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Transmission risk of vector-borne bacterial diseases (*Anaplasma* spp. and *Ehrlichia canis*) in Spain and Portugal

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Abstract

Background Ehrlichiosis and anaplasmosis are vector-borne bacterial diseases produced by intracellular rickettsial species of the genus *Ehrlichia* and *Anaplasma*. *Ehrlichia canis* and *Anaplasma* spp. (*A. platys and A. phagocytophilum*) have reported cases of zoonotic transmision and are the main bacterial agents of canine ehrlichiosis and anaplasmosis. They normally present an asymptomatic or mild course in domestic and wild animals with some lethal cases reported. The main vector of these diseases in Europe are the castor bean tick (*Ixodes ricinus*) and the brown dog tick (*Rhipicephalus sanguineus*), although only in the latter, the main host is the domestic dogs. The aim of this work is to apply an integrative approach to convert ecological niche models (ENMs) into potential transmission risk models and understand the relative contribution of the two potential vectors (*R. sanguineus* and *I. ricinus*) to spread both diseases in the Iberian Peninsula and Balearic Islands.

Results Two ENMs meeting all criteria were successfully generated for *R. sanguineus* and *I. ricinus* with human footprint being the most relevant explanatory variable. The novelty of the study lies in the combination of independent ENMs for both species to estimate the disease transmission risk of specific bacteria (*E. canis*, *A. platys* and *A. phagocytophilum*). Only the transmission risk maps that had higher contribution of *R. sanguineus* than *I. ricinus* showed relevant and positive significant correlations between risk and seroprevalence in either of the two species of bacteria ($R \geq 0.4$; $p < 0.05$). Regarding *Anaplasma* spp., the map having 10% contribution of *I. ricinus* (10I) and 90% of *R. sanguineus* (90R) inferred 47.4% of infected dogs in very high-risk areas. In the case of *E. canis*, the model showing a proportion of 25I-75R showed better validation power (53.4% of infected dogs in very high-risk areas).

Conclusion The validation approach used in this study produced a good approximation to understand the relative contribution of the two tick species in bacterial disease transmission in dogs in the Iberian Peninsula and Balearic Islands. *Rhipicephalus sanguineus* appears as the main transmitter of both diseases in the study area (90% and 75% for anaplasmosis and ehrlichiosis respectively), in accordance with its higher abundance and host preference. This estimate may help veterinary staff, clinicians and owners to optimize the control of these diseases in certain vulnerable areas, and thus reduce the risk of infection in risk areas.

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Keywords Ecological niche models, Future projections, Transmission risk, *Rhipicephalus sanguineus*, *Ixodes ricinus*, *Anaplasma* spp., *Ehrlichia canis*, Spain, Portugal

Background

Ehrlichiosis and anaplasmosis are vector-borne bacterial diseases affecting different types of blood cells from domestic, farm and wild animals with life-threatening cases reported in humans [1–4]. The etiologic agents described so far comprised intracellular rickettsial species of the genus *Ehrlichia* and *Anaplasma*. The main vector of these pathogens are ticks of the genus *Ixodes* spp., *Rhipicephalus* spp. and *Dermacentor* spp., arachnids with a widespread range across the globe known to parasite domestic and wild animals [1, 5–8].

Ehrlichia canis, *Anaplasma phagocytophilum* and *Anaplasma platys* are the main bacterial agents of canine monocytic ehrlichiosis, granulocytic anaplasmosis and canine cyclic thrombocytopenia respectively [9]. *A. phagocytophilum* is more typically found in granulocytes of rumiants and horses, and *A. platys* and *E. canis* are a usual pathogen in dogs' platelets and monocytes respectively [1, 10]. All of them present an asymptomatic or mild course with some exceptions [11, 12]. These species have reported cases of zoonotic disease in different countries [13–15].

Both the castor bean tick (*Ixodes ricinus*) and the brown dog tick (*Rhipicephalus sanguineus*) have been frequently reported as transmitter of these diseases in dogs, although only the latter is considered the main domestic host [10, 16–18]. In fact, *A. platys* is a pathogen mostly transmitted by *R. sanguineus* whereas *A. phagocytophilum* is usually found in *I. ricinus* [1]. In the same way, the main transmisor of *E. canis* is *R. sanguineus* although there are several cases reporting *I. ricinus* transmission [10, 17, 19].

