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Ecological niche modeling as a tool for prediction of the potential geographic distribution of *Bacillus anthracis* spores in Tanzania

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ABSTRACT

Introduction: Anthrax is caused by the spore-forming, Gram-positive bacterium *Bacillus anthracis*. The aim of this study was to predict the potential distribution of *B. anthracis* in Tanzania and produce epidemiological evidence for the management of anthrax outbreaks in the country.

Methods: The Maxent algorithm was used to predict areas at risk of anthrax outbreaks based on the occurrence and environmental data in Arusha and Kilimanjaro regions; the model was later transferred to predict the entire country. Seventy percent of the occurrence data were used to train the model, while 30% were used for model evaluation.

Results: Four regions of northern Tanzania are predicted to have a high risk for anthrax outbreaks, while the southern and western regions had low-risk areas. Soil type (56.5%), soil pH (23.7%), and isothermally (10.4%) were the most important variables for the model prediction, and the most significant soil types were solonetz, fluvisols, and lithosols.

Conclusions: A strong risk level across districts of the Tanzania mainland was identified in this study. A total of 18 districts in Tanzania Mainland are predicted to be at very high risk of an anthrax outbreak occurrence. These findings are important for policymakers to effectively mount targeted control measures for anthrax outbreaks in Tanzania.

Introduction

Bacillus anthracis, the causative agent of anthrax in wildlife, livestock, and humans, is a soil-borne, spore-forming and Gram-positive bacterium (Mullins et al., 2011). Upon entry into a susceptible host, the spores germinate into vegetative cells, which replicate rapidly in the bloodstream resulting in septicemia (Dragon and Rennie, 1995). The septicemic infection leads to hemorrhage in the host, which results in blood oozing into the soil (Steenkamp et al., 2018). It is speculated that death of the susceptible host occurs due to a tripartite toxin produced by this bacterium (Smith and Keppie, 1954). The disease can be peracute, acute, or chronic depending on the host susceptibility, immunity status of the host, and size of the spore inoculum; however, the peracute form is the most common infection in herbivores, while scavengers such as dogs may be infected without showing symptoms (Acha and Szyfres, 2005). In humans, the skin form is the most common (FAO-OIE-WHO, 2008).

Disease transmission pathways are a complex system that involves several agents of dispersion. In wildlife conservation areas such as Serengeti, Ngorongoro Conservation Area, Kilimanjaro, Arusha, and Mkomazi national parks, it is not possible to rapidly and properly dispose of anthrax-infected carcasses. Bloody

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vultures contaminate water bodies through bathing after opening up and feeding on anthrax-contaminated carcasses (Blackburn et al., 2010). It can also be dispersed by insects such as necrophagous flies, which play a crucial role in spreading anthrax (Blackburn et al., 2014). Hugh-Jones and De Vos (2002) reported the role of blow flies, which feed on fluids of the anthrax-contaminated carcass and deposit their feces or regurgitate liquids on leaves of vegetation near the carcass, ready for transmission to another animal. However, biting/hemophagic flies are also considered to transmit anthrax among wild animals and livestock (Food and Agriculture Organization of the United Nations, 2003) and even to humans (Fasanella, 2013). The infection in humans occurs when *B. anthracis* penetrates through skin abrasions or mucous membrane when a person comes into contact with an infected animal (Klous et al., 2016) or animal products, through the inhalation of spores, or through the consumption of raw or undercooked infected meat (Bengis and Frean, 2014).

The disease burden and economic impact of anthrax in domestic animals is not yet fully documented (Lewerin et al., 2010). However, it is estimated that 2000–20 000 human anthrax cases are reported annually worldwide (Khomenko et al., 2013), with more cases occurring in Africa, Asia, the USA, and Australia (Fasanella et al., 2014). China reported 112 000 human cases during the years 1956–1997 (Chen et al., 2016). In 2004, the Pollino National Park in Italy reported animal deaths due to anthrax, accounting for 81 cattle, 15 sheep, nine goats, 11 horses, and eight deer (Garofolo et al., 2011). In Zambia, 521 human cases and five deaths (case fatality rate of 0.95%) were reported in 2011 (Hang'ombe et al., 2012). Kenya reported 53 deaths of Grevy's zebra in 2006 (Muoria et al., 2007) and Uganda reported 500 deaths of wildlife and 400 deaths of domestic animals in 2004–2005 (Coffin et al., 2015). In 2016, Tanzania experienced a large anthrax outbreak in Monduli District in the region of Arusha affecting 21 humans, 109 wildebeest, 21 Grant's gazelles, one rabbit, 10 cattle, 26 goats, and three sheep (Mwakapeje et al., 2017).

In favorable environmental conditions, the bacteria from drained blood form spores, which can remain dormant for an extended period of time in the soil, possibly decades, until they affect a new susceptible host (Driks, 2009). Studies on the environmental suitability for the persistence of spores have shown that soil parameters such as alkalinity, calcium and high organic matter contents (Dragon and Rennie, 1995; Hugh-Jones and Blackburn, 2009), elevation, precipitation, temperature, and vegetation biomass (Blackburn et al., 2007; Joyner et al., 2010) may support the extended survival of *B. anthracis* spores in the environment. In a previous retrospective study by the present authors' group, it was established that recurrence of anthrax outbreaks in human, livestock, and wildlife interface areas of northern Tanzania were highly correlated with cycles of short rainfall followed by dry and hot weather (Mwakapeje et al., 2018). However, the spatial ecology and anthrax outbreak pattern in the country are not well understood. Other studies have reported that areas with an ambient temperature above 15.5 °C (Munang'andu et al., 2012), and a cyclic rainfall pattern with high evaporation potential characterized by calcareous soil (Winsemius et al., 2006) tend to favor long-term survival of the *B. anthracis* spores, causing frequent anthrax outbreaks in such areas.

Ecological niche modeling is a tool for identifying geographic and ecological areas suitable for species persistence based on the environmental variables of known occurrence sites (Phillips and Elith, 2010). During modeling of species distribution, presence-only or both presence and absence data may be used. The use of both presence and absence data has been shown to improve the model performance in some cases (Brotons et al., 2013). Nevertheless, absence data are challenging to verify (Gu and Swihart, 2004) and therefore a modeling technique with presence data only (Anderson et al., 2002) can be employed. However, the species can be absent from the suitable habitat for historical reasons or due to failure to disperse to those areas (Holt, 2003). Various presence-only modeling techniques to predict the geographic distribution of *B. anthracis* spores have been employed, such as Maxent (maximum entropy) (Chikerema et al., 2013) and GARP (genetic algorithm for the rule-set prediction) (Barro et al., 2016). Comparing correlative models such as Bioclim, GARP, and Maxent using the same input data, Maxent was found to give the best predictions (Tarkesh and Jetschke, 2012). Therefore, in this study, Maxent (Phillips et al., 2006) was used to model *B. anthracis* spores persistence and its spatial distribution using presence-only data.

The aim of this study was to predict the potential geographic distribution of *B. anthracis* spores in Tanzania and produce epidemiological evidence for the management of anthrax outbreaks in Tanzania. This information will provide a better ecological and epidemiological understanding of frequent anthrax outbreaks in the most at-risk areas. It will also help to zone the country based on risks and inform decision-makers in the effective allocation of resources for targeted preventive and control measures, such as intensified surveillance, community awareness, improved diagnostic capacity, and livestock vaccination against anthrax in the identified high-risk areas (Kracalik et al., 2017a).

