



Assessment of monthly infection risk of heartworm infection in Colombia: integrative ecological niche modeling of *Culex quinquefasciatus* and *Dirofilaria immitis*

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ABSTRACT

Heartworm disease (*Dirofilaria immitis*) is a globally distributed vector-borne zoonosis affecting canids and felids, which can be fatal by compromising the cardiorespiratory system. This study analyzes the annual and monthly infection risk in Colombia by integrating ecological niche modeling for *Culex quinquefasciatus*—the most important and widely distributed vector in the country—with the temperature-dependent number of *D. immitis* generations within the vector. Results identified the human footprint (78 %) as the primary determinant of vector distribution, surpassing climatic variables and confirming the synanthropic nature of transmission. The monthly analysis revealed sustained potential transmission year-round in lowlands and coastal areas, contrasting with a marked thermal barrier in the Andean region, where altitude limits parasite development despite the presence of the vector. External validation confirmed the model's robustness, locating 84.68 % of reported cases within very high-risk zones. Heartworm infection in Colombia is a non-seasonal urban phenomenon, strictly modulated by altitude. These findings call for replacing seasonal prophylaxis with continuous preventive protocols and prioritizing epidemiological surveillance under a One Health approach along the country's main demographic corridors.

1. Introduction

Heartworm disease, caused by *Dirofilaria immitis*, is a zoonotic vector-borne disease. Its definitive hosts are domestic and wild canids and felids, and its vectors are mosquitoes of the family Culicidae. It is a complex and progressive disease that affects the host's cardiorespiratory system, potentially becoming chronic and leading to acute, life-threatening conditions. Humans can also be affected, acting as accidental [or incidental] hosts, in whom single or multiple benign and asymptomatic pulmonary nodules occasionally develop (Noack et al., 2021).

This disease has a cosmopolitan distribution, predominating in regions with tropical and/or subtropical climates. Its presence depends on the interaction between environmental factors—such as average temperatures and high humidity that favor vector survival—, the presence of microfilaremic reservoirs, and anthropogenic factors. The latter include irrigated agriculture, human intervention through the creation of transport networks and new urbanizations, the formation of microclimates, the existence of large populations of uncontrolled reservoirs (such as wild canids and stray dogs), and the movement of companion animals, among others (Morchón et al., 2022).

The Americas is one of the continents where the disease is present,

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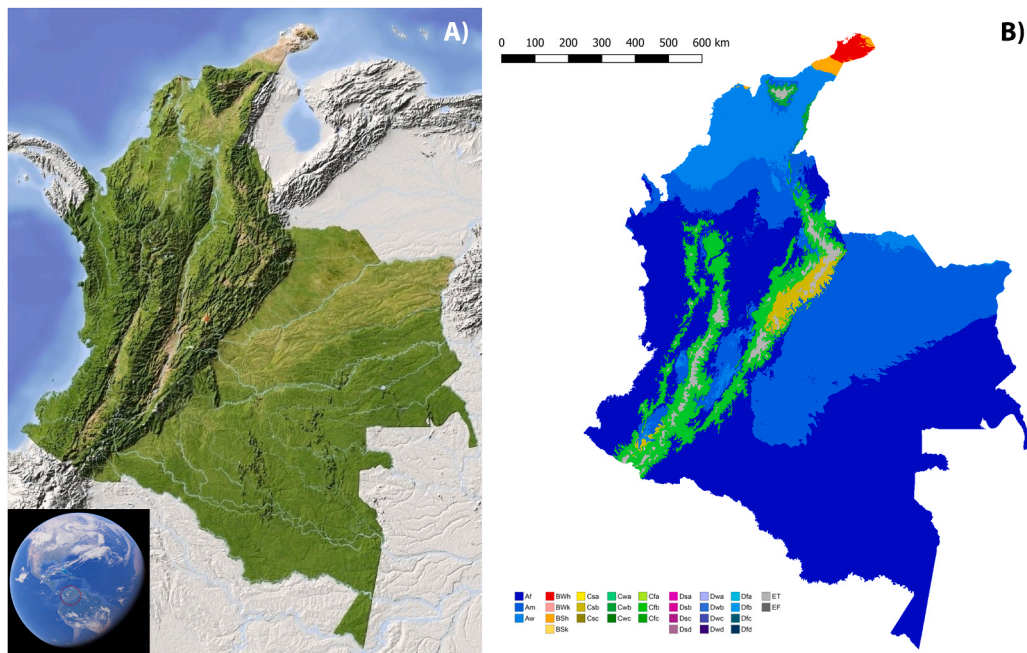


