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COVID-19 Screening among International Travelers in Kinshasa, Democratic Republic of Congo: A Multicenter Cross-Sectional Study

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Abstract

The emergence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in 2019 rapidly escalated into a global health emergency and pandemic. The spread of the virus, affecting millions, was largely facilitated by the ease of international travel. To balance public health measures with essential cross-border mobility between the Democratic Republic of Congo (DRC) and other countries, a traveler surveillance program was implemented. This study aimed to review the first six months of COVID-19 pandemic surveillance by screening international travelers in Kinshasa. A multicentric cross-sectional study was conducted between August 2020 and February 2021 across six COVID-19 screening sites affiliated with the National Institute of Biomedical Research (INRB). Data collected included sociodemographic characteristics, travel history, RT-PCR test results, and viral sequencing information. Among the 190,809 travelers included in the study, 4.7% tested positive for SARS-CoV-2. Most positive cases were between the ages of 21 and 60. Outbound travelers exhibited a higher positivity rate (6.1%). The predominant variant detected was 20E (EU1). Multivariate analysis identified age > 80, female gender, and outbound travel as factors significantly associated with increased infection risk. These findings underscore the critical role of targeted traveler surveillance in miti-

gating the international spread of imported and exported infectious diseases.

Keywords

COVID-19, Surveillance, International Travelers, Pandemic, Variants

1. Introduction

The relative tranquility in global health was disrupted in December 2019 by the emergence of Coronavirus Disease 2019 (COVID-19), an acute respiratory infection caused by the novel coronavirus SARS-CoV-2 [1]. In response to its swift global transmission, increasing case numbers and fatalities, and mounting pressure on healthcare systems, the World Health Organization (WHO) declared the outbreak a public health emergency of international concern and, later, a pandemic [2]-[5].

Transmission occurs primarily via respiratory droplets, with airborne spread playing a significant role. Notably, 30% to 50% of infections are asymptomatic, complicating detection and facilitating undetected transmission [6]-[9]. Domestic and international population mobility was a key driver of the global spread. The appearance of novel SARS-CoV-2 variants further underscored the virus's dynamic nature and its potential for rapid evolution until it reached a continent that was previously unaffected by this disease, namely Africa. The first African case of COVID-19 was detected in Egypt in 2020, and since then, the disease has spread to several African countries, with 10000 people affected with the alpha variant. This spread of the disease has been the result of the virus being imported by international travelers [5] [10]-[17].

In the early stages of the pandemic, many countries with limited prior experience implemented a range of control measures. As a result, Africa too has intensified its measures and strategy to combat the disease, focusing on physical distancing, border lockdowns, travel restrictions, and public space closures [18] [19].

The Democratic Republic of the Congo (DRC) reported its first COVID-19 case in the capital, Kinshasa, on March 10th 2020, in a Congolese traveler from Europe [5]. Subsequent cases were similarly linked to international travel, with most cases concentrated in one of Kinshasa's communes before local transmission took hold and spread progressively through national travel to other provinces. However, Kinshasa remained the epicenter where the number of COVID-19 cases was considerably high, with 320 out of 332 cases in DRC.

In response to this situation, a series of public health interventions was instituted, including the declaration of a health emergency, lockdowns, curfews, closures of public spaces, and restrictions on gatherings and travel [5] [20] [21].

Although initially effective, these measures imposed severe social, economic, and political costs [20]-[22], which led to the measures being lifted, with the risk of an increase in the number of cases following the importation of the disease and

the introduction of new variants by travelers. This is why it was imperative to set up more sustainable strategies. Consequently, the DRC adopted targeted surveillance protocols based on WHO guidance and the International Health Regulations (IHR). These included systematic screening of international travelers in Kinshasa, isolation of positive cases, and restriction of movement until recovery and virological clearance were confirmed [23]-[34]. Kinshasa is the capital and a commercial crossroads with a large flow of travelers estimated at 1,000,000 a year.

The aim of this study is to review the first six months of pandemic surveillance of COVID-19 through the screening of international travelers in Kinshasa.

2. Materials and Methods

2.1. Study Design and Setting

A multicentric cross-sectional study was conducted in Kinshasa, the capital of the Democratic Republic of the Congo (DRC), between August 2020 and February 2021 as part of a national surveillance program monitoring international travelers during the COVID-19 pandemic. The study was implemented through a collaboration involving the Ministry of Public Health, Hygiene, and Prevention; the Multisectoral Committee for the Response to SARS-CoV-2; the Microbiology Service of the University Clinics of Kinshasa; and the National Institute for Biomedical Research (INRB). Sampling sites included six locations affiliated with the INRB: N'djili International Airport, INRB headquarters, Batetela, Ngobila Beach, Ngaliema Clinic, and Cinquantenaire Hospital.