Materials and methods

Study areas

The study was conducted in the Arusha and Kilimanjaro regions of northern Tanzania, where the occurrence data for anthrax outbreaks were collected for whole-country modeling. The region of Arusha lies on the Kenyan border at latitude −3.36667 and longitude 36.683330, with an elevation of 1415 m above sea level. The population size of this region was estimated to be 1 694 310 in 2012 (2012 census) (The Minister of State — Planning and Parastatal Sector Reform, 1998). This region encompasses the savannahs and part of the Great Rift Valley. It has wildlife protected areas including the Ngorongoro Conservation Area (NCA), which contains the massive Ngorongoro Crater, and Arusha National Park, which covers volcanic Mount Meru. Manyara National Park, Grumeti Game Reserve, and Lake Natron Game Reserve are also found in this region. Meru, Ngorongoro, and Monduli districts were selected for this study.

The Kilimanjaro region is located in the northern part of the Tanzania mainland, south of the equator at 2°25′ and 4°15′; longitudinally it lies between 36°25′30″ and 38°10′45″ east of Greenwich and the region has an elevation of 2400 m above sea level. The 2012 census estimated a population of approximately 1 640 087, with an average annual population growth of 1.8% (Tanzania 2012 Population and Housing Census). The region has three ecological zones: lowland (1500 m and below), highland (1501–3000 m), and forest (3001 m and above) (Reform, 1998; Census, 2013). Kilimanjaro Region is bordered to the north and east by Kenya, to the south by Tanga Region, to the southwest by Manyara Region, and to the west by Arusha Region. The selected study districts in this region were Hai, Moshi Rural, Rombo, and Siha districts. Figure 1 illustrates the study area and the distribution of the occurrence data.

Anthrax occurrence data

A database of 192 mixed cases of human ($n = 68$), wildlife ($n = 21$), livestock ($n = 80$), and environmental ($n = 23$) samples was constructed from sporadic anthrax outbreaks, which occurred in different places of Arusha and Kilimanjaro regions in northern Tanzania between October 2016 and March 2018. This information was used to map risks of anthrax outbreaks for the whole of Tanzania.

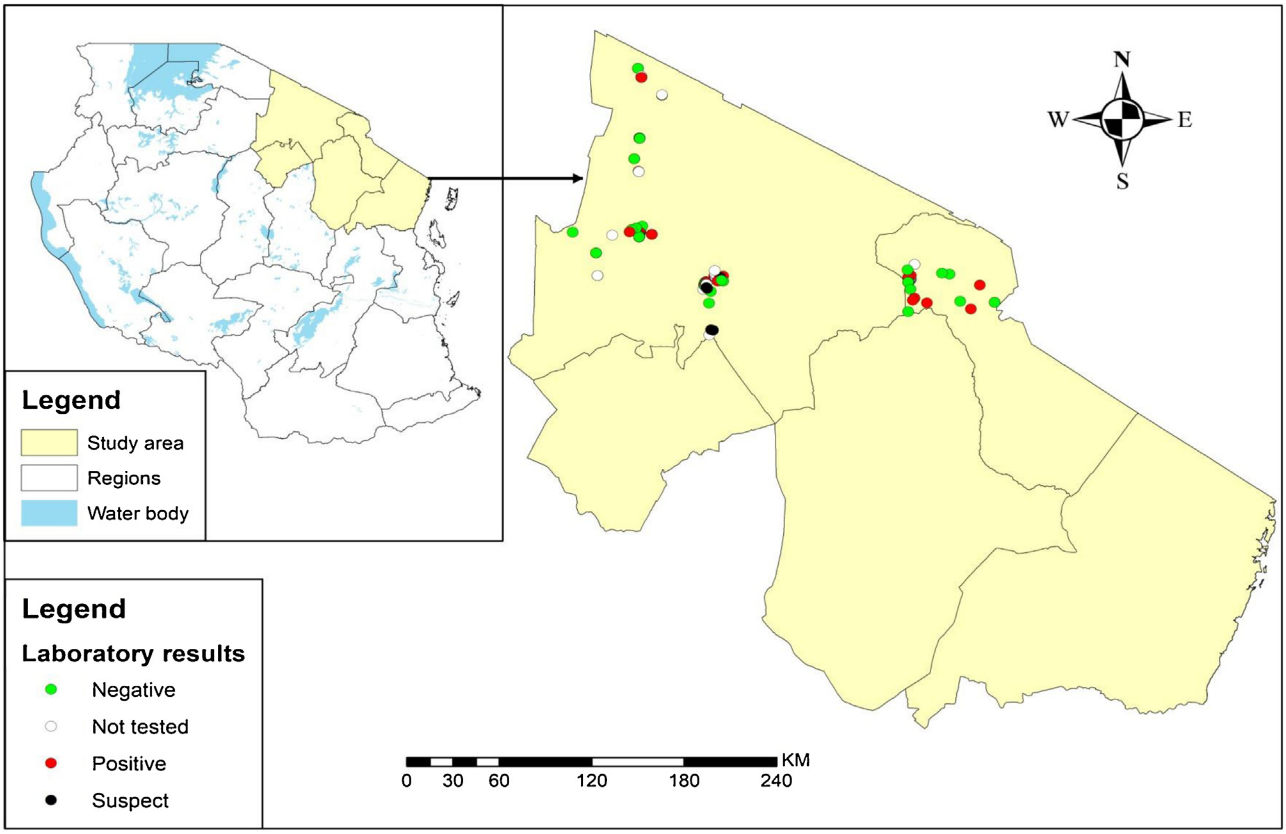

Figure 1. Map showing the study areas and distribution of the laboratory results in the areas sampled in northern Tanzania.

It is standard practice under normal circumstances during outbreaks that specimens for laboratory analysis are not taken from all suspected human cases; rather, a few are collected for confirmation of the existence of an outbreak. All specimens with errors in geo-coordinates and missing information were omitted from the database. Therefore, a total of 108 (56.25%) specimens were maintained in the database, of which 44 (40.74%) tested positive for *B. anthracis*. The positive cases for anthrax were linked to the geo-coordinates (latitude/longitude) that were collected either at a residence of a human suspected case or at a burial point of an animal carcass (livestock or wildlife) if a suspected human case reported any livestock death in the period 2 weeks prior to data collection, then geo-coordinates were collected at the carcass disposal site using a handheld global positioning system (GPS) machine. It should also be noted that on some occasions recording of the same geo-coordinates of outbreaks was repeated in different time periods; this also contributed to the lower number of occurrence data in the final database compared to what was recorded initially.

The collected data were stored in a Microsoft Excel spreadsheet. This was edited and the records with geo-coordinate errors, and the specimens which were not tested and those with negative laboratory results were removed from the dataset. A final version containing the geo-coordinates and positive laboratory results was saved in comma separated value (CSV) format, while environmental covariates were saved in ESRI ASCII format for further analysis in Quantum GIS software. Figure 1 shows the map of Tanzania illustrating the distribution of the geographical position of the sampled areas with the laboratory results of the collected specimens, following sporadic anthrax outbreaks in northern Tanzania. However, occurrence data from a small sampled area were used for model calibration and then to predict the habitat suitability of anthrax spores for the whole country.

Environmental covariates

A total of 21 climatic variables, as summarized in Table 1, were obtained from the 1-km grid Africlim database. These consisted of two categories of data: (1) temperature variables including annual mean temperature (BIO1), mean diurnal range (BIO2), isothermally (BIO3), temperature seasonality (BIO4), maximum temperature of warmest month (BIO5), minimum temperature of coldest month (BIO6), temperature annual range (BIO7), mean temperature of wettest quarter (BIO8), mean temperature of driest quarter (BIO9), mean temperature of warmest quarter (BIO10), mean temperature of coldest quarter (BIO11); (2) precipitation variables including annual precipitation (BIO12), precipitation of wettest month (BIO13), precipitation of driest month (BIO14), precipitation seasonality (BIO15), precipitation of wettest quarter (BIO16), precipitation of driest quarter (BIO17), precipitation of warmest quarter (BIO18), precipitation of coldest quarter (BIO19), moisture index arid quarter (MIAQ), and potential evapotranspiration (PET) (obtained from http://doi.org/10.1111/aje.12180). The variables were obtained under the current scenario that comprises monthly measurements obtained from weather stations around the world between 1950 to 2000 modeled under the 4.5 RCP (representative concentration pathways) scenario. Furthermore, 1-km grid soil type and soil pH data obtained from the ISRIC African soil database were also included; soil pH was included as a predictor variable because it has been shown that epidemics of anthrax are associated with an alkaline pH (Dragon and Rennie, 1995). Soil type as a categorical variable was also included in the model,

Table 1
Bioclimatic variables used for modeling by Maxent software.