The distribution of these diseases is cosmopolitan and subject to multiple social and environmental factors that make them dynamic both spatially and temporally [20]. In southern Europe, these diseases are considered endemic, with their main vectors widely distributed throughout the territory [21, 22]. The seroprevalence of *Anaplasma* spp. in domestic dogs in Spain is 5.1% and in Portugal 4.7%, with the highest seroprevalence mainly located in southern regions [22–25]. In relation to *E. canis*, mean seroprevalences in Spain and Portugal are similar, being 4.3% in Spain, with the highest seroprevalences reported towards the east, and 4.1% in Portugal, with high seroprevalences in the south [23, 25–27]. In addition, there are several reports on the occurrence of these diseases in cats and different species of ungulates and wild carnivores. In Portugal, seroprevalences of *Anaplasma*/*Ehrlichia* spp. in cats range from 0.6 to 5.4%, being the highest in the south [28, 29]. On the other hand, the prevalences of *A. platys* and *E. canis* in red foxes (*Vulpes vulpes*) are 14.5% and 2.9% respectively [30]. In Spain, the reported prevalence of *A. phagocytophilum* for wild ungulates (roe deer, red deer, fallow deer and wild boar) in the north was 24.2%, while in the south it was 9.2% [31, 32].

Eco-informatic tools such as ecological niche models (ENMs), have great potential to model infection risks of vector-borne disease and perform disease control and prevention [33]. ENMs of ticks transmitting bacterial diseases have been inferred to assess the geographic distribution and anticipate range expansions considering environmental variables such as temperature, precipitation, between others [34–37]. However, there is still work to do to improve estimations through niche model integration from different vectors or even considering the biology of the pathogen in the transmission cycle [33, 38].

Previous vector-borne disease risk models have shown great potential to produce realistic estimations, including those weighting ENMs from the vector with the biological characteristics of the parasite [39–41]. Other predictions of vector's distribution patterns have joined observations from different species to estimate potential risk areas [42]. However, that approach can be controversial if vectors include species with different ecological requirements because they violate the theoretical assumptions of niche modelling [43]. The problem therefore arises when addressing diseases transmitted by more than one vector, as the two cases described above, and where we cannot join observations from different species with distinct ecological preferences (i.e. *I. ricinus* is present in the eurosiberian whereas *R. sanguineus* in the mediterranean-atlantic region) to produce risk models.

In this study, we apply an integrative approach to convert ENMs into potential transmission risk models to assess the transmission risk of ehrlichiosis and anaplasmosis in areas where more than one vector occurs. We develop an approximation to understand the relative contribution of two potential vectors (*R. sanguineus* and *I. ricinus*) to spread both diseases in the present and future projections in dogs from the Iberian Peninsula and Balearic Islands. The model can be extrapolated to other domestic and wild species in other regions.

Methods

Study area

The territory established as the study area is the Iberian Peninsula (40°14'24" N 4°14'21" W), comprising the continental part of Spain and Portugal, and the Balearic Islands (39°30'00.0"N 3°00'00.0"E) (Spain). These territories are located in southeastern Europe, very close to the African continent, although separated by the Strait of Gibraltar. The Canary Islands, the Azores and Madeira, overseas territories of Spain and Portugal, have not been taken into account in this study due to their particular biogeographical characteristics, which are very different from those of the mainland territories. The Iberian Peninsula (590,000 km^2) is mostly surrounded by water, to the east and south by the Mediterranean Sea, to the north by the Cantabrian Sea and to the west by the Atlantic Ocean. The Balearic Islands, with 4,992 km^2, are an archipelago in the Mediterranean Sea made up of the islands of Mallorca, Menorca, Cabrera, Ibiza and Formentera [44, 45].

Most of the Iberian Peninsula is made up of a large central plateau with an average altitude of 600 m, together with large mountain ranges and hydrographic basins that provide it with a wide variety of environments. On the plateau we find three large basins, the Duero River which drains the northern sub-plateau, the Tajo River which drains the region between the central system and the Montes de Toledo (central peninsular), and the Guadiana River, which collects the waters of the southern sub-plateau. Two other major basins are the Ebro River in the north and the Guadalquivir River in the south. Finally, we must consider the numerous basins that start from the external mountain systems and flow into the sea, such as the North basin, which flows into the Atlantic, the South basin, which flows into the Mediterranean, as well as the Segura, the Jucar-Turia and the Eastern Pyrenees. The mountain ranges that divide the peninsula are the Cantabrian Mountains, the Pyrenees, the Iberian System, the Central System and the Baetic System [44, 45].

In terms of climatology, the northeast of Iberia is a region of mild winters, cool summers and high rainfall and humidity throughout the year; the Levantine area (east coast), a Mediterranean area with hot, dry summers and mild winters; the south, a region of African influence with a hot, dry climate and summer drought; while the central plateau is characterized by intense heat in summer and cold winters with rainfall normally concentrated in spring and autumn [46].

