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Paper

Ecological niche modeling of epidemiological significance ticks: an experimental study with the modleR workflow in Brazil

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Abstract

Spotted fever rickettsioses are tick-borne diseases of major epidemiological importance worldwide. Ticks can interact pathogenically with humans through endemic foci or sporadic epidemic outbreaks. Novel analytical tools and decision-making frameworks for tick-borne disease surveillance may improve resource allocation and enhance the response capacity of public health services.

In this study, we characterize and model the bioclimatic suitability of three tick species—*Amblyomma aureolatum*, *A. ovale*, and *A. sculptum*—across Brazil. The climatic niche of each species was quantified using four modelling algorithms (BIOCLIM, GLM, Maxent, and SVM) implemented within an automated modelling workflow (modleR). A total of 585 occurrence records were retained for modelling: 55 for *A. aureolatum*, 120 for *A. ovale*, and 410 for *A. sculptum*, covering the entire Brazilian territory.

Amblyomma sculptum exhibited a broader tolerance to temperature and precipitation variability, suggesting a wider potential distribution range compared to the other two species. This species was primarily associated with grassland habitats, such as those in the Cerrado biome. In contrast, *A. aureolatum* and *A. ovale* were more strongly associated with forested areas, particularly along the Atlantic Forest coastal region.

The modelling outputs presented here provide valuable insights to support targeted health surveillance and intervention strategies for tick-borne diseases in Brazil.

Keywords

Tick-Borne Diseases, Spotted Fever, Ecological niche, Climate niche modeling, ModleR

Introduction

Ticks are hematophagous ectoparasites that infest a wide range of vertebrate hosts and serve as vectors for numerous pathogens (Pérez De León et al., 2014). As cosmopolitan organisms, ticks can cause disease in humans through both endemic transmission and rapidly resolved outbreaks (Gilbert, 2021; Guglielmone et al., 2006). Among tick-borne diseases, rickettsioses are particularly notable due to their significant medical and epidemiological relevance, especially in endemic regions. Spotted fever (SF) is a major public health concern in several countries. In Brazil, three species of *Amblyomma* ticks—*A. aureolatum*, *A. ovale*, and *A. sculptum*—are recognized as the principal vectors of SF (Oliveira et al., 2016; Szabó et al., 2013). Among the rickettsial pathogens, *Rickettsia rickettsii* is the most virulent and lethal species, frequently reported in southeastern Brazil, including the northern region of Paraná state (Durães et al., 2021). The transmission dynamics of SF in Brazil are shaped by distinct ecological interactions between ticks and their vertebrate hosts. In the enzootic cycle, *A. sculptum* is closely associated with equids and capybaras (*Hydrochoerus hydrochaeris*), which serve as major amplifiers of *R. rickettsii* (Bitencourth et al., 2016). Conversely, *A. aureolatum* plays a prominent role in urban-forest interfaces, particularly in Atlantic Forest remnants

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near São Paulo, where domestic dogs (*Canis lupus familiaris*) act as key reservoirs (Ogrzewalska et al., 2012; Pinter et al., 2004). *A. ovale*, in turn, is associated with *R. parkeri*, a less pathogenic rickettsial agent responsible for milder forms of SF, with transmission cycles involving domestic dogs and forest environments beyond the Atlantic Forest (Bitencourth et al., 2021; Moerbeck et al., 2016). Despite growing knowledge, critical gaps remain in the understanding of alternative transmission cycles and the ecological determinants of SF across Brazil.

New analytical and decision-support tools can enhance tick-borne disease surveillance by improving the targeting of public health interventions and identifying ecological drivers of transmission in understudied or epidemiologically silent regions. Such approaches can help strengthen preparedness and response capacity (Montenegro et al., 2017; Rodrigues et al., 2022). Ecological niche modelling has become a powerful method for predicting the potential distribution of vectors and pathogens, providing valuable insights for public health decision-making (Estrada-Peña, 2008; Peterson, 2008). Nevertheless, studies applying this approach to tick-borne diseases in South America remain limited (Acevedo-Gutierrez, 2018; Donalisio et al., 2020; Estrada-Peña, 2008; Estrada-Peña et al., 2014; Lippi et al., 2021; Oliveira et al., 2017a, 2017b; Polo et al., 2020).

Here, we present climate suitability models and validate spatial predictions based on existing ecological knowledge of the climatic (temperature and humidity) and environmental (biome) requirements of the three *Amblyomma* species implicated in the transmission of SF in Brazil.