Fig. 1. Localization (A) and climates according to the Köppen Climate (B) in Colombia. (EF: Ice cap, ET: Tundra, Dfc: Subarctic, Dfb: Warm-summer humid continental, Dfa: Hot-summer humid continental, Dwc: Monsoon-influenced subarctic, Dwb: Monsoon-influenced warm-summer continental, Dwa: Monsoon-influenced hot-summer continental, Dsc: Subarctic with dry summer, Dsb: Warm-summer continental with dry summer, Dsa: Hot-summer continental with dry summer, Cfb: Marine west coast (temperate oceanic), Cfc: Subpolar oceanic, Cwa: Monsoon-influenced humid subtropical, Cwb: Subtropical highland (humid subtropical with dry winter), Csc: Cold-summer Mediterranean, Csb: Warm-summer Mediterranean, Csa: Hot-summer Mediterranean, BSk: Cold semi-arid (steppe), BSh: Hot semi-arid (steppe), BWk: Cold desert, BWh: Hot desert, Am: Tropical monsoon, Aw: Tropical savanna, Af: Tropical rainforest).

with prevalences varying greatly by country and climatic region (Genchi and Kramer, 2020). In North America, the United States is the country where the disease is best studied, harboring hyperendemic regions in the Southeast and the Mississippi Valley (Smith et al., 2022; American Heartworm Society, 2025). In Canada, it is located in the southwest, where a slow but continuous northward expansion of risk has been observed (McGill and Leighton, 2019; Jacobson et al., 2020).

In Central and South America, environmental factors facilitate uninterrupted transmission year-round (Labarthe and Guerrero, 2005; Esteban-Mendoza et al., 2020). In Mexico, heartworm infection is considered a hyperendemic veterinary problem on the Gulf Coast and in the Caribbean, with a mean national prevalence of 7.5 % (Zumaquero et al., 2020; Bedoya et al., 2022; Hay-Parker et al., 2025). A similar situation occurs in the Caribbean islands, where local prevalences in dogs of 40–60 % have been reported, particularly in animals without prophylaxis living outdoors (Noack et al., 2021).

In South America, the disease is distributed throughout the subcontinent, with higher incidence in the northern and central regions, with Brazil being the best-studied country showing the highest prevalences in the north (Labarthe and Guerrero, 2005). In Colombia, studies are scarce, although they indicate a heterogeneous epidemiological landscape. In the Colombian Caribbean, high prevalences (34.1–53.2 %) are reported (Badillo-Viloria et al., 2023). However, lower prevalences have been shown in cities such as Barranquilla (11.3 %) and Bucaramanga (6.3–10.8 %), Cartagena (3 %), and even lower in Medellín, Pereira, and Bogotá (Labarthe and Guerrero, 2005; Mccown et al., 2014; Muñoz and Daza, 2020; Esteban-Mendoza et al., 2020, 2024; Badillo-Viloria et al., 2023). It has also been reported that the human population is in contact with the parasite, with a seroprevalence of 6.71 % in Bucaramanga (Esteban-Mendoza et al., 2020) and 9.54 % in the Tikuna Indian community in the Colombian Amazon (Vieira et al., 1998), highlighting the zoonotic risk of the disease.

