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RESEARCH ARTICLE

Spatial prediction of immunity gaps during a pandemic to inform decision making: A geostatistical case study of COVID-19 in Dominican Republic

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Abstract

Background: To demonstrate the application and utility of geostatistical modelling to provide comprehensive high-resolution understanding of the population's protective immunity during a pandemic and identify pockets with sub-optimal protection.

Methods: Using data from a national cross-sectional household survey of 6620 individuals in the Dominican Republic (DR) from June to October 2021, we developed and applied geostatistical regression models to estimate and predict Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) spike (anti-S) antibodies (Ab) seroprevalence at high resolution (1 km) across heterogeneous areas.

Results: Spatial patterns in population immunity to SARS-CoV-2 varied across the DR. In urban areas, a one-unit increase in the number of primary healthcare units per population and 1% increase in the proportion of the population aged under 20 years were associated with higher odds ratios of being anti-S Ab positive of 1.38 (95% confidence interval [CI]: 1.35–1.39) and 1.35 (95% CI: 1.32–1.33), respectively. In rural areas, higher odds of anti-S Ab positivity, 1.45 (95% CI: 1.39–1.51), were observed

The findings and conclusions in this report are those of the author(s) and do not necessarily represent the official position of the U.S. Centers for Disease Control and Prevention.

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with increasing temperature in the hottest month (per°C), and 1.51 (95% CI: 1.43–1.60) with increasing precipitation in the wettest month (per mm).
Conclusions: A geostatistical model that integrates contextually important socioeconomic and environmental factors can be used to create robust and reliable predictive maps of immune protection during a pandemic at high spatial resolution and will assist in the identification of highly vulnerable areas.

KEYWORDS
COVID-19, immunity against SARS-CoV-2, model-based geostatistics, pandemic, predictive mapping, spatial analysis

INTRODUCTION

The impact of the ongoing Coronavirus disease (COVID)-19 pandemic, caused by Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), has highlighted the need for better preparedness against pathogens with pandemic potential. The ability to rapidly assess and understand population-level immune response and the resulting protective immunity is essential for the design and implementation of prevention and control interventions during a pandemic [1]. A key challenge is the timely availability of reliable and accurate epidemiologic data, especially in areas with sub-optimal population immunity that could represent a risk of fuelling localised outbreaks [1]. To address this limitation, research has explored the use of disease mapping and predictive modelling to maximise the usefulness of available data [2]. Geostatistical modelling provides a flexible framework that enables the combination of a variety of spatial datasets to make predictive inferences, including the ability to describe and detect areas where the population-level immunity against emerging (novel) pathogens is likely to be low [2].

COVID-19 spread rapidly across the Dominican Republic (DR) since the first laboratory confirmed case was identified on 1 March 2020. As of 29 November 2023, there were approximately 667,075 cumulative cases of COVID-19 in the DR with 4384 related deaths [3], representing one of the highest disease burden for countries in the Caribbean region. As part of the national emergency response, the DR adopted strict public health policies to address the pandemic [4]. The extent and impact of the implementation of the national public health measures against COVID-19 have been highly variable across the country [4]. A national COVID-19 vaccination campaign was launched in late February 2021, and by August 2021, the COVID-19 vaccine coverage was 52.3% for one dose, 36.2% for two doses and 5.3% for three doses [5]. At that time, the most widely administered COVID-19 vaccines in the DR were Sinovac (∼90% of doses), Oxford/AstraZeneca and the Pfizer/BioNTech vaccines [6].

Our previous studies conducted in the DR at national and regional levels estimated that 85.0% (95% CI 82.1–88.0) of the population aged ≥5 years had SARS-CoV-2 spike (anti-S) antibodies (Ab), which could result from infection, vaccination, or both, with seroprevalence varying from 78.7% (95% CI 75.0–82.2) to 90.4% (95% CI 86.1–93.8) between regions [7,8]. Our current study extends the previous work by using geostatistical methods to estimate and predict population immunity for the whole country at high spatial resolution. The identification of sub-national areas with predicted low anti-S Ab seroprevalence may help national authorities to assess future epidemic risks and guide the targeting of interventions such as vaccine prioritisation and health messaging. The primary aim of this study was to demonstrate the application and utility of geostatistical modelling to describe and predict the geographical distribution of population immunity to SARS-CoV-2 during a pandemic and identify areas that are likely to have sub-optimal population immunity. Specifically, the objectives were (i) to identify, characterise and model geographical patterns of anti-S Ab seropositivity at the household level using environmental and sociodemographic risk factors and (ii) to predict anti-S Ab seroprevalence in the DR in locations where seroprevalence data were not available.

METHODS

Study area

The DR is located in the eastern part of the island of Hispaniola in the Caribbean. Most of the country's area (48,671 km^2) corresponds to the mainland and 159.4 km^2 to adjacent islands. The 31 provinces and the Santo Domingo national district are divided administratively into municipalities, district municipalities, sections and barrios/parajes (Figure 1). In 2021, the total population was approximately 11 million [9]. Approximately 20% of the population reside in rural areas [9].

The DR has a tropical climate, with varying topography and a large variety of microclimates [10]. The average annual temperature is 25°C, with August being the hottest month and January the coldest. The areas with the highest humidity are in the north because they are influenced by the Atlantic Ocean [10].

