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Crimean-Congo Hemorrhagic Fever (CCHFV) Risk Modeling for Cameroon based on the Spatial Distribution of its Endemic Tick Vectors and Suitability of the Ecological Niche for Purpose of Disease Surveillance

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Abstract: Crimean Congo Hemorrhagic Fever Virus (CCHFV) is a severe tick-borne infection mainly transmitted to livestock and humans by ticks of the Nairovirus genus and family Bunyaviridae. This life-threatening pathogen is geographically diverse and found in many parts of the world including West Africa, Asia, and Europe. This tick-borne infection is highly pathogenic and recognized as the most medically important tick-borne disease affecting humans. Modeling the spatial distribution of the tick vectors of thislife-threatening human diseases, is vital to appreciating the ecological determinants of CCHF infections and spread as well as providing a planning framework for CCHFV surveillance and control programs in countries which have not yet experienced major outbreaks such as Cameroon. This research, incorporates the maximum entropy modeling approach (Maxent) to model the risk vulnerability of the local populations across Cameroon to the Crimean Congo hemorrhagic fever virus (CCHFV) by modeling the ecological niche suitability and geo-spatial distribution of CCHFV tick vectors found in the study area. Further, this paper accesses the geospatial distribution of risk, human vulnerability,and ecological niche suitability of eightdifferent CCHFV tick vectors specifically, Amblyomma variegatum,Hyalomma dromedarii, Hyalomma rufipes, Hyalomma truncatum, Rhicephalus sanguineus, Rhipicephalus annulatus, Rhipicephalus decoloratus, Rhipicephalus microplus. Thepreliminary outputs of the model clearly show evidence of CCHFV tick vector geolocation preferences in terms of its ecological niche suitability in Cameroon. The final model resultspresent a foundation and creates a road map for CCHFV surveillance which is vital for health personals monitoring diseases as well as stressing the importance of incorporating geospatial attributes to dynamic diseases surveillance efforts and control programs in Cameroon.

Keywords: Crimean-Congo hemorrhagic fever virus, Ecological niche, Tick vectors, Vulnerability, Spatial distribution, Maxent, Modeling, and Disease surveillance.

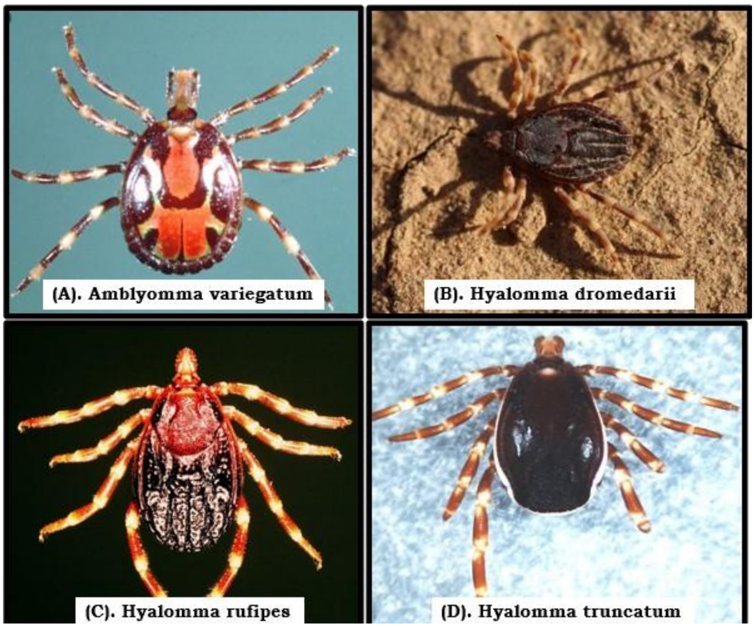
Résumé: Le virus de la fièvre hémorragique de Crimée-Congo (CCHFV) est une infection grave transmise par les tiques. Ce virus est principalement transmisaubétail et aux humains par les tiques du genre Nairovirus et de la famille des Bunyaviridae. Cet agent pathogène potentiellement mortel est géographiquement diversifié et se trouve dans de nombreuses régions du monde, notamment en Afrique de l'Ouest, en Asie et en Europe. Cette infection transmise par les tiques est hautement pathogène et reconnue comme la maladie transmise par les tiques la plus importante sur le plan médical chez l'homme. La modélisation de la distribution spatiale des tiques vecteurs de cette maladie humaine potentiellement mortelle est essentielle pour apprécier les déterminants écologiques des infections et de la propagation de la CCHF, dans le but de fournir un cadre de planification pour les programmes de surveillance et de contrôle de la CCHFV dans les pays qui n'ont pas encore connu d'épidémies majeures comme le Cameroun. Cette recherche intègre l'approche de modélisation de l'entropie maximale (Maxent) pour modéliser la vulnérabilité au risque des populations locales à travers le Cameroun au virus de la fièvre hémorragique de Crimée-Congo (CCHFV) en modélisant l'adéquation de la niche écologique et la distribution géospatiale des vecteurs de tiques CCHFV trouvés dans la zone d'étude. En outre, cet article accède à la distribution géospatiale du risque, de la vulnérabilité humaine et de l'adéquation de la niche écologique de huit vecteurs de tiques CCHFV différents, en particulier Amblyomma variegatum, Hyalomma dromedarii, Hyalomma rufipes, Hyalomma truncatum, Rhicephalus sanguineus, Rhipicephalus annulatus, Rhipicephalus decoloratus, Rhipicephalus microplus. Les résultats préliminaires du modèle montrent clairement des preuves des préférences de géolocalisation des vecteurs de tiques CCHFV en termes de pertinence de la niche écologique au Cameroun. Les résultats finaux du modèle présentent une base et créent une feuille de route pour la surveillance de la CCHFV qui est vitale pour les personnels de santé surveillant les maladies et soulignant l'importance d'incorporer des attributs géospatiaux aux efforts dynamiques de surveillance des maladies et aux programmes de contrôle au Cameroun.

Mots clés: Virus de la fièvre hémorragique de Crimée-Congo, Niche écologique, Vecteurs de tiques, Vulnérabilité, Distribution spatiale, Maxent, Modélisation et Surveillance des maladies.

