

CAPÍTULO 11

Generación de nuevo conocimiento durante la pandemia: un aporte del Instituto de Investigaciones Biológicas del Trópico (IIBT)

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Generación de nuevo conocimiento durante la pandemia: un aporte del Instituto de Investigaciones Biológicas del Trópico (IIBT)

Salim Mattar, Bertha Gastelbondó-Pastrana

El IIBT tiene dos décadas investigando las enfermedades emergentes y reemergentes. El instituto ha contribuido con el conocimiento sobre los síndromes febriles relacionados con las ETVs en humanos. Dentro de su trayectoria ha investigado sobre fiebres hemorrágicas vectores importantes en salud pública como: roedores, garrapatas, mosquitos y murciélagos.

En 2020 con la abrupta entrada de la pandemia, el IIBT puso a disposición de la región y el país toda su experiencia científica e infraestructura tecnológica para contribuir al control de la pandemia por SARS-CoV-2. Estos aspectos le permitieron al grupo IIBT generar publicaciones resultado de los diferentes proyectos de investigación asociados a COVID-19. En este capítulo se dan a conocer los resúmenes de los productos de nuevo conocimiento generados por el instituto durante la pandemia por SARS-CoV-2. Se encuentran relacionados artículos con colaboraciones a nivel nacional e internacional <https://www.unicordoba.edu.co/index.php/instituto-de-investigaciones-biologicas-de-tropico/>

Se destacan los primeros reportes en temas de reactividad cruzada serológica entre SARS-CoV-2 e infección por virus Zika, confirmación molecular de la transmisión de SARS-CoV-2 humana hacia perros y gatos por primera vez en Colombia. Antes de la aplicación masiva de las vacunas, el grupo contribuyó con el primer trabajo sobre la inmunidad de rebaño y abrió un interesante debate académico. El grupo publicó el primer reporte de reinfección por SARS-CoV-2 en Colombia, también sobre la presentación

de casos clínicos de COVID-19, reinfecciones por otros virus respiratorios y publico el primer avance en fase preclínica sobre la inmunogenicidad de una vacuna de RBD contra SARS-CoV-2.



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ARTÍCULO DE ACTUALIZACIÓN

Consenso de grupo *Ad-hoc* sobre recomendaciones para la evaluación y controles de calidad para el diagnóstico molecular y serológico de la infección humana por SARS CoV-2

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Grupo *Ad-hoc* de la Asociación Colombiana de Infectología y la Asociación Colombiana de Virología

Resumen

Se formulan recomendaciones de un grupo de consenso de expertos sobre los criterios para evaluar el desempeño diagnóstico (tamaño y selección de muestras para sensibilidad y especificidad analíticas, criterios para establecer límites de detección, criterios para establecer el estándar de oro para las serologías) que deberían ser tenidos en cuenta al evaluar y validar las pruebas diagnósticas para SARS CoV-2. Con el propósito de asegurar la calidad de las pruebas serológicas a utilizar en el país, se recomienda la participación en un programa de control de calidad externo, que garantice la idoneidad y desempeño en la realización de las pruebas diagnósticas serológicas y moleculares durante esta pandemia, ya que su uso tiene profundas implicaciones para las medidas de intervención clínicas individuales y de seguimiento y control en salud pública.

Palabras clave: Pruebas diagnósticas, SARS CoV-2, COVID 19, control calidad laboratorio

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INTERNATIONAL SOCIETY FOR INFECTIOUS DISEASES

Short Communication

Serological cross-reactivity using a SARS-CoV-2 ELISA test in acute Zika virus infection, Colombia

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ABSTRACT

Objectives: We investigated seroreactivity by using a commercial SARS-CoV-2 ELISA test in samples collected from different groups of individuals, including patients diagnosed to have Dengue, Zika, and Chikungunya infection between 2015 and 2019, from an endemic area in the Caribbean Colombian region.

Methods: A total of 127 sera samples obtained from six different groups of individuals were included in this study: Group A: patients with confirmed SARS-CoV-2 infection; Group B: patients with symptoms suggestive of COVID-19 or asymptomatic contacts with confirmed patients; Group C: patients with acute or recent dengue virus infection; Group D: patients with acute Zika virus infection; Group E: patients with previous Chikungunya virus infection; and Group F: individuals with exposure to spotted fever group rickettsiae.

