

# Beyond invasion: land use influencing bovine tuberculosis (bTB) infection as a function of ecosystem services

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## Research article

**Keywords:** encounter rate, host movement, invasive species, land use, proportion of Prosopis, species evenness

**Posted Date:** December 18th, 2019

**DOI:** <https://doi.org/10.21203/rs.2.19140/v1>

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# Abstract

**Background:** Changes in land use and associated ecosystem change have been described as one of the causal drivers in emerging and re-emerging of infectious diseases, but there is a notable scarcity of scientific knowledge to show whether, and how, land use change plays this role. Land use change may include the invasion of non-native woody species. We studied how and to what extent *Prosopis juliflora*, a most powerful invasive woody species, influences the prevalence of bovine tuberculosis (bTB) in cattle in the Afar Region, Ethiopia between November 2013 and April 2016. We examined the potential underlying mechanisms by which ecological consequences of land use, such as an invading woody species, alters the risk of bTB transmission.

**Methods:** A total of 2550 cattle from 102 herds were investigated for the presence of bTB using the comparative intradermal tuberculin test (CITT). Landsat images from 2014 were used to quantify the proportion of different land use types by applying a k-means unsupervised classification, and analyzing this within a buffer of 16km from the location of each cattle herd. A generalized linear model was used to quantify the relationship between bTB prevalence and the proportion of land use types. Then, multiple regression tree analyses were used to identify the most important land use predictor accounting for the variation in bTB prevalence.

**Results:** A model averaging analyses identified the proportion of *P. juliflora* as a significant risk factor for increasing bTB prevalence in cattle ( $b=12.2$ ,  $95\%CI=8.9-15.5$ ,  $p<0.001$ ), and multiple regression tree analysis identified the proportion of *Prosopis* as the most important land use predictor of bTB in cattle.

**Conclusions:** The loss in host species evenness and the increase in cattle movement as a consequence of the loss of palatable grasses in *Prosopis* areas could be potential mechanisms accounting for the observed higher bTB prevalence in these areas. Given the projected spread of *Prosopis*, land use changes and associated changes in host community composition could affect the risk of infectious diseases, which is important for decision makers when formulating disease control strategies.

## Background

In recent years, evidence suggests that land use practices drive emerging, re-emerging and further spreading of zoonotic diseases [1, 2, 3]. For instance, high percentages of forest edges nearby herbaceous cover increased exposure to tick vectors [4]. Vittor et al. (2006) found that the conversion of rain forests to agriculture has led to a re-emergence and increased incidence of malaria. Cleared land creates areas where water can become stagnant, providing breeding sites for mosquito species capable of parasite transmission [5]. A low proportion of riparian forest has been identified as an important predictor of whirling disease, due to increase stream sedimentation, thus, increasing habitat for oligochaetes [6]. Increased forest fragmentation was also associated with an increased risk of Lyme disease by creating suitable habitats for hosts [7]. Another study demonstrated that increased forest deforestation reduced the prevalence of *Trypanosoma cruzi*, etiologic agent of Chagas disease in

humans, in wildlife by reducing the abundance of mammalian reservoir hosts [8]. Therefore, understanding the underlying mechanisms how the risk of disease relates to the land use is important, both for predicting disease dynamics, and to provide valuable insights into successful control measures. Despite growing awareness that disease emergence may be related, at least in part, to land use [9], this study focuses on vector-borne diseases, while there is a notable scarcity of scientific knowledge to show whether, and how, ecological change plays this role on aerosol-borne animal diseases. Here, we examined the relation between the proportion of land use and bovine tuberculosis (bTB) prevalence in cattle, and explored the underlying mechanisms accounting for these observations.

Bovine tuberculosis (bTB), caused by *Mycobacterium bovis*, is a zoonotic disease of human, livestock and wildlife [10, 11], and cattle serve as the main host for the bacteria [12]. The disease is an important case of concern with potential public health, conservation and economic importance, since it can affect international trade of animals and animal products [13]. Inhalation of *M. bovis* is the principal route to bTB transmission and is facilitated by direct or indirect contact between infected and healthy animals. The direct or indirect interaction between hosts has several points at which alteration of the landscape could influence disease dynamics. Land use/cover could potentially influence bTB prevalence through direct effects on the host community composition, host densities and host contact networks. For instance, low proportion of forest, grassland, and other natural habitat due to anthropogenic influence has been associated with a number of ecological complications, resulting in reductions of biodiversity [14, 15]. Recent studies have shown that a reduction in biodiversity may increase the prevalence and transmission of bTB, as non-competent mammalian hosts at higher levels of biodiversity may dilute pathogen transmission, a mechanism termed the dilution effect [16, 17, 18]. Thus, it is important to distinguish between these processes, to understand how changes in land use indirectly affect pathogen transmission, and to be able to formulate control actions that minimize future disease outbreaks.