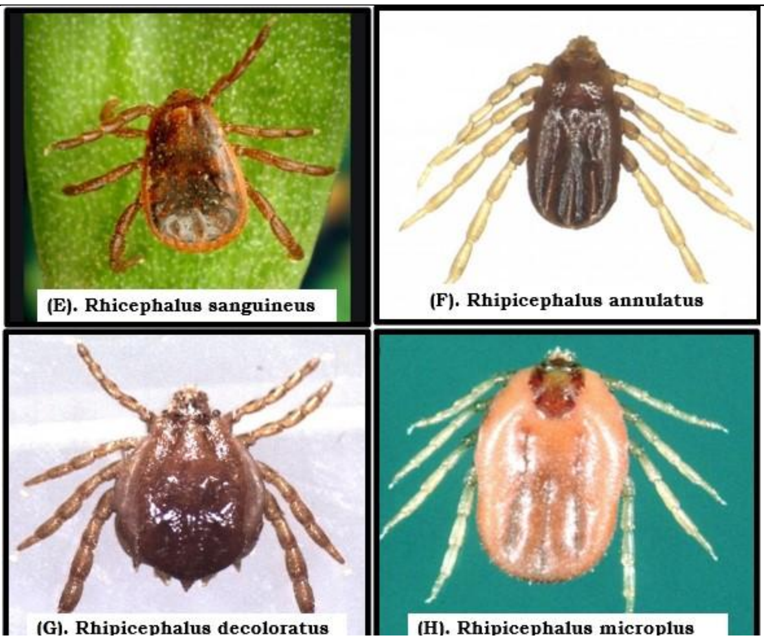
Introduction

Crimean-Congo hemorrhagic fever virus (CCHFV) is an emerging zoonotic infectious tick-born viral *Nairovirus* genus of the family *Bunya-viridae,* that causes serious illnesses and potentially hemorrhaging symptoms in humans (Mark A. Deka 2017, Chinikar et al. 2009). This virus, cited in some epidemiologic literatures as the Asian Ebola, is highly pathogenic and poses a serious challenge to public health. The Crimean-Congo hemorrhagic fever virus (CCHF) was initially diagnosed or identified in the Crimean region in 1944 (Hoogstraal H. 1979, Whitehouse 2004). Further study of the virus over time indicated a correlation between the virus and another virus that was causing hemorrhagic disease outbreaks in the African Congo basin, giving the virus its current name Crimean-Congo hemorrhagic fever (Han N. and Rayner S. 2011, Ergonul O. 2006). CCHFV has a high fatality rate (Yu-Chen et al. 1985, Sun-Bul et al. 2016), and incredibly difficult to treat, manage or prevent (Whitehouse 2004, Ardalan et al. 2006 and Chinikar et al. 2010). CCHFV transmission is similar in fashion to that of the Lassa fever and the Ebola virus (Leblebicioglu et al. 2016) and is the most widespread tick-born arboviral infection of humans in the world (Ergonul, 2012). This disease is endemic to many geographic regions from Asia, Europe, Middle East to Central and West Africa (Ergonul. 2006). The disease is considered to be spreading across the globe with increasing reports of new human infections in the sub-Saharan West African countries such as Senegal, Mauritania, Burkina Faso and Ghana (Chrisholm K, et al. 2012, Camicas J, et al.1990, Nemes z, et al. 2004). In Central Africa for instance, human CCHFV infections have recently been documented after being dormant for some decades (Grard G, et al. 2011).

Human contraction of this virus usually occurs through infected tick bites, consumption of infected meat, drinking unpasteurized milk from infected cattle and direct exposure to infected blood (Alavi-Naini et al .2006). While in infected animals there are no apparent manifestations, animals play a crucial role in the disease transmission and distribution cycle (Messina et al. 2015). Although the hard ticks (Ixodids) serve as vectors for CCHFV, livestock such as sheep, goats, cattle, horse, camels ducks, pigs, and chickens, are serve as amplifier host for the CCHFV tick vectors. A variety of Ixodid ticks (Acari: Ixodidae) such as Amblyomma variegatum **(A)**, Hyalomma dromedarii **(B)**, Hyalomma rufipes**(C)**,Hyalomma truncatum **(D)**, Rhicephalus sanguineus**(E)**, Rhipicephalus annulatus **(F)**, Rhipicephalus decoloratus **(G)** and Rhipicephalus microplus **(H),** illustrated in (**Figure. 1A –H**, below) in the Pan-African region have been document to carry the CCHF virus, however only a few species specifically Ixodid tick members of the genus Hyalomma have been reported to be the primary vector transmitter of the CCHF virus to humans (Maltezou and Papa. 2010). These Ixodid ticks prefer hot and dry semi-arid regions and are flourishing in many parts of African, Cameroon inclusive (Lutomiah J. 2014, Makio A et al. 2014) and (Messina et al. 2015). Human infections are rare and most common amongst people living with or amongst and working with livestock for example slaughterhouses, who are more expose and likely to get tick bites.



(**Figure .1)** Tick Vector Species **A-D**



(Figure .1) Tick Vector Species **E-H**

Human to human transmissions are possible especially amongst health care workers and people who come in contact with fluids of other infected humans. There is no available human cure or vaccine for CCHFV. Currently treatment is mostly supportive, and prevention can be achieved through the vaccination of livestock, use of pesticides and wearing of protective gear when in close proximity to livestock or infected individuals (Messina et al. 2015) and (Mark A. Deka 2017).

The emergence of CCHF disease and the population of Ixodid ticks in the environment is influenced by four main factors; Abiotic (Climate and temperature), Biotic factors (landcover and animal host), movement (area accessible for ticks on the ecological time scale, which could be limited by biogeographical barriers) and the habitat preference of the animal host (Arrontes 2005). Through the modeling of these factors, theseasonality, spatial distribution of CCHFV risk, human vulnerability, distribution of tick vectors and the ecological niche preference of CCHFV tick vectors, has been identified in geographic space.

Earlier research on the CCHF virus in Cameroon has not been comprehensive enough to provide frameworks of CCHFV risk vulnerability models that can be used for target actions in the case of an outbreak. With the changing climate and increasing resilience and emergence of the CCHF virus in some countries in Africa, it is imperative that a comprehensive risk model be created which can be used by health professionals to monitor and survey potential hotspots or high-risk areas. Earlier research reports documenting serological evidence of CCHFV in Cameroon focused mainly on certain parts of the country although the virus is a threat to all Cameroonians across the country (Ghogomu A. et al. 1989), (Paix MA. 1988), and (Serge A. et al. 2018). In Cameroon, researchers have made advances in comprehending as well as mapping the spatial distribution of various diseases and the characteristics of their vectors for example Malaria research (Rogers DJ. et al 2002) and (Moffet A. et al 2007), However, there has been little research on CCHFV risk vulnerability or the geospatial distribution of its tick vectors specifically at a country wide scale.

Other studies have isolated incidents of infection and location specific evidence of CCHFV antibodies in Cameroonians (Maurice Y. 1967), (Zeller HG. Et al. 1989), (Lebreton M. et al. 2006), (Rissmann M. et al. 2017) and (Sadeuh -Mba et al. 2018) but none has modeled the potential risk vulnerabilty of Cameroonians to CCHF virus at a country wide scale. As such, given the absence of comprehensive country wide analysis and diagnosis, its ever more important that health professionals and disease surveyors remain vigilant. This research seeks to provide a framework that will guide and support CCHFV surveillance in Cameroon.

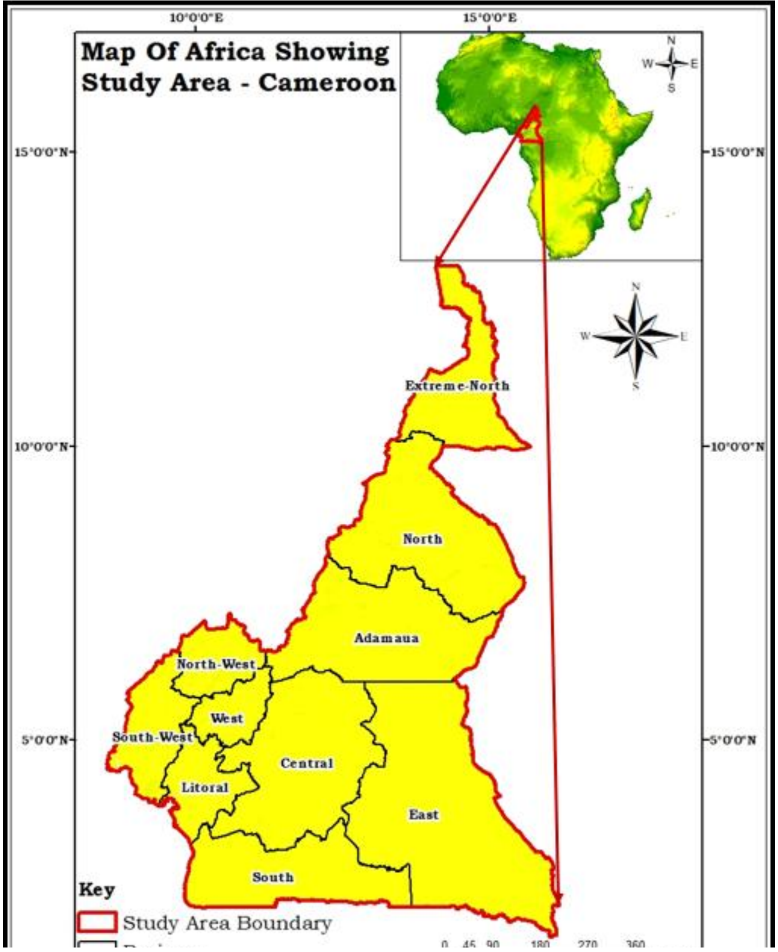
In populations endemic to the CCHF virus, incident outpatient report data has laid a foundation for understanding, diagnosing, managing, identifying hot spots and recognizing population most vulnerable to CCHF virus, thereby enabling a more focused preventive approach, hence limiting the spread and vulnerability. Surveillance for CCHF virus in both human and vector populations provides an opportunity for monitoring the likelihood of an outbreak and quickly identifying potential and likely hotspots.