Results: Overall, group A, group B, and group D showed seroreactivity to SARS-CoV-2 in 92%, 75%, and 26% of samples, respectively; furthermore, group C, group E, and group F showed 100% seroreactivity.

Conclusions: We found 26% of serological cross-reactivity in patients with acute Zika virus infection by using a commercial SARS-CoV-2 ELISA test. Further studies are needed to evaluate whether serological cross-reaction is maintained with time in nonacute patients with previous exposure to the Zika virus and its effect in SARS-CoV-2 serosurveys in endemic areas for this arbovirus.

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SHORT REPORT

Open Access



Epidemiological and viral features of a cohort of SARS-CoV-2 symptomatic and asymptomatic individuals in an area of the Colombian Caribbean

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Abstract

Background: Severe acute respiratory syndrome Coronavirus 2 (SARS-CoV-2) is an emerging viral pandemic disease. In the last 6 months, SARS-CoV-2 has caused millions of reported cases and hundreds of thousands of deaths. As other world regions, South America has not contained the pandemic's advance since it lacks the hospital and economic capacities. Public health implications of transmission, while the asymptomatic/presymptomatic infection is a critical concern at the current pandemic.

Objective: Describe the socio-demographic, clinical, and viral features of a cohort of SARS-CoV-2 infected individuals from the Colombian Caribbean.

Methods: Six hundred eighty-six clinical samples of suspected SARS-CoV-2 infection cases and contacts individuals from several hospital centers in the department of Córdoba, Colombia, were received at our laboratory between April 9th and May 16th, 2020. RNA was extracted using lysis buffers and spin columns. The samples were tested for SARS-CoV-2 by reverse transcription real-time polymerase chain reaction (RT-qPCR) using commercially available multiplex real-time PCR assay for simultaneous detection of 3 target genes of SARS-CoV-2 (Allplex™, 2019-nCoV assay, Korea). Viral copies quantification was done using a standard curve constructed from serially diluted of a SARS-CoV-2 positive control. Statistics descriptive methods were used.

Results: Thirty-five nasopharyngeal samples were positive for SARS-CoV-2 infection; the average age was 43 (range, 1–95 years). Seventeen of 35 (49%) of the patients showed symptoms. Most of them had a cough, fever, and odynophagia; three of the patients reported having arthralgia. Only two patients required hospitalization. None of the patients had known co-morbidities. RT-qPCR results show that two of the symptomatic patients had significantly higher RNA copies than the rest. Eighteen of 35 (51%) individuals were asymptomatic, and the average age was 30

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BRIEF REPORT



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Severe Acute Respiratory Syndrome Coronavirus 2 Seroprevalence Among Adults in a Tropical City of the Caribbean Area, Colombia: Are We Much Closer to Herd Immunity Than Developed Countries?

Salim Mattar^{1*}, Nelson Alvis-Guzmán³, Evelyn Garay⁷, Ricardo Rivero¹, Alejandro García¹, Yesica Romero¹, Jorge Miranda⁴, Ketty Galeano¹, Fernando de la Hoz¹, Katy Martínez¹, German Arrieta¹, Álvaro A. Faccini-Martínez², Camilo Guzmán¹, Hugo Kerguelien¹, María Moscoso¹, Hector Contreras¹, and Verónica Contreras³

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A serological survey was carried out in Montería (500 000 population), a mid-size city in Colombia. An overall prevalence of 55.3% (95% confidence interval, 52.5%–57.8%) was found among a sample of 1 368 people randomly selected from the population. Test positivity was related to economic characteristics with the highest prevalence found in the most impoverished areas, representing 83.8% of the city's population. We found a prevalence that might be associated with some important level of population immunity.

Keywords: coronavirus; ELISA; infectious disease transmission; poverty areas; socioeconomic status.

Colombia (503 million inhabitants) identified its first case of coronavirus disease 2019 ((COVID-19) severe acute respiratory syndrome coronavirus 2 [SARS-CoV-2] infection) on March 2, 2020, and by October 14, 2020 it had reported 930 159 cases (incidence, 17 539 per 100 000 people) and 28 306 deaths (mortality, 5339 per 100 000 people), with variations for incidence

Seroprevalence studies are essential because they allow a more reliable estimation of the population infected after COVID-19 epidemics and estimate the likelihood of a second peak of transmission [2]. Colombia, according to the website <https://serotracker.com/data>, has no reported seroprevalence studies of SARS-CoV-2.

