Magnitude and factors related to SARS-Cov-2 infection in the indigenous population of four municipalities in the department of Cordoba, Colombia

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Abstract

Background: The indigenous population has worse health indicators than the non-indigenous population, especially concerning infectious diseases. This study aims to analyze the magnitude and factors related to SARS-CoV-2 infection in the indigenous people of four municipalities in the Cordoba department.

Methods: a descriptive study was designed, whose population consisted of all the inhabitants of the four selected municipalities who agreed to participate, to whom a questionnaire of sociodemographic data, symptoms, vaccination and an RT-PCR test to evaluate infection was applied. From the secondary source of information, data were extracted from people who self-recognized themselves as indigenous population. A uni- and bivariate analysis of the information was performed.

Results: the prevalence of infection was estimated at 1.6%. The most important antecedents for infection were the presence of diabetes and asthma. Being a migrant and belonging to the subsidized regime were related to the presence of infection. Vaccination coverage of at least one dose was 90%. The most commonly reported symptom was cough.

Conclusion: The prevalence of SARS-CoV-2 infection in the indigenous population of the four prioritized municipalities is low. Being a migrant and having health insurance under the subsidized system were associated with a higher prevalence of infection.

Keywords: Indigenous population, Coronavirus, SARS-CoV-2, Vulnerability.

Background

According to estimates by the Economic Commission for Latin America and the Caribbean (ECLAC), an estimated 58 million people belonging to 800 indigenous peoples live in Latin America [1].

In Colombia, according to the results of the National Population and Housing Census 2018, a total of 1,905,617 inhabitants of the territory are self-recognized as indigenous, representing 4.4% of the total national population. Specifically in the department of Córdoba, there is a total census of 202,621, which represents an increase of 34.1% of the indigenous population with respect to the 2005 Census [2].

Traditionally, it has been established that the probability of illness and death of indigenous peoples is greater than that of the non-indigenous population [3], which, along with less

access to health institutions and medical services in general, makes them more vulnerable to any event that threatens their health [4, 5]. Likewise, life expectancy for this population has been estimated to be 5 to 10 years lower than that of the general population [6, 7].

First identified in China in 2019, the Sarcov-2 virus spread rapidly, causing acute respiratory disease, prompting the World Health Organization (WHO) to declare it a pandemic and to establish guidelines for states to contain its spread and mortality. The COVID-19 epidemic was declared a public health emergency of international concern by the WHO on January 30, 2020 [8].

Indigenous tribes are more vulnerable to epidemics due to worse social, economic, and health conditions than non-indigenous populations, which may increase the potential for the spread of diseases, which, along with a high immunological vulnerability, has led to the decimation of indigenous populations over time [9, 10]. This was proven during the H1N1 influenza pandemic of 2009, when the mortality rate in indigenous people was 4.5 times higher than that of the non-indigenous population, according to a study in Brazil [11].

According to Cortés-Gómez et al., indigenous peoples experience the impact of structural factors that explain their increased vulnerability to COVID-19, compared to the general population; such as structural violence, understood as social stratification harmful to the satisfaction of the basic needs of a social group, and institutional racism, which is a cultural form that justifies this inequitable access [12].

Thus, the Constitutional Court pronounced in Auto 004 of 2009 that the Colombian indigenous peoples are especially vulnerable and at high risk of the COVID-19 pandemic,

due to their historical condition of misery, poverty, and malnutrition, without the need for a virus to decimate or exterminate them demographically [13].

Worldwide evidence on the magnitude and factors associated with SARS-CoV-2 infection is scarce, especially in Colombia, specifically in the department of Córdoba, which has been identified as one of the regions with the highest increase in the indigenous population in its territory.

The objective of this study is to determine the magnitude and factors related to Sarcov-19 infection in the indigenous population of four municipalities in the Department of Córdoba.

Methods

Design: a descriptive, analytical, secondary source study was carried out.

Reference population: the reference population consisted of all the inhabitants of the four municipalities selected within the framework of the royalty project entitled: "Strengthening the Department of Córdoba with mechanisms to manage the diagnosis and handling of SARS-COV-2 through the implementation of a direct RT-PCR molecular test in the municipalities of Sahagún, Tuchín, Chinú, and San Andrés de Sotavento."

Sample size: a convenience sample was taken from the inhabitants of the four selected municipalities for a total of 18,000 RT-PCR tests performed.