Materials and methods

Ecological Niche Modelling based on climatic predictors

Ecological niche modelling was conducted based on climatic predictors for*Amblyomma aureolatum , A. ovale*, and *A. sculptum* using the modleR package (Sánchez-Tapia et al., 2017, 2020) within the R statistical environment (R Core Team, 2014). A correlative spatial approach was employed to explore relationships between species occurrences and bioclimatic variables, while acknowledging that biotic and abiotic factors beyond the scope of this study may also influence tick distribution (Estrada-Peña et al., 2016). Our analysis focused exclusively on climatic variables, excluding other potentially relevant drivers such as host availability (biotic) or terrain features (abiotic, e.g., elevation, slope). While these factors are recognized as important, their exclusion is consistent with established recommendations for large-scale tick distribution modelling, which emphasize climate as the dominant determinant due to limited and scale-dependent host data (Booth, 2018; Elith & Leathwick, 2023; Estrada-Peña et al., 2016; Peterson, 2011). Additionally, the use of non-climatic predictors is constrained by the complex ecology of the target species (Estrada-Peña, 2008). For instance, although animal hosts such as equines, domestic dogs, and capybaras are essential to enzootic cycles (Labruna, 2009; Oliveira et al., 2016), incorporating them into models is methodologically challenging due to anthropogenic biases in their distribution (Polo et al., 2020).

For each species, five algorithms were applied to identify areas environmentally like those where the species has been recorded, based on non-random associations between occurrence data and environmental conditions (Anderson et al., 2003). These included three presence-only or presence-background methods—Bioclim, Maximum Entropy (MaxEnt), and Mahalanobis Distance (Mahalanobis)—implemented via the *dismo* R package (Species Distribution Modeling, 2024). Additionally, two presence-absence methods were employed: Support Vector Machines (SVM) and Generalized Linear Models (GLM). The number of pseudo-absences was set to 100 times the number of presence points, with sampling restricted to a spatial buffer defined by the maximum distance between presence pairs, thus delimiting the accessible area for each species (Barbet-Massin et al., 2012; Peterson, 2011; VanDerWal et al., 2009).

Model performance was assessed using two standard evaluation metrics: the Area Under the Curve (AUC) of the Receiver Operating Characteristic (ROC) and the True Skill Statistic (TSS). AUC, a threshold-independent metric, is derived from plotting sensitivity against 1-specificity, and values above 0.8 are considered indicative of good model performance (Fielding & Bell, 1997; Swets, 1988; Mason & Graham, 2002). TSS is a threshold-dependent metric measuring agreement between observed and predicted presences and absences across various thresholds, with values above 0.6 considered acceptable (Allouche et al., 2006).

Only models meeting both criteria (AUC > 0.8 and TSS > 0.6) were retained. To assess model generality, occurrence datasets were partitioned via cross-validation with five subsets and one run per species, using 50% of occurrences for testing. Each partition was used for model fitting and spatial projection, enhancing robustness.

A 70% cut-off threshold was applied to convert continuous suitability scores into binary predictions. This conservative threshold balances model inclusivity with predictive accuracy, emphasizing specificity to reduce false positives and prevent overprediction—particularly critical for species with narrow distributions (Allouche et al., 2006; Jiménez-Valverde & Lobo, 2007). Additionally, this approach helps mitigate potential sampling biases from pseudo-absence generation, which might otherwise include unobserved presences (Barbet-Massin et al., 2012).

Finally, a consensus model was built to quantify prediction uncertainty by generating a binary consensus map based on the frequency of agreement among model outputs, using a majority threshold (≥0.5) defined by the consensus level parameter (Sánchez-Tapia et al., 2017, 2020).

Tick records

Georeferenced occurrence records for the three tick species across the Brazilian territory (between 5°16'N–33°45'S and 73°59'E–34°47'W), covering a land area of approximately 8,455,508 km^2, were compiled from three main sources: (i) direct scientific collaborations, (ii) a review of specialized literature, and primarily (iii) specimen records from biological collections accessed via the Global Biodiversity Information Facility (GBIF, https://www.gbif.org/) spanning the period from 1990 to 2019. All geographic coordinates were standardized to the WGS84 datum.

In accordance with the taxonomic revision by Nava et al. (2014), which reclassified *Amblyomma cajennense* as a complex of six species including *A. sculptum*, we consolidated historical records of *A. cajennense* (pre-2014)—excluding those from the Amazon biome and its ecotones—with post-2014 records of *A. sculptum*. This unification was performed using the rbind function in the modleR package, treating them as a single taxonomic unit henceforth referred to as *A. sculptum*.