Variable code	Variable description	Unit
1. Temperature variables		
Bio1	Annual mean temperature	°C
Bio2	Mean daily temperature	°C
Bio3	Isothermally (Bio2/Bio7) × 100	–
Bio4	Temperature seasonality (standard deviation × 100)	°C
Bio5	Maximum temperature of warmest month	°C
Bio6	Minimum temperature of coldest month	°C
Bio7	Temperature annual range (Bio5–Bio6)	°C
Bio8	Mean temperature of wettest quarter	°C
Bio9	Mean temperature of driest quarter	°C
Bio10	Mean temperature of warmest quarter	°C
Bio11	Mean temperature of coldest quarter	°C
PET	Potential evapotranspiration	mm
2. Precipitation variables		
Bio12	Annual precipitation	mm
Bio13	Precipitation of wettest month	mm
Bio14	Precipitation of driest month	mm
Bio15	Seasonal rainfall (coefficient of variation)	mm
Bio16	Precipitation of wettest quarter	mm
Bio17	Precipitation of driest quarter	mm
Bio18	Precipitation of warmest quarter	mm
Bio19	Precipitation of coldest quarter	mm
MIMQ	Moisture index moist quarter	N/A
MIAQ	Moisture index arid quarter	N/A
DM	Number of dry months	Months
LLDS	Length of longest dry season	Months

N/A, not applicable.

because the influence of soil type on *B. anthracis* spores persistence is ecologically documented and it is speculated that there is a significant relationship between the soil type and the extensive presence of anthrax outbreaks in certain areas (Griffin et al., 2014).

Model development

A pairwise Pearson correlation analysis for environmental variables was done using ENMTools (Warren et al., 2010). This was done in order to reduce multicollinearity of the environmental variables, and only variables with a lower than ±0.75 were retained for model fitting. After this procedure, the non-correlated environmental variables were chosen for the development of a species distribution model. The candidate variables identified included isothermally (BIO3), temperature seasonality (BIO7), moisture index arid quarter (MIAQ), potential evapotranspiration (PET), soil type (Sanchez et al., 2009), and soil pH.

A Maxent model was fitted using 100 bootstrap runs with 70/30 partition percentage for the training/testing datasets. Default Maxent model parameter settings were used (auto features, convergence threshold of 0.00001, maximum number of background points = 10 000, regularization multiplier = 1) (Phillips and Dudík, 2008). In order to train Maxent, one fold was used to fit a model and the remaining folds were treated as independent data for the evaluation of the predictive ability of the model performance (testing). A masked file was created and used in the model development in order to constrain the selection of background values, and the performance of the model was then evaluated. In each iteration, the contribution of every single variable to the general distribution was determined by Jackknife statistical technique, which allowed the variables with the greatest influence on the probability of persistence of *B. anthracis* and spatial distribution in Tanzania to be identified. However, the resolution of the resulting risk models was optimally maintained at 1 km.

Model evaluation

Several methods exist for the evaluation of model accuracy, but the most common method involves the area under the receiver operating characteristics curve (AUC) (Hanley and McNeil, 1982a). A successful model has an AUC value close to 1.0, and the higher the AUC, the better the model distinction of the presence from absence of a species; models with no clear distinction have an AUC close to 0.5 (Hanley and McNeil, 1982b). Evaluation of the critical individual environmental predictors in the model development was done by jackknife test, and response curves were also used to show how each environmental variable affects the Maxent prediction and how the logistic prediction changes as each environmental variable is varied, by keeping all other variables at their average sample value. Figure 2 illustrates a summary of the model development process and methods used to obtain significant variables for modeling.

Results

In the Maxent model, an AUC of 0.93 was obtained, indicating that the model had 'excellent' ability to predict the presence of *B. anthracis* spores in the most at-risk areas of the Tanzania mainland (Figure 3). The test indicated that the difference between the AUC from model prediction and the AUC at random was statistically significant, showing that the model performed better than random prediction.

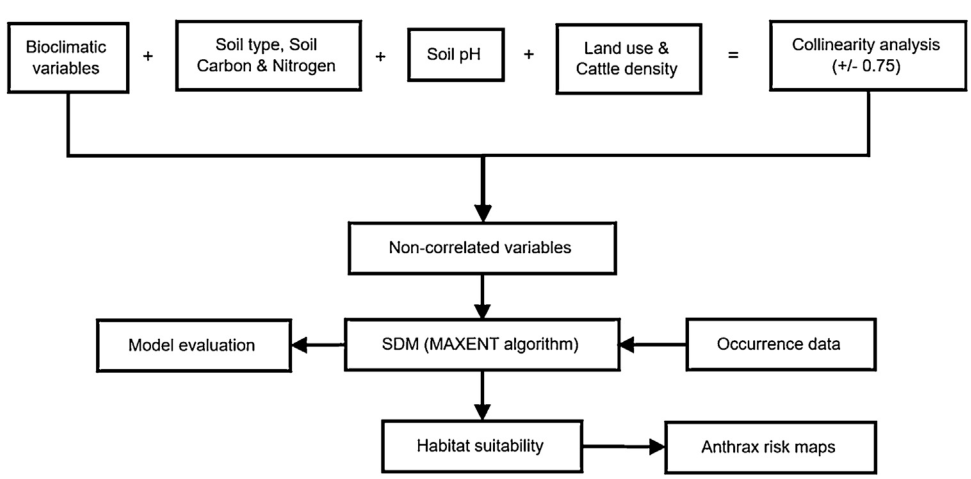

Figure 2. Flowchart indicating the model building process and potential variables included.

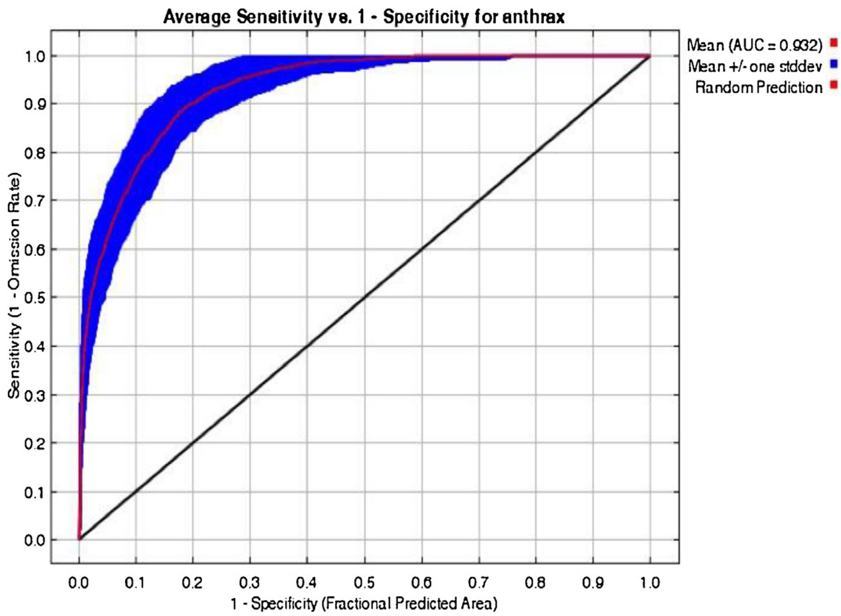

Figure 3. Average receiver operating characteristics (ROC) and related area under the curve (AUC) of the 100 bootstrap replicates.

