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GEOGRAPHIC RISK DISTRIBUTION MAPPING OF TICK-BORNE DISEASES IN CAMEROON

CARTOGRAPHIE DE LA DISTRIBUTION GEOGRAPHIQUE DES RISQUES DE MALADIES TRANSMISES PAR LES TIQUES AU CAMEROUN

Reni Bibriven **LILA**

ABSTRACT

Tick-borne diseases pose a significant health threat to humans and animals in Cameroon. This country is home to various tick species capable of transmitting diseases such as African swine fever, Anaplasmosis, Lyme disease and Congo-Crimean Hemorrhagic fever. Climate, habitat, tick geographic distribution, host availability, and human behavior impact Tick-borne disease dynamics. Despite research advancements, gaps remain in identifying ecological tick habitats and mapping environmental risk distribution, particularly in remote areas of third world countries. This study examined environmental and ecological factors influencing tick populations, environmental niche suitability and

disease transmission. The methodology used is based on an advanced species distribution entropy modeling approach to analyze and visualize tick-borne disease geographic risk distribution in Cameroon's North-West, West, Adamawa, and Northern Regions. The results reveal Environmental preferences of tick-borne disease vectors, Geographic distribution of disease risk and high-risk areas for targeted surveillance and control.

Keywords : Ticks, diseases, Niche, Distribution, Cameroon.

RÉSUMÉ

Les maladies transmises par les tiques (MTT) constituent une menace sanitaire importante pour les humains et les animaux au Cameroun. Ce pays abrite diverses espèces de tiques capables de transmettre des maladies telles que la peste porcine africaine, l'anaplasmoze, la maladie de Lyme et la

fièvre hémorragique Congo-Crimée. Le climat, l'habitat, la répartition géographique des tiques, la disponibilité des hôtes et le comportement humain ont un impact sur la dynamique des maladies transmises par les tiques. Malgré les avancées de la recherche, des lacunes subsistent dans l'identification

des habitats écologiques des tiques et la cartographie de la répartition des risques environnementaux, en particulier dans les zones reculées des pays du tiers monde. Cette étude a examiné les facteurs environnementaux et écologiques influençant les populations de tiques, l'adéquation des niches environnementales et la transmission des maladies. La méthodologie utilisée est basée sur une approche avancée de modélisation de l'entropie de la distribution des espèces pour analyser et visualiser la distribution géographique des risques de maladies transmises par les tiques dans les régions du Nord-

Ouest, de l'Ouest, de l'Adamawa et du Nord du Cameroun. Les résultats révèlent les préférences environnementales des vecteurs de maladies transmises par les tiques, la répartition géographique du risque de maladie et les zones à haut risque pour une surveillance et un contrôle ciblés.

Mots-clés : Tiques, maladies, Niche-Distribution, Cameroun.

INTRODUCTION

Tick-borne infections are widespread viral zoonosis of medical importance, posing a significant health threat globally (Spengler et al., 2019: 70). Despite this, tick-borne diseases are not always prioritized in disease surveillance and control campaigns in Sub-Saharan Africa.

The increasing spread of tick-borne diseases, including their ability to emerge or re-emerge in new areas, is a public health issue due to the infectious potential of viral vectors and the severity of infections like Crimean-Congo hemorrhagic fever, which has limited treatment options (Tipih et al., 2020:137).

Changes in environmental and climatic variables alter the distribution of tick-borne infection vectors, highlighting the influence of ecological niche favorability on host and vector dynamics (Estrada-Peña et al., 2015:1; Gale et al., 2010: 1859). Limited livestock disease surveillance at African borders allows the importation of tick-infected livestock and viral pathogens into neighboring countries (Motta et al., 2017: 14). The discovery of *Rhipicephalus* (*Boophilus*) *Microplus* in Cameroon is concerning, as it is a vector of *Babesia bovis*, a severe cattle tick-transmitted disease (Awa et al., 2015: 117; Silatsa et al., 2019: 10).

In Cameroon, 53 Ixodid hard tick species have been identified, with most research focusing on ticks that transmit infections to livestock, domestic animals, and humans (Ragenau 1951: 441). Tick-borne zoonotic infections pose a significant threat to

livestock production and human health (Jongejan 2004:3).

Research in Cameroon has evolved to assess environmental factors favoring tick infections, considering climate change and viral vector adaptability (Ngnindji-Youdje et al., 2022: 82; Abanda et al., 2019: 1). However, gaps exist in research coverage, with most studies concentrated on principal livestock rearing areas and urban areas, leaving large parts of the country unstudied and increasing vulnerability (Silatsa et al., 2019: 1).

This research aims to address gaps in tick-borne infection vulnerability studies by assessing distribution and analyzing environmental factors in four regions of Cameroon. Changes in environmental stability and bio-ecology disrupt disease patterns and vector behavior, expanding zoonotic viral vector niches (Mild et al., 2010: 199). Climate change influences migratory birds carrying immature tick vectors, expanding vector distribution. Four key factors contribute to Tick-borne disease spread and Ixodid tick populations: climate, land cover dynamics, animal hosts, and movement (Arrontes 2005: 57).

In livestock rearing areas, incident outpatient report data aids in understanding and managing tick-borne infections, identifying hotspots and vulnerable populations (Mark 2017: 68). Surveillance in human and vector populations helps monitor outbreak likelihood and identify hotspots.