Sampling: A stratified sampling was carried out by municipality and township using proportional or fixed allocation, according to the size of the population, based on the data of the DANE 2020 population projection, as follows:

Initially, the populations of the four study municipalities were added together, and the percentage weight of each was determined. Subsequently, this percentage was extracted from the total sample.

Similarly, for the municipalities of Tuchín and San Andrés de Sotavento, the percentage weight of the population of the townships was identified based on the total inhabitants of each municipality, and this percentage was extracted from the sample size chosen for each municipality.

For the municipalities of Sahagún and Chinú, for which the name of the townships are known but not their population, a fixed allocation was carried out, taking the size of the urban center from the 2020 DANE data.

Finally, the data collection for the unit of analysis, which was each of the inhabitants of the populations included in the study, was done at convenience, ensuring that they met the eligibility criteria, see Table 1.

Subsequently, from the secondary source of information where demographic data, history, symptoms, vaccination status, and RT-PCR test results were consolidated, all participants from the four municipalities that participated in the study and who are self-recognized as belonging to one of the indigenous groups were selected.

Table 1. Sample size by municipality

Municipality	Total population assessed	Sample of the	Percentage of the

		indigenous population	population analyzed
Chinú	2924	76	2.6%
Sahagún	8167	116	1.42%
San Andrés de Sotavento	3583	1327	37%
Tuchín	3218	1139	35.39%
Total	**17892**	**2661**	**14.87%**

103

104 **Data collection process**

105 **Identification of the indigenous population:** analogous to what was done by the National
106 Administrative Department of Statistics (DANE), self-recognition was used to capture the
107 ethnic belonging of the participants; this implies that each person recognizes himself/herself
108 as belonging to one of the ethnic groups or none of them [2].

109 **Demographic data:** the information was collected by the study field staff, trained for this
110 purpose, using the individual notification form of basic data of the information subsystem
111 SIVIGILA, of the National Institute of Health, in case of finding any patient with respiratory
112 symptoms, the Acute Respiratory Infection by new virus format, Cod INS 346, was also filled
113 out. These instruments were used to obtain information comparable to that reported at the
114 national level. The data collection process was carried out between January and July 2022.

115 **Laboratory tests:** the assay called "DirectDetectTM SARS-CoV-2 Detection Kit (PCR-
116 Fluorescence Probe)" was used. The technology platform on which Coyote Bioscience

designed the DirectDetectTM SARS-CoV-2 Detection Kit, is based on the Free qPCR Assay technology, which allows the release of nucleic acids from the clinical sample, reverse transcription and nucleic acid amplification reaction in the same tube. This technology allows DNA and RNA samples to be analyzed in the same tube, shortening the overall reaction time compared to other platforms where the reactions must be run in separate processes. The DirectDetectTM SARS-CoV-2 Detection Kit (PCR-Fluorescence Probe) assay is being evaluated by the WHO for use as an IVD for the detection of SARS-CoV-2 genome with the EUL mechanism. The DirectDetectTM SARS-CoV-2 Detection product is a real-time RT-PCR test designed to qualitatively detect SARS-CoV-2 virus nucleic acids in a nasopharyngeal/oropharyngeal swab or sputum sample from individuals who meet the criteria for COVID-19 as dictated by the Center for Disease Control. This test targets the ORF1ab gene and N gene of the SARS-CoV-2 virus, which offers an additional aid for the diagnosis of SARS-CoV-2 genome in infected patients, and can be used for epidemiological surveillance. This test adopts combined rRT-PCR methods with fluorescent probes to detect conserved regions of the SARS-CoV-2 ORF1ab and N genes, using specific primer pairs and fluorophore-labeled probes, respectively, for each gene.

Vaccination data: at the time of the evaluation of the sociodemographic data of the study participants, the vaccination status was inquired with the question: Have you received any vaccination against COVID19? and if so, the brand and number of doses received were inquired, in all cases in which the participants had their vaccination card with them, these data were contrasted with those in the document. If there were differences, the information on the card was used.

Statistical analysis: continuous variables are presented according to their distribution as mean ± standard deviation or median ± interquartile range, and categorical variables as percentages. The Chi-square test was used to calculate associations between the probability of having a positive test and sociodemographic, background, and health insurance conditions. A value of $p<0.05$ was taken as significant. The data were processed in SPSS version 25.

Ethical considerations: the Research and Ethics Committees of the Remington University Corporation evaluated and endorsed the study and all its procedures.