METHODS

This study aimed to estimate the prevalence of SARS-CoV-2 past infections in Montería. A population-based serological study was carried out over a random sample ($n = 1368$) of the population selected from all city areas. The neighborhood population size weighted the sample. The steps to select the sample were as follows: (1) blocks of houses were randomly selected from every neighborhood (10 neighborhoods); (2) a list of houses in every selected block was developed, identifying every house with a particular number; and (3) house-to-house visits were made in the city's neighborhoods, taking the even numbers. Adjoining houses were not visited. No attempt was made to identify whether participants had antecedents of suspected or confirmed COVID-19 infection or disease, nor whether they had been a contact of the confirmed case(s). The number of samples taken by neighborhoods fluctuated between 55 and 428. The blood samples were taken by health staff trained for epidemiological fieldwork. Once the blood samples were obtained, the tubes were sent to the University of Córdoba laboratory, where they were centrifuged. The enzyme-linked immunosorbent assay (ELISA) test was carried out by microbiologists who are experts in this type of test.

Sera were analyzed using Ingezip COVID 19 DR test (Ingenasa; Eurofins, Madrid, Spain), a dual recognition ELISA detecting semiquantitatively total SARS-CoV-2 virus N-nuclein-specific antibodies (immunoglobulin [Ig]G, IgM,

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Article

High Prevalence of SARS-CoV-2 in an Indigenous Community of the Colombian Amazon Region

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Abstract: Introduction. COVID-19 is a pathology caused by the SARS-CoV-2 virus. The World Health Organization (WHO) has reported more than 225 million cases and 4.5 million deaths worldwide. Objective. To describe the seropositivity, spatial distribution, and clinical and sociodemographic variables of SARS-CoV-2 in a community of the Colombian Amazon region. Methods. In December 2020, a cross-sectional observational study was carried out in a population located in the Colombian Amazon in the municipality of Mitú. Sociodemographic and clinical data were taken. Besides, 589 blood samples were taken, and an antibody detection was carried out with an ELISA and a recombinant protein N antigen of SARS-CoV-2. Results. A seropositivity of 57.6% was observed. The highest proportion of the infection is located in inter-municipal transport zones. The bivariate analysis did not show differences in the SARS-CoV-2 infection rate concerning the variables sex, age range, and the presence of comorbidities ($p > 0.05$). The bivariate and multivariate analysis showed that being symptomatic and presenting neurological manifestations of the upper respiratory tract are clinical variables associated with SARS-CoV-2 infection ($p < 0.05$). One of the causes of this virus's high spread in this community could be that 53.3% of the people were asymptomatic. Conclusions. Our data showed a high burden and transmission of SARS-CoV-2 in the indigenous community. This could be linked to cultural behaviors and the high infection rate in asymptomatic patients.

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Yellow fever reemergence in Venezuela – Implications for international travelers and Latin American countries during the COVID-19 pandemic

A.J. Rodríguez-Morales et al.

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Short Communication

Using serological studies to assess COVID-19 infection fatality rate in developing countries: A case study from one Colombian department

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ABSTRACT

This study describe the infection fatality rate (IFR) by COVID-19 by age groups in one department of Colombia. It used results from a serological survey to establish a closer estimation of the true proportion of infected people. It found an overall IFR of 0.24% quite lower than the overall CFR (5.6%). We conclude that CFR severely overestimate the lethality of COVID-19 in developing areas.

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The infection fatality rate (IFR) is a critical epidemiological parameter that allows assessment of the dynamics and virulence of any infectious agent and the quality of health services (Levin et al., 2020). There is still uncertainty about the true IFR of COVID-19 because detecting all infections and cases depends on the quality of

capacities. Thus, Colombia lacks accurate estimates on IFR (Hurtado-Ortiz et al., 2020). So far, only 3 Latin American countries—Argentina, Brazil and Chile—have informed IFR from serological surveys (Ioannidis, 2021). In this short report, we attempt to fill that gap by estimating IFR from a population-based serological survey in one