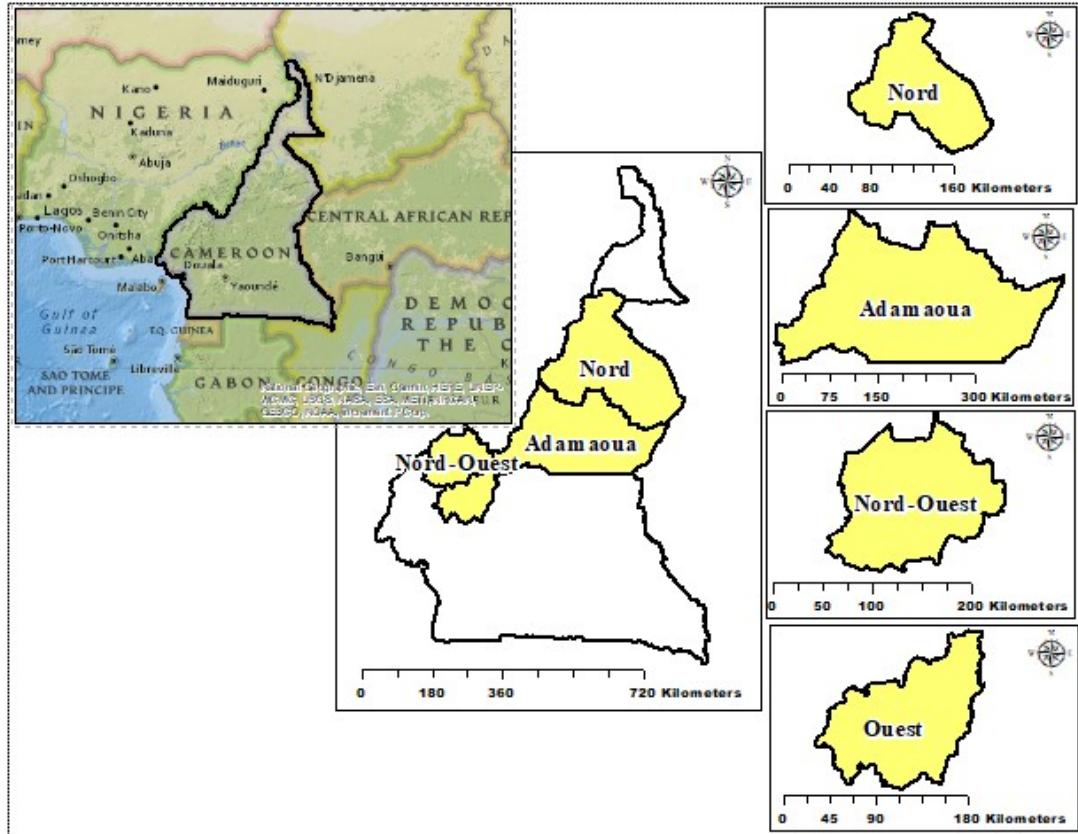
This research uses Maxent entropy modeling to assess environmental risk vulnerability associated with tick-borne infections in Cameroon.

1. STUDY AREA

Cameroon, located in Equatorial West Africa, spans 475,440 km², see (Fig. 1) and is known as “Africa in miniature” due to its diverse ecosystems, including mountains, deserts, rainforests, and coastlands. It lies between latitudes 2° and 12° North and longitudes 8° and 16° East, with five agro-ecological zones characterized by distinct climates and vegetation, ranging from arid savannas in the north to equatorial rainforests in the south (Kelly, RF., 2021: 781). Administratively, the country is divided into 10 regions see (Fig. 1) below, further subdivided into divisions and sub-divisions. Cameroon borders six countries and has a Gulf of Guinea coastline. Its climate features wet (May–October) and dry (November–April) seasons, with varying rainfall and temperatures. Major cattle production regions include the Northwest, Adamawa, West, and Far North, which collectively face significant risks from tick-borne

diseases. Cattle rearing is vital to these regions' economies, with the North-West Region and Vina Division alone reporting cattle populations of 546,508 and 176,257, respectively, in 2013 (Ngalim et al., 2015: 175; Motta et al., 2018: 1). Herd sizes range from 50 to 150 cattle, often grazed on communal pastures. Transhumance, a seasonal migration of livestock, is common during the dry season. This combination of geography, climate, and pastoral practices supports a variety of Ixodid tick species, posing challenges to livestock productivity and farmer livelihoods. Effective tick control and disease surveillance are essential for protecting human health, cattle, and local economies. Approximately 60% of the North-West Region is suited for livestock production, reinforcing agriculture's economic significance in rural Cameroon (Ngalim et al., 2015: 175).

Fig. 1: Map of Cameroon illustrating all Four Regions of Interest



2. METHODOLOGY

Tick-borne infections primarily persist in enzootic cycles, requiring specific host-vector interactions, such as animal-tick relationships, with humans serving as accidental hosts (Hoogstraal, 1979: 307). While human infections are rare, individuals in close contact with livestock, such as those in slaughterhouses, face higher exposure to tick bites or infected blood. Clinical manifestations of human tick-borne diseases are depicted in (Fig. 2) below. Human-to-human transmission can occur

through contact with bodily fluids of infected individuals, particularly affecting family members and healthcare workers. Certain diseases, like Crimean-Congo hemorrhagic fever virus, lack a cure or vaccine for humans. Current treatment relies on supportive care. Preventive measures include livestock vaccination, pesticide use, and wearing protective equipment when near livestock or infected individuals (Messina et al., 2015: 503; Mark, 2017: 68).

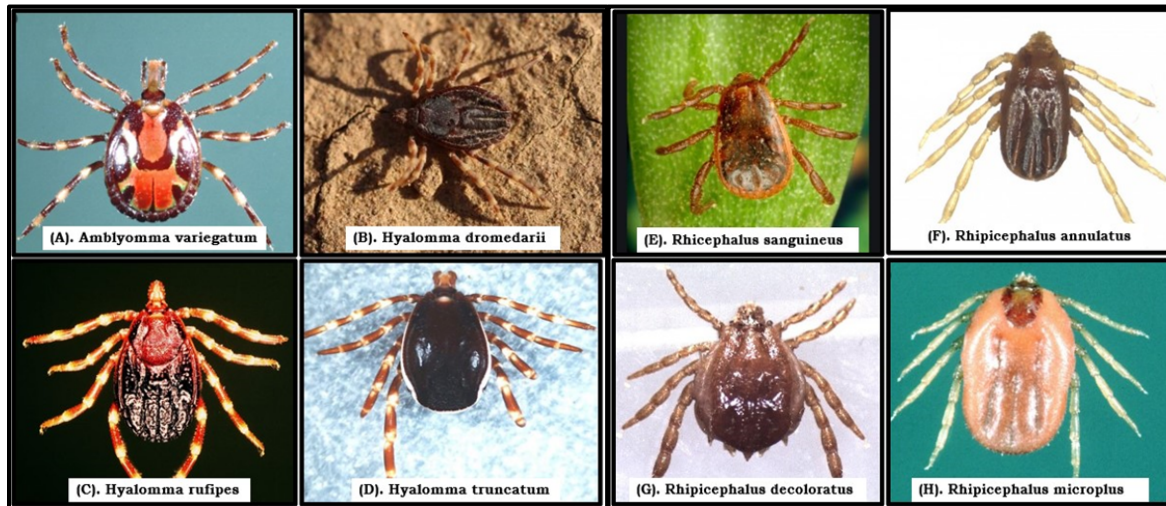
Fig. 2: Illustrates Clinical Signs and Symptoms of Some Tick-borne Infections



Many tick-borne diseases have been identified in hard ticks of the Ixodidae classification such as; Amblyomma, Hyalomma, Rhipicephalus and

Dermacentor, see (Fig. 3a-h). These ticks turn to act as reservoirs and carriers of tick related infections (Gargili et al., 2017:93, Spengler et al., 2016: 31).