Out of the 23 environmental variables, the following variables were identified as non-collinear: isothermally (BIO3), temperature seasonality (BIO7), moisture index arid quarter (MIAQ), potential evapotranspiration (PET), soil type (Sanchez et al., 2009), and soil pH. Table 2 indicates the percentage contribution of each of these variables, with soil type demonstrating the highest percentage contribution (56.5%), followed by pH (23.7%); hence the two variables (soil type and pH) in total contributed 80.2%. The Jackknife test helped to identify the variables contributing the most in the persistence and geographic distribution of *B. anthracis* spores in Tanzania.

The Jackknife test of variables indicated that omitting any of these six variables affected the regularization gain, AUC, and test gain in the model (Figure 4). Among the variables retained in the model, the soil type was the most important contributing variable to the model, followed by pH. However, pH decreased the gain the most when removed from the model. Therefore, by looking at the AUC of the Jackknife test, the most significant variables with scores of >0.7 (above fair) were soil type, soil pH, BIO3, and BIO7. Response curves for these variables with regard to their suitability for the prediction of *B. anthracis* spore geographic distribution are shown in Figure 5.

The response curve for soil pH showed that the probability of geographic suitability increased with the level of alkalinity (corresponding to high levels of calcium) in the soil.

The soil characteristics for the soil types that were identified as having the highest predictive power for *B. anthracis* spore survival (as shown in the response curve for soil types in Figure 5D and Table 3) were calcic cambisols (2), lithosols (9), eutric fluvisols (11), eutric histosols (16), and orthic solonetz (20). The soil type, soil pH, and isothermally were the most important variables; however, soil type was the single most important variable that accounted for 56.5% of the model prediction, with the following soil types identified as the most significant: solonetz, fluvisols, and lithosols.

Table 2
The percentage contribution and permutation importance of the variables used in Maxent modeling.

Variable	Percentage contribution	Permutation importance
Soil type	56.5	37.4
Soil pH	23.7	20.6
Bio3	10.4	26.8
MIAQ	5.2	9.4
PET	3.2	2.9
Bio7	1.1	2.9
Mask	0	0

Figure 6 shows a risk map indicating regions with very high, high, medium, and low probability of environmental suitability for persistence and spatial distribution of *B. anthracis* spores in Tanzania. The regions with stable areas of high and very high risk were Arusha and Kilimanjaro from the northern part of the country, while other regions like Mara, Manyara, Simiyu, and Singida had a few patches of high and very high risk areas. Regions like Dodoma, Mwanza, Dar es Salaam, Lindi, Mbeya, Rukwa, Katavi, and Kigoma were predicted to have a medium risk in a few locations, and the remaining regions in the country had a low risk of geographic suitability for *B. anthracis* spore persistence.

Discussion

Despite the fact that anthrax is a disease of both public and livestock importance in Tanzania, risk-mapping of the disease has not been used previously in the country. Consequently, there is no evidence-based allocation of resources for the prevention and control of the disease — bearing in mind that there are a lot of competing priorities for the distribution of financial resources in the country. Therefore, the findings of this study provide important insights for spatially allocating and prioritizing resources for anthrax surveillance, prevention, and control based on the predicted level of risk (very high, high, medium, and low) within each district. The district is an important administrative level for disease prevention and control policy implementation in Tanzania.

In this study, an ecological niche modeling technique was used to predict potential suitable habitat distribution of anthrax spores in Tanzania. This is the first study to present the potential risk distribution associated with *B. anthracis* spores in Tanzania using climatic and abiotic factors, such as soil type and soil pH. The regions of Arusha and Kilimanjaro had a higher risk (very high and high risk) of *B. anthracis* spore habitat suitability, as illustrated in the national prediction (risk map shown in Figure 6). The observations in the current study are in line with a previous report by Mwakapeje et al. (2018): in a retrospective

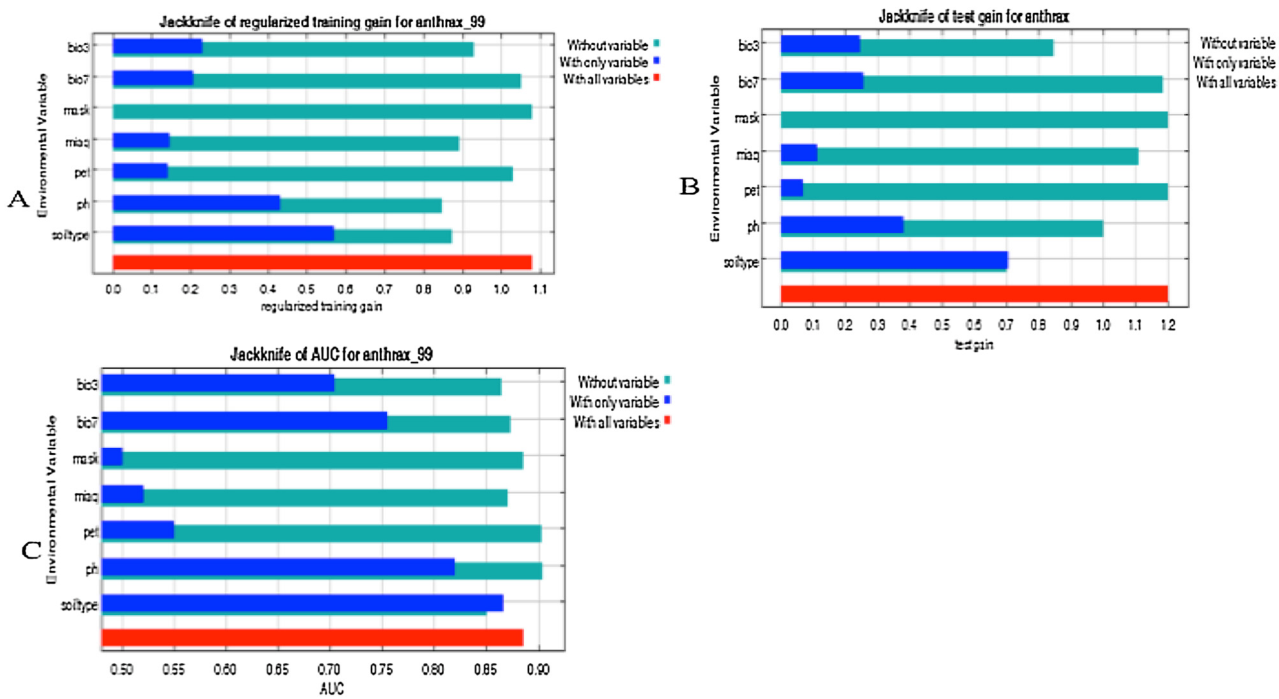

Figure 4. Jackknife tests of variable importance with (A) regularized training gain, (B) test gain, and (C) AUC. The light blue bars illustrate the model gain without variable inclusion, while the solid blue bars show its gain with the variable only.