To improve data consistency and reduce sampling bias, duplicate records from GBIF were removed, resulting in 889 unique occurrences (*A. aureolatum* = 103; *A. ovale* = 134; *A. sculptum* = 652). During the initial step of the modleR pipeline (setup_sdmdata), the number of records included in the modeling process was further reduced via automated cleaning, which removed exact duplicates and spatially correlated occurrences. This resulted in a final set of 585 validated records (*A. aureolatum* = 55; *A. ovale* = 120; *A. sculptum* = 410).

Bioclimatic variables

We utilized bioclimatic variables derived from monthly temperature and precipitation data spanning 1970–2000, obtained from the WorldClim platform version 2.0 (https://www.worldclim.org/data/worldclim21.html), at a spatial resolution of 2.5 arc-minutes (~5 km^2) (Hijmans et al., 2005). From the original 19 variables, four (BIO_08, BIO_09, BIO_18, and BIO_19) were excluded due to their combined temperature-precipitation metrics, which have been shown to introduce spatial artifacts (Broennimann et al., 2011; Samy & Peterson, 2016; Samy et al., 2016).

In the initial stage of the modleR workflow, we implemented data partitioning, pseudo-absence generation, and correlation-based variable selection. During pixel sampling in the calibration area (using the sample_proportion parameter, ranging from 0 to 1), we computed a correlation matrix with the findCorrelation function from the caret package (Classification And REgression Training), retaining the largest possible subset of abiotic variables with pairwise correlations below 0.70 (Sánchez-Tapia et al., 2017, 2020). This process selected four biologically relevant predictors:

BIO_02 (Mean diurnal temperature range)

BIO_04 (Temperature seasonality)

BIO_05 (Maximum temperature of warmest month)

BIO_15 (Precipitation seasonality)

All of which have previously been shown to influence tick life cycles (Szabó et al., 2013).

To improve both model performance and computational efficiency, we implemented a two-step environmental data processing strategy: Occurrence Data Cleaning and Bioclimatic Variable Processing. For occurrence cleaning, we applied the clean_uni function (Sánchez-Tapia et al., 2017, 2020), which enforces a one-record-per-pixel rule, eliminating duplicate environmental values within the same raster cells. This step reduced spatial autocorrelation artifacts while maintaining ecological representativeness (Aiello-Lammens et al., 2015).

Subsequently, all bioclimatic layers were spatially constrained using the crop function (from the raster package), applying the territorial boundaries of Brazil as the analytical mask (Hijmans, 2014). This spatial filtering step reduced computational load and eliminated extraneous environmental noise from neighbouring regions.

Together, these methodological refinements—occurrence thinning and spatial masking—ensured analytical rigor and operational efficiency, aligning with best practices for large-scale modelling of vector distributions (Petríc et al., 2023).

Data validation

The climate suitability models for each tick species were validated using a two-tiered approach, assessing: (i) climatic coherence (temperature and humidity ranges) and (ii) ecological coherence (distribution within Brazilian biomes). This dual validation framework aligns with established methodologies in ixodid tick research (Barbieri et al., 2015; Bitencourth et al., 2016, 2021; Guglielmone et al., 2003; Nava et al., 2014; Oliveira et al., 2016; Pinter et al., 2004; Szabó et al., 2013), ensuring that model outputs are consistent with known physiological tolerances and biogeographical distributions.

Limitations

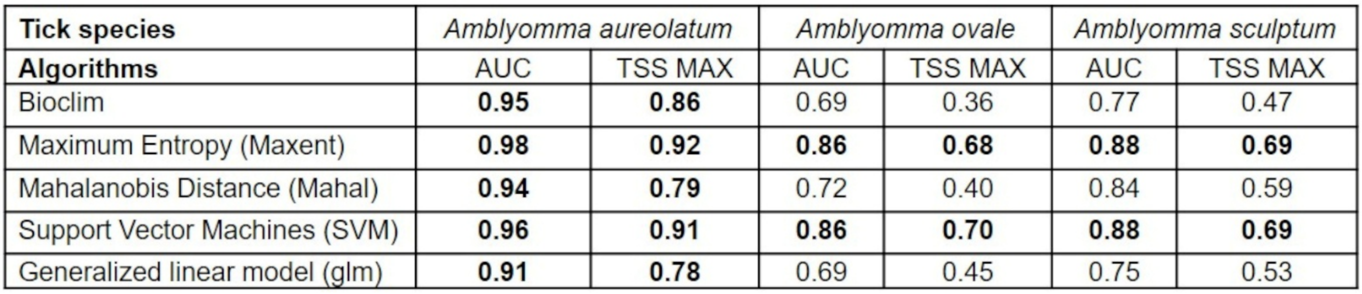
Due to the unavailability of independent occurrence data, external validation was not performed, which may limit the reliability of projections beyond the environmental conditions captured in the training dataset. This limitation is particularly relevant when extrapolating to non-analogous climates or under-sampled regions, where model performance cannot be independently assessed.