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LETTER TO THE EDITOR

Open Access

A first probable case of SARS-CoV-2 reinfection in Colombia




Whilken Novoa¹, Hollman Miller¹, Salim Mattar^{2*}, Álvaro A. Faccini-Martinez², Ricardo Rivero² and Hector Serrano-Coll³

Although reinfection by SARS-CoV-2 is a rare phenomenon, cases with suspected or possible reinfection by SARS-CoV-2 have recently been reported in different countries. In some cases, it is not clear whether the individual's RT-qPCR test remained positive for a prolonged

moved from the first place of infection 500 km away to another municipality bordering Brazil. He is a health care worker involved in public health activities related to the COVID-19 pandemic. On October 11, the patient-reported symptoms such as malaise, chills, headache,



SARS-CoV-2 vaccines: evolution and escape

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SARS-CoV-2 in eight municipalities of the Colombian tropics: high immunity, clinical and sociodemographic outcomes

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Background: Serological evaluation of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is an alternative that allows us to determine the prevalence and dynamics of this infection in populations. The goal of this study was to determine the clinical and sociodemographic dynamics of SARS-CoV-2 infection in a region of the Colombian Caribbean.

Methods: Between July and November 2020, a cross-sectional observational study was carried out in Córdoba, located in northeast Colombia in the Caribbean area. Eight municipalities with the largest populations were chosen and 2564 blood samples were taken. A commercial enzyme-linked immunosorbent assay was used with the recombinant protein antigen N of SARS-CoV-2. The people included in the study were asked for sociodemographic and clinical data, which were analysed by statistical methods.

Results: A seroprevalence of 40.8% was obtained for SARS-CoV-2 in the Córdoba region. In the bivariate analysis, no differences were observed in seropositivity against SARS-CoV-2 for gender or age range ($p > 0.05$). Higher seropositivity was found in low socio-economic status and symptomatic patients ($p < 0.0001$). A total of 30.7% of the asymptomatic patients were seropositive for SARS-CoV-2, which could be linked to the spread of this infection. In the multivariate analysis, seroconversion was related to poverty and clinical manifestations such as anosmia and ageusia ($p < 0.05$).

Conclusions: The high seropositivity in Córdoba is due to widespread SARS-CoV-2 in this population. The relationship between seropositivity and socio-economic status suggests a higher exposure risk to the virus caused by informal economic activities in low-income groups. Clinical manifestations such as anosmia and ageusia could be clinical predictors of infection by the new emergent coronavirus.



Vaccines for COVID-19 – Can we avoid living again in a ghost town?

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Clinical outcomes of patients hospitalized for COVID-19 and evidence-based on the pharmacological management reduce mortality in a region of the Colombian Caribbean



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ABSTRACT

Introduction: Despite the high volume of infections, some clinical aspects of this disease are still unknown. There are currently no studies in Colombia that describe the disease's clinical and treatment aspects in detail.

Objective: Describe the characteristics and clinical management of a group of admitted patients with SARS-CoV-2 infection in a private clinic in Montería, Córdoba-Colombia.

Patients and methods: A descriptive observational study was carried out between May and August 2020 in 209 hospitalized patients with a confirmed diagnosis of COVID-19. Upon admittance, clinical, sociodemographic characteristics, comorbidities, and complications were analyzed. Additionally, the effect of the following medications was described: 1-antibiotics (cefepime, piperacillin, tazobactam, meropenem, vancomycin)+low molecular weight heparin (LMWH)+corticosteroids (dexamethasone-methylprednisolone)+colchicine. 2- Antibiotic + LMWH + corticosteroids. 3- LMWH + corticosteroids. 4- LMWH + corticosteroids + colchicine. 5- Other treatments (Tocilizumab). **Results:** 107 (51%) of the 209 patients with a confirmed diagnosis of COVID-19 passed away. The main comorbidities related to mortality of these hospitalized patients with COVID-19 were obesity and kidney disease ($P < 0.05$). The main complications associated with fatal outcomes in this group of patients were Acute Respiratory Distress Syndrome (ARDS) and sepsis ($P < 0.05$). Furthermore, it was evidenced that the colchicine combination showed a significant difference in reducing mortality in hospitalized patients compared to the other therapeutic regimens ($P < 0.05$).

Conclusion: A mortality rate of 51% was found attributable to several factors such as advanced age, obesity, kidney disease, and an average time in days of late consultation. The implementation of the colchicine combination could reduce the mortality rate in this disease.