One of the other important pathways by which land use changes alter ecosystems is by the introduction of non-native species into novel landscapes [19, 20]. Incursion of non-native species is one of the most serious concern to natural ecosystems worldwide [21, 22, 23]. Recent evidence showed that land use changes due to invasion by invasive plant species affect the risk of exposure to diseases. For example, invasive plant species may increase the risk of infection to tick-borne diseases by increasing the density as well as the rate of encounter rate between ticks and their vertebrate hosts [24, 25]. Similarly, land use changes as a result of plant species invasions increase the risk of mosquito-borne diseases by providing favourable habitat for vector species [26], and providing a high-quality nutritional fruits and leaves for mosquito larvae [27]. *Prosopis juliflora* (further referred to as *Prosopis*) is among the most extremely invasive plants species globally, infesting over four million hectares of lands in arid and semi-arid part of Africa [28, 29, 30]. The species is native to Mexico, South America and the Caribbean. It was introduced in Ethiopia in the 1970s [31, 32] as a control mechanism to combat desertification [33; 34]. Around Awash in the Afar Region, about 30,000 ha of grassland, rangelands, water points and open *Acacia* woodland were estimated to be occupied by *Prosopis* [34]. Currently, the species is a most powerful invasive species, threatening biodiversity and mammalian host community structure [34]. As biodiversity loss is a predictor for the increase in bTB outbreaks [16, 17, 18], we expected that invasion of *Prosopis* might increase the

bTB prevalence through loss of non-competent or spillover mammalian hosts. The invasion by *Prosopis* reduces availability of palatable herbaceous species [34] which could increase the movement of cattle herds in search for pasture and increase the probability of contact with infected hosts. Moreover, areas that are currently invaded by *Prosopis* were important sources of forage for livestock in the dry season, leading to shrinkage of the range- and grasslands, and altering local host densities, and increasing contact among cattle herds. For instance, increased host movement have been repeatedly identified as one of the major risk factors for bTB infection in African cattle populations [35, 36, 37]. We, therefore, hypothesize that increasing *Prosopis* invasion can increase the risk of bTB infection by increasing contact among cattle herds. However, no study, to our knowledge, examined the effect of *Prosopis* invasion on the risk of disease transmission. Here, we explore the impacts of *Prosopis* invasion on bTB prevalence in cattle, and how these invasions may influence the key parameters of this host–pathogen interaction, leading to changes in bTB prevalence.

## Materials And Methods

### Study area

The field study was conducted from November 2013 to April 2016 in the Afar Region, Ethiopia, which is located in the Horn of Africa between 39°34' to 42°28'E longitude and 8°49' to 14°30' N latitude (Fig. 1). The region covers an area of 70,000 km<sup>2</sup>, divided into five administrative sub-regions, each of them comprising of several districts. The area has a bimodal rainfall pattern, with a long rainy season from July-September and a short rainy season from February-April. The mean annual rainfall ranges from 500 mm in the western escarpment to 150 mm in the eastern lowlands. The minimum and maximum annual temperature is 20 °C and 40 °C, respectively. The altitude ranges from 120 m below sea level in the north-east to 1500 m above sea level in the west [38].

Figure 1. Map of the study area illustrating the distribution of the districts in the Afar Region, Ethiopia.

### Study design and sample size determination

A cross sectional multi-stage sampling with 'sub-region' as the highest stage followed by 'district' (n = 17), and 'sub-district' (n = 34) as lowest sampling stages was used to select study villages. Study animals were obtained using a three-stage random sampling procedure. The 'village' within the sub-district was regarded as the primary unit, the 'herd' as secondary unit and 'individual animal' as tertiary unit. Herds of livestock in each sub-district were stratified into three groups based on herd size (large, medium and small) after calculating the average herd size of the sub-district. Herds (one herd from each stratum) and individual animals were selected randomly. A total of 102 livestock herds from 34 sub-districts (3 in each sub-district, one large, medium and small herd) were selected to identify bTB positive animals [37]. Informed consent was sought verbally from all livestock herders and herd owners. The total sample size per district was calculated using a 95% confidence interval at a 5% absolute precision following Thrusfield [39], which gave a total number of required animals of 2550. Herds (one herd from each stratum) and individual animals within herds were selected randomly.

# Tuberculin testing of cattle

To identify bTB positive animals, tuberculin skin testing was performed using Purified Protein Derivative (PPD, supplied by Prionics Lelystad B.V, Lelystad, The Netherlands). Bovine and avian PPDs were injected intradermally at two sites approximately 12 centimetres apart at the border of the anterior and middle thirds of one side of the neck. This was done after shaving the two sites using a razor blade. The skin thickness was measured with digital callipers prior to and 72 h after PPD injection. An animal was considered bTB positive if the reaction at the bovine site minus the reaction at the avian site was greater than  $\geq 4$  mm cut-off, according to the recommendations of the World Animal Health Organization [40]. In this study, livestock owned by one owner and/or his close relatives, in which, the animals shared common grazing sites, watering points, kept at night at a common site and moved together during migration, was considered as a single herd in the calculation of the herd prevalence. A herd was considered bTB positive if it had at least one tuberculin reactor animal [37, 40, 41, 42].