Results

Out of a total of 18,000 people surveyed in the framework of the macro project entitled: "Strengthening the Department of Córdoba with mechanisms to manage the diagnosis and handling of SARS-COV-2 through the implementation of a direct RT-PCR molecular test in the municipalities of Sahagún, Tuchín, Chinú, and San Andrés de Sotavento", a total of 2661 people who recognized themselves as belonging to one of the indigenous communities that are part of the four municipalities studied in the Córdoba department were registered, which corresponds to 14.78% of the studied population.

According to their sociodemographic characteristics, it was found that most of the people analyzed were female, with a median age of 36 years, most of them from the municipalities of San Andrés de Sotavento and Tuchín. Nearly 70% live in dispersed rural areas and, to a

lesser extent, in populated centers. 92% of the participants who recognize themselves as an indigenous population have health insurance under the subsidized regime. See Table 2.

Table 2. Sociodemographic characteristics of the population studied.

Characteristic	**Frequency (%)**
Age (median, interquartile range)	36 (26-54) years old
Sex	
Male	925 (34.7)
Female	1736 (65.2)
Municipality	
San Andrés de Sotavento	1324 (49.8)
Tuchín	1139 (42.8)
Chinú	76 (2.9)
Sahagún	116 (4.4)
Area of residence	
Dispersed rural	1831 (68.8)
Municipal capital	675 (25.4)
Populated center	101 (3.8)
No information	54 (2.0)
Health Regime	
Subsidized	2450 (92.1)
Contributory	163 (6.3)

Special	19 (0.7)
Uninsured	17 (0.6)

When analyzing the history of Sarcov-2 infection in participants who self-identified as indigenous, the most frequently reported comorbidity is diabetes, followed by asthma. 3.7% of the people reported working in the health sector. Nearly 20% reported having traveled to areas with a high prevalence of infection. Contact with another ill person or a confirmed case was reported by 1.3% and 3.0%, respectively. See Table 3.

Table 3. Frequency of history of SARS-CoV-2 infection

History of sarcov-2 infection	**Frequency (%)**
Comorbidities	
Asthma	6 (0.2)
COPD	3 (0.1)
Diabetes	49 (1.8)
HIV	1 (0.01%)
Work in the health sector	99 (3.7)
Travel to an area with high prevalence of infection	517 (19.4)
Contact with sick person	35 (1.3)

Contact with confirmed case	81 (3.0%)

Infection positivity and vaccination status

The RT-PCR tests applied to each of the participants reflect a prevalence of infection of 1.6%, which corresponds to 43 cases identified as positive.

90% of participants report having received at least one dose of vaccine. About 73% have received between two and three doses. Concerning the vaccine type, a homogeneous distribution can be observed, with only one person reporting having received Sinopharm. See Table 4.

Table 4. Vaccination status

Characteristic	Frequency	Percentage
Has received at least one vaccination	2193	90.7
How many doses?		
1	567	25
2	1141	50.2
3	506	22.3
4	16	0.7
Vaccine brand		
Astrazeneca	525	19.7

Janssen	474	17.8
Moderna	441	16.6
Pfizer	399	15
Sinopharm	1	0.01
Sinovac	340	12.8

Regarding the symptoms reported at the time of sampling, it is observed that the highest frequency is for cough, this difference being statistically significant for people with a positive and negative test. Fever and headache occurred at very low frequency, and sore throat and respiratory distress did not occur in people with positive tests. See Table 5.

Table 5. Symptoms reported at the time of sampling according to test result

Symptom	Positive (n (%))	Negative (n (%))	p value
Cough	7 (6.4)	103 (93.6)	0.002
Fever	2 (3.9)	49 (96.1)	0.199
Sore throat	0 (0)	57 (100)	0.391
Shortness of breath	0 (0)	1 (100)	0.984
Headache	2 (2.4)	80 (97.6)	0.385

The bivariate analysis for the factors related to SARS-CoV-2 infection shows that having migrant status and being insured under the subsidized health insurance scheme were related to a higher prevalence of infection in the indigenous population of the four municipalities. See Table 6.

Table 6. Factors associated with SARS-CoV-2 infection

Característica	**Positive (n (%))**	**Negative (n (%))**	**p value**
Sex			
Female	27 (1.6)	1709 (98.4)	0.423
Male	16 (1.7)	909 (98.3)	
Migrant status			
Yes	1 (20)	9 (80)	0.013
No	42 (1.6)	2609 (98.4)	
Health Regime			
Contributory	1 (0.6)	166 (99.4)	0.000
Subsidized	39 (1.6)	2411 (98.4)	
Special	1 (5.3)	18 (94.7)	
Uninsured	0 (0)	17 (100)	

Discussion

The main finding of this study was to determine the prevalence of SARS-CoV-2 infection and its related factors in a population that recognizes itself as indigenous in four municipalities of Córdoba department, prioritized within the framework of the project: "Strengthening the Department of Córdoba with mechanisms to manage the diagnosis and handling of SARS-COV-2 through the implementation of a direct RT-PCR molecular test in the municipalities of Sahagún, Tuchín, Chinú, and San Andrés de Sotavento."