2.2. Study Population

The study population consisted of all international travelers entering and leaving Kinshasa by air or river. Eligible participants included all international travelers aged > 3 years who were screened for SARS-CoV-2 in one of the sampling sites affiliated with the INRB, either before departure from or upon arrival in Kinshasa during the study period. Individuals who were missing information on the way of the trip, the type of traveler, and those who were not sampled or screened at non-INRB sites were excluded.

2.3. Data and Sample Collection

We collected data from the INRB central database extracted in CSV format from the INRB server. This database was established through a meticulous information collection process. Travelers pre-registered via the "inrbcovid.com" platform, completing an online form that generated a QR code linked to their identity. This code was encoded into a barcode for sample tracking and test result retrieval. A unique identification (ID) code linking test results with individual sociodemographic and clinical data enabled results to be reported online.

Sociodemographic data included ID code, age, sex, traveler category (incoming or outbound), origin (for incoming travelers), commune of residence (for outbound travelers), email address, nationality, and contact number. Clinical data were self-

reported and included symptoms such as fever, cough, chills, diarrhea, unexplained bleeding, headache, myalgia, vomiting, dyspnea, and abdominal pain. Additional variables included the sampling site, sample collection and result release dates, qRT-PCR test results, and any identified SARS-CoV-2 genotypes. Nasopharyngeal and oropharyngeal swabs were collected using sterile polyester swabs and placed in 3 mL of viral transport medium (VTM; COPAN ITALIA S.p.A). Samples were transported to the INRB at 4˚C in isothermal containers within 1 hour of collection.

2.4. Laboratory Analysis

The biological data archived and collected in the INRB tour operator monitoring database were obtained by routine laboratory analysis from the INRB team. Following the manufacturer's protocols, we extracted viral RNA using the Auto-Pure 32A automated system (Hangzhou Allsheng Instruments Co., Ltd) and Maccura viral RNA extraction kits. Then, we performed SARS-CoV-2 detection using qRT-PCR (Maccura Biotechnology, USA) with fluorescent amplification targeting the ORF, N, and E genes, detected through FAM, CYS, and ROX channels, respectively. Amplification conditions included reverse transcription at 50˚C for 15 min, enzyme activation at 95˚C for 2 min, followed by 40 cycles of amplification at 50˚C for 30 s and 40 ˚C for 10 min. Samples with cycle threshold (Ct) values < 30 were forwarded to the INRB Pathogen Genomics Laboratory for whole-genome sequencing. Viral cDNA was amplified using ARTIC primers for Illumina sequencing, and libraries were prepared using either the Illumina DNA Prep or Rapid Barcoding Kit and then sequenced on MiSeq or NextSeq platforms. For Oxford Nanopore sequencing, amplification was performed using ARTIC or Midnight primers, with libraries prepared using ligation or rapid barcoding kits and sequenced using MinION or GridION platforms.

2.5. Screening Implementation and Data Management

We began establishing screening stations in August 2020, starting at the INRB headquarters and expanding to decentralized units at Batetela, Cinquantenaire, N'djili International Airport, Ngaliema, and Ngobila Beach. The heads of the respiratory virology unit and the virology department supervised operations at each site. Staff processed on-site samples and transferred them to the INRB under a maintained cold chain. Each station had essential office and laboratory infrastructure, including printers, scanners, computers, and sampling kits. Station managers transmitted data to the head of the respiratory virology unit. We validated test results before release and centralized all records through the central data manager.

2.6. Statistical and Bioinformatics Analysis

The data were coded and then imported into R software version 4.3.2 for analysis. We summarized quantitative variables as means with standard deviations or medians with interquartile ranges (IQR), as appropriate. We reported categorical var-

iables as proportions. We stratified data by traveler category (incoming vs. outbound) and SARS-CoV-2 status (positive vs. negative). To compare means, we used Student's t-test, and to compare proportions, we applied Fisher's exact test.

We built a multivariable logistic regression model to identify factors associated with SARS-CoV-2 positivity, including age, sex, and traveler category as independent variables. We reported results as odds ratios (OR) with 95% confidence intervals (CI) and considered p-values < 0.05 statistically significant.

We used established bioinformatics pipelines to generate consensus genomes and assigned SARS-CoV-2 variants with Pangolin, Nextclade, and UShER to analyze viral sequences.