## Dung counts

Plots for dung counts were established using stratified random sampling. First, sub-districts were stratified according to vegetation type. 204 plots (6 in each of the 34 sub-districts) of  $100 \times 100$  m were laid out randomly in these vegetation types and were GPS geo-referenced. In each plot, we surveyed 50 transects of 100 m length and 2 m wide, and counted dung piles. Each pile of dung was attributed to a locally available wildlife species based on the size, shape and form of the pellets by using Stuart and Stuart [43], and with the help of experienced local trackers. The relative abundances of wild herbivores were estimated based on the frequency of faecal droppings found in the plot transects following Vicente et al. [44]. We divided each 100 m transect into 10 sectors of 10 m length. We defined sign frequency as the average number of 10-m sectors with the presence of wild herbivore droppings. Based on these frequencies, we calculated for each of the species the frequency-based indirect index (FBII):

Where  $s_i$  is the number of sign-positive sectors in the  $i$ th 100 m transect (i.e.,  $s_i$  varies between 0 and 10), and  $n$  is the number of 100 m transects considered (i.e.,  $n = 50$  for each plot; [44;18]).

## Questionnaire survey

Semi-structured interviews with the 102 herders and herd owners were conducted, gathering information on general herd management practices, livestock movement and herd size. Local agricultural officers, knowledgeable on local farming practices and who had received prior training on the administration and the scope of the questions assisted us during the interviews. The interviewer estimated the maximum movement distance of the livestock herd per day by tracing the herd movement in the area based on interview-derived information, bound by roads, streams, rivers or hills, village, district, sub-district, or region, wildlife habitat or park, or other physical indicators, which were located on a geo-referenced map. Subsequently, the maximum daily distance was calculated for sedentary and for the transhumance herds.

## Land use classification

We derive a land cover map from six Landsat 8 images (December 2014) with no cloud cover in the area of interest, obtained via the Centre Science Processing Architecture ordering interface ([espa.cr.usgs.gov](https://espa.cr.usgs.gov)). The description of the land use classes was based on the standard classes defined by the US Geological Survey [45]. Accordingly, we identified eight classes, namely, farmland, bushland, grassland, area covered by Prosopis, Acacia woodland, wetland, water bodies, and bare land (Table 1).

Table 1  
The description of the land use classes used in the Afar Region, Ethiopia.

<b>LULC classes</b>	<b>General description</b>
Farmland	Areas of land ploughed or prepared for crop growing (i.e., both areas identifiably under crop agriculture and land under preparation).
Bushland	Areas with shrubs, bush and small trees in which multiple stems and branches are produced from the base of the main stem.
Grassland	Areas covered primarily with different grass species and with herbaceous plant species, which are used as a natural grazing land, with scattered shrubs, bushes and trees.
Prosopis	Areas covered with <i>P. juliflora</i> , an invasive plant species with dark evergreen leaves and closed canopy cover throughout the year.
Acacia woodland	Areas dominated by Acacia species found along the major perennial rivers (Mile and Awash). The vegetation is usually evergreen (due to continuous water supply from the rivers) and serves as a dry season feed for livestock.
Wetland	Areas covered with swamps and wetlands
Water bodies	Areas with water bodies
Bare land	Areas with essentially no vegetative cover

Table 1. The description of the land use classes used in the Afar Region, Ethiopia.

We classified the images by means of a k-means unsupervised classification, using Erdas Imagine. Initially, 36 clusters were requested, for which the maximum number of iterations was set to 20, and the convergence threshold to 0.950. Subsequently, each of the 36 clusters was given one of the eight class labels, based on Google Earth imagery, resulting in a map with eight classes and its proportion.

Farmland and Prosopis were often grouped together, and therefore we performed a principal component analysis (PCA) using Landsat 8 bands 3 and 4 to separate these two classes. After the PCA, we applied another unsupervised classification to the first component. We then labelled the classes as Prosopis. We had difficulty to classify farmland, because different crops are in different developmental stages and have different spectral information. Therefore, we used the large commercial irrigation farms present in the area via Google Earth, and added them to our classification.

We constructed a reference set of 61 points, using Google Earth images. These reference points served as 'ground truth data' to define the accuracy of the classified map and calculate the kappa coefficient of agreement. We determined the proportions of the land use classes within a buffer of 16 km around each of the 102 study herds, which is the daily average distance of herd movement [37], using ArcGIS.

## Statistical analysis

Shannon's diversity index ( $H'$ ) was used to estimate mammalian species diversity as;

where  $p_i$  is the proportion of species  $i$ , and  $S$  is the number of species [46].

Pielou's index was used to estimate mammalian species evenness [46], which is most widely used in ecology [47].

where  $H'$  represents the Shannon diversity index, and  $S$  is the total number of species observed.

Biodiversity metrics were calculated using package `vegan` of R v3.2.0 [48].