The public health threat of CCHFV to Cameroonians in every region requires the need for a thorough environmental risk assessment. This research focuses on the modeling of the ecological niche suitability requirements of eight Ixodid tick CCHFV vectors in Cameroon in order to map thematically the spatial distribution of CCHFV risk vulnerability in Cameroon as a whole. Such maps can be used to support prevention programs and disease surveillance frameworks in different parts of the country. A Geographic Information Systems (GIS) and an environmental niche factor analysis was employed using the maxent entropy species distribution modeling approach to build spatial distributions, predictive habitat suitability's for the CCHFV Ixodid tick vectors , Amblyomma variegatum,Hyalomma dromedarii, Hyalomma rufipes, Hyalomma truncatum, Rhicephalus sanguineus, Rhipicephalus annulatus, Rhipicephalus decoloratus and Rhipicephalus microplus on a country wide scale. Further, acumulative model of the spatial CCHF virus risk vulnerability distribution for Cameroon was created based on the eight Ixodid tick CCHFV vectors' ecological niche suitability. The final out put model(s) can be used for informative purposes, assessment of risk vulnerability, identification of hotspots, creating target preventative measures and CCHF virus surveillance in Cameroon. This study contributes to the current knowledge of CCHF virus mapping in Cameroon and Central West Africa by creating models of risk vulnerability for eight Ixodid tick vectors at a very high spatial resolution and fine scale.

Method and Data

Study Area

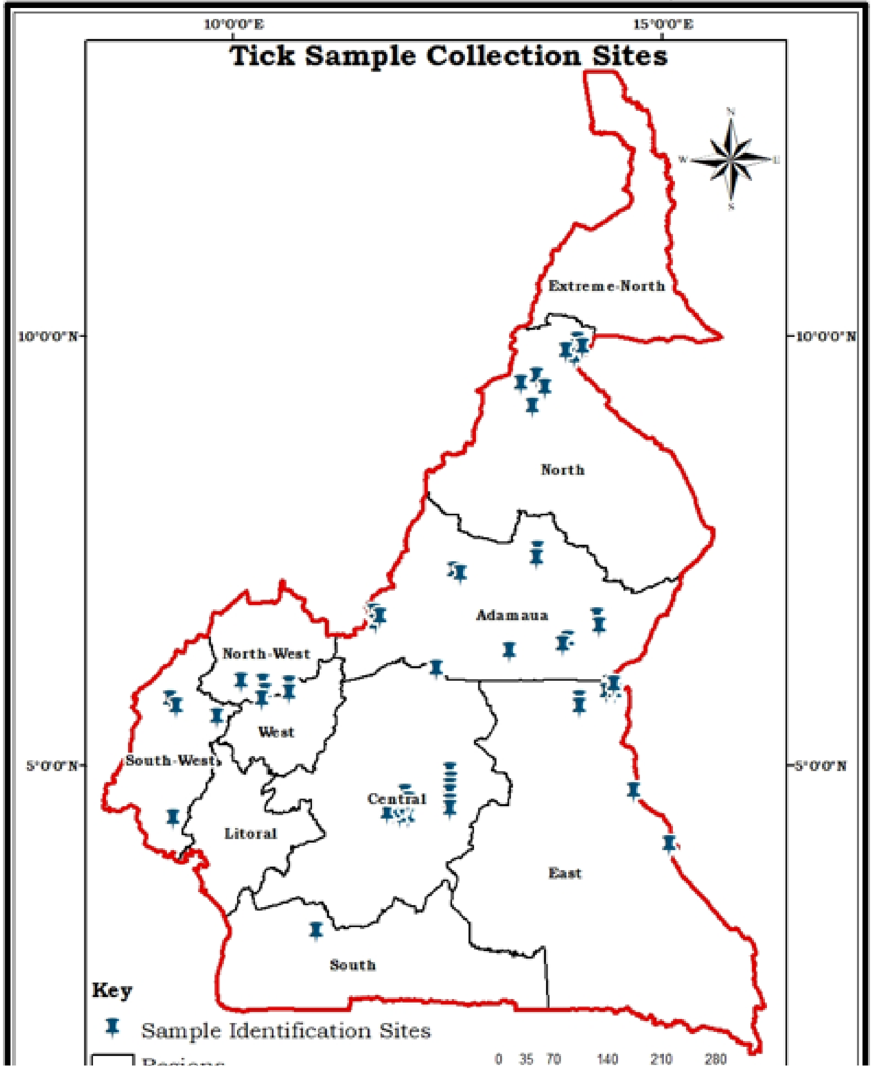
Cameroon is a country in Equatorial West-Africa. It extends from latitude $2^0$and 12^0 North and longitude8^0 and 16^0East illustrated in **(Figure. 2**, below**)**.It covers a land surface area approximately 475,000 km^2. Sometimes described as "Africa miniature" because it exhibits all the major climates and vegetation of the continent from, mountains, deserts to oceanic coastlands. Cameroon has five agro-ecological zones distinguished by the dominant physical, climatic and vegetation features. It also has several bio-geographical climates from the Arid Savannas in the north to the equatorial rainforest in the south. Highlands in the central Midlands and western parts of the country. These Unique combination of dominant and microclimates contribute to the flourishing boom in ecological systems and climate regional seasonality that supports a wide variety of Ixodid tick species. (Olivry JC. 1986).



(Figure. 2) Map of Cameroon Showing its Regions

Ixodid Tick Presence Data

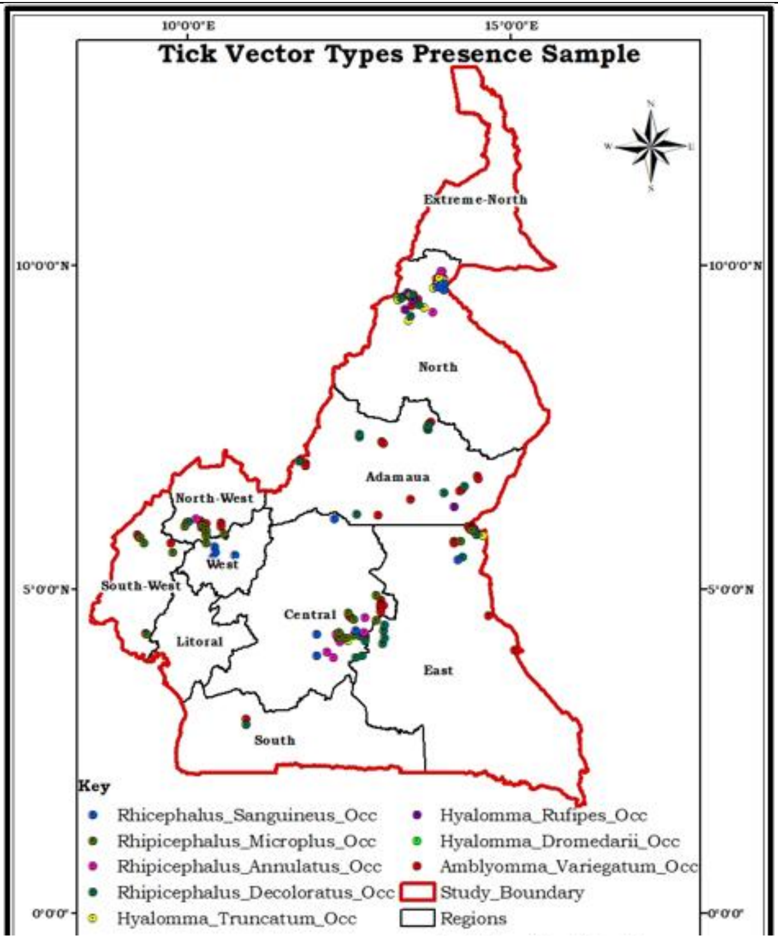
A database comprising of latitude and longitude coordinate locations of eight CCHFV tick vector species presence data was compiled from the analysis ofboth peer-reviewed literatures (Badia-Rius et al. 2019, Silatsa et al. 2019), and credible species databanks such as, GenBank records and Global Biodiversity Information Facility (GBIF; www.gbif.org). The Peer-reviewed literature of tick presence data was selected using the manual search guide described in (Micheal et al. 1996) and (Messina et al. 2015). The differentspecies of the tick vector presence data used for this analysis was collected spatially from a total of 53 sites across the five agro-ecological zones of Cameroon (Silatsa et al. 2019) as illustrated in (**Figure. 3**, below).