Ocurrence data

The list of occurrences for both tick species (*R. sanguineus* and *I. ricinus*) from Spain and Portugal (excluding Atlantic islands) was obtained through natural data repositories [18, 47, 48]. Localities referenced with geographic uncertainty > 1 km were disregarded. Additionally, postal codes of geolocalized observations of species reported in previous studies [49] were converted to latitude-longitude using the *geocode* function of tidygeocoder package [50] in R v4.2.3 [51]. Finally, in order to reduce spatial autocorrelation biases in observations' distribution and abundance, we overlap them with a 1 km^2 grid to consider only one observation per square.

Ecological niche modelling

The 15 bioclimatic variables (1970–2000) related with temperature and precipitation were downloaded from WorldClim v2.1 climate database at spatial resolution of 1 km^2, after discarding those that contain combination data from the two variables [52]. We used one independent set of climatic variables to calibrate the ENM model for *R. sanguineus* and another one for *I. ricinus.*

To improve model calibration and reduce collinearity between variables, we only included complementary variables with a correlation of less than 0.8 ($r < 0.8$) [53]. For the niche model of *R. sanguineus*, we included BIO_1 - Annual Mean Temperature, BIO_2 - Mean Diurnal Range [Mean of monthly (max temp - min temp)], BIO_3 - Isothermality (BIO_2/BIO_7) (×100), BIO_4 - Temperature Seasonality (standard deviation ×100), BIO_5 - Max Temperature of Warmest Month, BIO_{12} - Annual Precipitation, BIO_{15} - Precipitation Seasonality (Coefficient of Variation), BIO_{17} - Precipitation of Driest Quarter. In the case of *I. Ricinus*, we used the same bioclimatic variables excluding BIO_4 due to the new correlation appearing with BIO_2 when *I. ricinus* observations where considered. In addition, the environmental variables including vegetation (density of shrubs and herbaceous plants) were downloaded from EarthEnv [54] and human pressure (built environment, population density, electric power infrastructure, farmland, grazing land, roads, railways and waterways) from Socioeconomic Data and Applications Center [55]. All downloaded data layers were processed in ArcMap 10.8 to ensure uniform extent, resolution (1 km^2 per pixel) and coordinate system (GCS_WGS_1984).

Distribution models for the two tick species (*I. ricinus* and *R. sanguineus*) were performed using the kuenm approximation [53] of the MaxEnt software [56] in R [51]. MaxEnt is a maximum-entropy method that estimates habitat suitability based on the environmental conditions of the observations [56]. To model both tick species, we independently built 102 models with Kuenm for the following combination of parameters: 17 regularization multiplier values "M" (0.1–1.0 at 0.1 intervals, 2–6 at intervals of 1, 8, and 10), six possible combinations of three feature classes "F" (linear, quadratic, and product: l, q, lq, lp, qp, lqp) and a set of variables. The performance of the models created was assessed considering the significance (partial ROC), with 100 iterations and 50% data used for bootstrapping, omission rates (OR = 5%) and model complexity (Akaike information criterion - AIC) and validated with the mean ratio of the area under the curve (AUC) obtained with points of occurrence independent of the calibration (30% and 70% of total observations were used for testing and training data respectively). The best-fit model (final model) was generated using the extrapolation with clamping option, running ten replicates with the same parameters selected in the previous step and re-evaluated based on previous criteria.

Transmission risk maps development

The fulfilled the following points to develop the transmission risk maps: (1) Generate individual ENM in the form of raster layers for each vector (*Ixodes-Rhipicephalus*); (2) Weight the two ENMs in different proportions to produce transmission risk maps of both pathogens (*Ehrlichia-Anaplasma*); and (3) Validate the risk map according to seroprevalence data (see next section).

The resultant ENMs in the form of raster layers for both tick vectors were weighted to produce potential transmission risk of bacterial diseases in different proportions (*Ixodes-Rhipicephalus* (I-R); 0–100, 10–90, 25–75, 50–50, 75 – 25, 90 – 10, 100-0). Considering that each pixel in the raster contains the likelihood of the vector being present, the new combined suitability value for each pixel in the weighted model was estimated applying the formula:

$$ENM\ weighted = \frac{ENMi * I + ENMr * R}{100}$$

being *ENMi* and *ENMr* the output suitability value for *Ixodes* and *Rhipicephalus*, and I-R the proportion of contribution to the final model respectively.

For instance, if we consider the suitability value of *Ixodes* being 0.1 in one pixel of the species-specific ENM and that of *Rhipicephalus* being 0.4 in the same pixel but in its individual ENM (as there is one ENM for both of the two vectors), the new value for that pixel in a weighting scheme of 10I-90R would be something intermediate:

$$ENM\ weighted = \frac{0.1 * 10 + 0.4 * 90}{100} = 0.37$$

Two transmission risk maps were developed independently for each of the two species of bacteria (*E. canis* and *Anaplasma* spp.) analyzed in this study depending on validation results (see below).