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Original article

Seroprevalence of antibodies against to SARS-CoV 2 in umbilical cord blood in two hospital centers in Córdoba and Sucre, Colombia

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ABSTRACT

Introduction: Pregnant women continue to be vulnerable to COVID-19, and their immunosuppressed state could put them at greater risk of developing more severe forms of the disease. In Colombia and Latin America, there are few studies on the immune response of the newborn against SARS-CoV-2.
Aim: To determine the prevalence of SARS-CoV-2 infection in umbilical cord blood in two hospital centers in Córdoba and Sucre.

Methods: Between March and June 2021, a prospective descriptive cross-sectional study was carried out. Two hospitals from the departments of Córdoba and Sucre, located in the Northwest Caribbean area of Colombia, participated. Three hundred sixty umbilical cord blood samples were taken at the N hospitals. A commercial ELISA was performed to detect total IgG, IgM, and IgA antibodies against the N protein of SARS-CoV-2. The ethics committee approved the study of the participating institutions.

Results: Of 3291 women who gave birth in the hospital centers included in the study, 360 (11%) participated. Complete clinical data were obtained for 223 women. The mean age of the women was 24 years (range, 15–42). 29.4% (106/360) of the umbilical cord samples had total antibodies against SARS-CoV-2. Pregnant women did not have blood samples taken. 58% of the women were asymptomatic. There was no association between umbilical cord samples, clinical, epidemiological characteristics, and serological response to antibodies to SARS-CoV-2 ($p > 0.05$).

Conclusions: The prevalence of umbilical cord blood samples was 29.4% for total SARS-CoV-2 antibodies. The study provides essential aspects for the epidemiological approach to neonates infected with SARS-CoV-2.

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Immunogenicity and safety of a RBD vaccine against SARS-CoV-2 in a murine model

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ABSTRACT

Introduction: Although more than half of the world's population is already vaccinated, the appearance of new variants of concern puts public health at risk due to the generation of new immunogens against the virus as a crucial and relevant strategy in the control of these new variants.

Methods: A preclinical study used a potential vaccine candidate (RBD, SARS-CoV-2). Four groups of BALB/c mice were used, a control group, an adjuvant group, a group inoculated with one dose of RBD subunit protein, and the fourth group inoculated with two doses of RBD subunit protein.

Results: No inflammatory or cellular changes were shown in the mice's anatomopathological evaluation. Higher kinetics and 75% seroconversion were obtained in the mice inoculated with two doses of RBD ($P < 0.0001$).

Conclusions: The application of two doses of the RBD vaccine candidate in BALB/c mice proved safe and immunogenic against SARS-CoV-2.



scientific reports



OPEN Human-to-dog transmission of SARS-CoV-2, Colombia

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Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), the causative agent of the current COVID-19 pandemic, has evolved to have a wide range of hosts, including non-human primates, wild and domestic animals. The ACE2 protein has a high level of conservation and is the common receptor invertebrate species for a viral infection to occur; this receptor could give rise to anthroponotic events. This article describes the first event of symptomatic transmission in Latin America from a human to a dog by the B.1.625 lineage of SARS-CoV-2. We found 21 shared mutations in the complete genomes of viral sequences from owners and dogs. Further phylogenetic and molecular analysis showed that 100% co-localization of the clade helps to understand human-animal transmission. Prediction of the Spike protein structure of the sequenced virus and docking analyzes showed that the E484K mutation in the receptor-binding domain (RBD) could contribute to the viral affinity of ACE2. Therefore, close contact between SARS-CoV-2-infected humans and pets should be avoided to prevent the emergence of novel mutations of public health importance from anthroponotic events.