(Figure. 3) Tick Vector Sample Collection Sites

These Agro-ecological zones comprise of the Sudano-Sahelian zone (North plains with high temperatures, dry Savannahs and steppe vegetation), the High Guinea Zone (Adamawa plateau region), The Western Highlands Zone, which covers the West and North-West (low temperatures and high rainfall), the Humid forest mono modal rainfall (Coastal Lowlands), and Humid forest bi-modal rainfall (Southern plateau). Each zone exhibits its own distinct bioclimatic and environmental characteristics (Silatsa et al. 2019).

A sum of 172 tick vectors identifiedin 53 sampling sites, and on (GBIF), were extractedand mapped from peer-reviewed literature as in(Silatsa et al. 2019) and platforms such as Global Biodiversity Information Facility(GBIF; www.gbif.org),illustrated in (**Figure. 4,**below), (Messina et al. 2015a, 2015b and Silatsa et al. 2019).



(Figure. 4) Tick Vector Types Presence Sample

The identified tick vector presence data comprised of a sample of eight Ixodid CCHFV tick vectors namely, Amblyomma variegatum,Hyalomma dromedarii, Hyalomma rufipes, Hyalomma truncatum, Rhicephalus sanguineus, Rhipicephalus annulatus, Rhipicephalus decoloratus and Rhipicephalus microplus. The latitude and longitude coordinate positionsof each tick specie was identified and recorded using a global positioning system (GPS) (Badia-Rius et al. 2019) and (Silatsa et al. 2019) and subsequently used for modeling.

Environmental Layers

The geographic and environmental characteristics of each agro-ecological zone in Cameroon was analyzed using a geographic information system (GIS). Two unique categories of data were obtained from various peer- reviewed literature sources and platforms to calibrate the model. The two main data categories were classified into 'Abiotic variables' and 'Biotic variables'. The Abiotic variables included Climatic datasets (consisting of 19 bioclimate variables), outlined in (**Table. 1**, below), Topographic datasets (slope, aspect, terrain curvature, elevation and terrain roughness), Land-use land cover (LULC), Normalized Vegetation Index (NDVI), and an Enhanced Vegetation Index (EVI) while the Biotic variables included, Livestock Spatial Distribution (LSD) (cattle, sheep, goat, horse, duck, chicken), Population Distribution and Population Density. Interpolated climate data such as bioclimate data has increasing be used to model spatial distribution of vector-borne diseases (Kalluri et al. 2007) and (Beck LR. 2000). The interpolated climate layers were created by collecting weather station point data across the area of study and creating a blanket continuous climate raster using sophisticated smoothing algorithms. The most commonly used global interpolated climate data resource for species distribution modeling is WorldClim, assessable from the link (www.worldclim.org) last accessed oct 8, 2020 (Hijmans et al. 2005) and (Slater H, Michael E. 2012).

For this analysis,nineteen bioclim variables were extracted from monthly temperature and precipitation values at a spatial resolution of $1km^2$. The nineteen bioclimatic variables extracted from WorldClim included annual values such as mean temperature and precipitation, measures of seasonality (annual ranges in temperature and precipitation) and extreme or limiting environmental factors such as temperatures of the coldest and warmest months, and precipitation of the wettest and driest months. A normalized vegetation index (NDVI) as well as an enhanced vegetation index (EVI) were also included as important covariates in the model because of their crucial role in shaping the ecological niches of Ixodid hard ticks. These two metrics are also key indicators of the soil moisture conditions in the area of interest (Guerra et al., 2002) and (Randolph 2000). NDVI data was downloaded from the Copernicus Global Land Service archive accessible through the link https://land.copernicus.vgt.vito.be/, for 2012–2018 periods in 1 km spatial resolution. Population distribution and density raster datasets were extracted at the resolution of 1 km from the site WorldPop accessible through the link (www.WorldPop.org) last accessed September 23rd 2020. A 22 class Land-use landcover raster was extracted at a resolution of 1km from Global Land Cover 2000 Project and reclassified to five most important classes, including, dense evergreen forest, deciduous woodlands, forest/savanna mosaics, dry savannas and croplands.

(Table .1) Bioclim Covariates

Variables	**Data Resolution**
BIO1 =annual mean temperature (C) 30 arc-seconds,(1km)	
BIO2 =mean diurnal range (mean monthly (max temp – min temp) (C)30 arc-seconds,(1km)	
BIO3 =Isothermality (BIO2/BIO7) (_ 100) (_C)30 arc-seconds, (1 km)	
BIO4 =temperature seasonality (standard deviation _ 100) (_C) 30 arc-seconds, (1 km)	
BIO5 =maximum temperature of warmest month (_C) 30 arc-seconds, (1 km)	
BIO6 =minimum temperature of coldest month (_C)30 arc-seconds, (1 km)	
BIO7 =temperature annual range (BIO5–BIO6) (_C)30 arc-seconds, (1 km)	
BIO8 =mean temperature of wettest quarter (_C)30 arc-seconds, (1 km)	
BIO9 =mean temperature of driest quarter (_C)30 arc-seconds, (1 km)	
BIO10 =mean temperature of warmest quarter (_C) 30 arc-seconds, (1 km)	
BIO11 =mean temperature of coldest quarter (_C) 30 arc-seconds, (1 km)	
BIO12 =annual precipitation (mm)30 arc-seconds, (1 km)	
BIO13 =precipitation of wettest month (mm) 30 arc-seconds, (1 km)	
BIO14 =precipitation of driest month (mm) 30 arc-seconds, (1 km)	
BIO15 =precipitation seasonality (coefficient of variation) (mm)30 arc-seconds, (1 km)	
BIO16 =precipitation of wettest quarter (mm) 30 arc-seconds, (1 km)	
BIO17 =precipitation of driest quarter (mm) 30 arc-seconds, (1 km)	
BIO18 =precipitation of warmest quarter (mm)30 arc-seconds, (1 km)	
BIO19 =precipitation of coldest quarter (mm) 30 arc-seconds, (1 km)	

Each of these land cover classes where subsequently converted into separate raster layers. Five to pographic raster datasets including, Slope, Aspect, Elevation, Terrain Curvature and Terrain Ruggedness were extracted from a 1km resolution digital elevation model (DEM) of the study area to be used for model calibration. Finally, a high-resolution raster 1km livestock density and distribution data for (cattle, goat, horse, sheep, pig, duck, chicken) outlined in **(Table. 2**, below**)** were extracted from the database developed by the Food Agriculture Organization (FAO) accessible through the link (www.fao.org) last accessed Oct 12, 2020.