The persistence of the disease in the country is attributed to climatic factors, as well as agricultural intensification, landscape modification, and insufficient ecosystem protection—conditions that favor the vector

cycle—and the existence of uncontrolled hosts (Maggi and Krämer, 2019).

In the context of vector-borne disease control, Ecological Niche Modeling (ENM) has become a fundamental tool for minimizing infection risk. Based on Geographic Information Systems (GIS), these models allow for the generation of habitat suitability maps, identifying areas where environmental conditions are optimal for vector establishment (Deka and Heukelbach, 2021; Omar et al., 2021; Velu et al., 2023; Wouters et al., 2024). Regarding the study of infection risk for heartworm infection, recent studies have incorporated parasite development within the vector (number of generations of *D. immitis*) into ENM as a key variable for interpreting infection risk (González-Mohino et al., 2025; Rodríguez-Escolar et al., 2025). This approach has proven effective in generating more realistic and dynamic risk maps, allowing for predictions with greater spatial and monthly resolution throughout the year (González-Mohino et al., 2025; Rodríguez-Escolar et al., 2024a, 2024b, 2025).

The aim of the present study is to analyze the monthly dynamics of *D. immitis* infection risk in Colombia using ecological niche models. This analysis considers parasite development within the vector and its suitable habitat as variables, thereby providing a scientific basis for the implementation of control strategies and veterinary prophylaxis, taking into account its zoonotic aspect under a One Health perspective.

2. Materials and methods

2.1. Study area

Colombia (12° 27' N and 4° 13' S, 79° 00' W and 60° 50' W), located in northwestern South America, covers 1141,748 km² bordered by the Caribbean Sea (north), Venezuela and Brazil (east), Ecuador and Peru (south), and the Pacific Ocean (west) (Fig. 1A). The territory is traversed by the Andes, which split into three ranges (Western, Central, and Eastern Cordilleras), alongside isolated systems like the Baudó Mountains and the Sierra Nevada de Santa Marta (home to the 5775 m

Table 1
Analysis of the contribution of the 11 environmental and bioclimatic variables to the ecological niche model for *Cx. quinquefasciatus*.

Variable	Contribution (%)
Human footprint	78
Water bodies	11.8
Seasonality of temperature (BIO ₄)	8.5
Shrubs	0.7
Seasonality of precipitation (BIO ₁₅)	0.5
Annual mean temperature (BIO ₁)	0.3
Herbaceous	0.1
Annual precipitation (BIO ₁₂)	0.1
Annual temperature range (BIO ₇)	0
Irrigated crops	0
Rivers	0

Cristóbal Colón peak). These highlands contrast with the vast lowlands of the Orinoco and Amazon (east), and the Pacific and Caribbean plains (west and north). Hydrographically, Colombia comprises five major basins: Caribbean, Pacific, Amazon, Orinoco, and Catatumbo. Key fluvial systems include the Magdalena (the country’s largest river), fed by the Cauca from the Southwestern Mountain Range; the Atrato, flowing from the Western Cordillera to the Gulf of Urabá; and the Amazon River along the Brazilian border. Major lentic bodies include Lake Guamuez (southwest) and Lake Tota (east) (Ministerio de Ambiente y Desarrollo Sostenible, 2025). Table 1

According to the Köppen-Geiger classification, the predominant climate is tropical (A), differentiating between areas with tropical rainforest climate (Af), tropical monsoon climate (Am), and tropical savanna climate (Aw). On the other hand, minority climates exist, such as dry climate (B) in desert and semi-arid regions, and mountain climate (E), divided into tundra (ET) and frost (EF) in the Andean heights (Fig. 1B) (Climate Shifts, 2019; Rubel and Kottek, 2010).