Severe Acute Respiratory Syndrome coronavirus 2 (SARS-CoV-2), the etiological agent of the current COVID-19 pandemic is a novel virus belonging to the *Betacoronavirus* genus and it is genetically closer to bat coronaviruses than human SARS. For the reasons mentioned above, it is known as a viral zoonosis^{1,2}. Research on transmission mechanisms of the viruses focuses on person-to-person contact. However, domestic animals' susceptibility to this virus is still uncertain³. To date, 11 complete SARS-CoV-2 genomes isolated from dogs have been reported in the Global Initiative on Sharing All Influenza Data (GISAID), from oropharyngeal samples⁴. The mechanism for viral infections depends on the binding between SARS-CoV-2 S Protein Receptor Binding Domain (RBD) and angiotensin-converting enzyme 2 (ACE2) receptor, which is crucial for infection since it allows the internalization of the virion into host cells⁵. Recently, several SARS-CoV-2 variants have emerged with an enhanced affinity towards human ACE2⁶. Considering that ACE2 receptors are present in several animal species, interspecies infections could arise from human-to-animal contact. However, the efficacy of the cellular union depends on the affinity of the viral RBD towards the host's receptors^{7,8}. Recently, several variants of SARS-CoV-2 have emerged with an augmented infectious capacity and neutralization-escape ability, these variants carry mutations in the spike protein such as N501Y, E484K, and K417T which have been described to have a relationship with higher transmissibility and resistance toward natural-induced and vaccine-elicited neutralizing antibodies⁹⁻¹¹. In January 2021, a novel lineage identified as B.1.625 was reported in 5.8% of sequenced genomes in Colombia during the first trimester. Due to its rapid augment in prevalence and the identification of characteristic mutations in Spike's N-terminal Domain (NTD), Receptor Binding Domain (RBD) and S1/S2 accounting for increased transmissibility, drug-resistance and antibody escape it was a rapidly growing lineage that circulated through America and Europe. The B.1.625 lineage is now circulating in 10 countries, including Colombia, and continues to pose a threat to public health and vaccine efficacy¹²⁻¹⁴. It is still unknown if the emergence of novel variants of concern and interest with augmented transmissibility account for enhanced infectivity of non-human hosts. Research of a more significant scale under the "One Health" approach is needed to assess the feasibility of direct human-to-animal transmission of SARS-CoV-2 in domestic environments to understand better the dynamics of the viral infections and their risk towards other species, including humans. This research performs viral genome analysis through next-generation sequencing of two SARS-CoV-2 clinical isolates from a dog and its owner. Given

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First report and genome sequencing of SARS-CoV-2 in a cat (*Felis catus*) in Colombia

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BACKGROUND Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is a virus of zoonotic origin that can bind to ACE2 receptors on the cells of many wild and domestic mammals. Studies have shown that the virus can circulate among animals mutate, lead to animal-to-human zoonotic jump, and further onward spread between humans. Infection in pets is unusual, and there are few human-to-pet transmission reports worldwide.

OBJECTIVE To describe the SARS-CoV-2 infection in a domestic animal in Córdoba, Colombian Caribbean region.

METHODS A cross-sectional molecular surveillance study was carried out, oral and rectal swabs were taken from cats and dogs living with people diagnosed with coronavirus disease 2019 (COVID-19).

RESULTS SARS-CoV-2 was found in a cat living with a person with COVID-19. Genome sequencing showed that the B.1.111 lineage caused the infection in the cat. The owner's sample could not be sequenced. The lineage is predominant in Colombia, and this variant is characterised by the presence of the D614D and Q57H mutation.

CONCLUSION The present work is the first report of an infected cat with SARS-CoV-2 with whole-genome sequencing in Colombia. It highlights the importance of detecting SARS-CoV-2 mutations that could promote the transmissibility of this new coronavirus. There is still a significant information gap on human-to-cat-to-human infection; we encourage self-isolation measures between COVID-19 patients and companion animals. The findings of this study give a preliminary view of the current panorama of SARS-CoV-2 infection in animals in Colombia.

Key word: population surveillance - public health - one health - COVID-19 - viral zoonoses

SHORT REPORT

Open Access

Effectiveness of the CoronaVac® vaccine in a region of the Colombian Amazon, was herd immunity achieved?



Héctor Serrano-Coll^{1,2}, Hollman Miller³, Camilo Guzmán¹, Ricardo Rivero¹, Bertha Gastelbondo¹, Jorge Miranda¹, Ketty Galeano¹, Jhon Montaña-Restrepo³ and Salim Mattar^{1*}

Abstract

Introduction: Currently, more than 4.5 billion doses of SARS-CoV-2 vaccines have been applied worldwide. However, some developing countries are still a long way from achieving herd immunity through vaccination. In some territories, such as the Colombian Amazon, mass immunization strategies have been implemented with the CoronaVac® vaccine. Due to its proximity to Brazil, where one of the variants of interest of SARS-CoV-2 circulates.