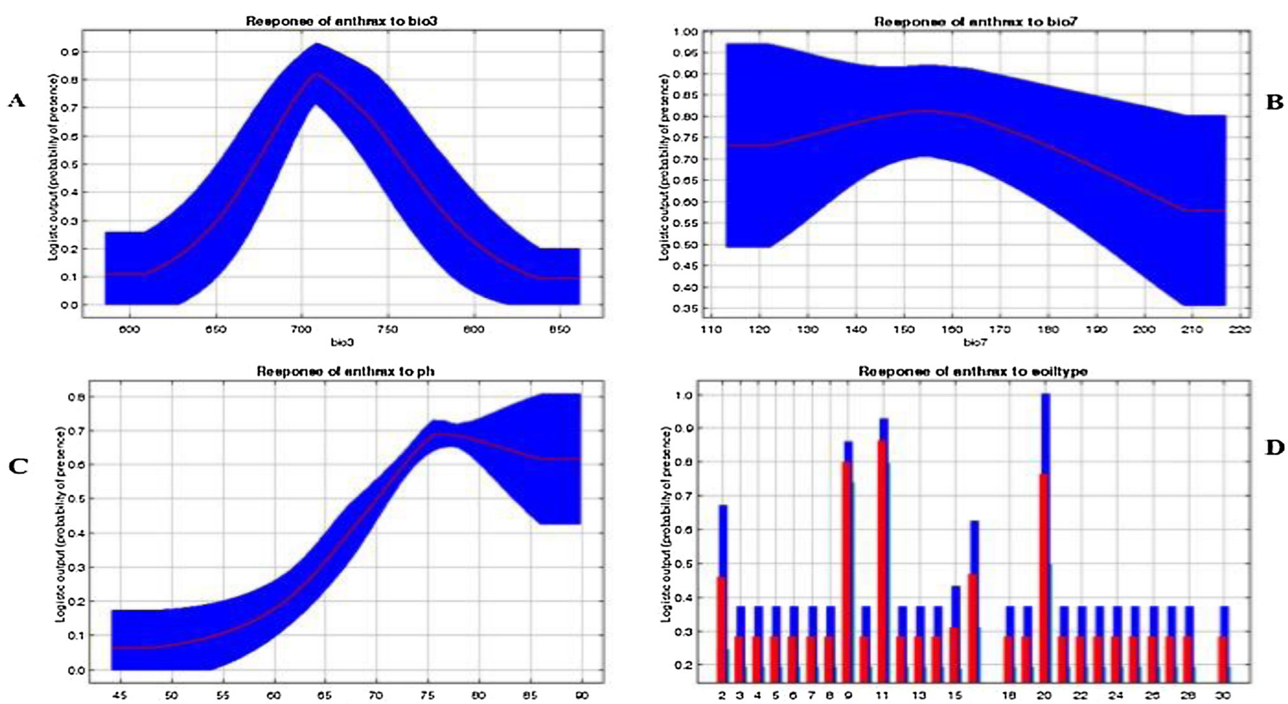

Figure 5. Response curves for the most significant variables in the Maxent model for the persistence of *Bacillus anthracis* in Tanzania: (A) BIO3 (isothermal), (B) BIO7 (annual temperature range), (C) soil pH, and (D) soil type. The red lines indicate the mean values, while blue areas denote 1 standard deviation limits, resulting from cross-validation model runs.

study (2006–2016), the incidence rate of human anthrax cases was found to be 7.88 per 100 000 population in Arusha Region, followed by 6.64 per 100 000 population in Kilimanjaro Region (Mwakapeje et al., 2018).

In the same predicted map, streaks of predicted very high and high risk were observed in Tanga, Coastal, Manyara, and Singida regions. From the predicted at-risk regions, the corresponding districts predicted with very high and high risks are indicated in Figure 7; these are Arusha Region (Ngorongoro, Monduli, Longido, Arusha Rural, and Meru), Kilimanjaro Region (Hai, Siha, Moshi Rural, and Rombo), Mara Region (Serengeti), Manyara Region (Simanjiro, Hanang, and Babati urban), Simiyu Region (Bariadi and

Table 3
Summary of soil types with a strong association to persistence and environmental suitability for *Bacillus anthracis* spores in Tanzania.

Soil code number	Soil type key	Soil type
20	So	Orthic solonetz
11	Je	Eutric fluvisols
9	I	Lithosols
2	Bk	Calcic cambisols
16	Oe	Eutric histosols

Itilima), Tanga Region (Kilindi), and Singida Region (Mkalama and Iramba). The areas within these regions are color-coded in the order of risk recognition. The ability to identify the risk associated with specific places and areas is extremely important for an efficient disease surveillance and control program.

In fact, some of the predicted districts with a high risk such as Hanang, Simanjiro, Itilima, Serengeti, Bariadi, Kilindi, Mkalama, and Iramba have had no reported anthrax cases through the surveillance systems. This might be attributed to the poor human and animal surveillance systems, leading to severe under-reporting and hence misleading disease burden information (Gibbons et al., 2014). Monduli and Ngorongoro are among the districts with a predicted high and very high risk of suitability for anthrax spores in Arusha Region, which corresponds with the recent frequent anthrax outbreaks in Monduli District; for instance in late 2016, a total of 130 wildlife carcasses, 39 livestock carcasses, and 21 human cases were confirmed to have been infected by anthrax (Mwakapeje et al., 2017). It is therefore envisaged that implementing targeted control measures based on the disease risk mapping will be more cost-effective, due to the reduced cost for carcass disposal, cost for laboratory reagents, and cost for outbreak management in general. It may also help in the implementation of a targeted livestock vaccination program and intensified human and animal disease surveillance, by focusing more closely on the predicted high and very high risk districts using the One Health approach (Cleaveland et al., 2017; Baum et al., 2017).

This model demonstrated that the environmental suitability for the persistence of *B. anthracis* spores was highly influenced by the soil type, pH, BIO3, BIO7, MIAQ, and PET variables, respectively. Apart from soil type and soil pH, other variables are categorized into temperature (BIO3 – isothermally, BIO7 – annual temperature range) and precipitation (MIAQ – moisture index arid quarter, PET – potential evapotranspiration) variables. Environmental variables such as soil and climate are postulated to favor and extend the survival of *B. anthracis* spores in the soil for a long period. This finding supports the results of other studies, which have shown that anthrax outbreaks are exacerbated by warmer temperatures, moist soils, and high organic matter content (humus) — these favor *B. anthracis* spore amplification (Dey et al., 2012).

It was found in this study that soil type and soil pH were the most significant variables for long-term persistence of anthrax spores in the identified high and very high risk areas. This is supported by other studies, which have shown that soil with high moisture, alkaline pH, and humus are suitable for anthrax spore germination and sporulation outside a mammal host; these are some of the critical variables that lead to the occurrence of anthrax outbreaks in animals, with spillover to humans (Kreuder Johnson et al., 2015). Other studies have documented that soil pH of more than 6.1 (alkalinity) in combination with calcium levels are