Suitability maps

The final consensus from our climate niche modelling produced three types of output per tick species: (i) continuous suitability maps illustrating potential distributions based on climatic affinities, with colour gradients indicating the elasticity of species–environment relationships (Sánchez-Tapia et al., 2017, 2020); (ii) uncertainty maps capturing model disagreement through maximum–minimum suitability intervals, where more intense colours highlight areas of greater algorithmic divergence (Samy et al., 2016); and (iii) binary maps derived by applying a probability cut-off threshold, delineating suitable (coloured) versus unsuitable (blank) habitats (Broennimann et al., 2011; Hijmans et al., 2005). All cartographic outputs were processed in QGIS-OSGeo4W 3.6.3-1 (QGIS Development Team, 2019), ensuring methodological alignment with current ecological modelling standards.

Results

Only the Maxent and SVM algorithms achieved acceptable predictive performance (AUC > 0.8 and TSS MAX > 0.6) across all three tick species and were therefore exclusively selected for the final suitability projections (see Table I).



Tick species	*Amblyomma aureolatum*		*Amblyomma ovale*		*Amblyomma sculptum*	
Algorithms	AUC	TSS MAX	AUC	TSS MAX	AUC	TSS MAX
Bioclim	**0.95**	**0.86**	0.69	0.36	0.77	0.47
Maximum Entropy (Maxent)	**0.98**	**0.92**	**0.86**	**0.68**	**0.88**	**0.69**
Mahalanobis Distance (Mahal)	**0.94**	**0.79**	0.72	0.40	0.84	0.59
Support Vector Machines (SVM)	**0.96**	**0.91**	**0.86**	**0.70**	**0.88**	**0.69**
Generalized linear model (glm)	**0.91**	**0.78**	0.69	0.45	0.75	0.53

TableI . Performance metrics (mean AUC and TSS MAX) of climate niche modelling algorithms and consensus models for the three epidemiologically important tick species in Brazil. Bold text indicates selected models meeting validation thresholds (AUC > 0.8, MAX > 0.6).

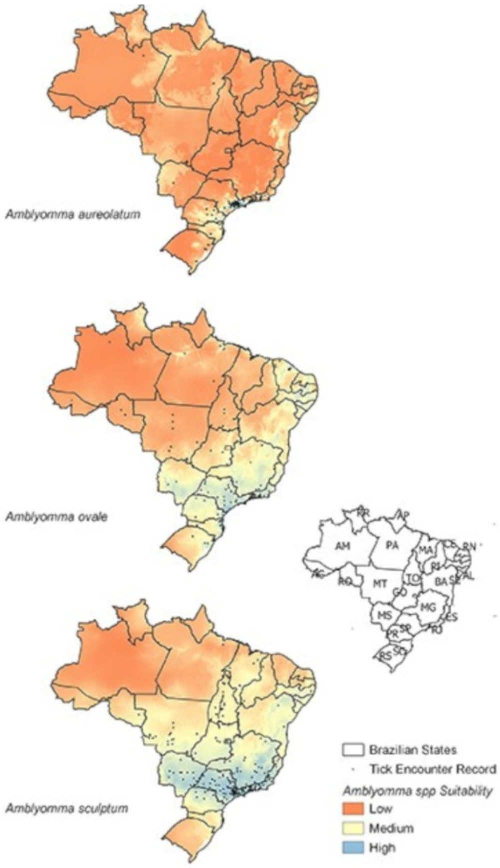


Figure 1 . Predicted climatic suitability distributions for three tick vectors of public health importance in Brazil: *Amblyomma aureolatum* , *A. ovale* , and *A. sculptum*. Suitability gradients reflect the probability of occurrence (0-1 scale) across Brazilian states.