SARS-CoV-2 spike antibody (anti-S) data

Data on anti-S Ab status (positive/negative) were obtained from a three-stage cross-sectional nationwide serosurvey conducted in the DR to identify the most common causes of acute febrile illness between 30 June and 12 October 2021.

FIGURE 1 Administrative map of the Dominican Republic at the province level (insert showing the location in the Americas. Base layers from: (https://www.diva-gis.org/gdata).

Full details about survey design and sampling methods have been reported elsewhere [7]. Briefly, the centroids of the 12,565 communities (locally called barrios or parajes, referred to here as clusters) in the DR were calculated using administrative shapefiles for these units. A spatially representative sampling method was implemented in R software [11] to select 134 clusters. This strategy for selection of clusters was conducted to ensure a wide spatial distribution of sampled communities across the country, that both urban and rural environments were equally represented, and that the two large urban areas of Santo Domingo and Santiago (approximately 35% and 10% of the national population, respectively) were not over-sampled. Household selection in urban clusters, where buildings are spread almost evenly within the cluster, was conducted using a grid sampling design. A grid with approximately 15 equally sized cells was created and overlaid over each cluster, with 15 households selected in closest proximity to the grid nodes. A second set of 8 households located in near proximity to a subgroup (every second location) of the 15 households was also selected (for a total of 23 households per cluster). In rural clusters, the spatially representative sampling method that was used to select the 134 clusters was implemented to select 23 households from a geo-referenced list of buildings generated in Google Earth Pro version 7.3.6.9345 [12]. Two provinces (containing 23 out of the 134 selected clusters) that were also participating in a linked study (prospective clinical surveillance of acute febrile infections (AFI) at two regional hospitals in San Pedro de Macoris and Espaillat provinces) were over-sampled with 60 households per cluster. A national target sample size of 7000 participants was estimated assuming a community-level seroprevalence of the most common AFI pathogens of ∼20% and a probable stratification of the final sample based on seven age groups (2–4, 5–9, 10–14, 15–19, 20–39, 40–59 and 60+ years), three major ethnic groups (70% mixed, 16% white and 13% black) and two residential settings (20% rural, 80% urban and peri-urban).

All household members aged ≥5 years were invited to participate in the survey. Standardised electronic questionnaires were administered to all participants using the Kobo Toolbox software (www.kobotoolbox.org) to collect self-reported demographics individual-level data including number, date and type of COVID-19 vaccine received. The Global Positioning System coordinates were captured for each household location. Venous blood samples were collected, processed as sera, and frozen at −80°C. Pan-immunoglobulin antibodies against SARS-CoV-2 spike were measured on Roche Elecsys SARS-CoV-2 electrochemiluminescence immunoassays that use a recombinant protein modified double-antigen sandwich format (Roche Diagnostics, Indianapolis, IN, USA). Assay performance measures were based on large non-manufacture-sponsored studies with specificity and sensitivity of 99.8% (CI 99.3–100) and 98.2% (CI 96.5–99.2), respectively [13,14].

This study was reviewed and approved by the National Council of Bioethics in Health, Santo Domingo (013-2019), the Institutional Review Board of Pedro Henríquez Ureña National University in Santo Domingo, and the Mass General Brigham Human Research Committee, Boston, USA (2019P000094). The study was registered at the Human Research Ethics Committee of The University of Queensland (2023/HE001506).

Administrative boundaries, socioeconomic and environmental data collection and processing

The socioeconomic and environmental covariate data considered for the analyses were identified based on review of published literature on drivers of SARS-CoV-2 transmission in different contexts [15,16]. These spatially referenced covariate layers were downloaded and extracted from different sources and processed as indicated in Supporting Information S1 and Table S1.

Geo-referenced datasets that included anti-S status, socioeconomic and environmental covariates were imported, processed and spatially integrated in ArcGIS software [17]. Data were extracted for each household location to define input parameters for the geostatistical models. To predict the probability of anti-S Ab positivity at unsampled locations, data on the covariates were extracted at the nodes of a regular 1 km × 1 km grid across the DR.

Exploratory methods and variable selection

Survey weighted seroprevalence of anti-S status and vaccination coverage by province were estimated, accounting for survey sampling design and probability weights. Individual COVID-19 vaccination status was used only for descriptive mapping and exploratory purposes and was not considered for prediction since there were no data available for individuals at unsampled locations. Correlations between environmental covariates were visually inspected using scatterplots and assessed using Spearman correlation coefficients. Non-spatial univariable logistic regression models were developed using R software R-4.0.3 [11] to examine the association between anti-S Ab (outcome variable) and the socioeconomic and environmental factors (covariates). For the highly correlated covariates (Spearman correlation coefficient ρ >0.7), those with the highest Akaike Information Criterion (AIC) value (i.e., lowest predictive power) in the univariable regression models were excluded. Covariates were normalised (centred around 0 with a standard deviation of 1) for scaling purposes by subtracting the mean from each value and dividing them by the standard deviation. Separate non-spatial multivariable logistic regression models were fitted for urban and rural areas, including the remaining explanatory variables as fixed effects and without considering the spatial dependence structure of the data. Variables with a p-value <0.2 in the non-spatial regression models were selected for inclusion in the final geostatistical models. Non-linear associations between predictors and the outcome variables were modelled using a piecewise approach and allowing the slope to varying across segments of the covariate values.