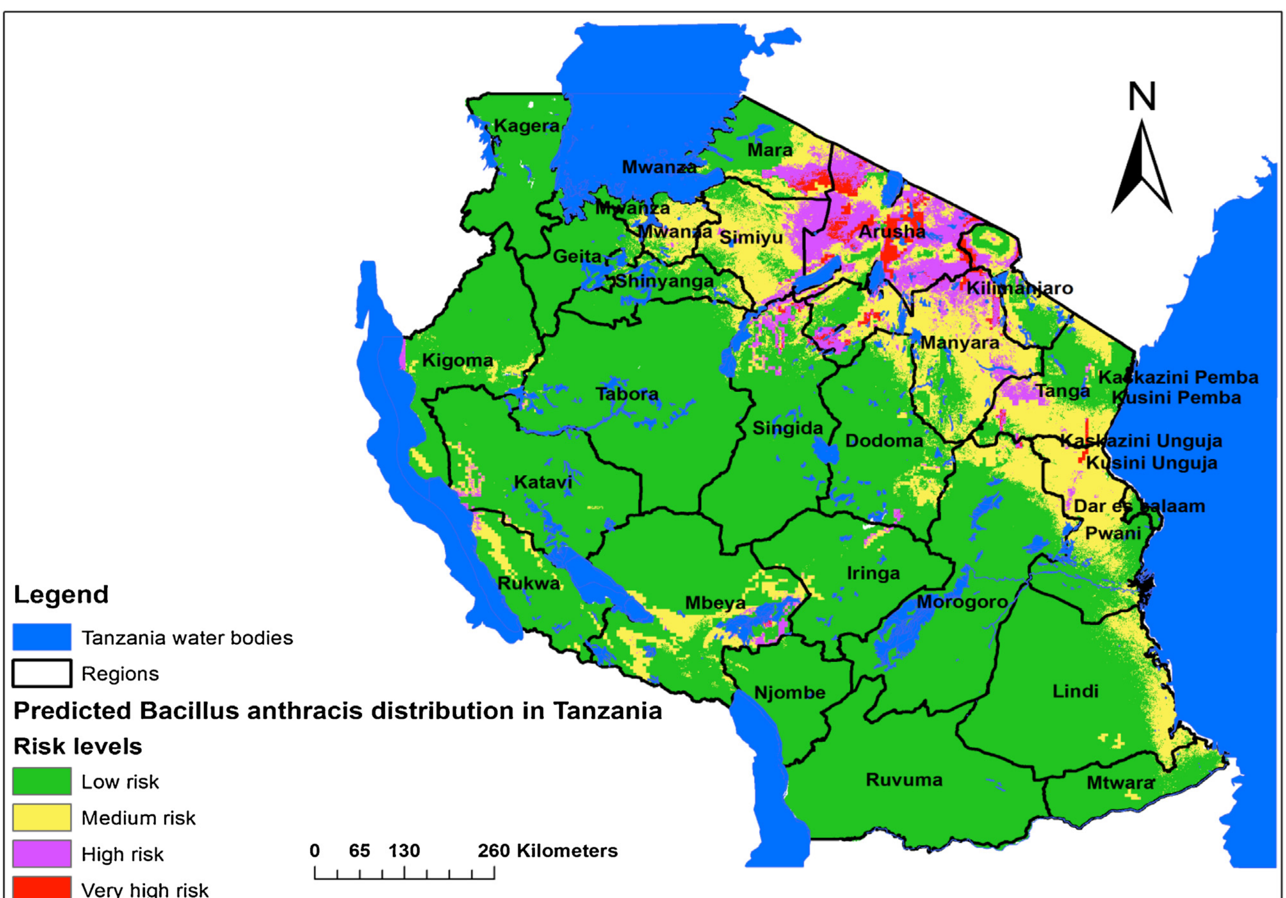

Figure 6. Risk map for the predicted environmental suitability of *Bacillus anthracis* spores within regions of the Tanzania mainland.

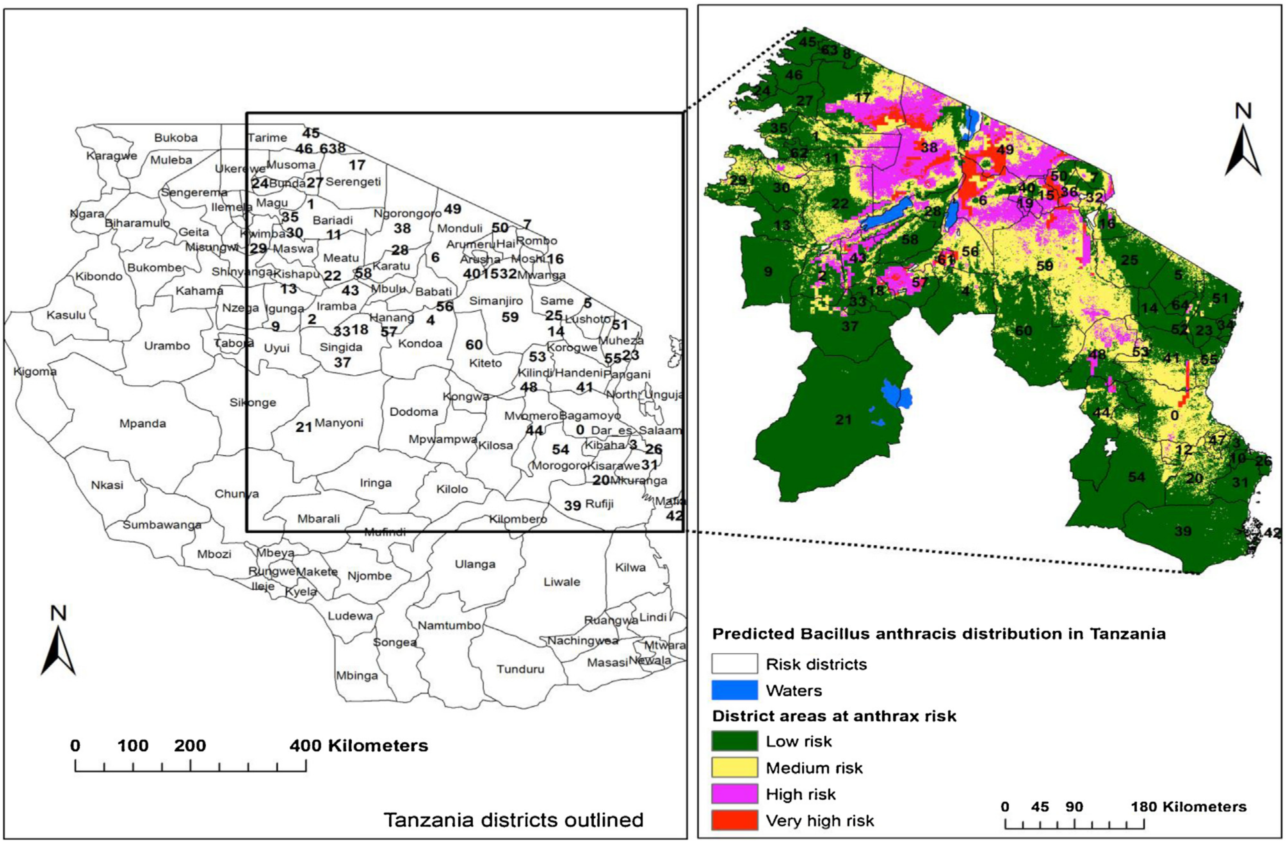

Figure 7. Risk map for the predicted environmental suitability of *Bacillus anthracis* spores distribution within districts in the very high risk regions of the Tanzania mainland.

important variables for the long-term survival of *B. anthracis* spores (Kracalik et al., 2017b). This type of soil is regarded as a natural reservoir for *B. anthracis* spores (Barro et al., 2016). This information is important for regional and district veterinary offices, as well as selected farming communities, to increase their awareness and the local relevance of predicted risks, the need to report unexpected livestock deaths, and also for livestock vaccination policy change.

Study limitations

During model building, factors such as livestock density, number of dry months, elevation, and length of the longest dry season were highly correlated with the most significant variables identified. Therefore, we are scientifically convinced that, apart from the identified most significant variables favoring the persistence of anthrax outbreaks in the areas with high and very high risk, there are other factors that contribute to anthrax-related deaths in Tanzania; for example the Gainer–Kolonin hypothesis of hyperacute deaths involving latent infections, climate stress, and severe seasonal biting-fly activity in the absence of suitable soils (Gainer, 2018). However, we still trust that the identified suitable environments for anthrax outbreaks are important regions and/or districts that should be given more attention, because they have been identified as hotspot areas for anthrax outbreaks in previous studies.

Conclusions

This study modeled the occurrence data and environmental variables to create risk maps with categorized risks, which assisted in establishing districts with very high, high, medium, and low risk of anthrax outbreak emergence in Tanzania. The results showed that northern Tanzania has a higher probability of the occurrence of anthrax outbreaks than other parts of the country. The most significant factors identified for anthrax persistence were soil type, soil pH, isothermality, mean temperature range, moisture index arid quarter, and potential evapotranspiration.

