282) had a PCR positivity duration between 11 to 20 days, with 13.9% (39/282) remaining positive after 46 days.

The median positivity duration between age groups was significantly different ($p = 0.009$) with those aged [35–45] years having the highest duration; 16 [IQR:10–26] days followed by those aged ≥ 46 years 15 [IQR:10–27] and equal for those aged [0–19] years 14 [IQR:8–17] days and [19–35] years 14 [IQR:7–19] days;. The median PCR positivity duration was higher in males as compared to females, with males having a PCR positivity duration of 16 [IQR: 11–26] days against 14 [IQR: 8–19] days in females, $p = 0.03$.

PCR positivity duration was not significantly different in asymptomatic and symptomatic patients, with the median positivity duration being 14 [IQR: 8–22] days in asymptomatic patients and 15 [IQR: 14–26] days in symptomatic patients, $p = 0.80$. The median positivity duration by age, sex, symptomatology and disease wave is shown on Table 3. We observed no correlation between baseline viral load and positivity duration ($r = 0.07$; $p = 0.33$). Following multivariate analysis, sex ($p = 0.03$), and epidemiological wave ($p = 0.02$) remained independent determinants of positivity duration.

Table 3 Positivity duration according to sociodemographic characteristics

	Median positivity duration	25%	75%	P value
Overall population	15	9	23	
By age range/years				
[0–19]	14	8	17	
[19–35]	14	7	19	0.008
[35–45]	16	10	26	
≥ 46	15	10	27	
By Gender				
Male	16	11	26	0.03
Female	14	8	19	
By Symptomatology				
Symptomatic	15	14	26	0.80
Asymptomatic	14	8	22	
Epidemiological wave				
Wave 1	15	13	22	< 0.0001
Wave 2	17	12	26	
Wave 3	9	6	12	

This table presents median positivity duration across age, gender and symptomatology. The medians were compared using Mann Witney U-test

SARS-Cov-2 positivity duration trend

Regarding the positivity duration globally, we observe that for the first wave, there was a greater representation of the participants from 0–21 days, for the second wave, participants were most represented as from above 21 days and for the third wave, we observed a net reduction of participants in all the ranges (Fig. 2).

The median positivity duration trend increased from the first wave driven by (the Original Wuhan strain) to the second wave (driven by the Alpha strain) from 15–17 days and decreased from the second to the third wave (driven by delta strain) from 17–9 days (Fig. 3).

Viral kinetics from first SARS-CoV-2 positivity and survival analysis

Considering baseline (mean: 24.7 ± 7.2 Ct) and last viral load (mean: 29.3 ± 5.9 Ct), the ΔCt (4.6 ± 1.3) and positivity duration (15 days) revealed a kinetic in viral decay of 0.3 ± 0.087 Ct/day. The survival analysis across different