Risk maps validation

In order to evaluate the reliability of the transmission risk models considering different I-R relative contributions, we performed two different approximations. For the first test, we considered all available seroprevalence estimates of the two bacterial diseases in different regions from the Iberian Peninsula [23–25]. Thus, we included seroprevalences from: (i) autonomous communities of Spain, (ii) provinces of “Castilla y León” and (iii) regions from Portugal. We discarded the three largest communities of Spain “Castilla y León”, “Castilla-La Mancha” and “Aragon” to avoid losing resolution. In parallel, we extracted values of risk from the same regions of Spain and Portugal using ArcMap. Finally, we performed a correlation between the two variables (seroprevalence and risk) to test which transmission risk map perform better predictions in R (based on the Spearman’s rank correlation coefficient and p-value).

For the second approach of validation, we used the natural jenk (breaks) classification method in ArcMap, with 5 classes relative to the probability of infection (“Very Low”, “Low”, “Medium”, “High” and “Very High”) with average risk intervals (“<0.15”, “0.15–0.27”, ”0.27–0.41”, “0.41–0.57”, “>0.57”). We then represented the number of georeferenced infected dogs in histograms by category to analyze which transmission risk map performed better predictions.

Future projections of transmission risk

The transmission risk maps were projected in MaxEnt [56] the bioclimatic variables of the future (time period range: 2081–2100) and best estimations regarding both parameters (multipliers and feature classes) and predictors (contribution of each tick to the risk model) for each of the two bacterial diseases. The RCP 8.5 scenario, which represents high CO_2 emissions in Europe [57], was assessed using the HadGEM3-GC31-LL model [58], to study the effect of climate change in the future. The risk in the present and the projected future risk were transformed into presence/absence binary maps using the 10th percentile threshold of the best proportion of occurrence records in each case, in order to perform a range-change analysis of the risk of *E. canis and Anaplasma* spp. infection in the future [59]. The percentage of cells that gained or lost risk of infection as a result of climate change was calculated for the maps projected to 2100 compared to the present map using the biomod2 package of the R software [60]. Finally, we measured the similarity between present-future bioclimatic conditions to assess the extrapolation risk and identify extrapolative areas using the function kuenm_mop of the kuenm package [53], being complementary analyses.

Results

Rhipicephalus sanguineus and *Ixodes ricinus* ENM

A total of 410/542 accurately georeferenced observations of *R. sanguineus* and *I. ricinus* from Spain and Portugal respectively were downloaded from different sources. After removing repeated observations in every 1 km grid, we ended up with a total number of 317/293 observations respectively to perform the ecological niche model for both species.

In the case of *R. sanguineus*, the environmental variables inferred significance in all 102 candidate models, 51 models met the omission rate criteria (model prediction power) and one of them met the criteria AICc (model complexity correcting for small sample size). The model M_0.3_F_lq with a mean AUC of 0.777 and meeting all criteria, was used to perform final suitability habitat maps (Fig. 1A).

For *I. ricinus*, the environmental variables inferred significance in all 102 candidate models, 5 met the omission rate and 2 of them met all criteria. We finally used the model M_5_F_lqp_Set_1 with best mean AUC (=0.792), the best model, between the two to perform final suitability habitat maps (Fig. 1B).

The percentage contribution of the variables selected ranged from 0.6% (Bio3) to 44.6% (human footprint) in the case of *R. sanguineus* and from 0.3% (Herbaceus) to 46.2% (human footprint) for *I. ricinus* suitability analysis (Table 1). Thus, human footprint seems to be the most important explanatory variable for both models as it has been shown in previous transmission risk maps for other diseases [41].

Table 1 Percent contribution of the variables selected in the ecological niche model of *Rhipicephalus sanguineus* and *Ixodes ricinus*. BIO1 = Annual Mean temperature, BIO2 = Mean diurnal range (Mean of monthly (max temp - min temp)), BIO3 = isothermality (Mean diurnal range (Mean of monthly (max temp - min temp))/ temperature Annual Range (Max Temperature of Warmest Month - Min temperature of Coldest Month)) (×100), BIO4 = temperature seasonality (standard deviation ×100), BIO5 = Max Temperature of Warmest Month, BIO12 = annual precipitation, BIO15 = precipitation seasonality (coefficient of variation), BIO17 = precipitation of driest quarter