2.2. Vector presence data

Occurrence points of mosquitoes belonging to the species *Culex quinquefasciatus*, one of the most relevant vectors transmitting *leishmaniasis* in the country (Dantas and Otranto, 2020; Cano-Pérez et al., 2022), were downloaded from the GBIF.org database (GBIF, 2025). Furthermore, it is one of the most widely distributed and abundant species available in this database. The occurrence points were superimposed on a grid with 1 km² resolution cells to reduce potential biases caused by spatial autocorrelation, using the resulting centroid of each positive cell for subsequent analysis. This spatial rarefaction process was essential because the initial 726 raw records exhibited extreme spatial clustering, with multiple records often sharing identical coordinates or falling within the same pixel. Consequently, the filtering procedure removed these redundant duplicates to avoid pseudoreplication, resulting in 38 spatially independent valid points that represent the true geographic extent of the species in the study area. This process was carried out using QGIS software version 3.34.15 (QGIS Development Team, 2025).

2.3. Bioclimatic and environmental data

Bioclimatic variables (1970–2000), related to temperature and precipitation, were obtained from the WorldClim database (WorldClim, 2025), including both current conditions and projections for 2100 under a climate change scenario. These variables were selected based on a multicollinearity analysis in R software version 4.4.2 (R Core Team, 2025), using the Pearson correlation coefficient. Of the 19 variables downloaded, those with a correlation equal to or greater than 0.8 were excluded. In accordance with the vector’s biology (Gorris et al., 2021), the variables selected for the study areas were: Annual Mean Temperature (BIO₁), Temperature Seasonality (BIO₄), Temperature Annual

Range (BIO₇), Annual Precipitation (BIO₁₂), and Precipitation Seasonality (BIO₁₅).

Additionally, the environmental variables included in the model were: rivers (USGEO, 2025), water bodies (HOTOSM, 2025), irrigated crops (FAO, 2025), human footprint (SEDAC, 2025), and herbaceous and shrub density (EarthEnv, 2025). All variables were downloaded and processed at a resolution of 1 km² (30 arc-seconds), with the same spatial extent (study area) and coordinate system (GCS_WGS_1984), using QGIS.

2.4. Habitat suitability models

To determine the habitat suitability of *Cx. quinquefasciatus* in Colombia, an ENM was generated using the MaxEnt algorithm (American Museum of Natural History, 2025), a predictive modeling tool based on the principle of maximum entropy that calculates the potential distribution of species using presence data (Philips et al., 2006).

A total of 102 candidate models were generated and evaluated. Their parameters reflect all combinations of 17 regularization multiplier configurations (from 0.1 to 0.9 and from 1 to 10), 6 feature class combinations (l, q, lq, lp, qp, and lqp), and one set of variables. From these candidate models, Kuenm selects the best fit based on three selection criteria: statistical significance (Partial_ROC < 0.05), omission rate (OR = 5 %), and model complexity using the corrected Akaike Information Criterion for small sample sizes (AICc ≤ 2). In addition, the Area Under the Curve (AUC) was also assessed, evaluating the general predictive capacity of the models. The AUC values were calculated internally by Kuenm using the standard MaxEnt procedure, which is based exclusively on presence records and 10,000 random background (pseudo-absence) points within the study area (default setting). The best-performing models met all these criteria simultaneously, including low omission rate, statistical significance, reduced complexity, and high AUC values.

2.5. Generations of *Dirofilaria immitis* month by month

The next step involved determining the development of the parasite within the vector on a month-by-month basis, using this information as a combined variable with the habitat suitability model to result in infection risk maps throughout the year. This variable represents the number of generations of *D. immitis* in the vector, calculated using a custom R script. We followed the methodology described by Genchi et al. (2005), González-Mohino et al. (2025) and Rodríguez-Escobar et al. (2025) for annual calculations, and further applied the adaptations to obtain monthly estimates as well. The number of generations for each month was calculated using daily mean temperature data from 1990 to 2016, obtained from the CHELSA database (CHELSA Climate, 2025). For the complete development of the parasite within the vector, it is established that an accumulation of 130 Growing Degree Days (GDDs) over 30 consecutive days is needed. For this to occur, a daily mean temperature of at least 14°C is required (Fortin and Slocombe, 1981).