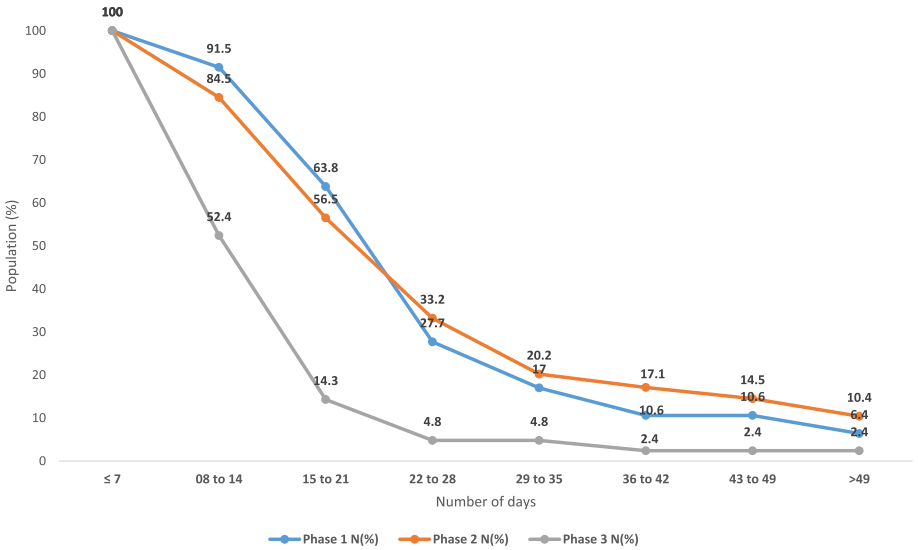

Fig. 2 Participants follow up trend with respect to waves

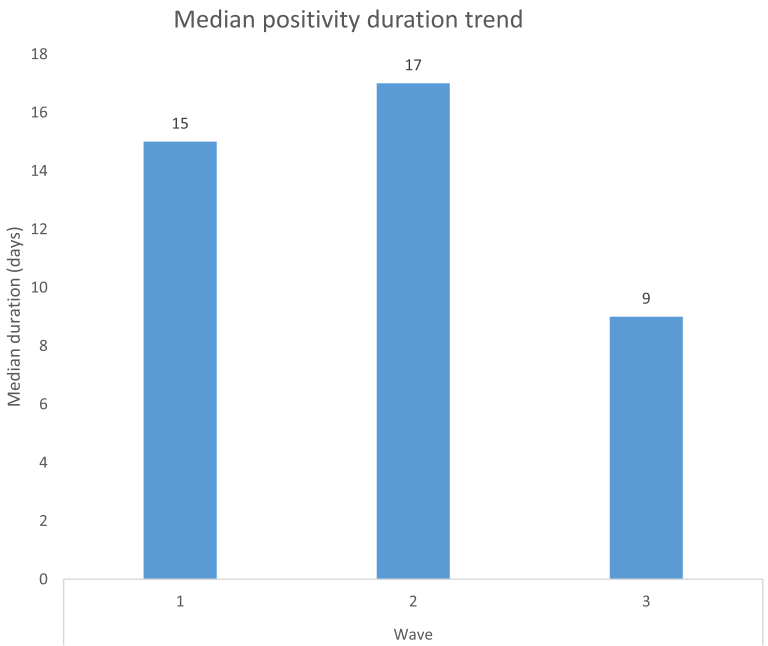

Fig. 3 Positivity duration trend

waves revealed highly significant differences in positivity duration distributions (Log Rank test, $\chi^2 = 60.300$, df = 2, $p < 0.001$). The mean survival times were highest in wave 2 (22.3, 95% CI: 19.8–24.8) and wave 1 (19.9, 95% CI: 15.5–24.3), while wave 3 had a notably lower mean positivity duration (9.4, 95% CI: 7.7–11.0). Median positivity duration for wave 1, wave 2, and wave 3 were 15, 17, and 9 days, respectively, indicating a significant decrease in positivity duration in wave 3. The overall mean positivity duration was 21 days (95% CI: 18.6–24.1), with a median of 15 (95% CI: 14–16); (Supplementary sheet, Fig. 4).

Discussion

The aim of this study was to describe viral dynamics and factors influencing positivity duration in SARS-CoV-2 infected patients in Cameroon, with respect to three

disease waves; first from March-September 2020, second from October 2020-May 2021, and third from June-October 2021.

Overall, mean viral load at baseline was moderate (24.8 Ct-value) and was similar between disease waves, with a mean Ct-value of 23.1±8.1 Ct in the first, 25.27±7.0 Ct in the second and 24.15±6.3 Ct in the third wave. This moderate level viremia could be justified by the fact that the study population was mostly comprised of healthy individuals, most of whom were travellers, as well as young and asymptomatic participants (84.4%). These results are concordant with previous reports [28] showing similar viremia trends. Elsewhere, the similar mean viral load between the waves showed that despite the new disease waves and emergence of new variants, the major changes were linked to disease contagiousness; however, it had less impact on disease severity, mortality and symptoms which are greatly predicted with viral load [29]. There were no significant differences in CT values at baseline, neither with respect to age rages nor sex, which is similar to other studies surely due to small sample size [30, 31]

With respect to symptoms, majority (84.4%) of our participants were asymptomatic in our general population, and also between the different waves. Amongst the symptomatic participants, the most presenting and significant symptom was cough ($p = 0.00065$), as also reported earlier [32, 33] to be one of the predictive symptoms of COVID-19 diagnosis. Not surprisingly, the mean viral Ct-value was significantly lower in symptomatic patients as compared to their asymptomatic counterparts. This is in line with literature and many other studies which describe the same findings [34]. One of the main determinants of disease symptomatology and severity is the viral load, with the peak in viral load corresponding to peak in symptoms [32, 35].

PCR positivity duration remains an important parameter in COVID-19 management as it can greatly guide management and de-confinement measures [36, 37]. Using serial PCR measures, we evaluated the overall duration for which participants remained positive. Overall, the median positivity duration was 15 days and was statistically different between disease waves (15 [IQR: 13–16] days in the first, 17 [IQR: 11–26] days in the second and 9 [IQR: 7–10] in the third wave, $p = 0.007$). These results are concordant with previous findings [28, 32] showing similar durations of SAR S-CoV-2 positivity. Furthermore, the different durations of positivity highlight the observation that third wave seems to present shorter disease durations as compared to the first and second wave, and as such should greatly change hospital durations and de-confinement periods and also prove collective immunity in the population. Additionally, participants were positive for a minimum of 3 days and maximum of 89 days which was similar between first (3 to 89 days) and second waves (3 to 86 days) but different from the third wave (3–29 days). These results are different from other studies which showed lower maximum positivity periods [33, 38]. Nonetheless, longer periods of positivity have also been described, with even cases of positivity after four months [39, 40].

As concerns factors influencing PCR positivity duration, age, gender and epidemiological wave were all found to influence duration of positivity on bivariate analysis. Notably, individuals 35 years and above showed a longer duration of positivity as compared to their younger counterparts. These might be due to decreasing immunity with increasing age or the presence of other co-morbidities or co-infections which could influence viral clearance [41]. Regarding gender, males appeared to have longer duration sof positivity as compared to females. This finding is similar to some existing data, and thought to be related to a difference in immune response in which females develop a higher immune response to infectious agents, reduced ACE-2 expression making them less susceptible to diseases [42]. Nitya Kumar et al, and ONUFEMMES-BUCREPS, 2020 [28] however did not find age nor gender to be significant to determinants of positivity duration in their studies.