Geostatistical multivariable regression models

Spatially-explicit models of anti-S Ab positivity were built in a geostatistical framework using the R package PrevMap [18]. Separate models were fit for urban and rural areas to allow for differences in the slope of covariate effects on anti-S Ab seroprevalence between these areas. To improve the computational efficiency of the models, households were aggregated to grid cells of 200 m × 200 m (anti-S positive cases were summed and divided by the total number of tested individuals in each grid cell). The models utilised the proportion of anti-S positives (binomially distributed) as the outcome variable, along with significant explanatory variables (variables with a p-value <0.2 in the non-spatial regression models), and spatially structured random effects. We estimated 95% confidence intervals (95% CI) and p-values for the odds ratios (OR) for the covariates in the final models.

The mathematical representation of the geostatistical model is provided below. It was assumed that the proportion of anti-S Ab positivity at each location j followed a binomial distribution, where Y_j is the number of positive anti-S Ab tests, n_j is the number of individuals tested for anti-S Ab, and p_j is the predicted seroprevalence of anti-S Ab at location j. The model structure was as follows:

$$Y_j \sim \text{Binomial}\left(n_j, p_j\right),$$

$$\text{logit}\left(p_j\right) = \alpha + \sum_{z=1}^{z} \beta_z \times \lambda_{zj} + s_j,$$

where α is the intercept, β is a matrix of covariate coefficients, λ is a matrix of z socioeconomic and environmental variables (fixed effects) at location j, and s_j are the geostatistical random effects to account for spatial variation in anti-S Ab positivity seroprevalence between locations not explained by the fixed effects. Parameter estimates for each model were obtained using the Monte Carlo maximum likelihood (MCML) method [18], which is a convolution-based low-rank approximation to the full Gaussian spatial process and is more computationally efficient for large spatial data.

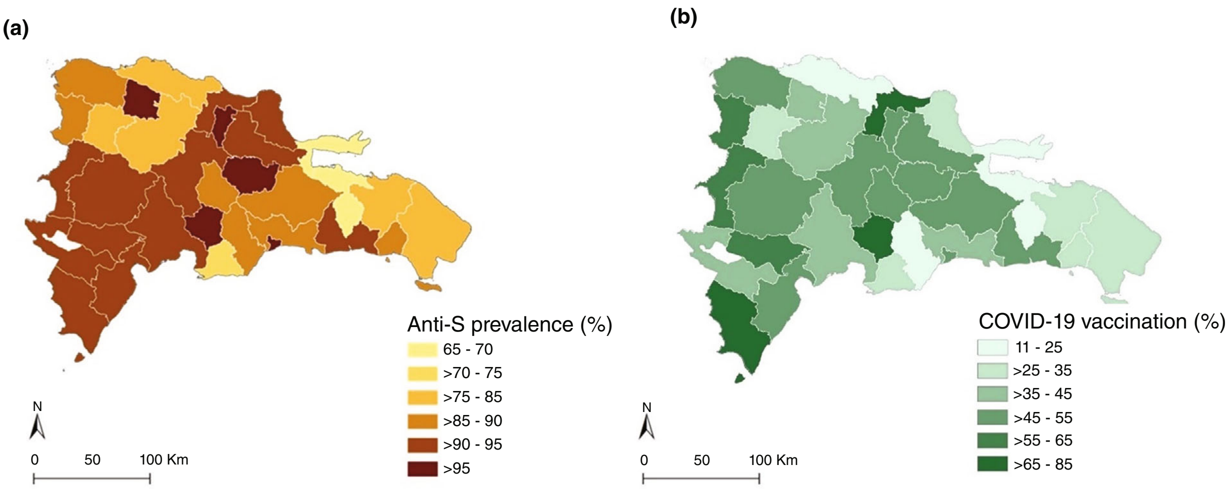

FIGURE 2 Geographical distribution of (a) adjusted Severe Acute Respiratory Syndrome Coronavirus 2 spike (anti-S) antibody seroprevalence and (b) Coronavirus disease (COVID)-19 vaccine coverage by province in the Dominican Republic, June–October 2021.

For both models, a burn-in of 5000 MCML iterations was used followed by 55,000 iterations, sampled at every 10th iteration to reduce autocorrelation. Predicted seroprevalence and exceedance probability based on threshold probability of 0.8 (represents the probability that the predicted seroprevalence of anti-S is above a threshold of 80%) at the sampled and predicted locations were generated. Convergence for all models was assessed visually based on inspection of Monte Carlo chains and autocorrelation plots.

Predicted seroprevalence of anti-spike ab

The predicted anti-S Ab positivity seroprevalence at the unsampled locations was estimated by fixing the model parameters at the corresponding MCML estimates from the fitted model [18]. ArcGIS was used to generate smoothed risk maps of the posterior distributions of the predicted seroprevalence and exceedance probability of anti-S Ab positivity of 0.8.

To determine the predictive performance of the models, a validation dataset was created for urban and rural locations separately by randomly withholding 25% of the data, fitting the model based on 75% of the data and then predicting anti-S Ab seroprevalence (with estimates of uncertainty) for the withheld subset. We estimated the root mean squared error (RMSE) by comparing the model-predicted seroprevalence in the withheld subset to the actual observed seroprevalence.