2.6. Risk maps and validation

To obtain the risk maps, the Raster Calculator tool in QGIS 3.34.15 was used to perform a pixel-by-pixel multiplication (weighting method) of the final *Cx. quinquefasciatus* ENM and the monthly *D. immitis* generation estimates. This approach assigned equal weight (50 %) to both variables, producing maps that represent infection risk throughout the year. The legend values were standardized across all monthly maps: the maximum value observed during the highest-risk month was designated as “high,” while the minimum value from the lowest-risk month was labeled as “low.” The midpoint between these extremes was defined as “medium.” These standardized labels were applied in QGIS to facilitate visual comparison and interpretation.

To validate the resulting risk map, the Jenks Natural Breaks



Fig. 2. Prediction of the average number of generations of *Dirofilaria immitis* in Colombia.

classification method was used to divide the data into five risk classes (“very high”, “high”, “medium”, “low”, and “very low”). Subsequently, to evaluate the correspondence with known infections, 211 presence points of positive cases (177 animals and 34 humans) were overlaid on the average risk map (Mccown et al., 2014; Otalora et al., 2022; Badillo-Viloria et al., 2023; Esteban-Mendoza et al., 2020, 2024). This allowed for the calculation of the percentage of infected individuals falling within each risk class.

3. Results

3.1. Ecological niche model

The final model selected for *Cx. quinquefasciatus* in Colombia (M8.F1.Set1.EC) presented an AUC of 0.916 and habitat suitability values ranging from 0 (low suitability) to 0.98 (high suitability) (Supplementary Figure 1). The variables with the highest contribution to the model are human footprint (78 %), water bodies (11.8 %), and temperature seasonality (BIO₄) (8.5 %). The remaining variables have contribution percentages lower than 0.7 %. The map reveals a marked geographical pattern where zones of highest suitability align with the Andean region and the Caribbean, coinciding with major urban corridors; this indicates highly favorable conditions in inland cities such as Bogotá, Medellín, Cali, and Bucaramanga, as well as in coastal centers like Barranquilla. In contrast, zones of lower suitability extensively dominate the eastern and southern half of the territory, corresponding to the Orinoco plains and the Amazon rainforest, where environmental conditions prove unfavorable for the species' establishment.

3.2. Number of generations

Regions with the highest number of *D. immitis* generations are located in the north-central part, covering the entirety of the Caribbean

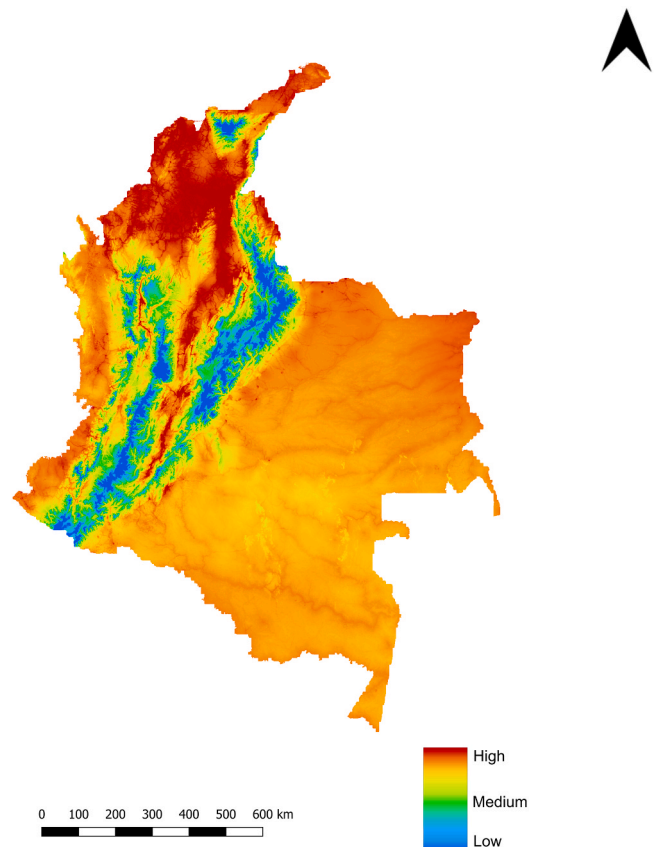


Fig. 3. Average infection risk map for heartworm infection in Colombia, constructed from the ecological niche model (ENM) of *Culex quinquefasciatus* suitability and the average number of extrinsic generations of the parasite within the vector.