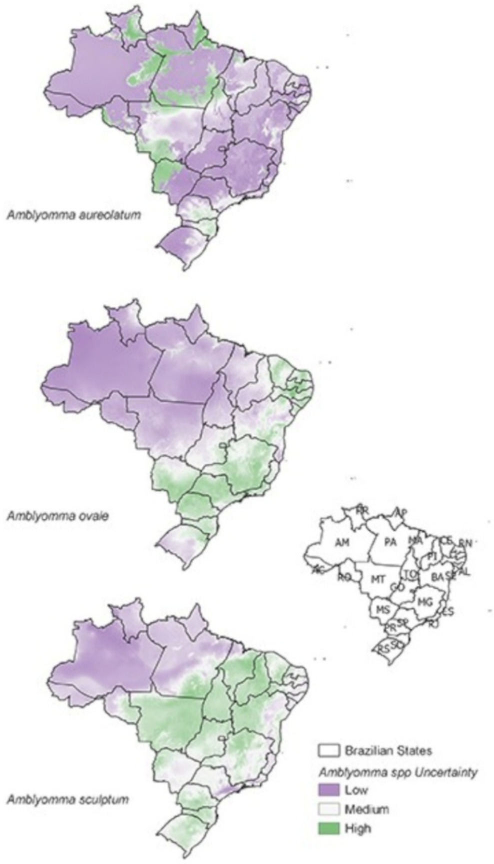


Figure 2 . Model uncertainty estimates for *Amblyomma aureolatum* , *A. ovale* , and *A. sculptum* distributions in Brazil, showing areas of highest algorithmic disagreement (maximum-minimum suitability intervals).

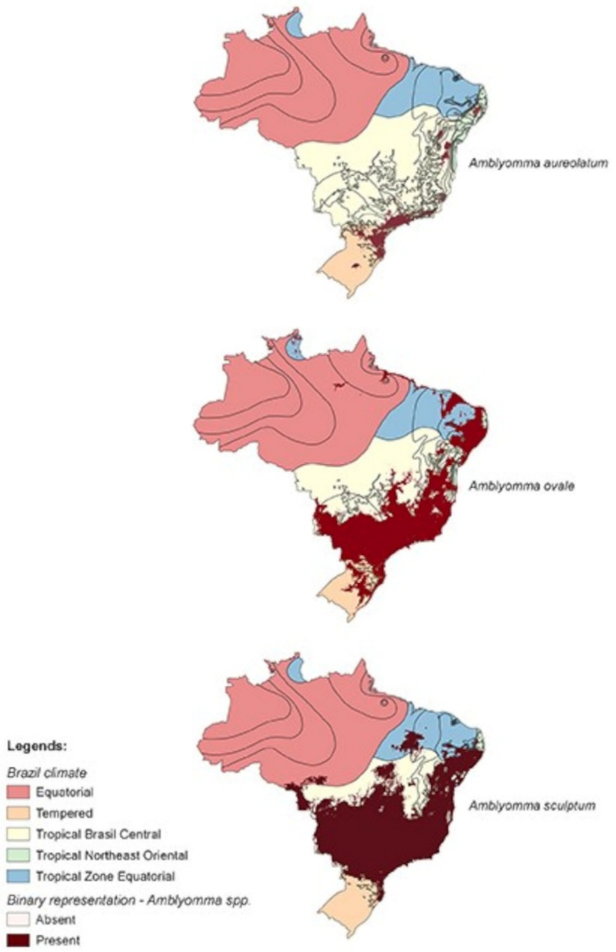


Figure 3 . Climatic coherence validation for *Amblyomma aureolatum* , *A. ovale* , and *A. sculptum* niche models, indicating regions where predicted distributions align with known bioclimatic tolerances.

Climate suitability models revealed distinct distribution patterns for each tick species and highlighted areas of uncertainty based on algorithmic disagreement (Figures 1 and 2). Validation of climate coherence further confirmed alignment between predicted distributions and known bioclimatic tolerances (Figure 3).

Amblyomma aureolatum exhibited high climatic suitability along the Atlantic coastal region of Brazil, particularly in the states of Santa Catarina, Paraná, São Paulo, and Rio de Janeiro (Figure 1). Model uncertainty was greatest in the Pantanal region of Mato Grosso and the Amazon biome (Figure 2).

For *A. ovale*, suitability was strongly associated with coastal areas from northern Santa Catarina to southern São Paulo, and extended inland to metropolitan São Paulo, the mountainous regions of Rio de Janeiro, the Zona da Mata in Minas Gerais, and the northern coast of Espírito Santo. Additional suitable areas included parts of the Cerrado (Mato Grosso do Sul and Goiás) and Caatinga biomes (Pernambuco, Paraíba, Rio Grande do Norte, and Ceará) (Figure 1). However, model uncertainty was generally higher across Brazil, except within portions of the Cerrado (Figures 2 and 3).

A. sculptum showed high climatic suitability in the plateaus of Paraná and São Paulo, the mountainous region of Rio de Janeiro, parts of Minas Gerais and Bahia, and the Cerrado regions of Mato Grosso and Mato Grosso do Sul (Figure 1). Areas of higher model uncertainty included the coastal regions of Rio de Janeiro, São Paulo, Bahia, and Sergipe, as well as portions of the Cerrado and Caatinga (Figures 2 and 3).