Fig. 3: Tick-borne Disease Vectors of the Amblyomma, Hyalomma, Rhipicephalus and Dermacentor Ixodidae classification and Family).



Source: World Health Organization (WHO) Report, 2022.

2.1. Data

2.1.1. Inventory Tick-borne Disease Vector Data and Sample Collection Locations

Tick vectors are adaptable organisms that thrive in various ecological niches globally. To conduct comprehensive research on tick populations, data must be collected from diverse environments, including urban livestock farms (e.g., Ngaoundere, Garoua, Bamenda) and remote areas

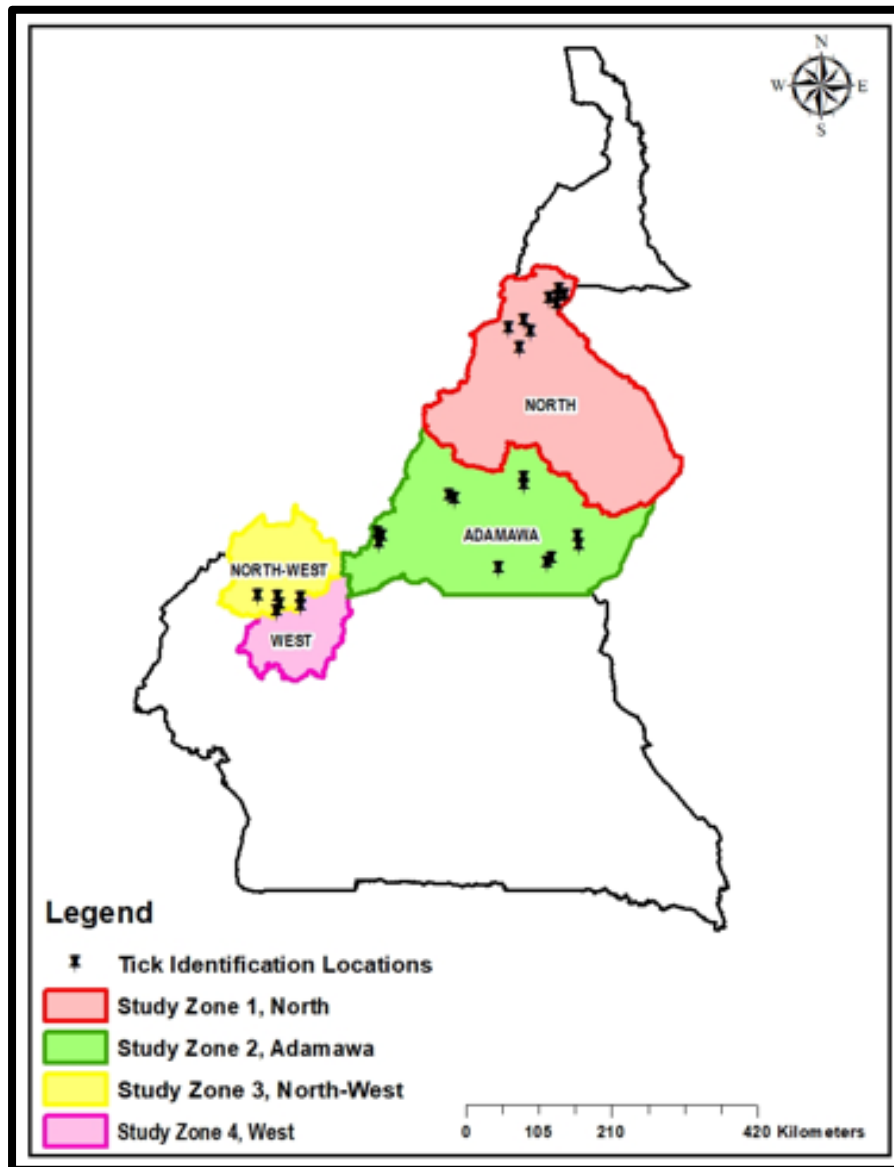
(e.g., Mayo Sava, Adamawa plateau, Benoué National Park). However, logistical and financial constraints require strategic site selection to ensure cost efficiency and accurate data collection. The criteria considered for the selection of tick sample collection site for this study included:

1. Geographical Location: Ticks have specific habitats; therefore, locations must be representative of where ticks are likely to be found (Ngangngang et al., 2021: 82).
2. Host Availability: Ticks require hosts to feed on, making livestock farms preferable for sample collection (Ngangngang et al., 2021: 82).
3. Tick Abundance: Environmental suitability affects tick populations; thus, sites with favorable niches should be prioritized to ensure sufficient sample sizes (Ngangngang et al., 2021: 82).

A sum of 27 tick sample locations (livestock farms) were identified within the study areas, and their respective latitude and longitude recorded. The tick

Sample collection used the “Removal from host” method, employing fine tweezers as recommended in the literature (Kaufman et al., 1980:102) see (Fig. 4)

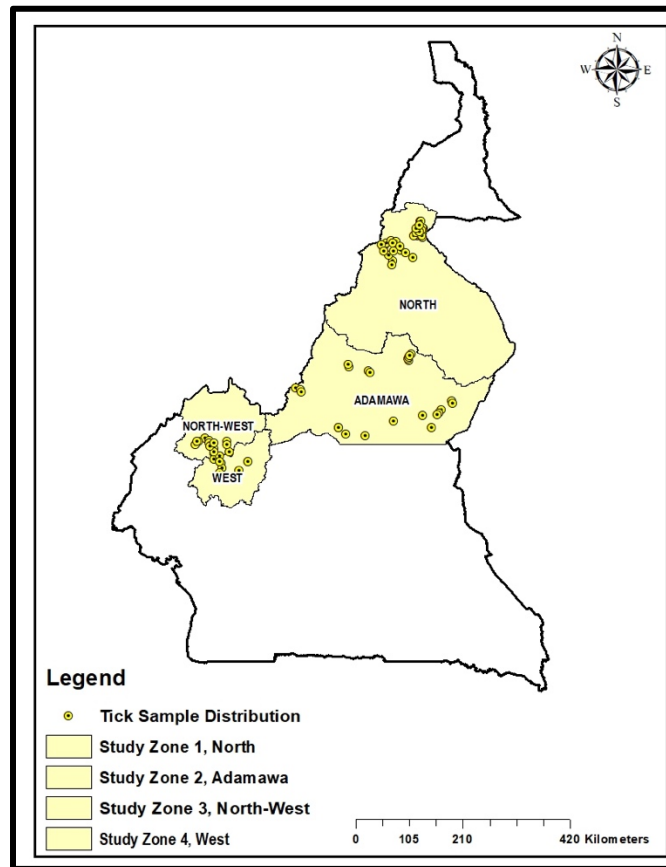
Fig. 4: Tick Vector Sample Collection Locations (Livestock Farms)