Coast, the Pacific littoral, the Amazon, and the Orinoco, concentrated in large cities. Conversely, a clear physiological barrier is observed in the Andean Region with a null or very low number of generations across its three mountain ranges (Fig. 2). The maximum is reached in March, with more than seven generations (Supplementary Figure 2). In all months, the maximum generations range between six and seven, with a minimum value of zero in all months. This minimum value is found in high-altitude zones, such as the peaks of the mountain ranges. The annual maximum average is almost seven generations, concentrated in large cities, especially Bogotá, Bucaramanga, and Barranquilla. The minimum value reaches zero in the highest altitude zones.

3.3. Potential risk of infection and validation

The mean potential risk of heartworm infection is shown in Fig. 3. There is an elevated risk of infection in the northwest zone, where cities with the highest population density are found. This risk decreases to medium-high values in the eastern zone corresponding to the Colombian Amazon. It reaches medium-low and very low values as altitude increases, as seen in the three major mountain ranges and the Cristóbal Colón peak in the north.

The monthly spatiotemporal analysis of infection risk evidences a marked seasonal stability, remaining medium-high throughout the year, especially in regions located in the northwest of the country (Fig. 4). Lowlands and coastal areas in regions such as the Caribbean, the Pacific, and the Orinoco exhibit constant maximum infection risk values across all 12 months of the year. Conversely, the Andean barrier acts as a permanent limiting factor, with infection risk remaining low throughout the year, regardless of the month. March shows the highest infection