Objective: To determine the effectiveness of the CoronaVac® vaccine in a population of the Colombian Amazon.

Methods: Between February 24, 2021, and August 10, 2021, a descriptive observational study was carried out in which a population of individuals over 18 years of age immunized with two doses of the CoronaVac® vaccine was evaluated. The study site was in the municipality of Mitú, Vaupés, in southeastern Colombia, a region located in the Amazon bordering Brazil. Results. 99% of the urban population of the Mitú municipality were vaccinated with CoronaVac®. To date, 5.7% of vaccinated individuals have become ill, and only 0.1% of these require hospitalization. One death was attributable to COVID-19 has been reported among vaccinated individuals, and the vaccine has shown 94.3% effectiveness against mild disease and 99.9% against severe infection.

Conclusions: The herd immunity achieved through mass vaccination in this population has made it possible to reduce the rate of complicated cases and mortality from COVID-19 in this region of the Colombian Amazon.

Highlights:

- CoronaVac® has shown 94.3% effectiveness against mild disease and 99.9% against severe infection in this indigenous population.
- CoronaVac® reduces the mortality rate from 2.2% in 2020 to 0.22% in 2021.
- The herd immunity was achieved through mass vaccination in this region of the Colombian Amazon.

Keywords: COVID-19 vaccines, Prevention, Post-exposure, Prophylaxis, Public health, Mass vaccination

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SARS-CoV-2 in eight municipalities of the Colombian tropics: high immunity, clinical and sociodemographic outcomes

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Background: Serological evaluation of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is an alternative that allows us to determine the prevalence and dynamics of this infection in populations. The goal of this study was to determine the clinical and sociodemographic dynamics of SARS-CoV-2 infection in a region of the Colombian Caribbean.

Methods: Between July and November 2020, a cross-sectional observational study was carried out in Córdoba, located in northeast Colombia in the Caribbean area. Eight municipalities with the largest populations were chosen and 2564 blood samples were taken. A commercial enzyme-linked immunosorbent assay was used with the recombinant protein antigen N of SARS-CoV-2. The people included in the study were asked for sociodemographic and clinical data, which were analysed by statistical methods.

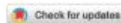
Results: A seroprevalence of 40.8% was obtained for SARS-CoV-2 in the Córdoba region. In the bivariate analysis, no differences were observed in seropositivity against SARS-CoV-2 for gender or age range ($p > 0.05$). Higher seropositivity was found in low socio-economic status and symptomatic patients ($p < 0.0001$). A total of 30.7% of the asymptomatic patients were seropositive for SARS-CoV-2, which could be linked to the spread of this infection. In the multivariate analysis, seroconversion was related to poverty and clinical manifestations such as anosmia and ageusia ($p < 0.05$).

Conclusions: The high seropositivity in Córdoba is due to widespread SARS-CoV-2 in this population. The relationship between seropositivity and socio-economic status suggests a higher exposure risk to the virus caused by informal economic activities in low-income groups. Clinical manifestations such as anosmia and ageusia could be clinical predictors of infection by the new emergent coronavirus.

Keywords: asymptomatic infections, economic conditions, informal social controls, public health, seroepidemiologic studies, social

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OPEN

Genomic epidemiology of SARS-CoV-2 variants during the first two years of the pandemic in Colombia

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Abstract

Background The emergence of highly transmissible SARS-CoV-2 variants has led to surges in cases and the need for global genomic surveillance. While some variants rapidly spread worldwide, other variants only persist nationally. There is a need for more fine-scale analysis to understand transmission dynamics at a country scale. For instance, the Mu variant of interest, also known as lineage B.1.621, was first detected in Colombia and was responsible for a large local wave but only a few sporadic cases elsewhere.

Methods To better understand the epidemiology of SARS-Cov-2 variants in Colombia, we used 14,049 complete SARS-CoV-2 genomes from the 32 states of Colombia. We performed Bayesian phylodynamic analyses to estimate the time of variants' introduction, their respective effective reproductive number, and effective population size, and the impact of disease control measures.