We quantified the relationships between bTB prevalence and proportion of land use in two separate analyses. First, we used a Generalized Linear Model to examine the effects of the proportion of land use on bTB prevalence as a binary response. From the global model, we constructed candidate models using  $\Delta AIC < 5$ , with the best approximating model having the lowest  $\Delta AIC$  [49]. We used model averaging to construct the final model based on the lowest Akaike weights of the different candidate models [50]. So, we analysed differences in host community composition as function of the proportion of land use type to examine the possible underlying mechanisms through which land use type altered bTB prevalence. Secondly, we used regression tree analyses to identify the most important land use predictors accounting for the variation in bTB prevalence. We used multivariate regression tree analysis because of its ability to deal with non-normal data, numerical and categorical data, as well as its ability to automatically consider the interactions among explanatory variables [51]. We carried out all analyses in R v3.2.2 [52].

## Results

Grassland was by far the dominant land cover followed by bushland (Fig. 2). Farmland, Prosopis and acacia woodland were often minor components of the landscape, but the major part of the main dry season grazing land, which is found in the Awash River basin, was covered by Prosopis, followed by acacia woodland (Fig. 2). The overall map accuracy of classification was 70%, and the kappa coefficient was 0.63.

Figure 2. Classification of land use types in the Afar Region, Ethiopia, on the basis of 2014 Landsat images.

## Land use and bTB prevalence

There was a significant positive relationship between the proportion of Prosopis and bTB prevalence, but bTB prevalence tended to be relatively lower in areas with a higher proportion of bushland (Table 2).

Table 2

Summary statistics of the final model, obtained through model averaging, with regression coefficient (b, 95% CI), Odds Ratio (OR, 95% CI) and p-value from the likelihood ratio test for the effect of proportion of land use on bTB prevalence in Ethiopian cattle.

Land use type	b (95% CI)	OR(95% CI)	p-value
Prosopis	12.2 (8.9–15.5)	20.4(7.9–52.7)	< 0.001*
Bushland	-0.06 (-1.2-0.6)	0.7(0.3–1.8)	0.279
Grassland	-0.01(-1.1-0.9)	0.9(0.5–2.5)	0.958
Acacia woodland	0.01(-2.8-6.8)	1.2(0.6–6.7)	0.935
Farmland	0.48 (-5.2-6.6)	7.2(6.3–8.2)	0.447
OR = Odds Ratio, CI = 95% confidence intervals; * P < 0.05; ** p < 0.01; *** p < 0.001			

Table 2. Summary statistics of the final model, obtained through model averaging, with regression coefficient (b, 95% CI), Odds Ratio (OR, 95% CI) and p-value from the likelihood ratio test for the effect of proportion of land use on bTB prevalence in Ethiopian cattle.

The multivariate regression tree analysis indicated that the proportion of Prosopis and bushland in the landscape were correlated with bTB prevalence (Fig. 3), with a higher bTB prevalence in cattle in areas with a higher Prosopis proportion. The first split of the multivariate regression tree was determined by the proportion of Prosopis, grouping 67 herds (average bTB prevalence was 1.7%) that had less than or equal to 1.3% Prosopis proportion. The second split was determined by proportion of bushland, grouping 12 herds (average bTB prevalence: 2.1%) that were located in areas with a bushland proportion < 26.6% (Fig. 3).

Figure 3: Pruned regression tree for predicting the prevalence of bTB prevalence with explanatory land use proportion variables. Each partition is labelled with the splitting rule and its value. Splitting statements are true to the left and false to the right. Terminal nodes are labelled with the predicted (mean) bTB prevalence value of the observations in the terminal group and the number of observations (n).

The regression tree analyses confirmed that the variable ranking first, i.e., the proportion of Prosopis, was also the variable that had a significant association with the bTB prevalence in the GLM. The regression tree analysis also included bushland proportion as the second important predictor variable after Prosopis, similar to the GLM.



# Land use and host community

Regression tree models also identified *Prosopis* proportion as the most important land use predictor contribute to the reduction in mammal species evenness (Fig. 4A) and livestock herd movement (Fig. 5A). We found that the mean species evenness (Pielou's species evenness,  $J'=0.76$ ) was the lowest recorded in the area with the highest proportion of *Prosopis* ( $>7\%$  cover), indicating that the proportion of *Prosopis* was correlated with a low species evenness in the landscape. When the proportion of *Prosopis* cover was  $<7\%$ , species evenness was positively correlated with the proportion of *Acacia* woodland (Fig. 4A).

The best explanatory variable correlated with Shannon's species diversity index was the proportion of grassland. When the proportion of grass was  $\geq 55\%$  the predicted mean species diversity was relatively high at 1.8 (Fig. 4B).

Figure 4. Pruned regression tree using proportion of land use type as a predictor for predicting A) species evenness,  $J'$  and B) Shannon's diversity,  $H'$ . Each partition is labelled with the splitting rule and its value. Splitting statements are true to the left and false to the right. Terminal nodes are labelled with the predicted (mean) value of the observations in the terminal group and the number of observations ( $n$ ).