The climatic suitability models demonstrated strong ecological validity for all three epidemiologically important spotted fever vector species in Brazil, aligning with established bioclimatic tolerances reported in the literature. *Amblyomma sculptum* exhibited the broadest environmental adaptability, showing greater tolerance to seasonal variations in temperature and precipitation across Brazil’s spring-summer (September–March) and autumn-winter (March–September) cycles. This physiological plasticity translated into a considerably wider potential geographic distribution compared to the other two species. In contrast, *A. aureolatum* and *A. ovale* exhibited narrower distributions, predominantly associated with areas characterized by lower annual temperature and humidity fluctuations (Figure 3). These niche distinctions likely reflect species-specific microclimatic adaptations that influence their respective roles in the dynamics of spotted fever transmission.

Model outputs further supported ecological coherence by aligning closely with known biome associations. *A. sculptum* displayed a marked affinity for grassland ecosystems, particularly within the Cerrado biome, consistent with its documented habitat preferences. In contrast, *A. aureolatum* and *A. ovale* were strongly associated with forested environments, especially remnant Atlantic Forest fragments along Brazil's coastal regions (Figure 4). These biome-specific preferences mirror each species' physiological requirements and host-seeking behaviours as observed in field studies.

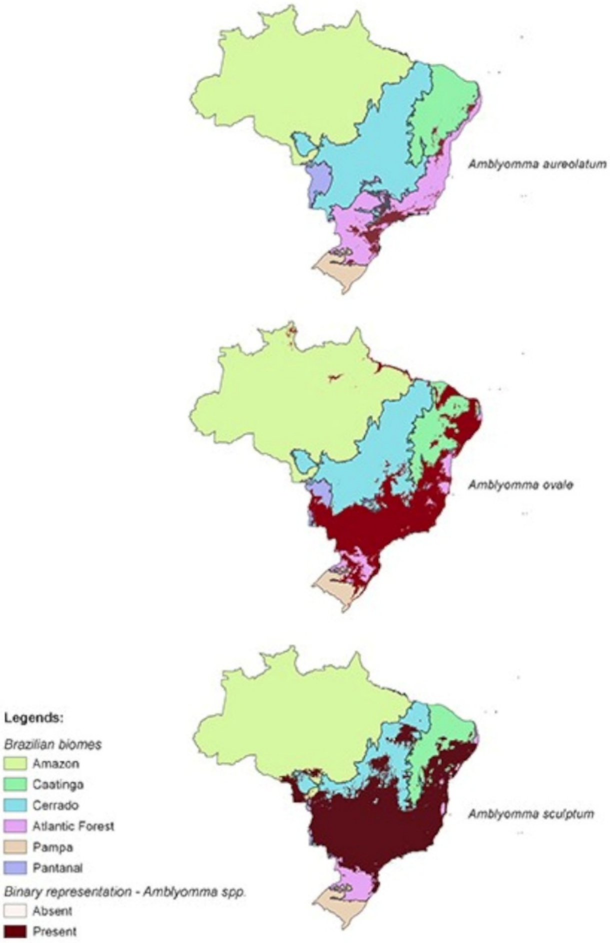


Figure 4 . Ecological niche validation of *Amblyomma aureolatum* , *A. ovale* , and *A. sculptum* across Brazilian biomes, showing species-specific associations with major vegetation types.

Discussion

Research on Brazil's rickettsiosis epidemiological profile has systematically advanced the understanding of ecological drivers in the disease's enzootic and epizootic cycles, providing a critical foundation for risk assessment across diverse spotted fever transmission scenarios (Durães et al., 2021; Montenegro et al., 2017). Although numerous studies (Bitencourth et al., 2016; Donalisio et al., 2020; Durães et al., 2021; Machado et al., 2018; Montenegro et al., 2017; Nasser et al., 2015; Oliveira et al., 2016, 2017a, 2017b; Szabó et al., 2013; Weck et al., 2016) have characterized the complexity of transmission, substantial knowledge gaps remain regarding the ecological determinants of vector-host-pathogen dynamics. Our modelling approach addresses these limitations by developing spatial tools to enhance surveillance capacity for rickettsial diseases across Brazil's heterogeneous landscapes.

Our climate suitability models revealed distinct distribution patterns among the three primary tick vectors of spotted fever in Brazil. *Amblyomma sculptum* and *A. ovale* demonstrated broader climatic suitability, while *A. aureolatum* exhibited more spatially restricted habitats. These results are consistent with existing literature on neotropical tick ecology (Bitencourth et al., 2021; Guglielmone et al., 2003; Nava et al., 2014), particularly regarding: (i) *A. sculptum*'s broad ecological plasticity across multiple biomes; (ii) *A. ovale*'s adaptability to both forested and ecotonal environments; and (iii) *A. aureolatum*'s dependence on narrower microclimatic conditions.