The categorized risks are important and will help to direct decision-makers with regard to resource allocation in a most cost-effective approach. The identified high-risk districts have to reduce mortalities in livestock and prevent the disease in humans through continued pre-outbreak targeted livestock vaccination, safe carcass disposal (preferably incineration) of animals that have died from anthrax, public awareness campaigns, the provision of relevant diagnostics for livestock and human care facilities, and intensified human and animal surveillance systems. These activities, if implemented effectively, will help to significantly control the existing devastating frequent anthrax outbreaks in the predicted high-risk areas of Tanzania.

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Conflict of interest

The authors declare no conflicts of interest.

Author contributions

ERM: conceptualized the study, collected specimens, participated in the laboratory confirmation of anthrax, participated in the data analysis and interpretation of the results, drafted the article, and addressed comments from the co-authors until the article was ready for submission to the peer review journal; SAN: participated in the conceptualization of the study, participated in the data analysis and interpretation of the results, and reviewed and commented on the article; GM: participated in the conceptualization of the study, participated in the data analysis and interpretation of the results, and reviewed and commented on the article; SA: participated in the conceptualization of the study, participated in the data analysis and interpretation of the results, and reviewed and commented on the article; LN: participated in the conceptualization of the study, participated in the data analysis and interpretation of the results, and reviewed and commented on the article; HEN: supervised the design of the study, and reviewed and commented on the article; RHM: supervised the design of the study, and reviewed and commented on the article; ES: supervised the initial design of the study, participated in the data analysis and interpretation of the results, participated in the conceptualization of the study, participated in drafting the article, and reviewed and commented on the article.

Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at https://doi.org/10.1016/j.ijid.2018.11.367.

References

Acha PN, Szyfres B. Zoonoses and communicable diseases common to man and animals: volume I. Bacterioses and mycoses. PAHO scientific and technical publication no. 580, I. 3rd ed. , doi:http://dx.doi.org/10.1590/S1135-57272005000300012 378 pp..

Anderson RP, Gómez-Laverde M, Peterson AT. Geographical distributions of spiny pocket mice in South America: insights from predictive models. Glob Ecol Biogeogr 2002;11(2):131–41, doi:http://dx.doi.org/10.1046/j.1466-822X.2002.00275.x.

Barro AS, Fegan M, Moloney B, Porter K, Muller J, Warner S, et al. Redefining the Australian Anthrax Belt: modeling the ecological niche and predicting the geographic distribution of *Bacillus anthracis*. PLoS Negl Trop Dis 2016;10(6), doi:http://dx.doi.org/10.1371/journal.pntd.0004689.

Baum SE, Machalaba C, Daszak P, Salerno RH, Karesh WB. Evaluating one health: are we demonstrating effectiveness?. One Health 2017;3:5–10, doi:http://dx.doi.org/10.1016/j.onehlt.2016.10.004.

Bengis RG, Frean J. Anthrax as an example of the One Health concept. Rev Sci Tech de l'OIE 2014;33(2):593–604, doi:http://dx.doi.org/10.20506/rst.33.2.2309.

Blackburn JK, McNyset KM, Curtis A, Hugh-Jones ME. Modeling the geographic distribution of *Bacillus anthracis*, the causative agent of anthrax disease, for the contiguous United States using predictive ecological [corrected] niche modeling. Am J Trop Med Hyg 2007;77(6)1103–10 77/6/1103 [pii].

Blackburn JK, Curtis A, Hadfield TL, O'Shea B, Mitchell MA, Hugh-Jones ME. Confirmation of *Bacillus anthracis* from flesh-eating flies collected during a West Texas anthrax season. J Wildl Dis 2010;46(3):918–22, doi:http://dx.doi.org/10.7589/0090-3558-46.3.918.

Blackburn JK, Van Ert M, Mullins JC, Hadfield TL, Hugh-Jones ME. The necrophagous fly anthrax transmission pathway: empirical and genetic evidence from wildlife epizootics. Vector Borne Zoonotic Dis 2014;14(8):576–83, doi:http://dx.doi.org/10.1089/vbz.2013.1538.

Brotons L, Thuiller W, Araújo MB, Hirzel AH. Presence-absence versus presence-only methods for predicting bird habitat suitability. Ecography 2013;27(4):437–48, doi:http://dx.doi.org/10.1111/j.0906-7590.2004.03764.x.

Census H. The United Republic of Tanzania, II. 2013.

Chen WJ, Lai SJ, Yang Y, Liu K, Li X, Lou, et al. Mapping the distribution of anthrax in mainland China, 2005–2013. PLOS Negl Trop Dis 2016;10(4), doi:http://dx.doi.org/10.1371/journal.pntd.0004637.

Chikerema SM, Murwira A, Matope G, Pfukenyi DM. Spatial modelling of *Bacillus anthracis* ecological niche in Zimbabwe. Prev Vet Med 2013;111(1–2):25–30, doi:http://dx.doi.org/10.1016/j.prevetmed.2013.04.006.

Cleaveland S, Sharp J, Abela-Ridder B, Allan KJ, Buza J, Crump JA, et al. One Health contributions towards more effective and equitable approaches to health in low- and middle-income countries. Philos Trans R Soc B Biol Sci 2017;372(1725), doi:http://dx.doi.org/10.1098/rstb.2016.0168.

Coffin JL, Monje F, Asiimwe-Karimu G, Amuguni HJ, Odoch T. A One Health, participatory epidemiology assessment of anthrax (*Bacillus anthracis*) management in Western Uganda. Soc Sci Med 2015;129:44–50, doi:http://dx.doi.org/10.1016/j.socscimed.2014.07.037.

Dey R, Hoffman PS, Glomski IJ. Germination and amplification of anthrax spores by soil-dwelling amoebas. Appl Environ Microbiol 2012;78(22):8075–81, doi:http://dx.doi.org/10.1128/AEM.02034-12.

Dragon DC, Rennie RP. The ecology of anthrax spores: tough but not invincible. Can Vet J 1995;36(5):295–301.

Driks A. The *Bacillus anthracis* spore. Mol Aspects Med 2009;30(6):368–73, doi:http://dx.doi.org/10.1016/j.mam.2009.08.001.

FAO-OIE-WHO. Anthrax in humans and animals. . p. 219, doi:http://dx.doi.org/10.2105/AJPH.30.3.299. www.who.int.

Fasanella A, Adone R, Hugh-Jones M. Classification and management of animal anthrax outbreaks based on the source of infection. Ann Ist Super Sanita 2014;50(2):192–5, doi:http://dx.doi.org/10.4415/ANN_14_02_14.

Fasanella A. *Bacillus anthracis*, virulence factors, PCR, and interpretation of results. Virulence 2013;4(8), doi:http://dx.doi.org/10.4161/viru.26517.

Food and Agriculture Organization of the United Nations. EMPRES transboundary animal diseases bulletin. EMPRES Transboundary Anim Dis Bull 2003;24:2–7.

Gainer RS. Spore concentration and modified host resistance as cause of anthrax outbreaks: practitioners' Corner Le coin des praticiens. Can Vet J 2018;59:185–7, doi:http://dx.doi.org/10.1590/S0074-02761985000200007.

Garofolo G, Serrecchia L, Corrò M, Fasanella A. Anthrax phylogenetic structure in Northern Italy. BMC Res Notes 2011;4:, doi:http://dx.doi.org/10.1186/1756-0500-4-273.

Gibbons CL, Mangen MJJ, Plass D, Havelaar AH, Brooke RJ, Kramarz P, et al. Measuring underreporting and under-ascertainment in infectious disease datasets: a comparison of methods. BMC Public Health 2014;14(1):1–17, doi:http://dx.doi.org/10.1186/1471-2458-14-147.

Griffin D, Silvestri E, Bowling C, Boe T, Smith D, Nichols T. Anthrax and the geochemistry of soils in the contiguous United States. Geosciences 2014;4(3):114–27, doi:http://dx.doi.org/10.3390/geosciences4030114.