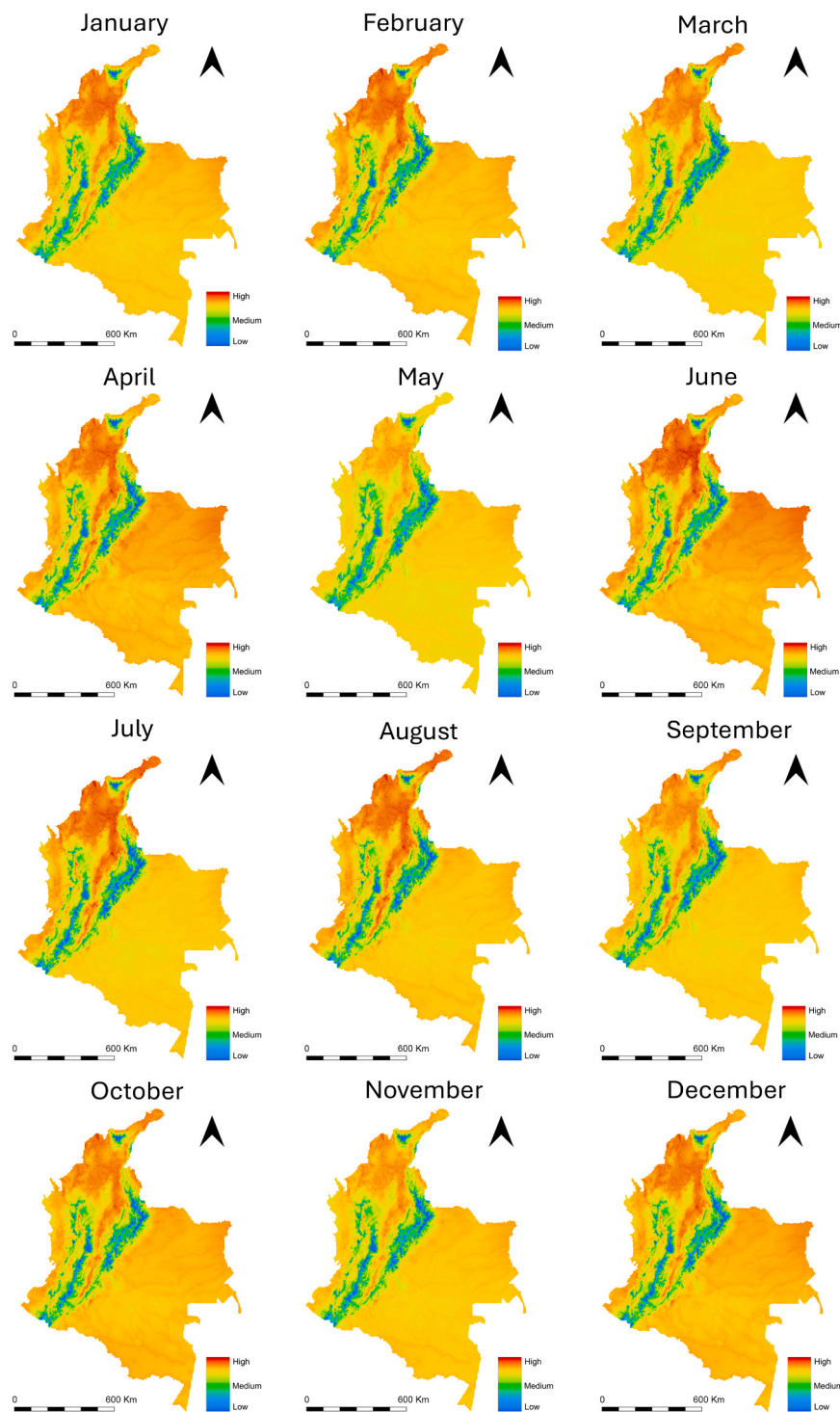


Fig. 4. Monthly infection risk maps for heartworm infection in Colombia, generated by combining the ecological niche model (ENM) of *Culex quinquefasciatus* suitability with the estimated monthly number of extrinsic parasite generations.

risk, while November shows the lowest.

To validate our results, dogs, cats, and humans infected by *D. immitis* were geolocated (Supplementary Figure 3). Of these, 84.68 % were found in zones of very high risk, 13.7 % in high-risk zones, and 0.81 % in both moderate and low-risk zones. Notably, no positive cases were recorded in the very low-risk zone.

4. Discussion

The present study constitutes, to the best of our knowledge, the first large-scale analysis in Colombia on the risk of heartworm infection under an ENM model for *Cx. quinquefasciatus*, integrating temperature-dependent *D. immitis* development in the vector (number of generations).

The choice of the species *Cx. quinquefasciatus* to carry out this analysis is based on: 1) its wide distribution in records available in

biological databases, which leads to greater statistical reliability of ecological niche modeling algorithms and reduces sampling bias inherent to less-studied sylvatic species; 2) its synanthropic ecological behavior and high ecological plasticity, allowing it to proliferate in urban and peri-urban environments where there is a higher density of definitive hosts and a susceptible human population; and 3) its role as one of the primary and most efficient vectors of *D. immitis* in tropical and neotropical regions, with a documented role in active transmission in Central and South America (Ahid et al., 2000; Torres-Chable et al., 2018; Camacho-Gómez et al., 2019; Dantas and Otranto, 2020; Cano-Pérez et al., 2022; García-Escobar et al., 2024).