RESULTS

Sample description and sample site locations

The dataset included 6620 participants aged ≥5 years from 3785 unique household locations in 134 clusters. Overall, 4131 (62.4%) were female and over half (3576, 54.0%) lived in urban areas. The mean age was 41.4 years with median and interquartile range of 40 and 35 years, respectively (range 6–97). The adjusted anti-S Ab positivity seroprevalence was above 65% for all provinces (Figure 2a). However, there was significant geographical heterogeneity across provinces, with lower anti-S Ab seroprevalence in the south-east and high anti-S Ab seroprevalence across the south-west regions (El Valle and Enriquillo Provinces). COVID-19 vaccine coverage (two or more doses) followed a similar pattern with the lowest coverage in the north and south-east of the country (Figure 2b).

The geographical distributions of the environmental and socioeconomic covariates are shown in Figures 3 and 4, respectively. Descriptive statistics of all covariates considered for the analyses are presented in Table S2. Based on data extracted at household locations, daily precipitation averaged over a year ranged from 0.11 to 0.27 mm with an average of 0.17 mm. The annual average of monthly temperature was 34.2°C, ranging from 25.9–41.3°C. The mean elevation and distance to water bodies were 157 m (range 0–1352 m), and 2.47 km (range 0–14.40 km), respectively. The most densely populated areas correspond to the two major urban areas of Santo Domingo in the south and Santiago in the north central region.

Five pairs of variables (annual average of monthly temperature/temperature in the coolest month, annual average of monthly temperature/temperature in the hottest month, population density/proportion of the population aged under 20 years, percentage of population without access to indoor toilet/adult illiteracy percentage and motorised travel time to healthcare facilities/walking only travel time to healthcare facilities) were identified with Spearman correlation coefficients ≥0.7. Results of the assessment of bivariate associations between the highly correlated covariates and anti-S seroprevalence are provided in Figure S1 and Table S3. Covariates significantly associated with the outcome, and also highly correlated were removed, retaining those with the lowest AIC (best predictive covariates). The socioeconomic and