2.7. Ethical Approval

The data in this study were extracted from database of COVID-19 surveillance during the pandemic authorized by the DRC's regulatory institutions, the Ministry of Public Health, Hygiene and Prevention, and the Multisectoral committee for the response to COVID-19. Hence, these data were archived in the absence of consent from travelers.

However, after review by the Ethics Committee of the School of Public Health of the University of Kinshasa, this study obtained ethical approval for data use in scientific publications (approval number ESP/CE/54/2025).

3. Results

3.1. Sociodemographic, Travel, and Travelers Characteristics

A total of 190,809 international travelers meeting the inclusion criteria were enrolled in the study. The most prevalent age groups were 41 - 60 years and 20 - 40 years, accounting for 47% (89,639/190,809) and 38% (71,624/190,809) of the study population, respectively. These same age groups also had the highest number of positive cases, with 46% (4141/8931) and 38% (3426/8931), respectively. The mean age was 42 years (±14.72). Males accounted for 65% (124,877/190,809) of travelers and 64% (5674/8931) of positive cases. Air travel was the most frequent way of the trip, accounting for 94.5% (180,277/190,809) and 92.4% (8344/8931) of positive cases. Outbound travelers predominated, accounting for 58% (110,674/190,809) and 74% (6646/8931) of positive cases (Table 1).

Table 1. General characteristics of participants and RT-PCR results.

Parameters	Total (%) N = 190,809	Negative N = 181,878	Positive N = 8931	p-value
Age (years)				0.012
<20	11,269 (5.9%)	10,737 (5.9%)	532 (6.0%)	
20 - 40	71,624 (38%)	68,198 (37%)	3,426 (38%)	
41 - 60	89,639 (47%)	85,498 (47%)	4,141 (46%)	
61 - 80	17,847 (9.4%)	17,048 (9.4%)	799 (8.9%)	
>80	430 (0.2%)	397 (0.2%)	33 (0.4%)	

Continued

Gender				<0.001
Male	124,877(65%)	119,203 (66%)	5,674 (64%)	
Female	65,932 (35%)	62,675 (34%)	3,257 (36%)	
Way of trip				<0.001
Air	180,277 (94.5%)	171,933 (94.5%)	8,344 (92.4%)	
River	10,532 (5.5%)	9,945 (5.5%)	587 (6.6%)	
Type of Travelers				<0.001
Incoming	80,135 (42%)	77,850 (43%)	2,285 (26%)	
Outbound	110,674 (58%)	104,028 (57%)	6,646 (74%)	

3.2. Origin of Travelers

Among inbound travelers with available origin data (n = 28,884), the majority of travelers came from Europe with 52.6% (15,200/28,884), followed by Africa with 22.3% (6,453/28,884), Asia with 12.7% (3,661/28,884), America with 12.2% (3,517/28,884) and Oceania with 0.2% (53/28,884). Travelers from Africa had a positive rate of 2.97% (192/6453), followed by America with 2.95% (104/3517), Europe with 2.04% (311/15200), and Asia with 1.91% (70/3661) (Figure 1). France, Belgium, the United States, and India were the leading countries of origin, accounting for 20%, 18.5%, 11.8%, and 7.2% of inbound travelers, respectively. The Republic of Congo, Kenya, and Cameroon were the African countries with the highest number of travelers, respectively 5.7%, 2.9%, and 2.5% (Figure 2).

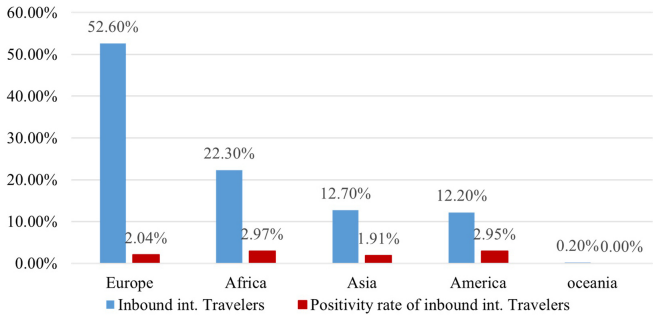

Figure 1. Distribution of inbound travelers and positivity rate by continent of origin.