A database of 93 tick vector species was compiled, including latitude and longitude coordinates recorded via a global positioning system for precise identification, see (Fig. 5) below. The identified species included *Amblyomma variegatum*, *Hyalomma dromedarii*, *Hyalomma rufipes*, *Hyalomma truncatum*, *Rhipicephalus sanguineus*, *Rhipicephalus annulatus*, *Rhipicephalus decoloratus*, and *Rhipicephalus microplus*. These tick samples were evenly distributed across the four areas of

interest for the research. The collected tick vector data was validated against peer-reviewed literature (e.g., Silatsa et al., 2019: 1) and reputable databases, such as GenBank and the Global Biodiversity Information Facility (GBIF; www.gbif.org). Additionally, the manual search guide outlined in Messina et al. (2015: 503) was used to cross-reference tick presence and sample site data, ensuring accuracy and reliability.

Fig. 5: Spatial Distribution of Tick Vector Samples within Areas of Interest



2.1.2. Biotic and Abiotic Environmental Data Layers

This study employed GIS tools to analyze the geographic and environmental characteristics of the four areas of interest, calibrating its model with abiotic and biotic variables. Abiotic variables included climate data, topographic datasets, land-use and land-cover, normalized vegetation index, and enhanced vegetation index, as summarized in **(Tab. 1)** below. Biotic variables encompassed livestock spatial distribution, population distribution, and density in **(Tab. 2)** below. The integration of these factors enabled the modeling of tick vector spatial distribution in the areas of interest. Climate data calibration used interpolated bio-climatic variables from WorldClim, covering annual means, seasonality, and extreme conditions (Mark, 2017: 68). Advanced smoothing analysis generated continuous climate rasters with a 1km² spatial resolution. Normalized vegetation index, and enhanced vegetation index data, sourced from the Copernicus Global Land Service archive (2012–2018),

provided insights into soil wetness, a critical factor for Ixodid tick habitats (Randolph, 2000: 217). Land-use data from the Global Land Cover 2000 Project categorized habitats into five groups: dry savannas, croplands, deciduous forests, evergreen forests, and forest/savanna mosaics. A Maximum Likelihood Classification approach was used to analyze Land use land cover data at 1km² resolution, converting land cover classes into raster layers for enhanced model precision. Topographic variables, including slope, aspect, and elevation, derived from a high-resolution DEM, were equally used to further enriched the model. Comprehensive livestock density and distribution data, including cattle, goats, and pigs, were integrated from the Food and agriculture organization databases (accessed Feb 7, 2024) at a 1km² resolution, adding depth to the biotic analysis. These detailed datasets and classifications supported the development of a robust model for understanding the ecological environments favoring tick vector habitats

Tabl. 1: Abiotic Variables (Topographic, Land cover coverage and Bioclim Covariates)

Variables	Data Resolution
Slope	(1km)
Aspect	(1km)
Elevation	(1km)
Terrain Curvature	(1km)
Terrain Roughness	(1km)
LULC Natural	(1km)
LULC Artificial	(1km)
NDVI Averages	(1km)
SWI	(1km)
EVI	(1km)
BIO1 = annual mean temperature ©	30 arc-seconds, (1km)
BIO2 = mean diurnal range (mean monthly (max temp – min temp) ©.	30 arc-seconds, (1km)
BIO3 = Isothermally (BIO2/BIO7) (_ 100) (_ C)	30 arc-seconds, (1km)
BIO4 = temperature seasonality (standard deviation _ 100) (_ C)	30 arc-seconds, (1km)
BIO5 = maximum temperature of warmest month (_ C)	30 arc-seconds, (1km)
BIO6 = minimum temperature of coldest month (_ C)	30 arc-seconds, (1km)
BIO7 = temperature annual range (BIO5 – BIO6) (_ C)	30 arc-seconds, (1km)
BIO8 = mean temperature of wettest quarter (_ C)	30 arc-seconds, (1km)
BIO9 = mean temperature of driest quarter (_ C)	30 arc-seconds, (1km)
BIO10 = mean temperature of warmest quarter (_ C)	30 arc-seconds, (1km)
BIO11 = mean temperature of coldest quarter (_ C)	30 arc-seconds, (1km)
BIO12 = annual precipitation (mm)	30 arc-seconds, (1km)
BIO13 = precipitation of wettest month (mm)	30 arc-seconds, (1km)
BIO14 = precipitation of driest month (mm)	30 arc-seconds, (1km)
BIO15 = precipitation seasonality (coefficient of variation) (mm)	30 arc-seconds, (1km)
BIO16 = precipitation of wettest quarter (mm)	30 arc-seconds, (1km)
BIO17 = precipitation of driest quarter (mm)	30 arc-seconds, (1km)
BIO18 = precipitation of warmest quarter (mm)	30 arc-seconds, (1km)
BIO19 = precipitation of coldest quarter (mm)	30 arc-seconds, (1 km)

WorldClim (1960-2000) and SRTM (shuttle Radar Topographic Mission)

Tabl. 2: Biotic Variables (Livestock and Population Density/Distribution Covariates)

Variables	Data Resolution
Population Density	(1km)
Population Distribution	(1km)
Goat	(1km)
Cattle	(1km)
Horse	(1km)
Pig	(1km)
Sheep	(1km)

GLCN (Global Land Cover Network (2014))

The biotic and abiotic environmental layers mentioned above were all pre-treated for consistency issues and transformed into ArcGIS raster layers with the same projections and pixel resolutions. In order to ensure that all of the raster layers aligned within a GIS environment to execute an ecological niche factor analysis using the highly sophisticated ecological species maximum entropy distribution algorithm “Maxent,” every single raster layer was then projected into the exact same coordinated system, WGS_1984_UTM_Zone_32N. (Jaynes 1957: 620; Mark 2017: 68; Phillips & Dudik 2008: 161).

2.2. SPECIES ENVIRONMENTAL DISTRIBUTION MODELING APPROACHES

Over the years, multiple techniques have been used for species distribution modeling, each addressing different analytical aspects of spatial factors influencing species locations. Methods like the Similarity Domain approach predict environmental suitability based on proximity to environmental spaces of the species under study. Species presence and background data techniques, akin to linear regression models, randomly select absence data from background pixels within the area of interest (Ferrier et al., 2003). Other methods, such as the Genetic Algorithm, generate binary predictions based on factor significance (Stockwell & Peters, 1999: 143).

