

Analysis of the current risk of *Leishmania infantum* transmission in Spain and Portugal using Ecological Niche Modelling and its future projection in climate change scenarios

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Background

Zoonotic diseases are among today's major emerging health problems for both humans and animals. These diseases are becoming increasingly common in Europe due to the effect of different aspects such as climate change, that allows the movement of vectors towards warming areas previously too cold, increased migration and travel by land, sea and air involving infected animals and humans, human activities, and inadequate management of diseases in animals and humans, among other factors [1]. Leishmaniasis is a vector-borne zoonotic disease caused by a protozoan parasite of the genus *Leishmania* spp. In Spain, as in other countries in the region, animal leishmaniasis is mainly due to *L. infantum*, with canids as its main sentinel host. The dynamics of this endemicity depend on environmental and bioclimatic factors that determine the survival of different species of the genus *Phlebotomus*, that act as vectors of the disease [2]. The aim of our study was to determine the risk of *L. infantum* infection in the Iberian Peninsula and its projection to 2080, using the Ecological Niche Modelling (ENM) methodology, taking into account the habitat suitability for the vectors.

Materials and methods

ArcMap 10.8 was used to process and edit all the variables to be used to determine the potential distribution of the vector (Bioclimatic, Human Footprint and vegetation types), as well as to represent the points of presence of *Phlebotomus perniciosus* [3] and Global Biodiversity Information Facility. The MaxEnt algorithm was employed to develop the *P. perniciosus* ENM. Once the model was generated, the infestation rate of *Leishmania* spp. in the phlebotomine sandfly was calculated using RStudio. By weighting the vector model and the infestation rate variable, we obtained an infection risk map of this disease in the Iberian Peninsula. This procedure was also repeated for 2040, 2060 and 2080. To validate the resulting risk maps, a regression analysis was performed between the average risk of infection and the prevalence of the disease in each of the autonomous communities of Spain and district of Portugal. Additionally, *L. infantum*-infected dogs in both Spain and Portugal were geolocated to observe the risk zone in which they lived.

Results

The highest risk of infection corresponds to the central and southwestern parts of the Iberian Peninsula, as well as the Mediterranean coast and the Ebro River basin. Furthermore, the risk increases in areas with high human pressure and in some areas of the northern coast of Spain. Regarding the validation of the risk map, the regression analysis revealed a positive and significant relationship between the mean risk of infection and the prevalence of the disease in the different autonomous communities. More than 80% of the dogs infected with *L. infantum* were in areas of high risk of infection, suggesting a good predictive capacity for our risk map. Future projections show a clear shift of the disease towards the north of the Iberian Peninsula.

Conclusions

The results obtained indicate a risk of infection of the disease in almost the entire peninsular territory. The methodology used takes into account the "One Health" perspective of the disease resulting in a predictive model, which is essential for the establishment of control measures by both clinicians and veterinarians to help reduce the risk of infection in animals and humans.

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