Among the three species, *A. aureolatum* displayed the most spatially restricted distribution, with occurrence strongly linked to remnants of the Atlantic Forest biome along Brazil's coastal mountain range. This biome has undergone severe deforestation and urbanization over the past five centuries (Joly et al., 2014; Marques & Grelle, 2021). Key ecological features characterizing *A. aureolatum*'s range include: (i) altitudes typically above 700 m a.s.l.; (ii) dense, closed-canopy forests with limited ground-level sunlight; (iii) mean annual temperatures below 23 °C; and (iv) consistently high relative humidity (Barbieri et al., 2015; Faccini et al., 2022). These bioclimatic thresholds help explain the fragmented presence of this tick in anthropogenically altered landscapes of the Atlantic Forest.

Climatic suitability for *A. aureolatum* aligns with medium-to-high elevation areas in Brazil—such as the Mar and Mantiqueira mountain ranges, the South Bahian Plateau, and the Diamantina Plateau (Barbieri et al., 2015). Its persistence is strongly influenced by the availability of hosts, particularly in well-preserved forest fragments (Barbieri et al., 2015; Bitencourth et al., 2021; Guglielmone et al., 2003). However, urban encroachment near forest edges has enabled domestic dogs (*Canis lupus familiaris*) to act as bridge hosts, introducing infected ticks into peri-urban areas (Ogrzewalska et al., 2012; Scinachi et al., 2017). This is especially concerning given *A. aureolatum*'s proven vector competence—adults infected with *R . rickettsii* can transmit the pathogen within 10 minutes of host attachment (Saraiva et al., 2014). These eco-epidemiological dynamics, exacerbated by biodiversity loss and increased human proximity to forest remnants, help explain the growing incidence of Brazilian spotted fever (BSF) (Oliveira et al., 2016; Pinter et al., 2004; Scinachi et al., 2017).

Amblyomma ovale exhibited the widest climatic suitability, covering nearly the entire Brazilian territory, corroborating previous findings (Barbieri et al., 2014, 2015; Bitencourth et al., 2016, 2021; Guglielmone et al., 2003; Moerbeck et al., 2016; Szabó et al., 2013). Phylogenetic analyses indicate two major clades corresponding to Brazil's major biomes—Cerrado/Caatinga and Atlantic Forest—with limited gene flow between populations (Bitencourth et al., 2016, 2021). *A. ovale* exhibits stage-specific host preferences: immatures feed primarily on small wild rodents, while adults parasitize free-ranging carnivores, especially domestic dogs in rural-urban interfaces (Guglielmone et al., 2003; Labruna et al., 2005; Sabatini et al., 2010; Szabó et al., 2010, 2012).

As with *A . aureolatum*, domestic dogs act as key bridge hosts, facilitating tick-human interactions and helping sustain infected tick populations in nature. In newly deforested or peripheral areas, dogs may act as invasive species—interacting with native wildlife and contributing to the decline of wild mammal populations. This shift promotes greater tick reliance on domestic hosts and enhances human exposure risk (Martins et al., 2016; Oliveira et al., 2017a, 2017b).

Amblyomma sculptum displayed the broadest climatic suitability across Brazil, in line with endemic areas reported in prior studies (Bitencourth et al., 2016; Paula et al., 2021). The known distribution of this species has been refined following the taxonomic revision of the *A. cajennense* complex, distinguishing *A. cajennense* (sensu stricto) in Amazonian regions from *A. sculptum* throughout much of the rest of Brazil (Nava et al., 2014). Although their ranges are distinct, these species coexist in transitional zones (Martins et al., 2016; Oliveira et al., 2017a, 2017b). *Amblyomma sculptum* shows high genetic diversity (Estrada-Peña et al., 2014; Nava et al., 2014) and is expanding in the Cerrado biome (Bitencourth et al., 2016), supported by its tolerance to Brazil's seasonal climatic variability (Durães et al., 2021; Labruna et al., 2002; Lemos et al., 1997; Oliveira et al., 2016).

Anthropogenic landscape changes have facilitated *A. sculptum*'s spread, including: (i) historical pasture expansion, (ii) loss of riparian forests, and (iii) increased host concentration (e.g., capybaras, small mammals) near human settlements. These alterations promote ideal conditions for zoonotic spill over (Luz et al., 2019; Martins et al., 2016; Sabatini et al., 2010; Szabó et al., 2009). The species' adaptability and success in human-modified environments make it a major public health concern.