BIOCLIM, introduced by Busby (1986: 1) and Nix (1986: 4), predicts environmental suitability by defining bioclimatic spaces favorable for species. Later, the Niche Suitability Environmental Factor Analysis transformed environmental spaces into favorable or unfavorable zones using species presence data and environmental suitability distribution (Hirzel et al., 2002: 2027).

This study integrates biotic and abiotic (Bioclim) data into the Maxent entropy algorithm (Jaynes, 1957), identifying tick vector ecological niche suitabilities as well as tick-borne disease hotspots. Maxent species entropy analysis, uses constraints and high entropy to

$$H(X) = -\sum P_i \log P_i \dots \dots \dots \text{Equation (1)}$$

Where, for a random variable X with different potential result, $N_1, N_2, N_3... N_x$ the presence probabilities are P_1, P_2, \dots, P_x , respectively (Yi et al., 2016: 260).

evaluate factor importance, converting environmental spaces into orthogonal favorable and unfavorable zones. While this study does not include comparative analysis with other models, this species entropy analysis was very effective in the identification of niche suitability for tick vectors in the areas of interest.

2.2.1. Maxent Entropy Ecological Niche Modeling

Geo-visualization of tick-borne disease hotspots was modeled using Maxent Species Distribution Entropy Software, (Phillips et al., 2006: 231). This tool predicts potential tick presence over large areas by analyzing environmental niche favorability with limited presence data. Favorability niches, where species thrive and expand without environmental constraints, were identified through variance analysis and extrapolation into unexplored geographic spaces. This method enables the prediction of suitability zones for tick vectors, highlighting potential disease hotspots. Such insights guide targeted surveillance and control programs in under-researched areas.

The Tick-borne disease hot spot distribution was modeled using Maxent species distribution entropy algorithm proposed in 1957 by Jaynes (Jaynes 1957: 620). Core to the objective of Maxent is predicting the distribution of species in unknown geographic space by using presence and background data. Maxent is particularly well-suited for modeling species distribution in areas with limited data, such as tick-borne disease vectors in under-studied regions. Also, This algorithm uses known information such as (tick vector presence data) to identify and extract the closest entropy distribution on an unknown distribution surface to that of the actual tick presence locations while at the same time being constraint by accompanying biotic and abiotic covariates (Phillips 2006: 231; Phillips et al., 2004: 655 & Mark 2017: 68). The Maxent species distribution entropy model algorithm can be expressed mathematically as follow;

Ninety-three tick vectors from 27 livestock farms were sampled and used for this analysis. Biotic and abiotic covariates were standardized into the same coordinate system and file format before being analyzed using the Maxent species distribution entropy algorithm. To optimize model accuracy, test filtration operations were conducted to identify and remove less impactful covariates, preventing dilution of results and improving predictive capability (Graham, 2003: 2809).

The initial algorithm test run highlighted biotic and abiotic covariates with insufficient contributions to predicting environmental niche favorability for tick-borne vectors. These variables were subsequently excluded from the model to enhance its accuracy and reliability

2.2.2. Model Calibration and Implementation

A randomization subset tool allocated 70% of tick vector presence data for model calibration and 30% for testing predictive accuracy. The data was projected onto potential endemic zones across the four study areas to analyze ecological niche favorability and disease potential hotspot distribution. Predictor variables, including abiotic and biotic covariates, were processed using a

regularization entropy algorithm to identify key influencing factors or covariates.

The Cross-validation tool was used to optimize model calibration by maximizing data utilization and addressing coordinate errors. To ensure robust results, ten replicate runs with random seeding were performed on the training data, while 10,000 background points were evenly distributed across the study areas to reduce collinearity errors. Threshold and regularization values were selected based on a series of set of rules as shown in (Tab. 3) below and multiple iterations conducted to ensure total coverage. Probabilistic estimation logistic algorithms for predictability were employed to ensure every pixel within the study area was encoded with prediction values of **0 (unsuitable)** and **1 (suitable)**.

The Jacknife permutations were used to identify abiotic and biotic covariates importance and relative contribution to the final model predictive capability. On completion of Jackknife analysis, three models were generated, first (without variables), second (with only one variable) and thirdly (with all variables).The Final model output, visualized the predicted geospatial distribution (probability) of possible tick-borne disease hot spots across the areas of interest as well as the environmental niche favorability across the four areas of study.

Tabl. 3: Executed Maxent Analysis Settings

Maxent Options	Optimization	Selected Setting	Maxent Optimization Options	Selected Setting
Produce Curves	Response	Yes	Write Plot data	Yes
Execute Jackknife		Yes	Extrapolate	Yes
Output format		Cloglog	Write plots	Yes
Random Seed		Yes	Maximum Iterations	1000
Remove Records	Duplicate	Yes	Convergence threshold	0.00001
Random test %		25	Default prevalence	/
Regularization Multiplier		1	Maxent Test Rule	Maximum test Sensitivity and Specificity
Maximum background points replicates		10,000	Add samples to back ground	Yes
Replicate test Execution form		Bootstrap	/	/

(Source: Lila Reni Bibriven 2024)

The Maxent species distribution entropy model generated a raster map where pixels encoded as (1) indicate favorable areas and (0) unfavorable areas, based on how well abiotic and biotic covariates matched the original tick vector presence data. The model performance was subsequently evaluated using the Area under the Curve of the Receiver Operating Characteristics (Van et al., 1998: 88). The Area under the Curve assessed the model's ability to predict tick vector presence within randomly selected geographic grid units by analyzing true positive and true negative rates. The resulting Receiver Operating Characteristics plot indicated model fitness, with values below 0.5 suggesting random performance and values close to or above

0.5 indicating strong predictive accuracy (Hijmans et al., 2005: 1965; Lachiche, 2009: 1675).

3. RESULTS

A spatial model of tick-borne disease hotspots was developed for the four areas of interest using environmental niche favorability data from 93 tick vectors. The model predicted areas with a high likelihood of disease prevalence by isolating ecological niche suitability for tick vectors. Maxent entropy analysis, after replicate runs, identified the contributions of the abiotic and biotic factors or covariate, as shown in the table of percentage contributions and permutation importance in (Tab. 4) below.

Tabl. 4. Analysis of Biotic and Biotic Variable Contributions to the Model Computation.