(Table .2)Topographic, Landcover coverage and Livestock Covariates

Variables	**Data Resolution**
Slope(1km)	
Aspect (1km)	
Elevation (1 km)	
Terrain Curvature(1 km)	
Terrain Roughness (1 km)	
LULC Natural (1 km)	
LULC Artificial (1 km)	
NDVI Averages(1 km)	
EVI (1 km)	
Population Density (1 km)	
Population Distribution (1 km)	
Goat (1 km)	

Cattle (1 km)
Horse (1 km)
Pig (1 km)
Sheep (1 km)
Chicken (1 km)
Duck (1 km)

Livestock densities were measured and calibrated in animal head counts per square kilometer. Once all the abiotic and biotic datasets had been converted to rasters with the same extent, coordinate systems and pixel resolutions, the next step was to perform an ecological niche factor analysis (ENFA) or an ecological niche model.

Ecological Niche Modeling

An ecological niche factor analysis is a species distribution model based on the niche modeling concept of Hutchinson in a multivariate statistical framework (Hutchinson GE. 1957). The ecological niche of a specie can be defined as those ecological conditions in which it can maintain population without immigration (Grinnell 1917). Specie ecological niches and associated potential geographic ranges can be approximated using correlative algorithms by analyzing known present point data to digital GIS data layers for a specific area, while summarizing the spatial variations of the GIS layers in a multidimensional environmental space (Guisan A. 2000).

Theecological niche of the CCHFV tick vectors for this research and their spatial distribution was modeled using the Maxent Entropy Method (Maxent). Initially proposed by Jaynes in 1957 (Jaynes 1957). The theory of maximum entropy is “based on the premise that when estimating the probability distribution, you should select that distribution which leaves you the largest remaining uncertainty that is the maximum entropy, consistent with your constraints” (Penfield 2010). The strength of maxent lies in its ability to effectively predict species distribution in space when only partial data for example presence data is available. Its goal is to predict specie distribution in geographic space by finding the entropy distribution closest to uniform, subject to constraints controlled by the abiotic and biotic variables under investigation (Philips SJ. 2006). When developing a maxent species distribution model, the more information is added to the calibration, the lower the level of uncertainty introduced into the output. The maxent extropy approach calculates the maximum entropy with dependence on known information (Philips and Dudik 2008), (Yi et al. 2016) and (Mark A. Deka 2017). A maxent entropy model can be expressed mathematically as follows.

- For a random variable $\boldsymbol{n}$withdifferent potential result, X_1, X_2, X_3 ,….. X_n, the presence probabilities are P_1, P_2,….P_n, respectively (Yi et al. 2016, 264).

$H(\xi)\sum Pilog\frac{1}{Pi} = -\sum PilogPi$……………………**Equation (1)**

The Maxent entropy algorithm is preferable for this species distribution modeling since the tick vector presence data is not homogenous throughout the study area. Also, the maxent entropy approach is effectively in predicting distribution even when presence data is incomplete or not representative of the entire study area (Nakazama et al. 2013).

For this research, the sampled172CCHFV tick vectorslocation presence data was converted into longitude (long) and latitude (lat) vector points on the map. In the model implementation process, only the tick vector presence points with accurate longitude and latitude coordinates were incorporated into the maxent model. Before incorporation into the maxent model, the abiotic and biotic environmental covariate variables were preprocessed in ArcGIS, QGIS and DIVA-GIS so that the final raster datasets have a consistent study area extent, coordinate system and cell resolution of 1km. Then, all the abiotic and biotic covariate raster layers were converted into an ASCII (text) file format using DIVA-GIS before uploading into maxent.

To isolate the abiotic and biotic environmental covariate with high ecological significance, a series of test runs were conducted in maxent. After a number of pre-analysis test runs, some of the abiotic and biotic covariates were removed from the model. This was done to avoid the problem of overparameterization which will prevent highly correlated covariates from influencing the model output hence reducing its predictive capability (Graham 2003), and (Morueta-Holme et al. 2010). From the preliminary results of the first test runs, nine of the nineteen bioclim covariate variables including, BioClim_2 -mean diurnal range (C) , BioClim_5 – max temperature warmest month, BioClim_6 -minimum temperature of the coldest month (C), BioClim_10 - mean temperature of the warmest quarter (C), BioClim_12 - annual precipitation, BioClim_13 -precipitation of the wettest month (m), BioClim_16 – Precipitation wettest Quarter (mm), BioClim_17 - Precipitation Driest

Quarter (mm) were eliminated from the model entirely because their percentage contribution and importance to the model was very small **(<1%).**

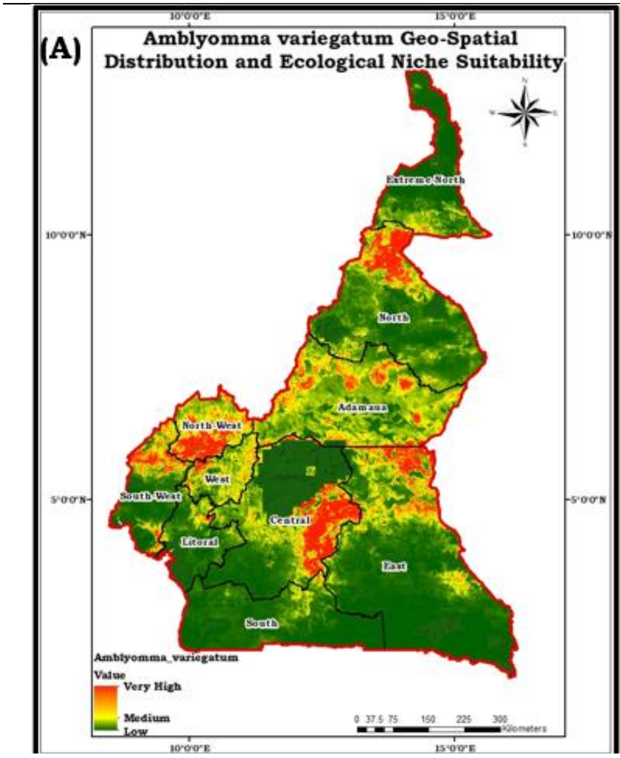
Model Calibration and Implementation

Sample data was divided into two parts, 70% to be used for the construction of the model, forming the functional associations between tick presence data and environmental covariates. 30% was utilized for testing the predictive capability of the model. The training regions were selected to be areas endemic to Ixodid ticks and the resulting model output was projected to the entire study area. The model calibration parameters included a random test percentage and a transformation of binary nature based on 10 percent of the tick presence data (*n*= 172; 30% for testing) for cross validation, ten replicate runs with random seeds to produce results with variations (Peterson 2008). A 10% training presence approach was chosen as the choice for the random test percentage. This technique addresses the problems of data points locational errors up to about 10% of the model tick presence data in case there are errors with the tick vector location sample data (Peterson 2008). A total of 10,000 random background points were specified to be distributed evenly through the study area to prevent collinearity. Selection of the convergence threshold and regularization values was carried out following the default rules and the number of iterations was chosen such that all models converged. The logistic algorithm was used to ensure that prediction probability estimates were between **0** (unsuitable) and **1** (Suitable), per map pixel. A jackknife analysis was also conducted to assess the percentage contributions and permutation importance for each of the abiotic and biotic covariates. Any significant decrease of the contribution value of the covariates from percentage contribution to permutation importance, implies that suitability heavily depends on a particular covariate variable. The final output of the model was a series of probability prediction maps, first, a general CCHFV riskvulnerability map for Cameroon based on total CCHFV tick vector spatial distribution across the study area and secondly, eight tick vector specie specific spatial distribution of risk vulnerability maps, where each pixel of the study area was evaluated with regards to niche suitability based on how closely the abiotic and biotic covariates match or converge with those of the original tick vector presence locations.