The movement of cattle herd was also correlated to proportion of *Prosopis* cover, with the greatest herd movement in areas with a higher proportion of *Prosopis* (Fig. 5A). Herds in areas with a proportion of *Prosopis*  $<1.3\%$  had the lowest mean herd movement (5.8 km/day). The regression tree showed that the proportion of bushland was the primary predictor differentiating herd size, eventually splitting into five groups of herd size, with smaller herds in areas with relatively more bushland (i.e.  $\geq 47\%$  cover; Fig. 5B).

Figure 5. Pruned regression tree using the proportion of land use type as a predictor for predicting A) herd movement and B) herd size. Each partition is labelled with the splitting rule and its value. Splitting statements are true to the left and false to the right. Terminal nodes are labelled with the predicted (mean) value of the observations in the terminal group and the number of observations ( $n$ ).

## Discussion

Measures of land use may be useful predictors of bTB risk at various spatial scales. Our study showed that bTB prevalence was positively associated with the invasion of *Prosopis*. Similarly, a regression tree model identified the proportion of *Prosopis* as important land use predictor for the prevalence of bTB. The invasive *Prosopis*, although only a minor proportion of the total area of the landscape, has invaded the majority of the dry season pastureland of the Awash River Basin and causes significant environmental damage and habitat destruction [33], and thereby indirectly regulates host community composition. The loss in host species evenness and the increase in cattle movement as a consequence of the loss of palatable grasses in *Prosopis* areas could be potential mechanisms accounting for the observed higher bTB prevalence in these areas.

Invasive species have the ability to change ecosystem processes [53] and decrease the abundance, structure and diversity of native species [54, 55]. Similarly, invasion of *Prosopis* has been shown to suppress the growth of grasses and other herbaceous species and reduce species diversity [33, 56, 57]. The low diversity of herbaceous plant species observed under the dense *Prosopis* canopy is associated with a lower light intensity and shorter light period received by the understorey native plant species as well through competition for soil moisture [56]. The influence of *Prosopis* on the palatable herbaceous species in highly invaded areas may contribute to the reduction in mammal species evenness that we observed, as abundance and distribution of mammal species is partly determined by the availability and quality of palatable plant species [58, 59]. Haregeweyn et al. [33] also reported negative impacts of *Prosopis* invasion on biodiversity in the Afar Region, as the invasion of *Prosopis* reduced the densities of wild animal species, such as oryx (*Oryx gazelle*), zebra (*Equus grevyi*), dik-dik (*Madoqua saltiana*), and kob (*Kobus ellipsiprymnus*) in response to a reduction of palatable plant species. As biodiversity loss is an explanatory factor of the increase in the bTB risk [16, 17, 18], bTB prevalence might increase through losses of non-competent or spillover mammalian host species. In pastoral areas of East Africa, the distribution and abundance of large grazers is negatively associated with the presence of cattle [60, 61, 62]. Odadi et al. [63] found that the preference of foraging habitat for cattle was lower in the presence of wild grazers. Loss of wild herbivores due to *Prosopis* invasion might increase encounter rates between susceptible and infected cattle herds. Such an “encounter increase” [64] might increase bTB infection risk.

Another way by which *Prosopis* may influence the prevalence of bTB is through livestock herd movement. Invasion of *Prosopis* species have been observed to suppress grass growth and reduce availability of herbaceous plant species [65]. The invasion by *Prosopis* reduces availability of palatable herbaceous species in the study area [34]. Several useful palatable plant species such as *Chrysopogon plumulosus*, *Cymbopogon schoenanthus*, *C. pospischilii*, *Andropogon canaliculatus*, *Eragrostis cylindriflore* and *Terapogon cenchriformis* are now on the verge of local extinction in areas due to *Prosopis* invasion [33, 34], which could increase the movement of cattle herd in search for pasture. Our study also showed that high proportion of *Prosopis* cover increased the movement of livestock herd. The herd moved more and grazed in larger areas, hence the probability of contact with either infected domestic or infected wildlife hosts increased, amplifying the chances for bTB infection [37]. Furthermore, *Prosopis* forms dense thorny thickets, which creates landscape barriers for host movement and decreases the permeability of the landscape. This can increase the encounter rates between susceptible and infected hosts, and thereby increase bTB transmission rates.

The dense canopies of *Prosopis* creates a soil that better retains humidity than surrounding non-*Prosopis* areas. Empirical studies conducted in Sudan showed that wind speed inside *Prosopis* plantation was reduced by 14%, while potential evaporation was reduced by 22% [66]. *M. bovis* has been detected in soil samples in East Africa [67], and experimental studies have confirmed that the bacteria can survive for multiple days outside hosts [68]. Kelly and Collins [69] suggested that the major factors influencing survival of the bacteria in soil is soil temperature and moisture, as high temperature causes desiccation, and negatively influence survival of the bacteria. Environmental persistence of *M. bovis* has been

proposed to play a role in the transmission of bTB in the UK [70]. Humid areas are also potential risk factors, and soils with higher levels of moisture and shade offer favourable conditions for *M. bovis* survival as demonstrated in Tanzania [71] and Zambia [72]. The moist and shaded conditions created by *Prosopis* can serve as propagating factors for *M. bovis*, by creating favourable conditions for the survival of the bacteria.