Variables	Percentage Contribution	Permutation Importance
precipitation of the wettest quarter	20%	7%
Precipitation of the warmest quarter	18%	6.6%
Isothermality	16.8%	23%
Min temperature of coldest month	10%	3.4%
temperature seasonality	9%	17%
precipitation of the coldest quarter	8.8%	6.3%
annual mean temperature	6.3%	0.3%
Goat population	6.2%	4.3%
Horse	5%	1.2%
Temperature annual range	4.6%	4.6%
population density	4.5%	2%
Cattle population	4.3%	9.7%
Lulc	3.3%	1.5%
Pig population	1.2%	0.2%
Slope	1.2%	0.8%
Sheep population	0.6%	1.4%

The maxent entropy model isolated crucial factors or covariates and their respective contributions to the overall model's ecological niche suitability prediction. The model computation produced the following contribution percentages; precipitation of the wettest quarter (20%), Precipitation of the warmest quarter (18%), Isothermality (16.8%), Min temperature of coldest month (10%), temperature seasonality (9%), precipitation of the coldest quarter

(8.8%), annual mean temperature (6.3%), Goat population (6.2%), Horse population (5%), Temperature annual range (4.6%), population density (4.5%), Cattle population (4.3%), Lulc (3.3%), Pig population (1.2%), Slope (1.2%) and Sheep population (0.6%).

Single covariate model replicate reruns were conducted on key environmental covariates, including bioclimate, livestock density, and

population density, to assess probabilistic risk distribution. After 10 replicate runs per variable, thematic maps illustrating environmental niche favorability and risk distribution were generated see (Fig. 6, Fig. 7, and Fig. 8) below. The calculated mean Area under the Curve of the Receiver-operating curve

plot for each environmental covariate was high at 0.838 (test Area under the Curve = 0.838, Area under the Curve standard deviation = 0.016), 0.804 (test Area under the Curve = 0.804, AUC standard deviation = 0.023) and 0.784 (test Area under the Curve = 0.784) respectively.

Fig. 6 : BioClimate Niche Favorability

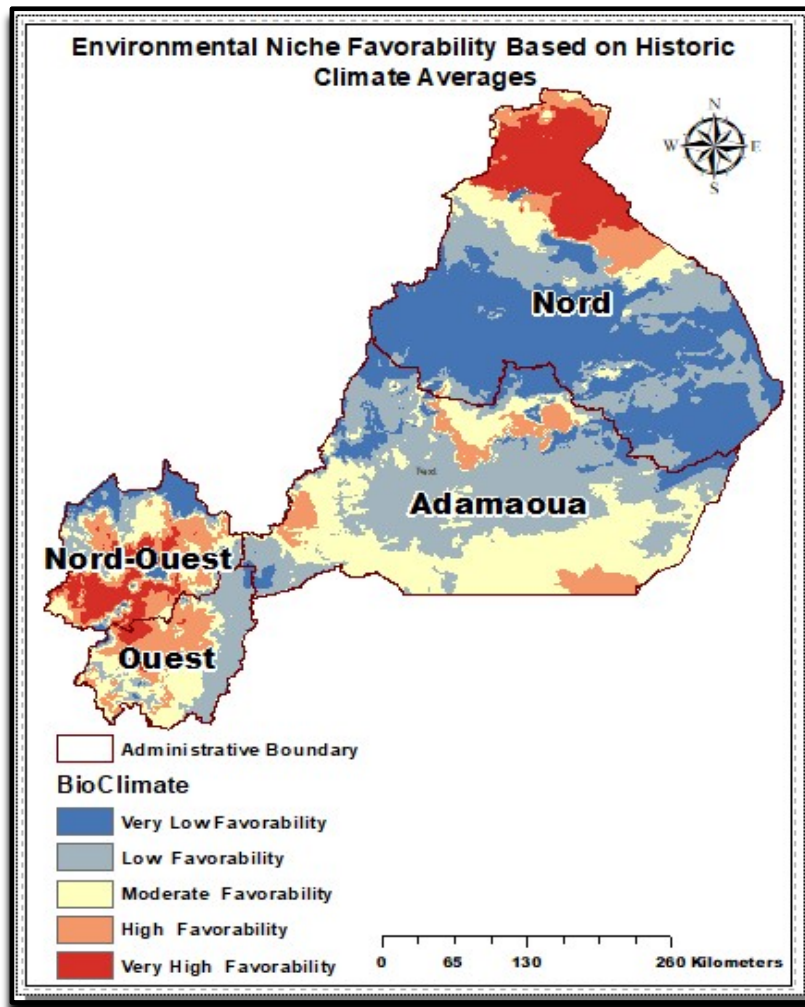


Fig. 7: Livestock Density Niche Favorability

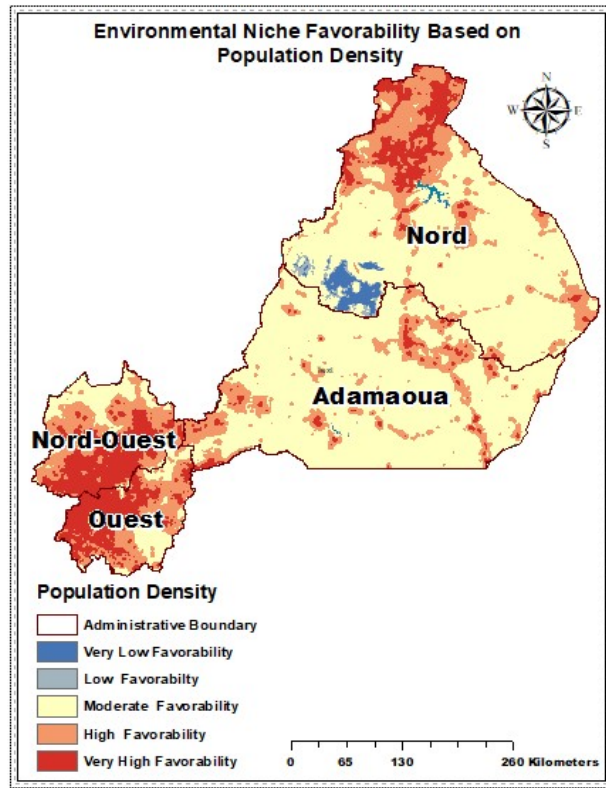
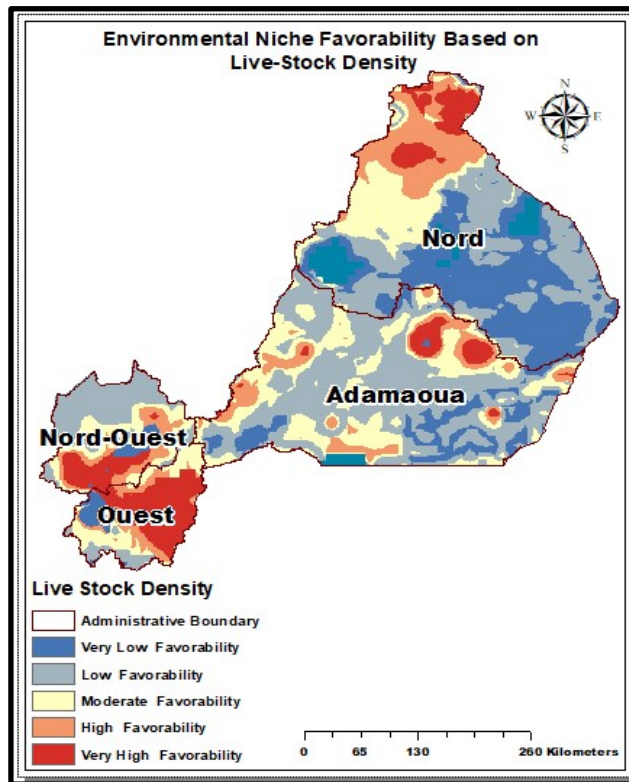