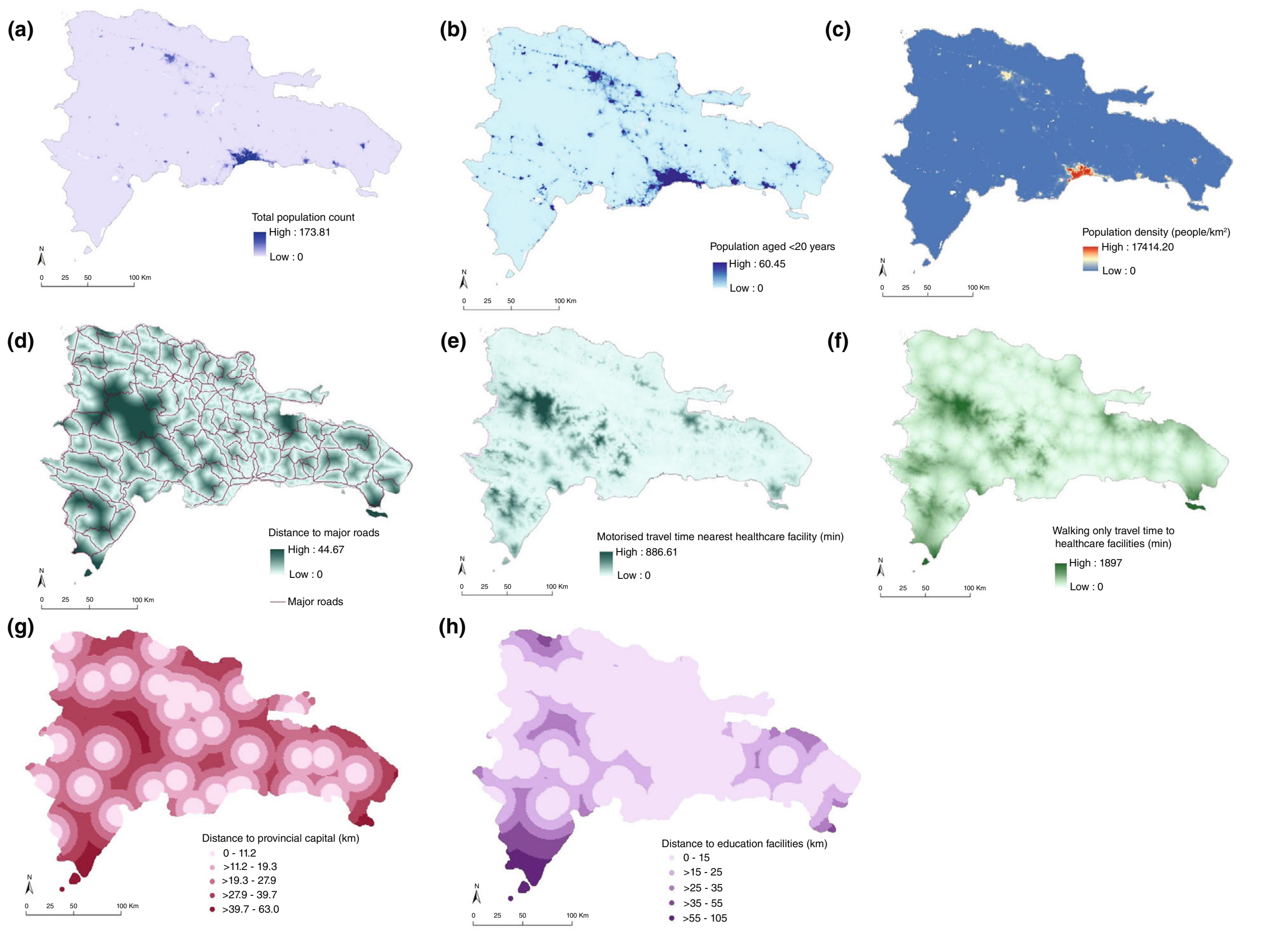

FIGURE 3 The geographical distributions of sociodemographic covariates in the Dominican Republic: (a) total population count, (b) proportion of population aged under 20 years and (c) population density (people/km^2) in 2020, (d) Euclidean distance to nearest major roads (km), (e) motorised travel time to nearest healthcare facility (min), (f) walking only travel time to healthcare facilities (min), (g) Euclidean distance to provincial capital (km) and (h) Euclidean distance to nearest education facilities (km). Details of spatial and temporal resolution of the spatial layer provided in Supporting Information S1. Base layers from: (https://www.diva-gis.org/gdata).

environmental covariates included in the final urban model were distance to provincial capital, walking only travel time to healthcare facilities, proportion of population aged ≤20 years, precipitation in the wettest month (August), built-up areas, unemployment rate and number of primary care units (PCU) per population (Table S5). Scatter plots of anti-S seroprevalence against covariates are presented in Figure 5. The final rural model included the following covariates: distance to inland water bodies, distance to provincial capital, distance to education facilities, elevation, precipitation in the wettest month, temperature in the hottest month (May), unemployment rate and number of PCU per population. An exploratory non-spatial model incorporating vaccination status was developed and is provided in Table S4.

Geostatistical model for anti-S seroprevalence

In the urban model, higher number of PCU per population was associated with the highest odds of being anti-S Ab positive (1.38, 95%CI: 1.35–1.39). Higher proportion of individuals aged ≤20 years was significantly associated with increased odds of anti-S positivity (OR: 1.35, 95%CI: 1.32–1.41). Odds of anti-S positivity increased by 1.33 (95%CI: 1.29–1.37) for each km increase in distance to the provincial capital. Odds of anti-S Ab positivity decreased significantly with longer walking travel time to the nearest healthcare facility and precipitation in the wettest month, with ORs of 0.86 (95%CI: 0.83–0.89) and 0.88 (95%CI: 0.86–0.90) for each 1 min increase in walking travel time and 1 mm in precipitation, respectively. Residing in built-up areas and, higher unemployment rates were not significant in the final urban model (Table 1).

In rural areas, odds of anti-S positivity were 1.45 (95% CI: 1.39–1.51) and 1.51 (95%CI: 1.43–1.60) with each 1°C increase in temperature in the hottest month and 1 mm increase in precipitation in the wettest month, respectively. Higher odds of anti-S Ab positivity were significantly associated with increasing PCU per population (OR: 1.44, 95%CI: 1.37–1.52). Distance to inland water bodies (per km) and

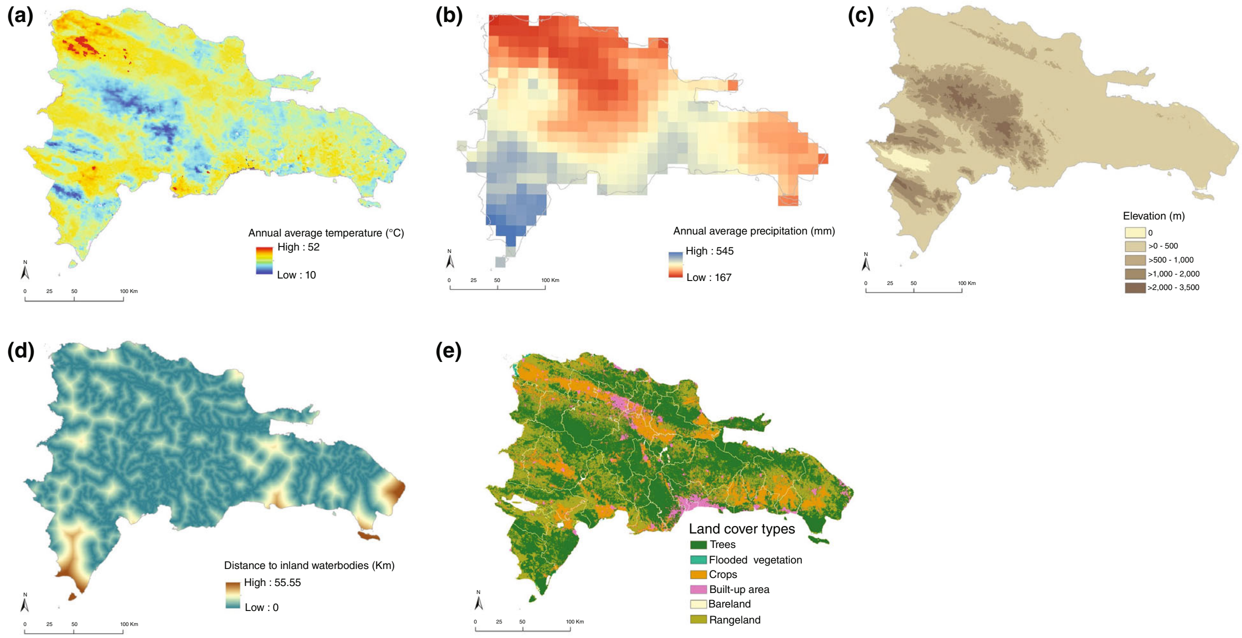

FIGURE 4 The geographical distributions of environmental covariates in the Dominican Republic: (a) annual average temperature (°C), (b) annual average precipitation (mm), (c) elevation (m), (d) distance to inland water bodies (km) and (e) land cover. Base layers from: (https://www.diva-gis.org/gdata).

