**SARS-CoV-2 Antibody Seroprevalence in Yaounde, Cameroon**

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# Summary

## Background

The degree of spread of severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) SARS-CoV-2 in many African countries is not well understood. Experience elsewhere suggests that official PCR case counts underestimate severalfold the true extent of community infection.

## Methods

In this cross-sectional community survey, households were the primary sampling unit, and their residences were randomly selected from an Open Street Map building footprint. Fingerprick blood samples were taken from adults and children above 5 and tested for antibodies against SARS-CoV-2 using the Abbott IgG/IgM PanBio test, a lateral-flow point-of-care test that detects IgG and IgM isotypes that bind to the SARS-CoV-2 nucleoprotein. We also administered questionnaires assessing sociodemographic information from the residents.

## Findings

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## Interpretation

The number of individuals in the Cité Verte population who have been challenged with SARS-CoV-2 infection is order of magnitude greater than the official case count.

However, a substantial population remains unexposed...

## Funding

GIZ

# Research in context

## Evidence before this study

## Added value of this study

Text

## Implications of all the available evidence

Text

# Introduction

Coronavirus disease 2019 (COVID-19) is caused by the severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2), which was identified for the first time in China at the end of 2019.1 The virus quickly spread globally, and the World Health Organization declared COVID-19 to be a pandemic on March 11, 2020. As at December 1, 2020, there have been over 67,000,000 notified cases, with over 1,500,000 reported deaths.2

Given the rapid spread of the epidemic in Europe and the Americas, and the handicapped response by countries with the richest health systems, the outlook for less developed countries, and sub-Saharan Africa in particular, seemed dire. High numbers of deaths were expected due to weaknesses in health systems, difficulties in enforcing hygiene measures, and perceived health vulnerabilities of the population.3,4 But the trajectory of the epidemic on the continent appears to have gone against expectation. Despite having over 2,200,200 infections as of December 1,2 Africa remains the least affected region and the mortality rate, even if not well documented, remains lower than expected.4

Several theories have been advanced to explain the seemingly mild trajectory of the SARS-CoV-2 epidemic in Africa: it has been hypothesized that sub-Saharan Africa's warm climate, young population, or cross-reactive immunity from other infections are mitigating factors.4 But an informed explanation of the epidemic trajectory requires accurate numbers on the actual extent of population infection. Was the spread of the virus largely impeded, or was virus spread widely without the majority of the population exhibiting clinical symptoms?

And, as is the case elsewhere,5 the officially reported case counts in Africa significantly underestimate the extent of spread.4

In this context, the use of serological antibody tests to detect exposure to SARS-CoV-2 is valuable. A number of validated SARS-CoV-2 antibody tests now exist on the market,6 and some of these are point-of-care lateral-flow immunoassays, which are affordable, easy to use and provide quick results. Although concerns about sensitivity and specificity remain, these antibody tests offer the opportunity to more accurately assess the prior infection rate of populations in regions where PCR-based testing has been uncommon.5

This report presents the protocol and results of our study using a lateral-flow immunoassay to assess the seroprevalence of anti-SARS-CoV-2 IgG and IgM antibodies in a region of Yaounde, the capital of Cameroon.

# Methods

## Sampling

On the basis of power calculations (with an assumed prevalence of 20%, a precision of 5% and a confidence level of 95%) we estimated 245 people would be sufficient. This sample was increased to 1000 people (>245 households) for improved precision.

Houses were randomly selected from a pre-processed set of all presumed residential buildings on an OpenStreetMap footprint7. However, some non-residential buildings were still encountered by the surveyors (XX%). In these cases, the next residential building to the right was used as a replacement.

In each household, all consenting residents between 5 and 80 years in each household were surveyed.

## Testing

The test used was the Abbott Panbio™ COVID-19 IgG/IGM Rapid Test Device, an immunochromatographic test for the qualitative detection of IgG and IgM antibodies to SARS-CoV-2 (with a manufacturer-estimated sensitivity and specificity of the test are 95.8% and 94% respectively).

The tests were performed on capillary blood which was collected from a finger prick from all the consenting participants. A questionnaire was also administered in tandem with the testing.

## Data analysis

**Seroprevalence estimation**

Seroprevalence values were weighted within each age or sex stratum to match the age-sex distribution of the Yaounde population, as sourced from the 2018 Cameroon DHS8.

We used the Rogan-Gladen formula to adjust IgG seroprevalence estimates to account for test performance.9 sensitivity estimate provided by Batra and others’ validation study of the Abbott test, which found a sensitivity of 91.5% (75 correct diagnoses out of 82 samples) when applied on sera collected from hospitalized COVID-19 patients 14 – 56 days post symptom onset.10 We measured specificity by applying the test on a panel of 246 pre-pandemic (2017) samples from hospital patients in Yaounde. The IgG test correctly diagnosed 230 of 246 samples (93.5% specificity).