Fig. 8: Population Density Niche Favorability.

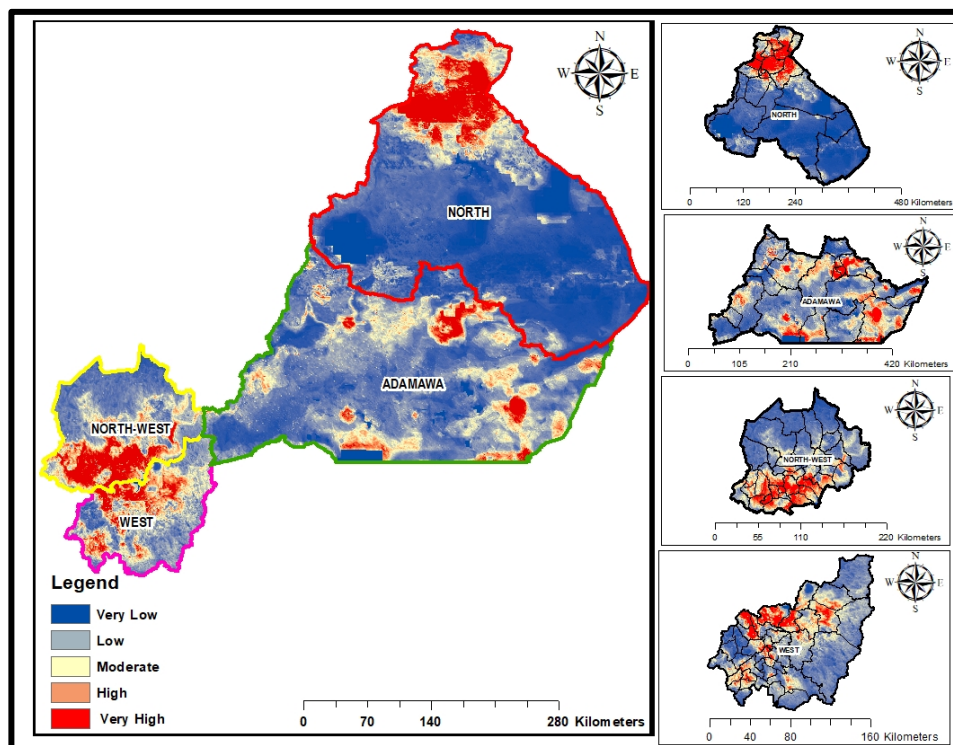


Cameroon's diverse biophysical environment significantly influences the distribution of tick-borne diseases. The thematic maps in (Fig. 6, Fig. 7, and Fig. 8) above illustrate how various environmental covariates create habitats supporting diverse tick species. Examining historical climate covariates, High humidity and temperatures enhance tick survival and reproduction, while seasonal rainfall promotes vegetation growth, providing habitats for ticks and hosts. Tick-borne disease prevalence is closely linked to livestock density and human activity. High livestock populations, see (Fig. 7) above, particularly in cattle ranching zones, increase tick infestations and transmission of diseases like African Tick-Bite Fever and Rickettsiosis. Finally, population density, see (Fig. 8) above, near agricultural areas further heightens exposure to tick bites, amplifying risks. Analyzing the correlation between environmental covariates and tick risk geographic distribution, will enables public health efforts to target high-risk areas, as identified through ecological data. This approach supports strategies to mitigate tick-borne disease risks, safeguarding human and animal health in Cameroon

3.1. Significant Variables and Model Performance

Further reruns were performed on the maxent entropy model, this time using covariates listed above which had a greater contribution to the model prediction capability. The resulting thematic map visualized tick-borne disease hot spots and probabilistic risk geographic distribution as illustrated in (Fig. 9) below. The Area under the Curve value for the computed high contribution covariates, indicated a strong model prediction performance with an Area under the Curve score of 0.867.

Fig. 9: Final Risk Susceptibility Model of Tick-Borne Disease Geographic and Environmental distribution for the four Regions of Interest



The thematic map in (Fig. 9) visualizes tick-borne disease risk across the four areas of interest, highlighting both observed tick presence and predicted risk in un-sampled areas. By comparing ecological conditions of known tick habitats with unexplored areas, the maps identify potential risk zones, offering a comprehensive view of disease distribution. (Fig. 9) shows zones suitable for ticks, even where their presence is unconfirmed, addressing gaps in under-studied regions.

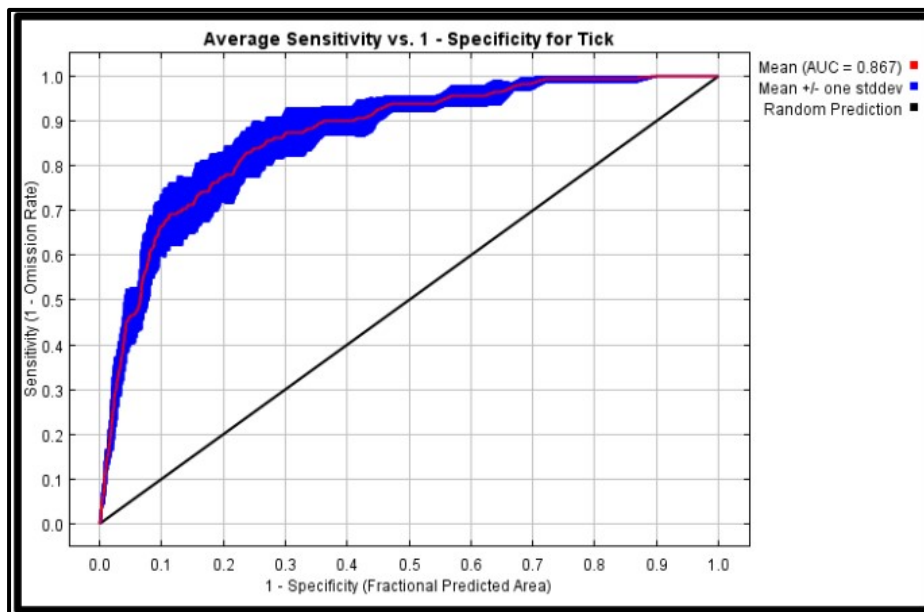
3.1.1. Model Evaluation and Validation

The maxent model was evaluated using the Receiver Operation Characteristic and Area under the Curve approaches. The Receiver-operating curve and the Area under the Curve model validation approaches have been utilized in various

research works from medical to geospatial to evaluate the predictive credibility of statistical models (Provost and Fawcett, 1997).