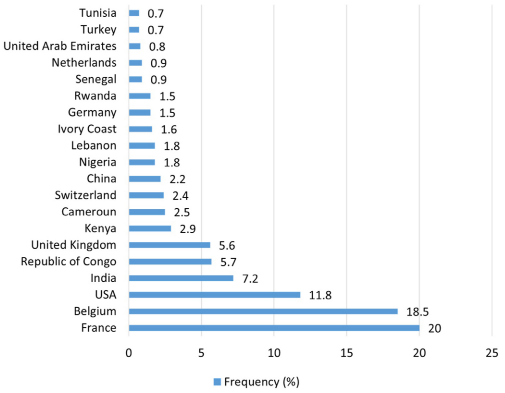

Figure 2. Countries of origin of inbound travelers.

3.3. Positivity Rate and Participants Characteristics

A total of 8,931 travelers tested positive for SARS-CoV-2, corresponding to an overall positivity rate of 4.7% (8,931/190,809). Female travelers exhibited a higher proportion of positive results, 4.9% (3257/65,932), compared to males, 4.5% (5674/124,877). The majority of positive cases were among air travelers and outbound individuals. Most positivity rates were 6.1% (6,646/110,674) among outbound travelers and 5.6% (587/10,532) among those traveling by river (Table 2).

Table 2. SARS-CoV-2 overall positivity rate and positivity rate by participant characteristics.

Parameters	Positivity rate (%)	p-value
Overall	4.7	
Type of traveler		0.01
Incoming	2.9	
Outbound	6.1	
Gender		0.06
Female	4.9	
Male	4.5	
Age (years)		0.01
<20	4.7	
20 - 40	4.7	
40 - 60	4.6	
61 - 80	4.5	
>80	7.7 (reference)	
Way of the trip		0.03
Air	4.6	
River	5.6	

3.4. Genomic Analysis

This study highlights that, over the period from August 2020 to February 2021, nine SARS-CoV-2 variants were identified among international travelers in Kinshasa. The variant "20A.EU1", currently designated as "20E (EU1)", was the predominant lineage identified (Figure 3).

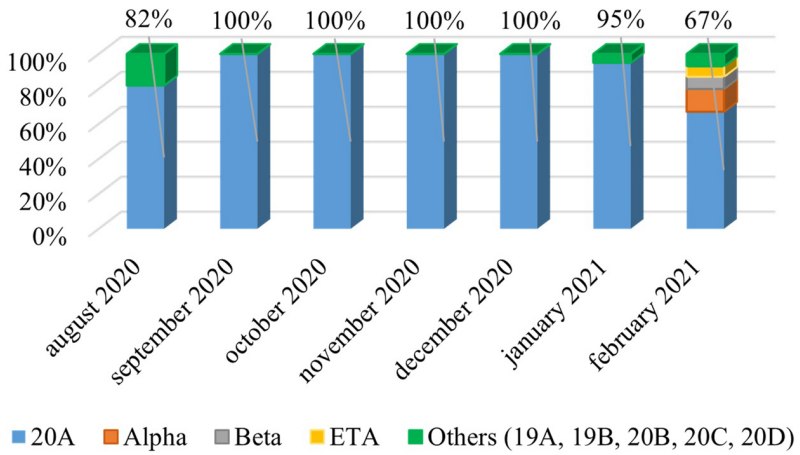

Figure 3. SARS-COV-2 variants detected during the study period.

3.5. Risk Factors for SARS-CoV-2 Positivity

Univariate analyses revealed significantly higher positivity among outbound travelers (6.1%) compared to incoming travelers (2.9%) (p = 0.01). Travelers aged > 80 years showed the highest positivity rate (7.7%) (p = 0.01), and those who traveled by river had higher positivity (5.6%) compared to air travelers (4.6%) (p = 0.03) (Table 2).

Multivariate logistic regression identified significant associations between positivity and traveler type, age, and gender (Table 3). Travelers aged > 80 years, female gender, and outgoing status were independently associated with increased odds of SARS-CoV-2 positivity.

Table 3. Association between participant characteristics and SARS-C0V positivity (multivariate analysis).

Parameters	ORa[1]	95% CI[1]	p-value
Age (years)			
>80	1	-	-
<20	0.37	0.13 - 0.60	0.002
20 - 40	−0.31	−0.50 - 0.10	0.002
41 - 60	0.24	0.11 - 0.36	<0.001
61 - 80	−0.05	−0.11 - 0.01	0.12
Gender			
Male	1	–	
Female	−0.07	−0.10 - 0.04	<0.001
Type of travelers			
Outbound	1	–	
Incoming	0.55	0.52 - 0.59	<0.001

[1]OR = Odds Ratio; CI = Confidence Interval.