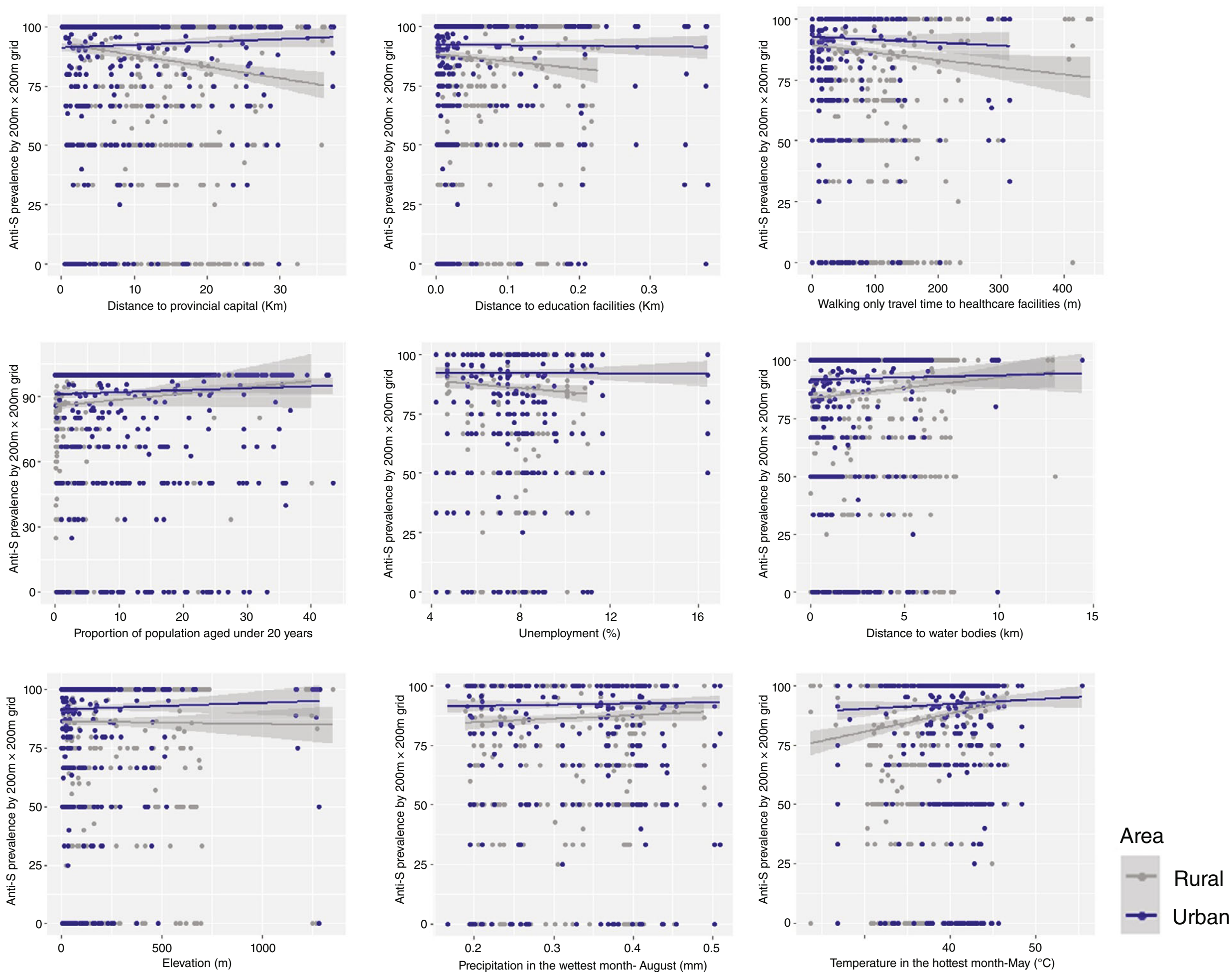

FIGURE 5 Scatter plots of Severe Acute Respiratory Syndrome Coronavirus 2 spike antibody seroprevalence against the covariates included in the models. The blue and grey dots and lines are for urban and rural areas, respectively.

TABLE 1 Odds ratios (ORs) and 95% confidence interval (95%CI) from the geostatistical models for anti-S positivity in urban and rural areas in the Dominican Republic, 2021.