Variable	Percent contribution Rhipicephalus sanguineus	Percent contribution Ixodes ricinus
BIO$_1$	4.96	6.96
BIO$_2$	12.48	11.23
BIO$_3$	0.60	2.28
BIO$_4$	14.35	-
BIO$_5$	2.21	7.48
BIO$_{12}$	7.25	1.21
BIO$_{15}$	5.89	4.06
BIO$_{17}$	6.10	18.24
Herbaceus	0.79	0.29
Human footprint	44.62	46.22
Shrubs	0.76	2.04

Risk maps validation

The validation of the potential weighted risk maps (based on the 7 different contributions from *E. canis* and *Anaplasma* spp.), showed a more relevant contribution of the brown dog tick than the castor bean tick in the transmission of both diseases, as expected due to its abundance and preference to parasite dogs (Fig. 2). Only the transmission risk maps that had higher contribution of *R. sanguineus* than *I. ricinus* showed relevant and positive significant correlations between risk and seroprevalence in either of the two species ($R \geq 0.4$; $p < 0.05$). Regarding *Anaplasma* spp.,

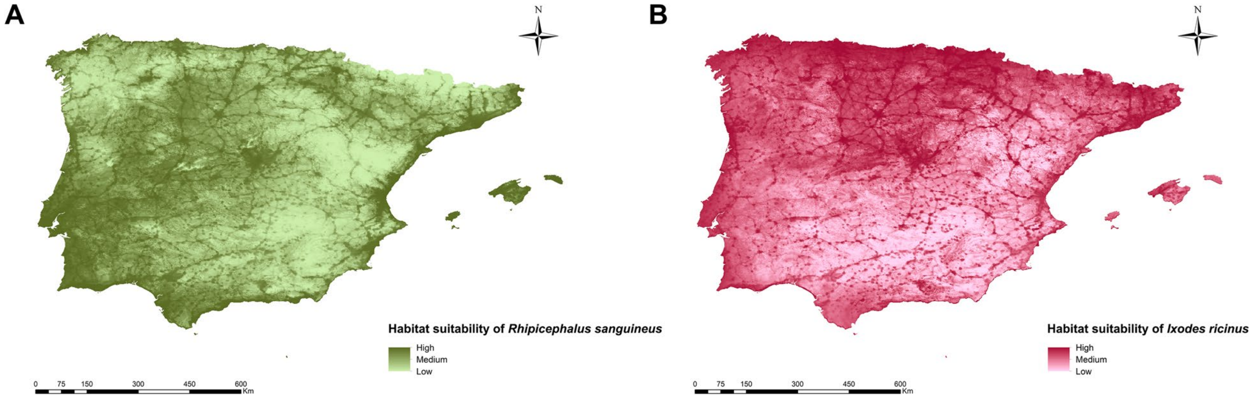

Fig. 1 Habitat suitability map for the two tick species considered in this study, with darker and slighter areas showing higher and lower suitability respectively. **A** *Rhipicephalus sanguineus* and **B** *Ixodes ricinus*

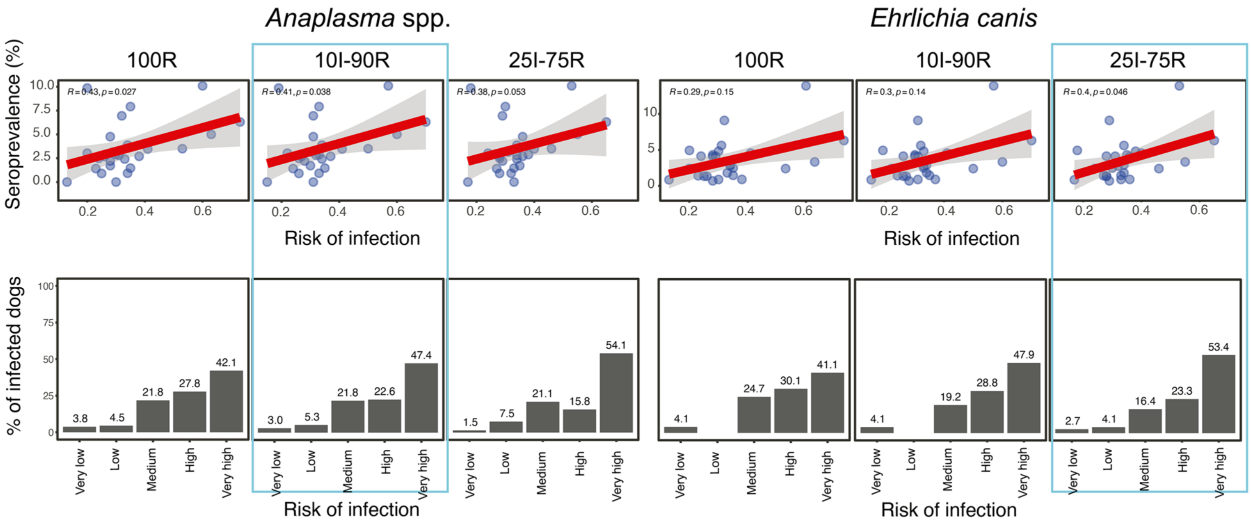

Fig. 2 Validation analysis of transmission risk maps using both seroprevalence data and % of infected dogs for the models having higher contribution of *Rhipicephalus sanguineus* than *Ixodes ricinus*. Weighting results for Ixodes-Rhipicephalus (I-R) include: 0–100 (100R), 10–90 (10I-90R), 25–75 (25I-75R). The final models selected for each of the diseases are marked in blue