According to sociodemographic characteristics, 65.2% of the population was female and 34.8% male, similar to a study conducted in the Wiwa indigenous community in northwestern Colombia [14]. However, according to the latest census data available, the indigenous population is distributed similarly for men and women [2].

The median age for the indigenous population analyzed was 36 years, with an interquartile range between 26 and 54 years, reflecting a young population, which could be related to a lower severity of infection, data comparable to those of indigenous populations in Brazil [15].

The presence of diabetes and asthma are reported as important antecedents for the infection, being the most frequently reported comorbidities in the population analyzed. These same conditions have been evidenced in different registries with indigenous populations [16-19].

In contrast to the study by Concha et al. [14], where SARS-CoV-2 infection was evaluated directly and indirectly, and 61/452 positive cases were reported by RT-PCR for a prevalence of infection of 13.5% [14], our study directly calculated a prevalence of infection of 1.6%. This difference may be due to several factors; first, most of the population analyzed in our study came from dispersed rural areas, where close contact and exchange with people from

other places are not as likely. On the other hand, the periods of data collection are located in different phases of the pandemic.

Regarding the sex of the population evaluated, no differences were found in SARS-CoV-2 infection, which is consistent with other Colombian studies evaluating seropositivity of infection in an indigenous community in the Amazon region or direct or indirect infection in indigenous communities in northern Colombia [14, 18].

Regarding the reported symptoms, it could be evidenced that these were self-reported at very low frequency, consistent with the findings of Concha et al. [14, 20]. A study by Sansone et al. found that symptom reporting differed according to ethnicity/race, the most important for the indigenous population being the presence of cough [21], similar to what was found in our study.

Vaccination coverage in the indigenous population is close to 91% of people who have received at least one dose, and 50% have received two doses, data close to what is found in the indigenous population of Brazil, whose coverage for December 2021 was 90% for one dose, but higher in people who had received two doses (85%) [22]. It is noteworthy in this regard that the Ministry of Health and Social Protection, aware of the importance of advancing the vaccination against covid-19 in ethnic groups, undertook various actions of dialogue and coordination in a joint effort between the Government and the different ethnic groups, recognizing their multiculturalism and the territorial characteristics that group them.

Among the factors independently associated with infection were being a migrant and being affiliated to the subsidized health care system. These aforementioned characteristics had already been foreseen in the scientific literature, which warned of the high vulnerability of

the indigenous population. In the case of migration, the effect that this had on their knowledge and cultural heritage to shape the notion of territory, often understood as freedom and struggle, was analyzed in detail, and how this could ultimately be a modulator of vulnerability [23].

The results of the present study should be analyzed in the light of the following limitations: first, the self-reporting of symptoms makes it possible that these data are subject to information bias, insofar as their reporting could generate stigmatization of the participant and, therefore, they preferred to hide them. It is possible that participants with greater severity of infection would have withdrawn their participation in the study; therefore, the analysis could have been limited to the mildest cases. The information on vaccination was contrasted, whenever possible, with the information contained in the vaccination card.

Conclusion: The prevalence of SARS-Cov-2 infection in the indigenous population of the four prioritized departments is low. Being a migrant, and having health insurance under the subsidized regime, were associated with a higher prevalence of infection.

Declarations

Ethics approval and consent to participate

The research and ethics committees of the Corporación Universitaria Remington evaluated and approved the study and all its procedures. All participants signed the informed consent form at the beginning of the study.

The current study is original and has not been published elsewhere in any form or language (partially or in its entirety). The results of the current study were presented honestly and without fabrication, falsification or inappropriate manipulation of data. No data, text, or theories of others are presented as if they were the author's ('plagiarism').

Consent for publication

Not applicable

Availability of data and materials

The data sets used and/or analyzed during the current study are available upon request to the corresponding author.

Competing interests

The authors declare that they have no competing interests. The funders had no role in the design of the study; in the collection, analysis, or interpretation of data; in the writing of the manuscript; or in the decision to publish the results.

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