Variables	Urban areas OR (95% CI)	Rural areas OR (95% CI)
Sociodemographic factors		
Distance to provincial capital (km)	1.33 (1.29–1.37)	0.87 (0.83–0.92)
Distance to provincial capital (km) (non-linear spline)	0.74 (0.68–0.80)	NA
Distance to education facilities (km)	NA	0.80 (0.73–0.88)
Distance to education facilities (km) (non-linear spline)	NA	0.86 (0.69–1.07)
Walking only travel time to healthcare facilities (min)	0.86 (0.83–0.89)	NA
Primary care units per population (ratio)	1.38 (1.35–1.39)	1.44 (1.37–1.52)
Proportion of population aged ≤20 years (%)	1.35 (1.32–1.41)	NA
Unemployment rate (%)	0.93 (0.91–0.95)	0.79 (0.75–0.83)
Environmental factors		
Distance to inland water bodies (km)	NA	1.21 (1.16–1.26)
Elevation (m)	NA	1.16 (1.11–1.22)
Average precipitation in the wettest month (August) (mm)	0.88 (0.86–0.90)	1.51 (1.43–1.60)
Temperature in the hottest month (May) (°C)	NA	1.45 (1.39–1.51)
Built-up area	1.20 (0.80–1.09)	NA
Variance of the spatially structured random effect	0.003 (0.003–0.01)	0.04 (0.03–0.06)
ϕ (Decay of spatial correlation)	38.94 (9.25–163.87)	3.43 (1.93–6.11)

Note: Statistically significant ORs are highlighted in blue (positive associations) and grey (negative associations).

elevation (per m) were also positively associated with anti-S Ab positivity, with ORs of 1.21 (95%CI: 1.16–1.26) and 1.16 (95% CI: 1.1–1.22), respectively. In contrast to urban areas, odds of anti-S positivity decreased significantly with increasing distance to the provincial capital, OR 0.88 (95%CI: 0.83–0.92). Furthermore, there was a significant negative association between anti-S positivity and increasing distance to the nearest educational facility (OR: 0.80 [95%CI: 0.73–0.88]) as well as increasing unemployment (OR: 0.80 [95%CI: 0.75–0.83]).

Predictive mapping of anti-S seropositivity

A national-level map was created by combining the urban and rural maps (Figure S2) for mean posterior distributions of predicted anti-S ab seroprevalence (Figure 6a). The model predicted significant spatial heterogeneity in anti-S Ab seroprevalence, with highest predicted seroprevalence (≥95%) in the south-west (particularly in Independencia and Barahona Provinces), and high predicted seroprevalence (90%–95%) in the south-central part of the country. Predicted seroprevalence was lowest (<80%) in the north and in the far south-west. The exceedance probability for anti-S Ab positivity seroprevalence greater than 0.8 is depicted in Figure 6b, showing that the predicted seroprevalence of anti-S Ab for most locations in the DR was highly likely to exceed 80%. The RMSE for the urban model was 9.11 and for the rural model was 6.81. Full R code for the geostatistical models is provided in https://github.com/Angelamcr2203/COVID-19.

DISCUSSION

In this study, we demonstrated the utility of a geostatistical approach to estimate and predict population immunity at high spatial resolution, identify pockets of lower population immunity that could be used to help guide targeted interventions, particularly vaccination campaigns. This approach and findings are valuable for improving our understanding of the immunological vulnerability of the local population at the time of the survey, as well as for informing preparedness strategies for future pandemics. While seroprevalence of anti-S Ab was generally high across the country at the time of the survey, there were areas with low predicted seroprevalence, with varying risk factor profiles, that could benefit from targeted interventions, particularly vaccine campaigns.

Variations in COVID-19 vaccination efforts and the effectiveness of mitigation strategies may be attributed to differences in primary healthcare coverage and healthcare system organisation [19]. Similar to other studies that have assessed socioeconomic vulnerabilities to COVID-19 [20], we found that in the DR, increasing number of PCU per population (i.e., proxy for access to healthcare) in both urban and rural areas, had a positive association with anti-S positivity. This suggests that improving access to PCU may support a better structure and organisation of the COVID-19 vaccination programme, improving equitable immune protection particularly for vulnerable populations with less equitable access. Similar to other countries, in the DR, there is limited availability of healthcare facilities in rural areas and/or challenging geographic accessibility including longer travel distances to healthcare and vaccination providers [21]. This situation may also impact vaccination coverage and resultant population immunity. It is therefore not surprising to discover that in urban areas, where there is potentially higher density of PCUs, anti-S Ab seroprevalence demonstrated a positive association with increasing distance to provincial capital and a negative association with increasing walking only travel time to healthcare facilities. In contrast, in rural settings, increasing distance to provincial capital and education facilities and higher unemployment rates were associated with lower odds of anti-S positivity. This finding is also supported by the low