within significant maps, the one having 10I-90R contribution proportion of (I-R) showed best estimates in the number of infected dogs in very high-risk areas (47.4%) (Figs. 2 and 3A). In the case of *E. canis*, the model showing a proportion of 25I-75R showed better validation power (53.4% of infected dogs in very high-risk areas) (Figs. 2 and 3B).

The visualization of the transmission risk maps of *Anaplasma* spp. (10I-90R) showed higher risk in urban areas with special incidence in those located along rivers and the coast (Fig. 4A). The mid-west territory also stands out as important transmission risk zone. For the case of *E. canis* (25I-75R) similar risk areas appear with the higher expected incidence of the northern part of the Iberian Peninsula, as expected due to the higher contribution of the vector *I. ricinus* to the model (Fig. 4B).

Future projections of transmission risk

The transmission risk map projected to the future (2100) of both bacterial diseases showed a northwest shift of the highest expected incidence (Supplementary Fig. 1). Again, the expected incidence in the future across the northern strip of the Iberian Peninsula increases for *E. canis* relative to *Anaplasma* spp.

In fact, when we estimate the magnitude of the risk-change we find that most habitat suitability gain occurs in the northwestern areas for both species (Supplementary Fig. 2A and B). There was a 77.9% loss (mostly in the

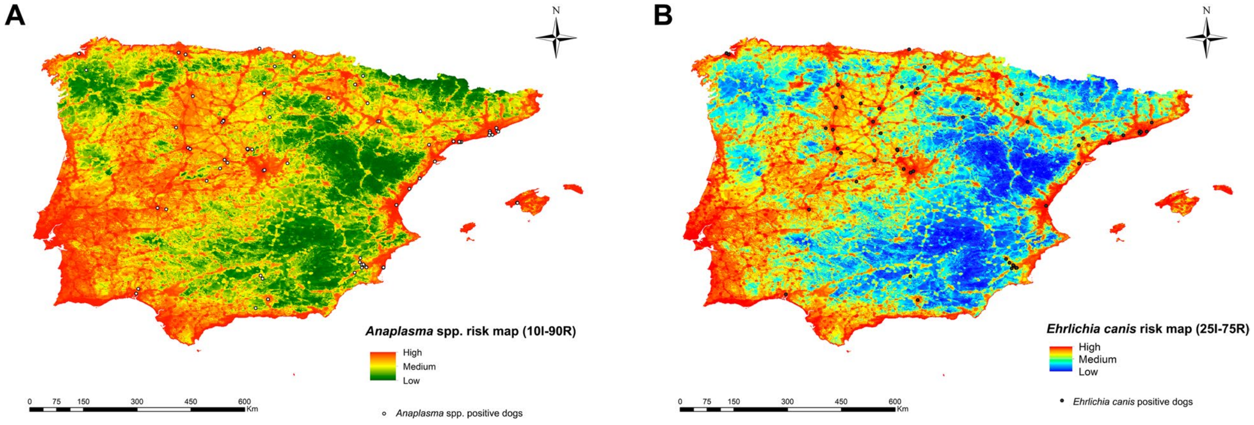

Fig. 3 Potential transmission risk maps of both diseases displaying the best power in the validation analysis, with infected dogs superimposed over the maps. **A** *Anaplasma* spp. and **B** *Ehrlichia canis*