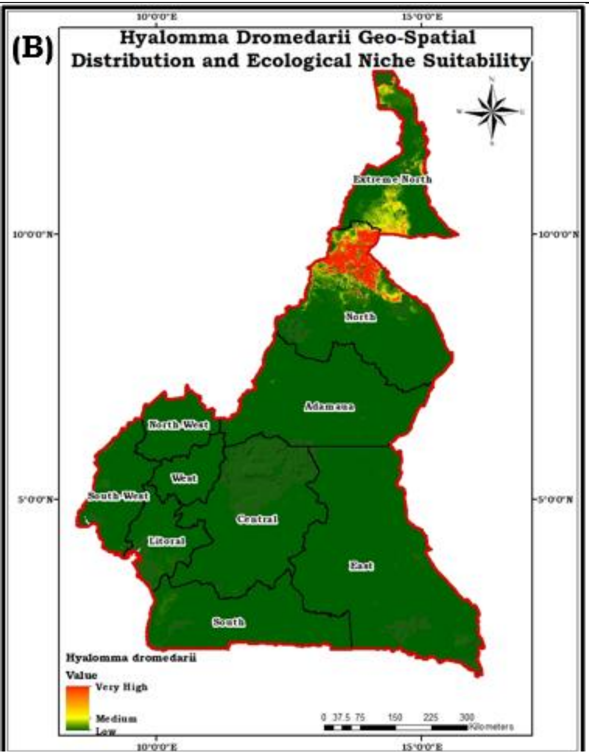
To access the predictive performance of the model, the area under the curve (**AUC**) score of the receiver operating characteristics (**ROC**) was calculated. An ideal predictive model will have an AUC value closer to **1.0**, while an AUC value of **0.5** signifies that the model distribution only occurred by random chance.

Results and Model Validation

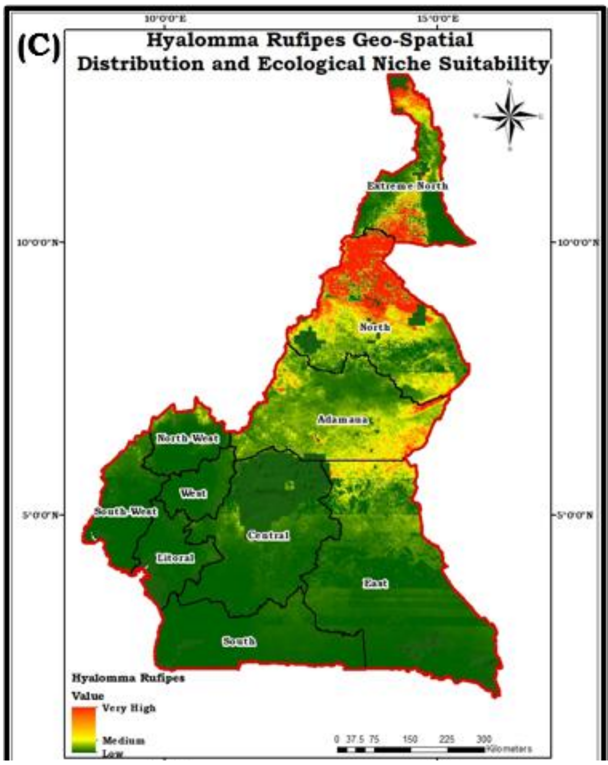
The maxent ecological niche factor analysismodel produced ten cumulative outputs, one model for the cumulative ecological niche suitability analysis of all tick samples (172) and an addition ofeightseparate specie specific ecological niche suitability models, illustrated in (**Figure. 5A – H**, below), predicting the areas with **(High)** and**(Low)** CCHFV risk vulnerability based on the spatial distribution of ecological niche suitabilityvariables forCCHFV tick vectors across Cameroon. The Bioclim covariates were somewhat surprisingly limited as only seven Bioclim parameters had a considerable contribution to the overall model, with the remaining 12 Bioclim covariates contributing **<1%** to the overall model. The maxent model results further showed that the sampled tick vectors' ecological niche suitability for the study area was greatly depended on the following factors, Bioclim_3 – Isothermality, Chicken, Bioclim_4 – Temperature Seasonality, Bioclim_19 – Precipitation of coldest quarter (mm), Bioclim_18 – Precipitation of warmest quarter (mm), Bioclim_1 – Annual mean temperature (c), Goat, Horse, Bioclim_7 – Temperature annual range (c), Cattle and Duck. The model was rerun one last time with only the factor that had reasonable contributions to the model output (listed above). The resulting output model was validated using the Area Under the Curve (AUC)model evaluation approach.