Gu W, Swihart RK. Absent or undetected? Effects of non-detection of species occurrence on wildlife-habitat models. Biol Conserv 2004;116(2):195–203, doi:http://dx.doi.org/10.1016/S0006-3207(03)00190-3.

Hang'ombe MB, Mwansa J, Muwowo S, Mulenga P, Kapina M, Musenga E, et al. Human–animal anthrax outbreak in the Luangwa valley of Zambia in 2011. Trop Doct 2012;42(3):136–9.

Hanley JA, McNeil BJ. The meaning and use of the area under a receiver operating characteristic (ROC) curve. Radiology 1982a;143(1):29–36, doi:http://dx.doi.org/10.1148/radiology.143.1.7063747.

Hanley JA, McNeil BJ. The meaning and use of the area under a receiver operating characteristic (ROC) curve. Diagn Radiol 1982b;143:29–36, doi:http://dx.doi.org/10.1148/radiology.143.1.7063747.

Holt RDR. On the evolutionary ecology of species' ranges. Evol Ecol Res 2003;5:159–78.

Hugh-Jones M, Blackburn J. The ecology of *Bacillus anthracis*. Mol Aspects Med 2009;30(6):356–67, doi:http://dx.doi.org/10.1016/j.mam.2009.08.003.

Hugh-Jones ME, De Vos V. Anthrax and wildlife. Rev Sci Tech de l'OIE 2002;21(2):359–83, doi:http://dx.doi.org/10.20506/rst.21.2.1336.

Joyner TA, Lukhnova L, Pazilov Y, Temiralyeva G, Hugh-Jones ME, Aikimbayev A, et al. Modeling the potential distribution of *Bacillus anthracis* under multiple climate change scenarios for Kazakhstan. PLoS One 2010;5(3), doi:http://dx.doi.org/10.1371/journal.pone.0009596.

Khomenko S, Rozstanlnyy A, Gogin A, Kolbasov D, Pinto J, Lubroth J, et al. Anthrax outbreaks: a warning for improved prevention, control and heightened awareness. Empres Watch 2013;37(September) Available from: http://www.fao.org/3/a-i6124e.pdf. [Accessed 26 August 2018].

Klous G, Huss A, Heederik DJJ, Coutinho RA. Human-livestock contacts and their relationship to transmission of zoonotic pathogens, a systematic review of literature. One Health 2016;2:66–76, doi:http://dx.doi.org/10.1016/j.onehlt.2016.03.001.

Kracalik I, Malania L, Broladze M, Navdarashvili A, Imnadze P, Ryan SJ, et al. Changing livestock vaccination policy alters the epidemiology of human anthrax, Georgia, 2000–2013. Vaccine 2017a;35(46), doi:http://dx.doi.org/10.1016/j.vaccine.2017.09.081.

Kracalik IT, Kenu E, Ayamdooh EN, Allegye-Cudjoe E, Polkuu PN, Frimpong JA, et al. Modeling the environmental suitability of anthrax in Ghana and estimating populations at risk: implications for vaccination and control. PLoS Negl Trop Dis 2017b;11(10):1–17, doi:http://dx.doi.org/10.1371/journal.pntd.0005885.

Kreuder Johnson C, Hitchens PL, Smiley Evans T, Goldstein T, Thomas K, Clements A, et al. Spillover and pandemic properties of zoonotic viruses with high host plasticity. Sci Rep 2015;5:1–8, doi:http://dx.doi.org/10.1038/srep14830.

Lewerin SS, Elvander M, Westermark T, Hartzell LN, Norström AK, Ehrs S, et al. Anthrax outbreak in a Swedish beef cattle herd—1st case in 27 years: case report. Acta Vet Scand 2010;52(1):7, doi:http://dx.doi.org/10.1186/1751-0147-52-7.

Mullins J, Lukhnova L, Aikimbayev A, Pazilov Y, Van Ert M, Blackburn JK. Ecological Niche modelling of the *Bacillus anthracis* A1.a sub-lineage in Kazakhstan. BMC Ecol 2011;11:, doi:http://dx.doi.org/10.1186/1472-6785-11-32.

Munang'andu HM, Banda F, Siamudaala VM, Munyeme M, Kasanga CJ, Hamududu B. The effect of seasonal variation on anthrax epidemiology in the upper Zambezi floodplain of western Zambia. J Vet Sci 2012;13(3):293–8, doi:http://dx.doi.org/10.4142/jvs.2012.13.3.293.

Muoria PK, Muruthi P, Kariuki WK, Hassan BA, Mijele D, Oguge NO. Anthrax outbreak among Grevy's zebra (*Equus grevyi*) in Samburu, Kenya. Afr J Ecol 2007;45(4):483–9, doi:http://dx.doi.org/10.1111/j.1365-2028.2007.00758.x.

Mwakapeje ER, Assenga JA, Kunda JS, Mjingo EE, Makondo ZE, Nonga HE, et al. Prevention, detection, and response to anthrax outbreak in Northern Tanzania using one health approach: a case study of Selela ward in Monduli district. Int J One Health 2017;3:66–76, doi:http://dx.doi.org/10.14202/IJOH.2017.66-76.

Mwakapeje ER, Høgset S, Fyumagwa R, Nonga HE, Mdegela RH, Skjerve E. Anthrax outbreaks in the humans — livestock and wildlife interface areas of Northern Tanzania: a retrospective record review 2006–2016. BMC Public Health 2018;18:106, doi:http://dx.doi.org/10.1186/s12889-017-5007-z.

Phillips SJ, Dudík M. Modeling of species distributions with Maxent: new extensions and a comprehensive evaluation. Ecography 2008;31(2):161–75, doi:http://dx.doi.org/10.1111/j.0906-7590.2008.5203.x.

Phillips SJ, Elith J. POC plots: calibrating species distribution models with presence-only data. Ecology 2010;91(8):2476–84, doi:http://dx.doi.org/10.1890/09-0760.1.

Phillips SJ, Anderson RP, Schapire RE. Maximum entropy modeling of species geographic distributions. Ecol Model 2006;190(3–4):231–59, doi:http://dx.doi.org/10.1016/j.ecolmodel.2005.03.026.

Reform, M. of S.-P. and P. S. Kilimanjaro region socio-economic profile. 1998.

Sanchez PA, Ahamed S, Carré F, Hartemink AE, Hempel J, Huising J, et al. Digital soil map of the world. Science 2009;325:680–1.

Smith H, Keppie J. Observations on experimental anthrax: demonstration of a specific lethal factor produced in vivo by bacillus anthracis [3]. Nature 1954;, doi:http://dx.doi.org/10.1038/173869a0.

Steenkamp PJ, Van Heerden H, van Schalkwyk OL. Ecological suitability modeling for anthrax in the Kruger National Park, South Africa. PLoS One 2018;13(1):1–13, doi:http://dx.doi.org/10.1371/journal.pone.0191704.

Tarkesh M, Jetschke G. Comparison of six correlative models in predictive vegetation mapping on a local scale. Environ Ecol Stat 2012;19(3):437–57, doi:http://dx.doi.org/10.1007/s10651-012-0194-3.

The Minister of State — Planning and Parastatal Sector Reform. The Arusha Region Socio — economic profile. 1998.

Warren DL, Glor RE, Turelli M. ENMTools: a toolbox for comparative studies of environmental niche models. Ecography 2010;33(3):607–11, doi:http://dx.doi.org/10.1111/j.1600-0587.2009.06142.x.

Winsemius HC, Savenije HHG, Gerrits AMJ, Zapreeva EA, Klees R. Comparison of two model approaches in the Zambezi river basin with regard to model reliability and identifiability. Hydrol Earth Syst Sci 2006;10(3).