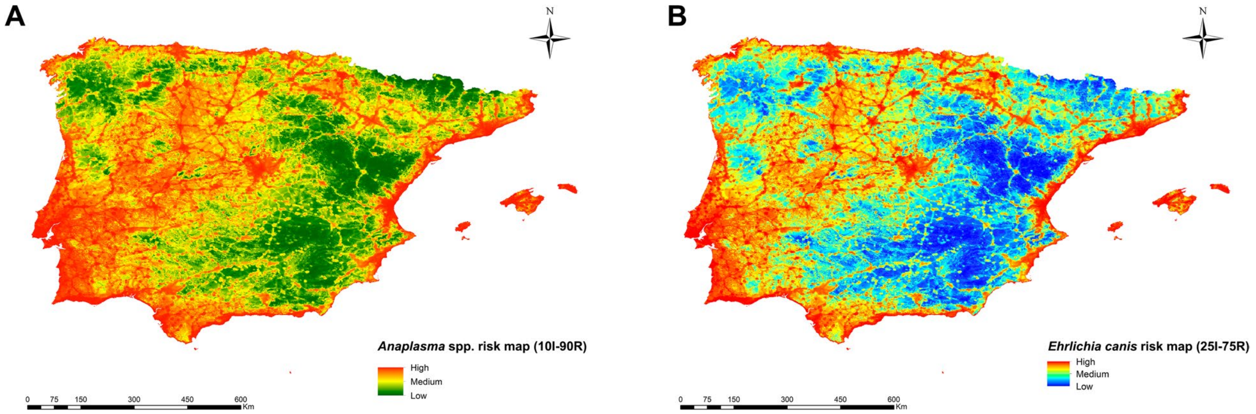

Fig. 4 Potential transmission risk maps of both diseases displaying the best power in the validation analysis. **A** *Anaplasma* spp. and **B** *Ehrlichia canis*

west) and 4.3% gain (mostly in the north) in the range of *Anaplasma* spp. whereas 79.8% and 2% respectively for *E. canis*.

However, the mop analysis revealed that strict extrapolation (values of 0) was occurring for the bioclimatic variables selected in both vectors (Supplementary Fig. 3A and B) across the whole territory of the Iberian Peninsula except for the northern strip.

Discussion

In this study we have estimated the potential geographic distribution of bacterial disease vector ticks in the Iberian Peninsula and Balearic Islands (*I. ricinus* and *R. sanguineus*) with veterinary and human interest. The novelty of the study lies in the combination of independent ENMs for both species to estimate the disease transmission risk of specific bacteria (*E. canis*, *A. platys* and *A. phagocytophilum*). The validation approach (both with seroprevalence and infected dogs) seems a good approximation to test the approximate contribution of both tick species in disease transmission and have detected which species is more important for the transmission of the disease in dogs in the Iberian Peninsula and Balearic Islands.

Previous studies in Europe that produced a ENM of both tick species with a larger study area, indicates that habitat suitability for both species is high over most of the Iberian Peninsula [34, 61]. These results coincide with our work, which presents habitat suitability at a resolution of 1 km, thus improving the accuracy of the model but in a smaller territory. The potential suitable areas for *R. sanguineus* and *I. ricinus* are concordant with their mediterranean and eurosiberian distribution respectively. In both ENMs, the most relevant variable of the potential distribution of the species is the human footprint (built environment, population density, electric power infrastructure, cropland, grazing land, roads, railways, and waterways). The second variable with the highest contribution is BIO_4 (Temperature Seasonality) for the *R. sanguineus* model and BIO_{17} (Precipitation in the driest quarter) for the *I. ricinus* model. Finally, the third variable with the highest percentage is the BIO_2 (Mean Daytime Temperature Range) for both models. The human footprint could favour a greater presence of various species of ticks carried by small mammals and birds, which can play an important role in the maintenance of tick populations. This fact may be related to the large number of these hosts in urban and suburban areas compared to natural areas due to the absence of predators in the former [18, 62, 63]. More data, including from wild animals, would be very important, but studies on these hosts are scarce and none at the national level, which limits their use in model validation and could influence future predictions. BIO_2 and BIO_4 are variables related to temperature, which is a key factor for the distribution and activity of both species [64, 65]. The contribution of BIO_{17} related with precipitation in the *I. ricinus* model may be associated with their presence in habitats with high relative humidity [65].

The representation of the potential distribution of the vectors (meeting the three criteria described in the results section) makes it possible to understand the relative contribution of them to spread bacterial diseases. This information can be compared with prevalence data estimated applying molecular tools to directly identify the pathogens in ticks [66, 67]. In this work, we use the weighting approach to observe that model combinations having higher contribution of *R. sanguineus* than *I. ricinus* produced better adjustment and between those, we selected the combination 10I-90R and 25I-75R to reliably reflect the potential transmission risk of anaplasmosis and ehrlichiosis respectively.