A determining finding of this research is the identification of the human footprint as the most influential macroecological variable (78 %) in the distribution of *Cx. quinquefasciatus*, significantly surpassing traditional climatic variables such as precipitation. This result is consistent with literature defining this culicid as an eminently synanthropic and ubiquitous species, whose ecology is linked to unplanned urbanization and the availability of artificial breeding sites rich in organic matter (Labarthe and Guerrero, 2005; Dantas-Torres and Otranto, 2020; Wilke et al., 2021). The fact that water bodies (11.8 %) are the second most important variable reinforces this association: vector persistence in Colombia does not depend exclusively on seasonal rainfall regimes, but on the constant water availability associated with human infrastructure and urban sanitation (Pires and Gleiser, 2010; Wilke et al., 2019). This explains the high habitat suitability observed in the dense urban corridors of the Andean region (Bogotá, Medellín, Cali) and the Caribbean Coast (Barranquilla), consolidating heartworm infection as a predominantly urban and peri-urban zoonosis in this country, as observed in other South American regions.

Weighting the vector model with the number of *D. immitis* generations reveals a stable infection risk dynamic across months due to tropical thermal stability, which permits an uninterrupted transmission cycle throughout the year. This complex interaction reveals that the highest infection risk may occur in zones with thermal permissiveness and urban vector suitability, such as Barranquilla, Cali, Bucaramanga, and Medellín—cities with low to medium altitude.

However, our results also evidence a strong thermal dependence inversely related to altitude, generating a spatial decoupling between vector and parasite in certain regions. In high-altitude zones, such as the Cundiboyacense high plateau (Bogotá), despite extremely high suitability for the vector *Cx. quinquefasciatus*, transmission risk is limited by mean temperatures that frequently do not exceed the 14°C threshold necessary for *D. immitis* development in the vector. On the other hand, the Andes Mountains act as a physiological barrier, while low-altitude zones such as the Caribbean, Amazon, and Orinoco act as natural incubators due to high temperatures.

The infection risk map in Colombia is robustly validated, as 84.68 % of georeferenced positive cases among infected animals and seropositive humans were located in zones classified as "very high risk." Conversely, the presence of medium-high risk in the Amazon, where *Cx. quinquefasciatus* suitability is lower, suggests the possible participation of alternative vectors such as *Aedes* spp. or other species (Labarthe and Guerrero, 2005) that could be sustaining the cycle in areas with lower human density but optimal thermal conditions for the parasite. It is also true that data on animals and people in contact with the parasite come mainly from reports in areas with access to medical and diagnostic services. Therefore, being able to study the presence of the disease in areas such as the Colombian Amazon would be of great interest in order to study its distribution in these areas and increase the validity of the risk of infection in this model.

5. Conclusions

This study demonstrates a continuous year-round risk of heartworm infection in Colombia, although it remains low in the mountainous zones that separate the very high-risk northern regions from the medium-high

risk Colombian Amazon. Consequently, these findings provide novel epidemiological insights into the transmission of this zoonotic parasite in the Neotropics. Furthermore, the study offers a validated predictive tool within the One Health framework, advocating for a paradigm shift in veterinary prophylaxis in the country, which must be continuous rather than seasonal. Moreover, we propose the use of these risk maps as essential tools for stratifying epidemiological surveillance, prioritizing vector control and diagnostic interventions in major urban centers of the northwest and central regions. This approach aims to prevent future zoonotic outbreaks and mitigate the impact of climate change on public health.

CRedit authorship contribution statement

Elena Carretón: Writing – review & editing, Supervision, Investigation. **Iván Rodríguez-Escobar:** Writing – review & editing, Writing – original draft, Visualization, Validation, Methodology, Investigation, Formal analysis, Data curation. **José Alberto Montoya-Alonso:** Writing – review & editing, Investigation. **Rodrigo Morchón:** Writing – review & editing, Writing – original draft, Visualization, Supervision, Resources, Project administration, Investigation, Conceptualization. **Manuel Collado-Cuadrado:** Writing – review & editing, Visualization, Investigation, Formal analysis. **Víctor Arcila-Quiceno:** Writing – review & editing, Investigation, Formal analysis. **Elena Infante González-Mohino:** Writing – review & editing, Writing – original draft, Visualization, Methodology, Investigation, Formal analysis, Data curation. **María Victoria Esteban-Mendoza:** Writing – review & editing, Investigation, Formal analysis.

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Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.vetpar.2026.110699.

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