## Conclusion

Our findings contribute to a growing body of literature that illustrates how land use change can alter the prevalence of diseases through altering the host species community composition, and density and mobility of hosts. The loss of biological diversity and the homogenization of host communities have the potential to increase the prevalence of and risk of exposure to zoonotic diseases. Removal of the invader could mitigate disease risk, coupled with the benefits of invasive plant removal to wildlife communities, suggesting a potential win-win scenario for biodiversity conservation and disease control. However, our results are a necessary first step towards understanding the role of invasive species on bTB risk and identifying the underlying mechanisms. More experimental studies including surveys of host communities in invaded and uninvaded areas by *Prosopis*, coupled with a *Prosopis* removal experiment are needed to distinguish between these pathways.

## Declarations

### Ethical Approval and Consent to participate

This study was approved by Haramaya University, Ethiopia (Reference number HUP14/559/15; 37). All animal owners gave verbal informed consent.

### Consent for publication

Not applicable

### Availability of supporting data

The authors declare that all data and material used in the publication will be available online.

### Competing interests

The authors declare that they have no competing interests.

### Funding

NUFFIC and Haramaya University

**Author Contributions:** Conceived and designed the experiments: SWD, WFdB, IMA, HHHTP, EEV. Performed the experiments: SWD. Analyzed the data: SWD, EEV. Wrote the paper: SWD. Reviewed the manuscript: SWD, WFdB, IMA, HHHTP, EEV, HB.

## Acknowledgements

We are grateful to NUFFIC for the financial support of the PhD scholarship through Wageningen University for the first author. We thank Haramaya University for the logistical support. We are also indebted to all field and laboratory staff who worked with us during tuberculin testing, habitat survey and laboratory work. Finally, we are grateful to all herders and herd owners who collaborated with us during the interviews and bTB testing.