The potential high-risk areas predicted with our models and the seroprevalence values available in the literature coincide with areas where the high human pressure and the average temperature throughout the year is high [23, 25]. Inland areas of the peninsula, mountainous and high-altitude places with low temperatures correspond to those with a lower risk of infection. Our infection risk map for *Anaplasma* spp., resulting from the 10I90R weighting of the models of both ticks, indicates that those areas with the highest risk of infection correspond to the northern plateau, southwest of the peninsula, the banks of the Ebro, the Mediterranean coast and the Balearic Islands and the Cantabrian coast. These results correspond to canine seroprevalence studies in Spain and Portugal, obtaining the highest values in Aragon (11.5%), Murcia (9.9%), Andalusia (8.9%), Extremadura (7.9%) and Valencian Community (6.9%) in Spain [23]; and the Algarve (10.1%) and Lisbon (6.3%) in Portugal [25]. In addition, it is worth noting the high prevalence in wild ungulates in the north of the peninsula with 24.2% [31]; and the seroprevalence in red foxes in Portugal of 14.5% [30]. Regarding the infection map for *E. canis*, obtained through the 25I75R weighting, the areas with a high risk of infection are the center-north of the peninsula, southern Portugal, the Mediterranean coast and the Balearic Islands, with highest seroprevalence areas in dogs being the Valencian Community (9.1%), Aragon (6.9%), Andalusia (5.9%) and Navarre (5.6%) in Spain [23]; and the regions of Algarve and Lisbon with 13.9% and 6.3% respectively in Portugal [25].

Regarding future predictions of transmission risks in both models, there is a loss of suitability in ~80% of the territory (mainly in the centre-east) and a shift of suitable habitats towards the north and west of the peninsula, potentially caused by the effects of global warming (e.g., increase in temperature) being more pronounced in specific areas or by surpassing tolerance limits of the species. These results are in line with projections made in European models for *R. sanguineus* and *I. ricinus*, where there is a loss and a north-western shift of habitat suitability in the future [34, 61]. The result of the mop analysis indicates that a strict extrapolation occurs in most of the Iberian Peninsula possibly because of using too many predictors, therefore, the presence of extrapolative areas makes future predictions in the Iberian Peninsula risky [34]. Thus, the higher uncertainty of performing these estimates urge caution in the interpretation of future scenarios.

The nature of the validation approach does not allow to exactly define the contribution from each vector, but it can point to the vector that contribute most to the transmission of the disease (*R. sanguineus* in the diseases we considered in this work for dogs in the Iberian Peninsula and Balearic Islands). The loss of resolution derived from seroprevalence and average risk estimations in large regions is the reason for discarding some big autonomous communities in Spain after preliminary analysis. Epidemiological studies focusing in smaller and random regions (normally this information is collected in urban/rural areas) and including both presence (prevalence) and absence data, may allow performing more accurate validations of the risk models proposed [68]. In addition, in order to have the whole scenario of the disease, it is important to validate these models using prevalence data from other organisms [30, 31]. Simultaneously, incorporating other potential hosts and their dynamics (i.e., birds; [69]), in the modelling approach herein developed, along with information on pathogen biology, may improve the infection risk estimates in accordance with the Biotic-Abiotic-Mobility principle [68].

Conclusion

We have been able to map the risk of infection of *Anaplasma* spp. and *E. canis* for the canine and potentially for the human population by the relative contribution of two potential vectors under current and future habitat conditions. *R. sanguineus* appears to be the main transmitter of both diseases throughout the Iberian Peninsula and Balearic Islands. This estimate may help veterinary staff, clinicians and owners to optimize the control of these diseases in certain vulnerable areas, and thus reduce the risk of infection in risk areas.

Abbreviations

ENMs	Ecological niche models

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s12917-024-04383-3.

Supplementary Material 1: Supplementary Figure 1. Potential transmission risk maps projected to 2100 of both diseases. A) *Anaplasma* spp.and B) *Ehrlichia canis*.

Supplementary Material 2: Supplementary Figure 2. Range change analysis showing areas of gain, loss and those that remain as in the present of the risk of infection of the two bacterial diseases. A *Anaplasma* spp.and B *Ehrlichia canis*.

Supplementary Material 3: Supplementary Figure 3. Results of the mop analysis showing extrapolation risk values for A *Rhipicephalus sanguineus* and B *Ixodes ricinus*.

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Authors' contributions

A.B.P, I.R.E. and R.M. helped in the conceptualisation. A.B.P., I.R.E., M.C.C., C.V., E.I.G.M. and R.E.H.L. helped with data analysis and visualisation. R.E.H.L., J.A.S.A. and R.M. helped in supervision. A.B.P., I.R.E. and R.M. wrote the manuscript.

A.B.P., I.R.E., R.E.H.L., J.A.S.A. and R.M. assisted in the editing and the final editing of the manuscript. All authors read and approved the final manuscript. I.R.E. and R.M. have contributed to the work in equal measure.

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Data availability

Data is provided within the manuscript or supplementary information files.

Declarations

Ethics approval and consent to participate

Not applicable.

Consent for publication

None.

Competing interests

The authors declare no competing interests.

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