### Risk factor analysis

For seropositivity risk factor analysis, we used logistic models with household random effects to account for within-household clustering. In the logistic models, the following prospective risk factors were analysed: sex, age, education, BMI group, occupation, contact with an international traveller since March 1st, contact with a suspected or confirmed COVID case since March 1st, presence of comorbidities (combining hypertension, respiratory illness, diabetes, tuberculosis, HIV, cardiovascular illness and “other illnesses” which were not explicitly listed in questionnaire), whether or not the respondent is the breadwinner, adherence to social distancing rules, location of the household (one of nine health zones), number of household members, and whether or not there are children in the household. Each variable was first analysed in a univariate model. Then variables with p < 0.10 for at least one factor level were entered into the multivariable analysis. All such variables are shown in the regression tables.

## Ethical considerations

The study protocol obtained the ethical clearance and the administrative authorization of the Ministry of Health of Cameroon. Every adult participant (21 years or above) signed an informed consent. For minors, a person with parental authority was asked to sign the consent form and, if the age was equal to or above 15 years, an assent was also requested. Questionnaires were coded and names of participants were recorded in a confidential list available only to the study team. Before starting the study, all the team members were trained on research ethics, good clinical practices and study protocol and procedures.

# Results

Global distribution of venomous snake species

Global variation in market antivenom availability

Populations lacking access to quality health care

# Discussion

“Concerns have been raised regarding the use of pointof-contact antibody tests for clinical decision making and for so-called immune passports. However, use of such tests for large-scale, population-based, seroprevalence studies is less controversial, provided that sensitivity and specificity are sufficiently high and appropriately corrected for.37,38 “ - https://www.thelancet.com/pdfs/journals/langlo/PIIS2214-109X(20)30387-9.pdf

“Our results have strong face validity, showing a high correlation with reported death rates, an increase over time as the pandemic progressed, and distribution by age, socioeconomic status, and household size that would be expected. “ https://doi.org/10.1016/ S2214-109X(20)30387-9

Important doubts exist regarding the use of rapid point-of-care antibody tests in clinical settings, due to their far-from-perfect specificity values (CITE). This is valid as a worry regarding clinical use, but it less important for population-based surveys, where estimates can be adjusted for sensitivity and specificity, as we have done here.

Confidence in our results is increased by the fact seropositivity showed the correlations with household size and COVID-like symptoms that would be expected.

Understanding what populations have already developed antibodies to SARS-CoV-2 is vital for public health planning. It allows to understand whether large-scale spread––additional waves of infection––are still possible. It also provides data that allows us to do a retrospective review of public health prevention measures: that is, it allows us to ask questions like: to what extent were these measures effective? And, how can hygiene measures be reinforced for future epidemics.

By studying a random sample of participants in a West African city, this study gives an idea of what levels of spread might be reasonable to expect in similar cities in Africa where serosurveys have not been done. The analysis therefore provides valuable data to inform practice and research.

While the estimates arrived at in this cannot serve as a stand-in for other African cities where serosurveys have not been done, we should expect that the extent of spread here (and especially the high degree of underreporting) should not be too far from what might be expected in similarly-dense African cities with like climates.

Other studies have shown similarly high extents of spread in African cities. A preprint from Nigeria showed that up to XX% of individuals in Niger state were positive for anti SARS-CoV-2 antibodies.

## Limitations

Future serosurveys might focus on some of the limitations of the present study.

Our study is limited by our lack of knowledge of the time since infection of each of the study participants. Because of this, our sensitivity estimates are crude, time-indifferent estimates. This is an important limitation because we know that even IgG antibody levels decline over time. However, one recent study found that IgG antibodies were present up to 8 months after infection.8

# Contributors

JL, DMP, and SIH conceived and planned the study. JL wrote the computer code, and designed and carried out the analyses with input from FMS and DMP. DJWe constructed the accessibility covariate data layer. JL produced all output figures. DJWi, DAW, NR, RRdC provided intellectual inputs into aspects of this study. All authors contributed to the interpretation of the results. JL wrote the first draft of the manuscript and all authors contributed to subsequent revisions.

# Declarations of interests

The authors declare no competing interests.

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# Figures and Tables

**Figure 1. Conceptual overview of vulnerability to snakebite envenoming.** Vulnerability can be considered as the intersection of populations who live within the range of venomous snakes which have no antivenoms available, cannot easily access health care, and have poor-quality health care in delivery of antivenoms or ensuring necessary stocks. The intersection of all three defines the most vulnerable peoples. The figure to the right indicates that these factors vary in space and that by overlaying these features, the most vulnerable populations can be identified spatially (represented here by the boxes outlined in black).

**Figure 2. Venomous snake species ranges, and number of medically important venomous snake species per 5 x 5km location for which no effective therapy is currently listed by WHO.** A: Categories one and two venomous snake species count ranging from low (1) to high (13). Light grey (Panel A), represents locations where no medically important venomous snake species are present; B: Categories one and two venomous snake species with no effective therapy, counts range from low (1) to high (7). Light grey (Panel B) represents locations where snake species present have effective therapies listed by WHO, and dark grey (Panel B) represents locations where no medically important venomous snake species are present.