Our models demonstrate strong congruence between predicted tick distributions and established ecological data (Donalisio et al., 2020; Guglielmone et al., 2006; Oliveira et al., 2016). *Amblyomma sculptum* exhibits preference for open habitats—sunlit pastures, riparian areas, and urban edges (e.g., parks, vacant lots)—reflecting its classification as a ruderal species (Barbieri et al., 2015; Bitencourth et al., 2021; Martins et al., 2016; Szabó et al., 2013). While initially associated with wild hosts such as tapirs (*Tapirus terrestris*) and capybaras (*Hydrochoerus hydrochaeris*), its adaptation to livestock and companion animals has firmly established it as a primary vector of *Rickettsia* spp. in human-modified landscapes (Guglielmone et al., 2006; Labruna et al., 2005; Labruna, 2009; Martins et al., 2016; Oliveira et al., 2016; Rodrigues et al., 2022; Szabó et al., 2013). In contrast, *A. aureolatum* and *A. ovale* maintain more specialized ecological requirements, with distinct altitudinal niches and dependencies on preserved forest ecosystems

(Barbieri et al., 2015; Bitencourth et al., 2021; Faccini et al., 2022; Guglielmone et al., 2003; Scinachi et al., 2017). Nevertheless, both species are increasingly affected by domestic dog-mediated dissemination of infected tick populations at forest-urban interfaces (Labruna et al., 2005; Sabatini et al., 2010; Szabó et al., 2010, 2012).

Conclusions

Our study demonstrates that the three primary tick vectors of spotted fever in Brazil exhibit considerable tolerance to thermal and precipitation gradients, resulting in broader potential distributions than previously recognized. This finding is supported by both ecological niche models and biological collection records. While climate suitability modelling alone cannot establish direct correlations with disease transmission dynamics, our results are consistent with growing evidence of elevated rickettsiosis risk—particularly in south-eastern Brazil. Importantly, we advocate for the systematic inclusion of uncertainty mapping in vector distribution studies and propose that scientific journals mandate such analyses to enhance the reliability of risk assessments.

In line with similar research efforts in Brazil, our findings offer practical insights to support tick-borne disease surveillance initiatives under the Unified Health System (SUS). We highlight that areas characterized by high model uncertainty in tick vector distribution should be prioritized by public health authorities. These uncertain zones may hypothetically correspond to ecotonal regions (e.g., Cerrado-Amazon transition zones) or landscapes undergoing rapid anthropogenic transformation, where conventional modelling approaches may inadequately capture habitat suitability for arthropod reservoirs. Notably, these regions often coincide with historically underreported areas for human spotted fever cases.

To mitigate this potential surveillance bias, we propose a tiered adaptive surveillance strategy based on model confidence levels:

(i) High suitability + Low uncertainty: maintain routine surveillance for spotted fever;

(ii) Medium suitability + High uncertainty: implement targeted sampling of vectors and hosts (e.g., ticks, capybaras, equines, domestic dogs) for PCR and serological testing; train primary healthcare personnel to recognize atypical symptoms; and conduct fine-scale environmental risk mapping at the municipal level;

(iii) Low suitability + High uncertainty: deploy community-based monitoring tools (e.g., participatory syndromic surveillance); establish referral protocols to tertiary centres with diagnostic capacity; and ensure logistical support for laboratory confirmation during suspected outbreak alerts.

This tiered framework aims to optimize resource allocation while addressing the limitations of current modelling approaches, particularly in frontier expansion zones and epidemiologically silent areas.

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Ethical approval

The models presented in this study were developed using exclusively publicly available scientific data and biological collection records obtained from open-access repositories. As no human or animal subjects were involved, ethical review board approval was not required for this research.

Conflicts of interest

The authors declare that there are no conflicts of interest.

Author Contributions

Conceptualization: CMR; Methodology: CMR; Formal analysis: DSM, GSG and SVO; Investigation: CMR, GSG and SVO; Writing original draft preparation: CMR; Writing, review, and editing: CMR, ACD and LG; Visualization: CMR and DSM; Supervision: LG; Project administration: CMR and LG; Funding acquisition: ACD and LG. All authors have read and agreed to the published version of the manuscript.

Data availability

The data associated with the findings of this study, including tick specimen records and the climate models supporting these findings, are openly accessible through the Global Biodiversity Information System (GBIF) at https://www.gbif.org/ and the WorldClim platform at https://www.worldclim.org/data/worldclim21.html, respectively. Additionally, data pertaining to biomes and climatic ranges within the Brazilian territory can be obtained from the Brazilian Institute of Geography and Statistics (IBGE) via their official website at https://www.ibge.gov.br/geociencias/downloads-geociencias.html. Furthermore, the statistical metrics used to select among the various algorithm scripts for running the climate models in ModleR are provided in the Supplementary Material accompanying this article.

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