Concerning viral kinetics, after comparing baseline viral load and positivity duration among our participants, we observed a kinetic in viral decay of 0.3±0.087 Ct/day. Also, the results of the survival analysis suggest similar positivity duration patterns regardless of Baseline CT categories which can be due to the fact that positivity duration can vary from one individual to another and also depends on the treatment.

Regarding the trend of positivity duration from the different waves we included in our study, we observed an increase in median positivity duration from 15 to 17 from the first wave to the second wave which was driven by the Alpha strain. Furthermore, we observed a decrease in median positivity duration (17-9) from the second to the third wave. These results are similar to other findings [43]. In the same move, we can predict the median positivity duration for the next strain which was Omicron to be lesser than the others. The decrease in positivity duration from one wave to another can be justified by collective immunity (due to multiple/cumulative viral exposure) [44] and increasing number of those vaccinated [44, 45]. Studies show that combination of a previous SARS-CoV-2 infection and a respective vaccination, called hybrid immunity, appears to grant the greatest protection against SARS-CoV-2 infections despite that several knowledge gaps remain regarding this issue [46]. Following multivariate analysis, gender and disease

epidemiological wave, remained independent factors affecting PCR positivity duration.

Study limitations

The main limitation of our study is the absence of important clinical data such as anthropometric parameters, medical history of participants (co-infections, comorbidities) and healthcare provided during infections. Due to the retrospective collection of data for the most part of our population, such data was absent and unfortunately could not be included in our analyses. Nonetheless, our predominantly young population in the study (63% less than 45 years), suggests a rarity of some clinical events, which may have greatly influenced viral dynamics. Also, although we did not perform any analysis on immune response, to accompany the observed findings, vaccination coverage in the country was low during this period, suggesting little influence of vaccination. However, natural immunity from previous covid-19 infections especially in the third-wave, or even pre-existing immunity to SARS-Cov-2 as shown in previous studies [10], may have contributed to the observed findings.

Conclusion

From this population of individuals living in the capital city of Cameroon during the three first waves of COVID-19 pandemic, the duration of SARS-CoV-2 positivity is about 15 days, indicating a viral clearance around 2 weeks for optimal confinement or prevention of transmission at community-level. However, men and/or the elderly stand at higher risk of prolonged infection. For personalised monitoring of COVID-19, the viral decay (0.3 Ct daily) suggests specific confinement period according to individual baseline viremia. At the public health level, the variability of the positivity duration of SARS-CoV-2 positivity from the first to the third wave suggests a need for continuous surveillance for updated prevention and control strategy and natural immunity should be taken into consideration for public health policy regarding SARS-CoV-2.

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s12879-025-11048-5.

Supplementary Material 1

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Authors' contributions

J.F., A.M.K.N, A.D.N., C.C.A.,E.G.J., Y.B., D.T., N.F., M.C.T.T., A.C.K., G.A.B., S.C.D.N., W.L.T.P., D.H.G.A., N.K.E., E.M., R.A.N.M., M.S.S., J.O.O., C.N.O., C.A., L.C., M.M.S., F.C.S., Y.B., E.G.H.E., A.K.N., V.C., N.D., A.N. and C.F.P. wrote the main manuscript. J.F., A.M.K.N, A.D.N. and C.C.A. collected, analyzed the data and prepared figures. J.F., A.M.K.N, A.D.N. and C.C.A initiated the manuscript. All the authors revised and approved the final manuscript.

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Data availability

All data generated or analysed during the current study are not publicly available due to the fact that the data contain potentially identifying or sensitive participant information. In this study, participants were assured that `All the information collected is kept private and confidential' and that `only authorized study staff will have access to this information.'This approach to access study data was approved by the National Ethics Committee of Cameroon (CNERSH) (N° 2020/09/1292/CE/CNERSH/SP), which requires that we release data from Cameroonian studies only after they have provided their written approval for additional analyses. As such, data for this study will be available upon request, with written approval for the proposed analysis from the CNERSH. To request these data, individuals can contact CNERSH secretary, email: setcominae@gmail.com.

Declarations

Ethics approval and consent to participants

This study was conducted in conformity with the core principles of the Helsinki declaration. An administrative authorization was obtained from the CIRCB; ethical clearance was obtained from the Institutional Ethics Committee for Research on Human Health of ESS-UCAC (ref N° 2021/020431/CEIRSH/ESS/MBC) and from the Cameroon national committee for human health research (N°2020/05/1227/CNERSH/SP). Written informed consent were obtained from all the participants.

Informed consent for the study was obtained from parents/guardians of child participants. Data were processed using unique identifiers to ensure confidentiality; laboratory results were returned to participants. All positive patients were referred to the take-care centres.

Consent for publication

Not applicable

Competing interests

The authors declare no competing interests.

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