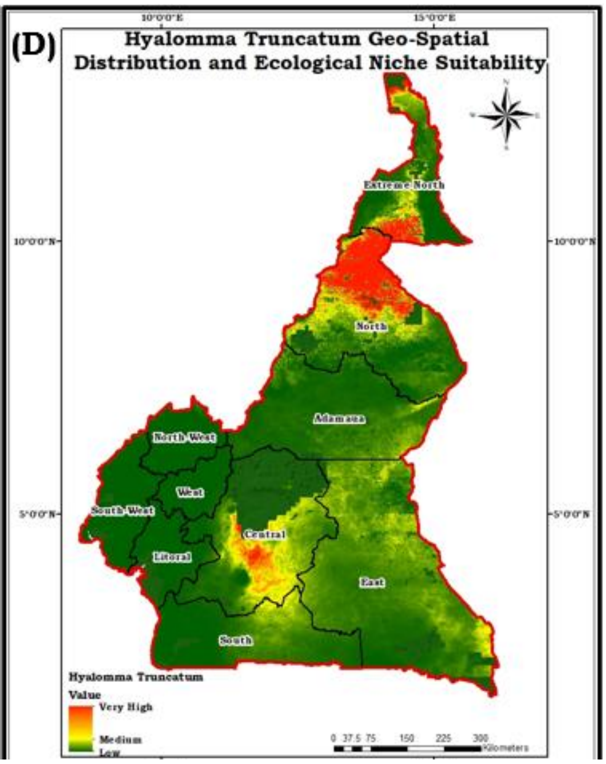
(Figure. 5a) Amblyomma Variegatum



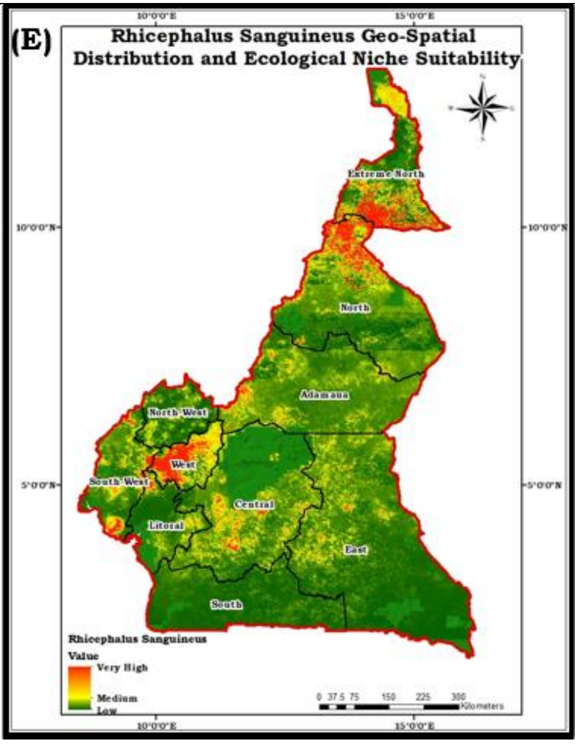
(Figure. 5b) Hyalomma Dromedarii



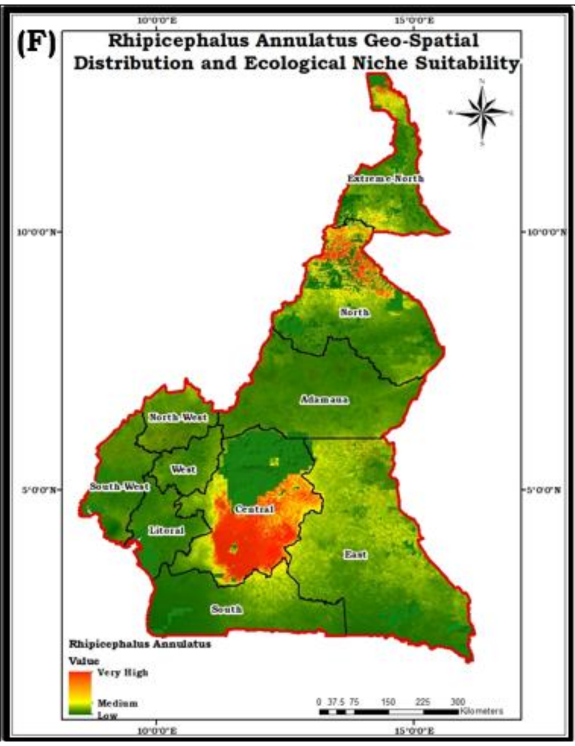
(Figure. 5c) Hyalomma Rufipes



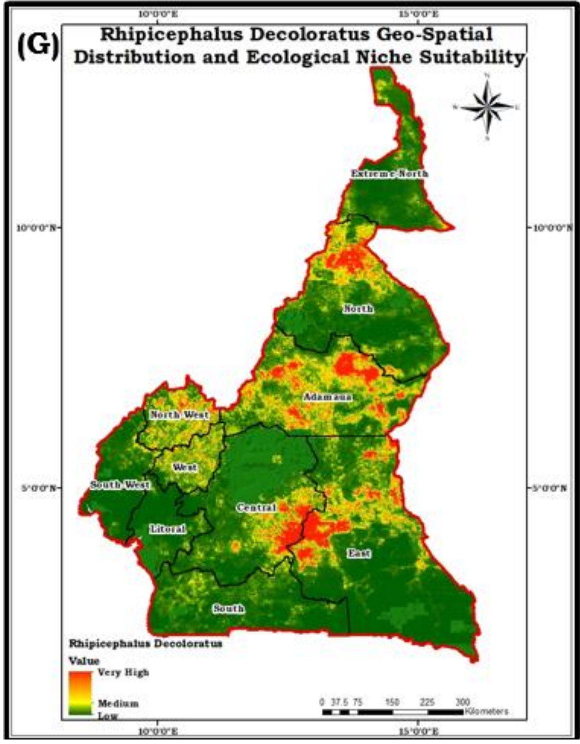
(Figure. 5d) Hyalomma Truncatum



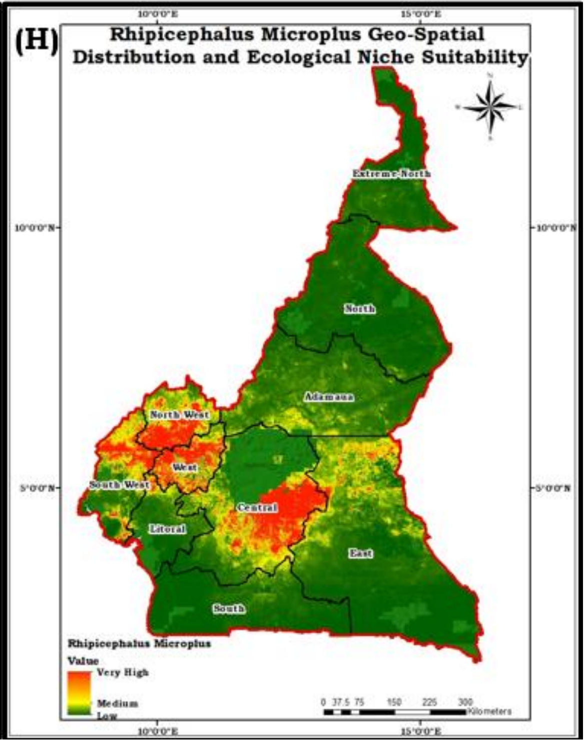
(Figure. 5e) Rhicephalus Sanguineus



(Figure. 5f) Rhicephalus Annulatus

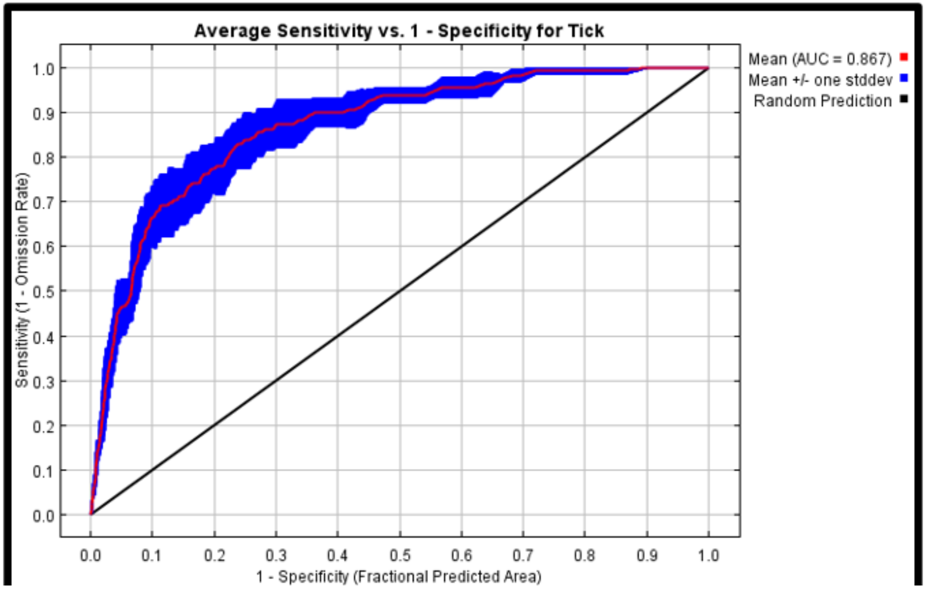


(Figure. 5g) Rhicephalus Decoloratus



(Figure. 5h) Rhicephalus Microplus

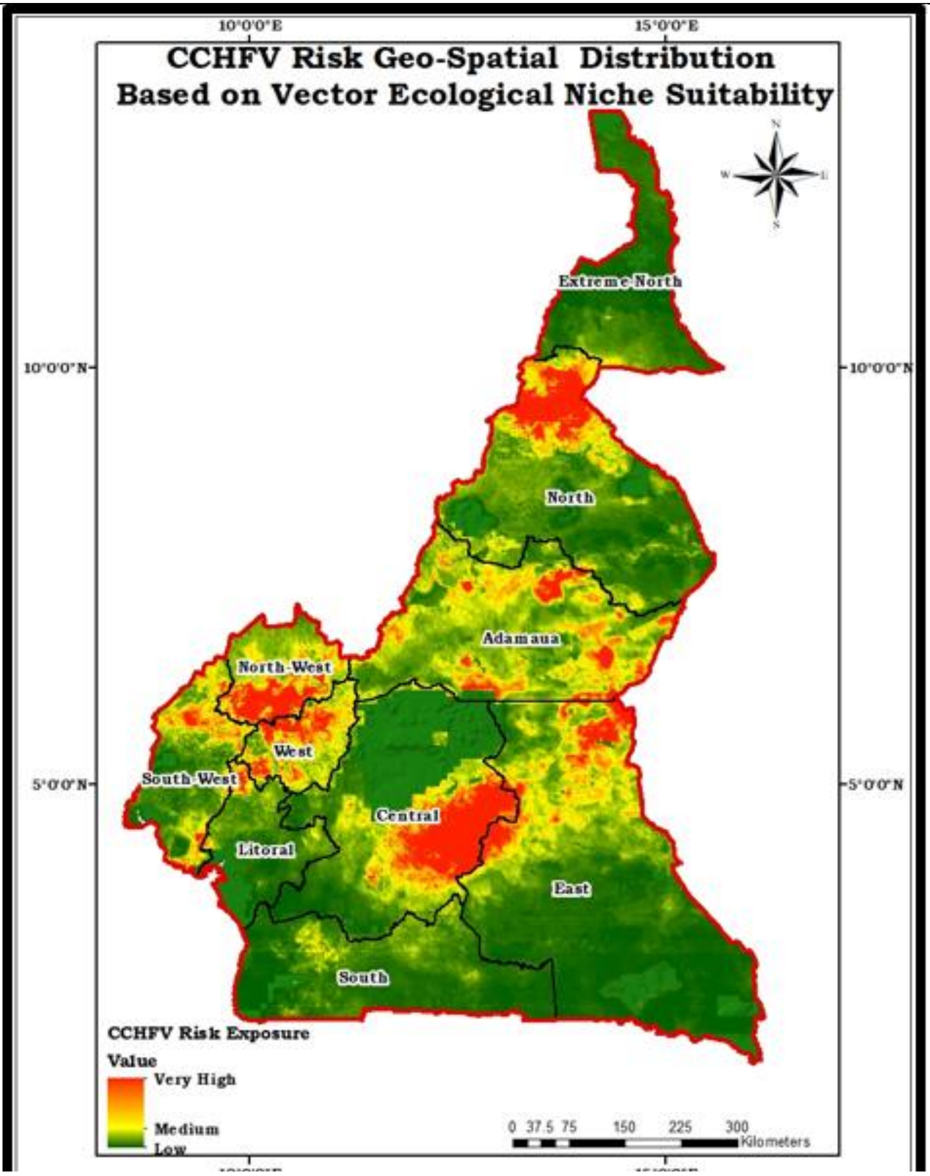
The accuracy of the models was determined by calculating their respective Areas Under the Curve (AUC) using the Receiver Operating Characteristics Curve (ROC) model validation approach, (Fawcett 2006; Nandi & Shakoor 2009) and observing the number of CCHFV tick vectors that fall within the various categories of the Crimean-Congo Hemorrhagic Fever Virus risk vulnerability model. The ROC operator characteristic is useful in representing the quality of the deterministic or probabilistic distribution and forecast system while the AUC characterizes the quality of the forecast system by demonstrating the system's ability to anticipate accurately the presence or absence of a pre-defined event, (Negnevitsky 2002). In an ROC curve, the false positive rate is plotted on the x- axis and false negative rate plotted on the *y*- axis. When calculating the ROC value, AUC values closer to **1.0** indicate high levels of accuracy of the model while results closer to **0.5** indicate inaccuracies in the overall model (Yilmaz 2010). When the AUC of the receiver operating characteristic (ROC) was calculated for this research, the mean of the ROC plot was **0.867** (test AUC = **0.867**, AUC Standard Deviation = **0.027**) asillustrated in (**Figure. 6**, below).



(Figure .6) The receiver operating characteristics (ROC) curve plotting the average area under the curve (AUC) for “Abiotic” and “Biotic” covariates after ten replicate runs.

The high AUC values indicate that the models’ predictive probabilities are accurate, and the high AUC value **(0.867)**,has not occurred by some random chance (Fielding and Bell 1997) and (Phillips and Dudik 2008), as such can be replicated successfully.

The final model outputas illustrated in (**Figure. 7**, below),was very successful in predicting the spatial distribution of suitability of the ecological niche for CCHFV tick vectors as well as the potential current and probabilistic spatial distribution of CCHFV risk vulnerability in Cameroon. Hence, laying a road map for CCHFV surveillance,prevention, and mediation as well as management frameworks in the event of a major CCHFV outbreak by monitoring hotspots and clusters on the tick vector pathogen ecological niche suitability and spatial risk vulnerability probability distributionModels.



(Figure. 7) CCHFV Risk Vulnerability Model Based on Tick Pathogen Vector Distribution and Ecological Niche Suitability

Discussion and Conclusion

Crimean-Congo hemorrhagic fever virus is an immense public health threat especially to health personnel and livestock industry workers in countries across West and Central Africa. The tremendous potential of the CCHFV to cause nosocomial outbreaks in Cameroon in association with the limited available treatment and management options for the infected clearly underscores the need for constant CCHFV surveillance in Cameroon (Lwande OW. Et al 2012) and (Akuffo et al 2016). CCHFV circulation in Cameroon has been repeatedly reported in wild and domestic animals in Cameroon from the early 1980’s to most recently in 2017 based on serological (Maurice Y. 1967), (Zeller HG. Et al. 1989) (Lebreton M. et al. 2006), (Rissmann M. et al. 2017) and molecularevidence (Rissmann M. et al. 2017). With respect to humans, anti-bodies have been documented in Cameroonians in urban settings particularly in the Northwestern regions and Northern parts of Cameroon Paix MA. Et al. 1988) and (Gonzalez JP. et al 1989). The recent