**Figure 3. Proportion of each HAQ Index decile.** Population living within the range of (left) one or more medically important venomous snake species (either category); (right) one or more medically important venomous snake species (either category), for which no effective therapy is listed.

**Figure 4.** **Average travel time to nearest major city for populations living within snake ranges.** Light grey pixels represent areas without the presence of venomous snake species of medical importance.

**Figure 5.** **Vulnerable population hotspots.** This map indicates the absolute numbers of people living in areas within the range of one or more medically important venomous snake species, and more than three hours away from major urban centres, for HAQ Index deciles 1-3. A: pixel-level vulnerability surface (vulnerability to all species of medically important snakes). B: Aggregated administrative level two vulnerability to all species of medically important venomous snakes. C: Aggregated administrative level two vulnerability to only those species for which no effective therapy is currently listed by WHO.

**Table 1. Vulnerable population count.** Country-level count of vulnerable peoples living within the range of one or more medically important venomous snake species, for which no effective therapy exists, and more than three hours urban centers with a population ≥50 000 provided per HAQ Index decile [ranging from 1 (low) to 10 (high)]. Please see Supplementary File 1 for vulnerability estimates not incorporating antivenom availability.

# Additional Files

Supplementary file 1:

**Figure 1. Schematic overview of the methods.** Overview of the methods representing input data (green, snip diagonal corner rectangle), analyses (orange, rectangle), intermediate outputs (blue, rounded rectangle, dashed) and final outputs (yellow, rounded rectangle).

**Table 1: Ranked species requiring range validation.** Species requiring range validation are prioritised based on medical category, number of out-of-range records, and average distance (decimal degrees) of out-of-range records. Species with an asterisk are species for which we provide a recommended amended range within our analysis (see Supplementary File 2 for range visualisations).

**Figure 2: Venomous snake species ranges and their overlap based upon proposed, amended ranges.** A: Categories one and two venomous snake species count ranging from low (1) to high (13); B: Category one venomous snake species count ranging from low (1) to high (8); C: Category two venomous snake species count ranging from low (1) to high (11). Grey represents locations where no venomous snakes within the different aggregations are to be found.

**Figure 3: Numbers of species with no listed antivenom, split by medical importance.** Each panel represents the number of venomous snake species per 5 x 5km cell for which no species-specific antivenom exists. Panel A: Category one medically important species; Panel B: Category two medically important species, ranging from low (blue, 1 species) to high (red, 7 species); Panel C. Both category one and category two medically important species, ranging from low (blue, 1 species), to high (red, 7 species).

**Figure 4: Proportion of each HAQ Index decile population living within ranges of medically important snake species.** A) One or more snake species (either category); B) One or more Category one species; C) One or more Category two species; D) One or more species lacking listed antivenoms (either category); E) One or more Category one species lacking listed antivenoms; F) One or more Category two species lacking listed antivenoms.

**Figure 5: Population time-delay plots, per HAQ Index decile.** Separate plots per HAQ Index decile (1-10), showing the percentage of the population living within n hours from urban centres with a population ≥50 000. Three letter codes represent each countries ISO3 code; numeric values following ISO3 codes (where applicable), represent the Food and Agriculture Organisation (FAO) Global Administrative Unit Layers (GAUL) code (administrative level one).

**Figure 6:** **Vulnerable population hotspots.** This map indicates the absolute numbers of people living in areas within the range of one or more medically important venomous snake species, and more than three hours away from major urban centres, for HAQ Index deciles 1-10. A: pixel-level vulnerability surface (vulnerability to all species of medically important snakes). B: Aggregated administrative level two vulnerability to all species of medically important venomous snakes. C: Aggregated administrative level two vulnerability to only those species for which no effective therapy is currently listed by WHO.

**Table 2:** **Vulnerable population count.** Country-level count of vulnerable peoples living within the range of one or more medically important venomous snake species for which no effective therapy exists and more than three hours urban centers with a population ≥50 000, provided per HAQ Index decile [ranging from 1 (low) to 10 (high)].

Table 3. Genus inclusion list.

Table 4. Covariates used to construct each Multivariate Environmental Similarity Surface.

**Figure 7. Visualisation of MESS construction and record evaluation process.** Panel A represents a stacked output of 100 MESS iterations, with cell values ranging from 0 to 100, generated using occurrence records within the currently accepted expert opinion range (black outline). Panel B represents a binary version of the stacked output (A), in which cells with a value ≥95 in (A) are classified as being cells of environmental interpolation, and cells <95 in (A) are classified as being cells of environmental extrapolation. Out-of-range records are then overlaid on top of the new binary surface (Panel C), and are classified as being MESS +ve or MESS –ve. Records which are MESS +ve contribute towards a new range recommendation (Panel D).

Supplementary file 2:

Species inclusion lists, incorporating species MESS, amended ranges or original EORs, where applicable.

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