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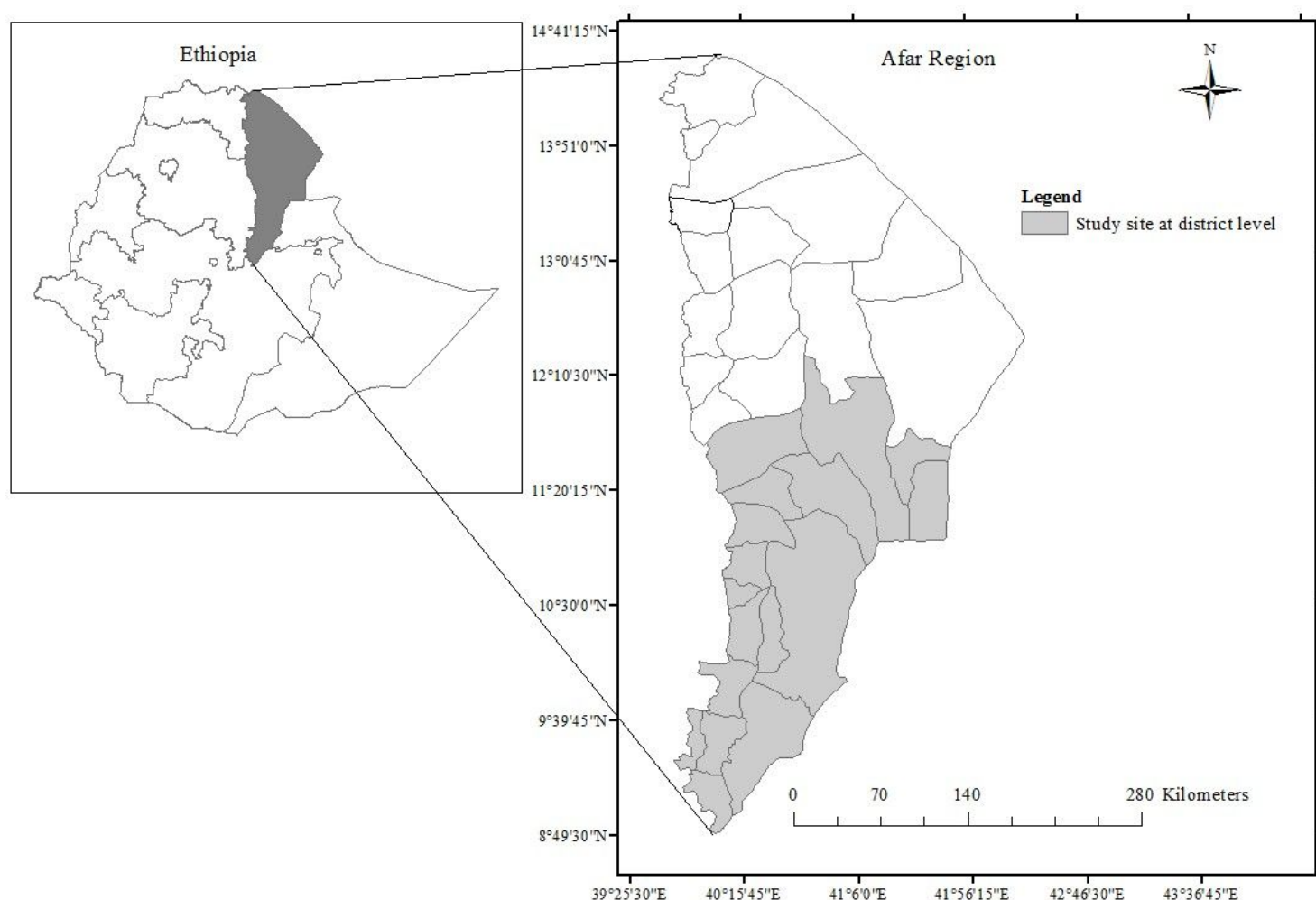
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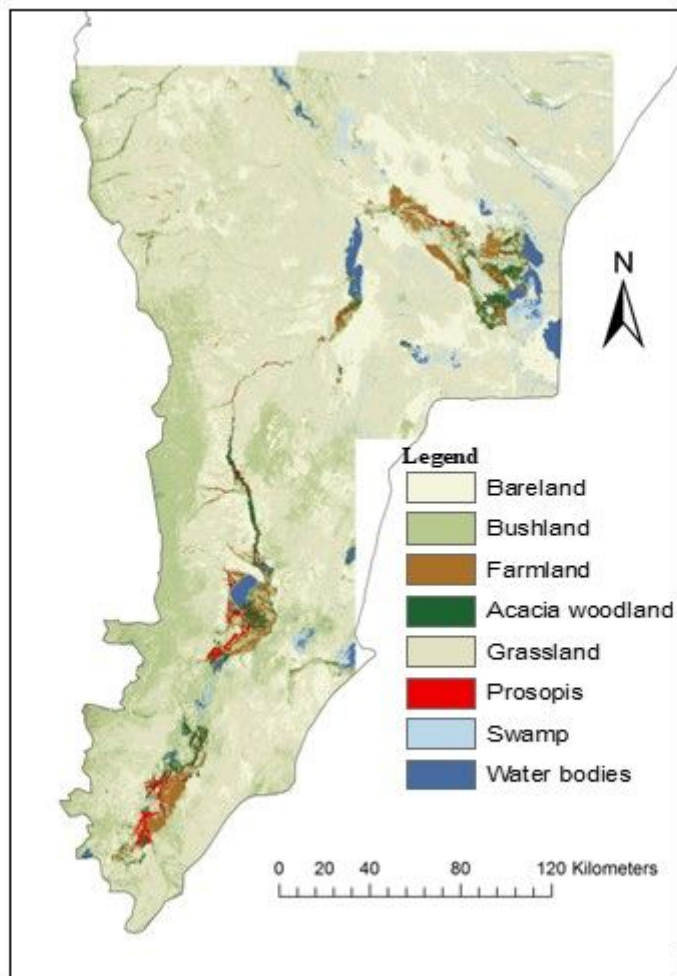
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## Figures



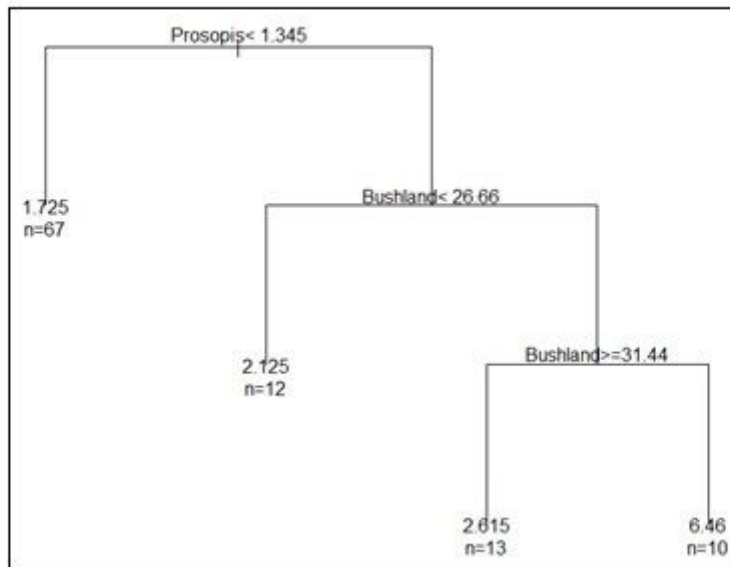
**Figure 1**

Location of the study area illustrating the distribution of the districts in the Afar Region, Ethiopia.