Results Here, we detect a total of 188 SARS-CoV-2 Pango lineages circulating in Colombia since the pandemic's start. We show that the effective reproduction number oscillated drastically throughout the first two years of the pandemic, with Mu showing the highest transmissibility (Re and growth rate estimation).

Conclusions Our results reinforce that genomic surveillance programs are essential for countries to make evidence-driven interventions toward the emergence and circulation of novel SARS-CoV-2 variants.

Plain Language Summary

Colombia reported its first COVID-19 case on 6th March 2020. By April 2022, the country had reported over 6 million infections and over 135,000 deaths. Here, we aim to understand how SARS-CoV-2, the virus that causes COVID-19, spread through Colombia over this time and how the predominant version of the virus (variant) changed over time. We found that there were multiple introductions of different variants from other countries into Colombia during the first two years of the pandemic. The Gamma variant was dominant earlier in 2021 but was replaced by the Delta variant. The Mu variant had the highest potential to be transmitted. Our findings provide valuable insights into the pandemic in Colombia and highlight the importance of continued surveillance of the virus to guide the public health response.

The high price that Colombia has paid for its lack of biotechnological sovereignty

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During the COVID-19 pandemic, Latin American countries suffered the collapse of their health systems. This was caused by the high demand for care for those infected, which in parallel was added to the care of patients with other types of diseases. The excess demand for health services caused medical and laboratory supplies to decline rapidly. In this sense, the shortage was a reality, and thus, imported molecular diagnostic equipment, supplies, and kits soon became scarce. The COVID-19 pandemic disclosed a health crisis caused by an insufficient systematic policy of appropriating scientific knowledge. Without a model of scientific knowledge, there are few possibilities for consolidating markets for technologies such as diagnostic methods for new infectious agents, medicines, vaccines, and medical devices, among others.

The effects of this asymmetry in the availability and access to technologies and biotechnologies were essential for many countries, especially low-income countries, to suffer high rates of excess mortality from COVID-19. A systematic review and meta-analysis on excess mortality from COVID-19 from 79 countries found an overall excess mortality of 104.84 (95% CI: 85.56–124.13) per 100,000 in-

During the COVID-19 pandemic, it became clear that rich countries had priority access to vaccines; this "VIP" treatment was caused by the monopoly of the large pharmaceutical companies that distributed the vaccines then. The pandemic demonstrated, in the lower-middle-income countries of Latin America, little investment in research, development, and innovation activities, which shows an imbalance in the levels of competitiveness. We pay dearly in the pandemic for dependence on other countries. It was demonstrated that Latin American countries must develop systematic and continuous strategies based on research, development, and innovation activities at their different maturity levels that allow increasing the number of patents and biotechnological developments to shape a universal public health crisis better.

Scientific autonomy is justified because it promotes progress and benefits society. Access to medicines and health supplies is essential to achieve total health coverage. The increase in costs and the scarcity of medicines are some problems that third-world countries face.⁴ Significant social, economic, and environmental achievements can be obtained if Latin America deci-



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Original Article

Not all respiratory infections were SARS-CoV-2 during the pandemic, analysis in a clinic on the Colombian Caribbean coast



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ABSTRACT

Introduction: Acute Respiratory Infections (ARIs) are considered one of the leading causes of morbidity and mortality worldwide. Children under five and older adults are most likely to die from this cause.

Objective: To describe the behavior of infection by respiratory viruses other than SARS-CoV-2 during the pandemic in a clinic in the Colombian Caribbean.

Methods: This descriptive and retrospective study evaluates the characteristics, associated comorbidities, and requirements of hospitalization or Intensive Care Unit in patients diagnosed with respiratory viral infections treated at IMAT OncoMedica clinic from July 2020 to August 2022.

Results: This study evaluated 351 patients with respiratory symptoms, observing an exponential increase in cases of respiratory infection as of April 2022, with a high proportion of syncytial virus infections mainly in children under 18 years of age (22.1%) and Human Rhinovirus/Enterovirus in patients with solid tumors and hematological disorders (48.8%), the latter was associated with a higher rate of hospitalization and ICU requirement in the individuals evaluated.

Conclusions: Respiratory viruses other than SARS-CoV-2, such as Rhino/Enterovirus, RSV, and adenovirus, are circulating in the population at a clinic on the Colombian Caribbean coast. The findings should motivate public health authorities to conduct more thorough surveillance in the rest of the state.

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