plasma sample survey conducted between 2005 and 2012 of the Pigmies inhabiting the Eastern forest region in Cameroonrevealed the presence of seroprevalence CCHFV anti bodies (Sadeuh -Mba et al. 2018). Majority of the CCHFV research papers in Cameroon have cited the reports of CCHFV antibodies historically centered in urban settings (Foupouapouognigni Y. et al. 2011), which may have given the false impression this was simple an urban disease. With the detection of antibodies in the Pigmies in the East forest, a population that has lived in the forest for over 20,000 years mainly as hunters and gatherers (Gonzalez JP. et al. 1989), seems to suggest we have not fully understood the level of prevalence of CCHFV and its current spread in Cameroon.

The main purpose of this analysis, was to analyze the special distribution of CCHF virus tick vectors across the five agro- ecological zones of Cameroon in order to produce models of CCHFV potential risk vulnerabilitymodels that can be used for CCHFV surveillance and response guide in the event of a major outbreak of the virus in Cameroon. Knowledge of where the tick vectors live and flourish, is a crucial requisite for understanding other eco-regions or zones where they can survive as well as spread whatever diseases they carry for example CCHFV. With increasing availability of high resolution and inexpensive quality abiotic and biotic data over large areas, more and more analysis aimed at modeling various species distributions has been on the rise. In Central and West Africa for example, prior research papers have made advances in understanding and modeling the spatial distribution of diseases and their vectors for example Malaria research (Rogers DJ. et al. 2002) and (Moffet A. et al. 2007). However, there has been little research on CCHFV modeling at a country wide scale. Previous studies have isolated incidents of infection and location specific evidence of CCHFV antibodies (Maurice Y. 1967), (Zeller HG. Et al. 1989), (Lebreton M. et al. 2006), (Rissmann M. et al. 2017) and (Sadeuh -Mba et al. 2018) but none has modeled the potential risk vulnerability of Cameroonians to CCHF virus at a country wide scale by modeling the ecological niche suitability distribution of a wide variety of CCHFV tick vector species found in Cameroon.

This research paper attempts to breach that scholarly research gap. CCHFV like its tick vectors relies on some complex interactions between suitable environmental conditions, host, and favorable abiotic and biotic covariates for its viral maintenance . Modeling the geographic extent of the CCHF virus can be a daunting task due to the complex nature of the virus (i.e. insufficient detection due to absence of symptoms in its animal host), which is why this research attempts that modeling endeavor by mapping the potential spatial distribution of the tick vectors and potential virus risk vulnerability and exposure in Cameroon. No, such comprehensive research has been done for Cameroon at a very high resolution and fine scale, which makes this research topic so relevant for risk management currently. It is very likely that some Cameroonians are currently infected with CCHFV considering that testing facilities and disease awareness are still limited to the public. Broad species sampling among humans, livestock, and wildlife as well as virological analyses of CCHFV tick vectors would be of great interest in identifying the transmission hotspots of CCHFV in Cameroon. Such investigations would provide baseline data to set up and optimize a national CCHFV surveillance and control in Cameroon. Conclusively, the final model results of the maximum entropy modeling approach of this research could serve as a vital tool for health programs like the ones mention above and local government administrators looking to maximize the viability, efficiency, and effectiveness of disease prevention, control, and surveillance programs for example CCHFV across Cameroon.

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