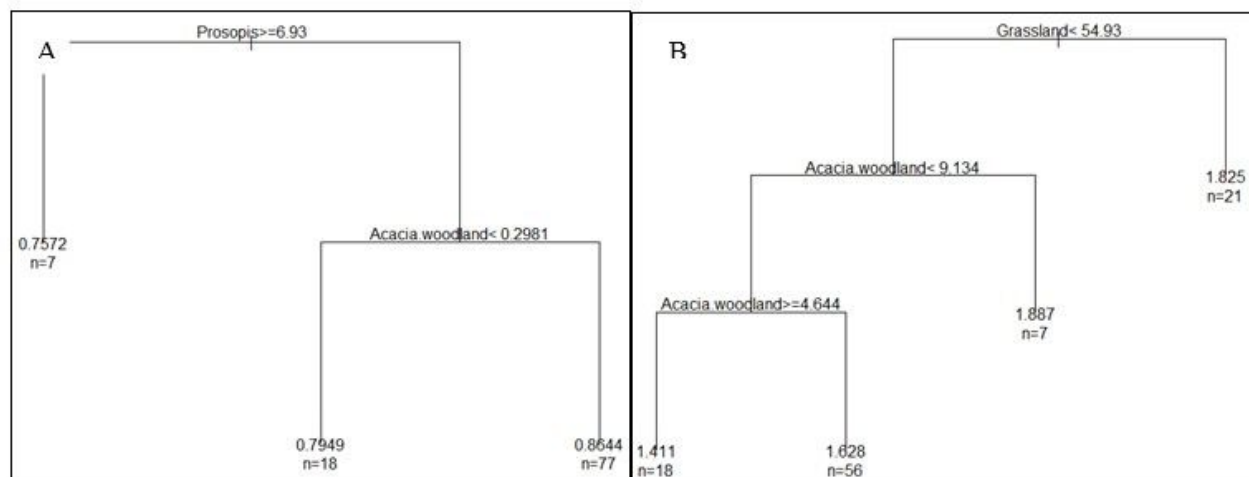
**Figure 2**

Classification of land use types in the Afar Region, Ethiopia, on the basis of 2014 Landsat images.



**Figure 3**

Pruned regression tree for predicting the prevalence of bTB prevalence with explanatory land use proportion variables. Each partition is labelled with the splitting rule and its value. Splitting statements are true to the left and false to the right. Terminal nodes are labelled with the predicted (mean) bTB prevalence value of the observations in the terminal group and the number of observations (n).



**Figure 4**

Pruned regression tree using proportion of land use type as a predictor for predicting A) species evenness,  $J'$  and B) Shannon's diversity,  $H'$ . Each partition is labelled with the splitting rule and its value. Splitting

statements are true to the left and false to the right. Terminal nodes are labelled with the predicted (mean) value of the observations in the terminal group and the number of observations (n).

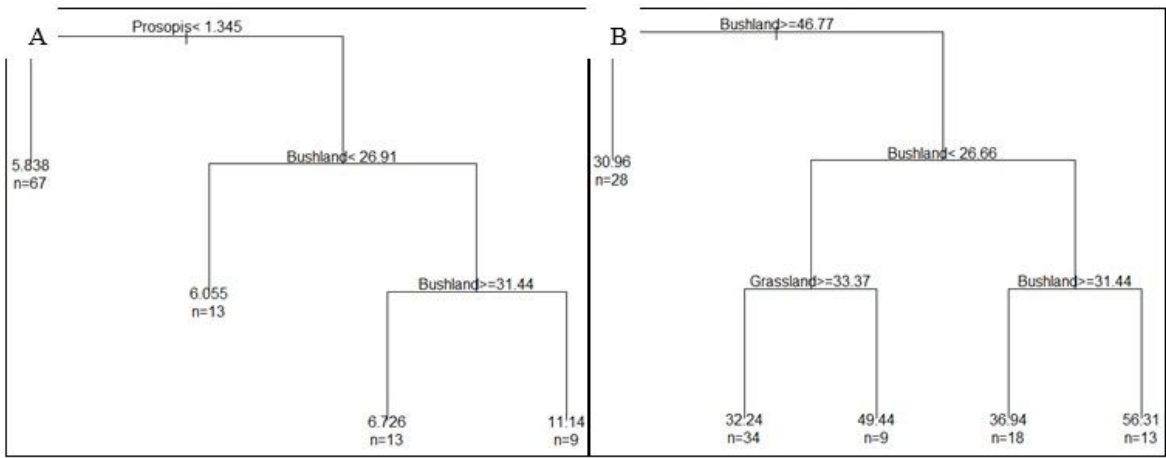


Figure 5

Pruned regression tree using the proportion of land use type as a predictor for predicting A) herd movement and B) herd size. Each partition is labelled with the splitting rule and its value. Splitting statements are true to the left and false to the right. Terminal nodes are labelled with the predicted (mean) value of the observations in the terminal group and the number of observations (n).