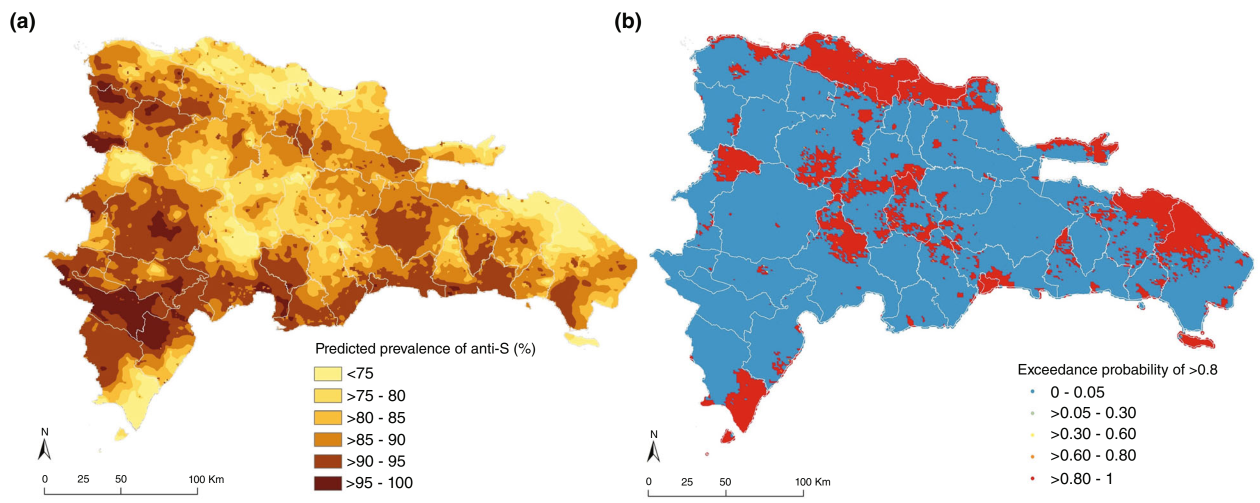

FIGURE 6 Spatial distribution of predicted seroprevalence (a) of Severe Acute Respiratory Syndrome Coronavirus 2 spike (anti-S) antibody seroprevalence in the Dominican Republic 2021 (b) and of exceedance probability of 80% seroprevalence.

predictive seroprevalence of anti-S Ab in mountainous areas in provinces located on the border with Haiti such as Elías Piña, where military carts had to facilitate transportation of medical supplies during the vaccination programme [22].

Precipitation during the wettest month (August) was found to be a significant environmental factor influencing anti-S Ab positivity. However, the association exhibited a contrasting pattern between urban and rural areas, with higher precipitation significantly reducing the odds of anti-S positivity in urban areas, while rural areas showed significantly higher odds. Furthermore, higher temperature during the hottest month displayed a positive association with anti-S positivity only in rural areas. Several studies have examined the effect of climatic variables on COVID-19 incidence with mixed results that varied considerably in effect sizes, significance levels, weather indicators, regions and time periods [15,16,23]. To date, there is still limited evidence on how environmental factors may be influencing transmission risk, vaccination coverage or other factors underlying COVID-19 immunity [24]. This contrasting evidence reinforces that drivers influencing transmission and access to health care might vary between settings.

There was a positive association between anti-S seropositivity, and the proportion of the population aged ≤20 years. Because those aged ≤16 years did not have access to the COVID-19 vaccine in the DR by the time of our survey [6], this relationship may be explained partially by the likelihood of infection in the younger population [25]. Also, it has been observed that younger populations may have increased likelihood of being infected relative to older age groups as a result of greater social connectivity. Generally, older people exhibit greater awareness of the pandemic and are more likely to comply with suggested behaviours and regulations because infection may result in a higher risk of severe and fatal outcomes for them [26].

This study had several strengths, including the spatial sampling design that allowed us to maximise the spatial dispersion of the selected clusters. Also, the availability of accurate geo-referenced anti-S Ab data at the household level, facilitating analysis at a fine spatial scale. However, there were several limitations, such as challenges in interpreting a positive anti-S result, as it was difficult to determine whether this was due to infection, vaccination, or both; nevertheless, it serves as an indicator of immune protection. Also, anti-S seroprevalence constantly evolves as a result of the complex interplay between further vaccine doses, repeated infections and waning immunity from both vaccination and infections. Lastly, while our data provide granular spatial insight into SARS-CoV-2 infection or vaccination, substantial transmission of Delta and Omicron variants between survey sampling and the present time has likely markedly impacted population immunity and seroprevalence [27]. While our findings may not reflect the current spatial epidemiology of anti-S Ab in the DR, we have demonstrated the value of predictive risk mapping for informing pandemic response.

CONCLUSIONS

Identifying areas with low population immunity helps highlight areas in need of additional resources, investment and targeted interventions, and provide valuable insights into the adequacy and equity of vaccine provision during a pandemic and how this needs to be addressed for subsequent outbreaks of other emerging infectious diseases. These findings pave the way for further research aimed at enhancing our understanding of the dynamics of anti-S over time and across diverse settings.

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CONFLICT OF INTEREST STATEMENT

Eric J. Nilles is the PI on a US CDC funded U01 award that funded the study, and Colleen L. Lau, Adam Kucharski, Devan Dumas, Michael de St. Aubin, Angela Cadavid Restrepo, Helen J. Mayfield, Salome Garnier, Marie Caroline Etienne, William Duke, Gabriela Abdalla, Bernarda Henriquez and Margaret Baldwin, have received salaries, consultancy fees or travel paid through this award. Emily Zielinski Gutiérrez and Beatriz Lopez are employees of the US CDC. Bernarda Henriquez, Cecilia Then Paulino, Lucia de la Cruz, Farah Peña and Ronald Skewes Ramm are employees of the Ministry of Health and Social Assistance, Dominican Republic, that was subcontracted with funds from the US CDC award. Adam Kucharski is supported by the Welcome Trust, UK. We declare no other competing interests.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available from the corresponding author (Eric J. Nilles), upon reasonable request.

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SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

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