When the Area under the Curve of the tick-borne disease hotspot model was plotted, the results indicated a high accuracy and predictive capability rate of **0.867** with an Area under the Curve standard deviation of **0.027** as illustrated in the curve plot in (Fig. 10) below. Considering the Receiver-operating curve and the Area under the Curve plot thresholds of = or < **0.5** signifying **random fitness** and > **0.5** or **closer to 1.0** signifying **perfect fitness**, it can be concluded that the tick-borne disease hotspot geospatial distribution model is very predictive and acceptable as accurate probabilistic tick-borne disease risk environmental distribution within the four areas of interest for this research (Phillips and Dudik 2008: 161).

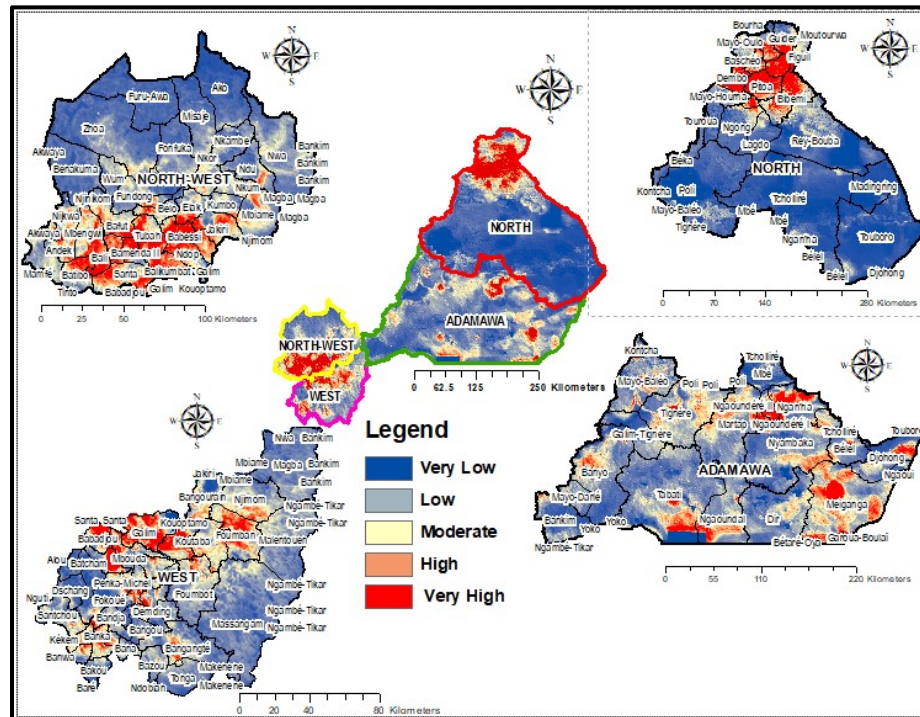
Fig. 10: Tick-Borne Disease Risk Susceptibility Model Receiver-operating curve and Area under the Curve Validation Curve



Further, thematic maps were used to geo-visualized the spatial distribution of risk at a sub-divisional level to identify risk dynamics within each administrative sub-division. The final model risk distribution at the sub-divisional level is visualized in (Fig. 11) below.

The sub-divisional risk distribution map can be vital in timely identification and deployment of resources for awareness, prevention, management and surveillance of livestock, considering the high resolution and precision of risk model at the administrative boundary level.

Fig. 11: Sub-Divisional Tick-Borne Disease Risk Distribution Map



4. DISCUSSION

This study utilized an integrated approach combining GIS analysis with the Maxent entropy modeling technique to map the ecological niche favorability of tick-borne disease vectors. Ninety-three tick vectors were sampled from 27 urban and rural cattle-rearing sites, selected based on geographic location, host availability, and tick abundance for cost-effective precision. Abiotic such as precipitation, temperature and biotic such as livestock density variables were pre-processed into ArcGIS raster layers and analyzed in the Maxent algorithm environment. The model identified precipitation of the wettest quarter as the most influential factor for tick environmental niche suitability at (20%) and demonstrated strong predictive accuracy with an overall Area under the Curve score of 0.867. Tick-borne diseases in Cameroon pose significant public health risks, especially to livestock and people interacting with

them. Diseases like Crimean-Congo hemorrhagic fever virus, which lack effective treatments, underscore the need for continuous surveillance. While serological and molecular testing has documented tick-borne diseases in Cameroon (Maurice 1967: 395; Gonzalez et al., 1989: e0010217), most research has focused on urban areas, neglecting remote zones with potential high-risk probabilities. The research addresses these gaps by generating high-resolution thematic maps to visualize the spatial probabilistic risk distribution of tick-borne disease, accounting for under-researched areas. These maps will inform strategies to manage and prevent tick-borne diseases by identifying hotspots and guiding control efforts. Understanding ecological niche preferences and the geospatial distribution of tick vectors enhances disease surveillance and management amid evolving climatic and ecological dynamics.

CONCLUSION

In conclusion, thematic cartographic maps generated from this entropy analysis using maxent, can be used to identify tick-borne disease risk spatial distribution and hotspots in Cameroon. These maps can guide targeted interventions like vaccinations and public awareness campaigns. Unlike previous studies in Cameroon, this research offers a broader, high-resolution geo-visualization view of the risk across multiple regions within Cameroon. By identifying high and potential risk areas, this study supports evidence-based decision-making for tick-borne disease prevention and control in Cameroon as well as global effort to combat tick-borne disease spread in humans and animals. Further research needs to be conducted to improve the spatial localization of potential hotspots for tick diseases by broad collection of serology samples from humans, livestock as well as virology of tick vectors across the country. However, such advanced clinical analysis are beyond the privy of this study.

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