4. Discussion

This study processed surveillance data on COVID-19 in international travelers extracted from a pre-established database. A limitation of the study was the lack of important information, including clinical data and country of origin in some cases. This prevented a full investigation of risk factors and limited the implementation of specific measures based on the prevalence of COVID-19 in the countries of origin. These data were derived from the traveler's subjective online declaration at the time of registration. Nevertheless, the study generated interesting results on COVID-19 in Kinshasa. This is one of the first studies on COVID-19 among travelers to the DRC. Its main objective was to review the first six months of COVID-19 pandemic surveillance by screening international travelers in Kinshasa.

Thus, the present study shows that most international travelers fell within the 41 - 60 (47%) and 21 - 40 (38%) age groups. This pattern mirrors findings from the literature. Tsuboi *et al.* reported similar age distributions in Japan, with 48.6% of travelers aged 20 - 39 and 34.9% aged 40 - 64 [35]. In Canada, Lunney *et al.* found that the 18 - 34, 35 - 49, and 50 - 64 age groups accounted for 25.8%, 22.2%, and 37.7% of cases, respectively [36]. These age groups, often engaged in work,

study, or business travel, tend to move frequently and, therefore, face increased exposure to infection.

More than 60% of inbound travelers did not report their country of origin, which limits geographic analysis—a challenge that Lunney *et al*. also noted in Canada [36]. Most travelers who provided this information came from Europe, likely due to direct flight availability and ongoing commercial ties with the DRC. The study period overlapped with the vacation season, which likely contributed to increased travel among members of the Congolese diaspora returning home. The Republic of Congo, Kenya, and Cameroon are African countries fairly close to the DRC, which most often serve as transit countries before reaching the DRC. Consequently, some travelers might eventually list them as their countries of origin. Also, given the significant flow of international travelers to these countries, the risk of importation of the disease was increased.

None of the travelers reported symptoms at the time of testing. This trend aligns with research in the DRC and elsewhere showing a high proportion of asymptomatic cases [6]-[8]. In addition, some travelers may have concealed symptoms to avoid travel bans or quarantine requirements, as documented by Lunney *et al*. in Canada [36].

We observed a 4.7% SARS-CoV-2 positivity rate, which exceeds the 3.6% and 2.15% reported by Zhang *et al*. [34] and Lunney *et al*. [36], respectively. Zhang's study targeted symptomatic or high-risk individuals, while Lunney's included only incoming, voluntarily tested travelers. In our cohort, 92.4% of positive cases occurred among air travelers, consistent with findings by Lunney *et al*., who reported that 90% of tested travelers arrived by air. We also found that outbound travelers accounted for 74% of positive cases, possibly because most incoming travelers had already undergone testing at departure and were less likely to test positive again on arrival in Kinshasa.

Travelers from Africa exhibited the highest positivity rate (2.97%), followed by those from the Americas (2.95%) and Europe (2.04%). These findings contrast those from Japan, where Tsuboi *et al*. reported much higher positivity rates among travelers from Asia, Europe, and the Americas [35]. These differences likely reflect varying levels of travel intensity and regional ties. Japan, for instance, maintains dense commercial and human exchanges with Asia, which may explain higher positivity among Asian travelers.

We identified the 20A (EU1) variant, later renamed 20E (EU1), as the most prevalent strain during the study. This variant, linked to Europe's second wave, appeared frequently among international travelers and likely spread globally during holiday-related surges in mobility. The WHO classifies this lineage under the Alpha variant. Increased travel during this period likely enabled its rapid international spread, underscoring the role of travel in viral dissemination.

We also found that age, gender, and traveler type were significantly associated with the risk of testing positive. Specifically, travelers aged 80 or older, female travelers, and outbound travelers faced the highest risk. Lunney *et al*. identified

older age as a key risk factor [36]. Pustahija *et al*. observed increased risk among older males and those with preexisting conditions [15]. Reduced immune function and comorbidities may explain the elevated risk in older adults.

5. Conclusion

This study demonstrates that international travelers significantly influence the transmission of SARS-CoV-2. Traveler surveillance is crucial in identifying asymptomatic cases and enables timely public health responses. Our findings offer a practical framework for enhancing epidemic preparedness and implementing rapid, effective traveler monitoring systems in future outbreaks.

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Institutional Review Board Statement

The study did not require ethical review, as data collection occurred under the national COVID-19 response protocol.

Informed Consent Statement

As part of the national COVID-19 response, the data used in this study are authorized for research publication.

Data Availability Statement

All data supporting the findings are available from the corresponding or senior authors upon request.

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Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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