Can we predict the potential distribution of Phytophthora cinnamomi far from its native habitat?

The Andalusian case

INTRODUCTION

- Phytophthora cinnamomi is one of the 100 most dangerous invasive species in the world. From New Guinea, region where this oomycete is thought to be native, it spread towards many regions in the northern hemisphere, included the Iberian Peninsula\(^1\). In Andalusia, this pathogen is causing root rot and decline in cork oak (Quercus suber) and holm oak (Quercus ilex) forests and agroecosystems.\(^2\)

AIM & HYPOTHESES

- In this work, we used Environmental Niche Models (ENMs) in order to predict the potential distribution of P. cinnamomi.
- P. cinnamomi is present in the soil (resting spores) and in plant tissues (mycelium). Ecological niche models depend on the assumption that species distribution is in equilibrium with the prevalent environmental conditions within a given region. P. cinnamomi is an alien pathogen in the Iberian Peninsula, but it had time enough to establish itself and consequently, its presence will be more probable where it finds good abiotic and / or biotic conditions to succeed and/or when human activities favor its spreading.

MATERIAL & METHODS

- The study area is Andalusia (southern Spain), region with an extension of 87,669 km\(^2\). This region is a very diverse territory located in the southern part of the mid-latitudes of north hemisphere.\(^3\)
- We used both presence and presence-absence records of P. cinnamomi in Andalusia from a complex dataset based on the Andalusian Forest Monitoring Network, the Forest Phytosanitary Alert Network, data from two published papers P.\(^4\) and our field data from research projects. In all, n=188 (presence, n=88; absence, n=100)\(^5\).
- Ten factors were selected for explain the distribution of P. cinnamomi. We checked for multicollinearity using the Pearson Correlation and the Variance Inflation Factor (VIF). The modelling framework is applied at a resolution of 250 meters.\(^6\)
- We fitted a set of models based of regression-based methods, and machine learning algorithms: Generalized Linear model (GLM), Generalized additive model (GAM), and Maxent (using presence-only data, and generating random background points).\(^7\)
- We calculated the ROC/AUC, a standard measurement of accuracy in Species Distribution Models derived from the confusion matrix.\(^7\)
- The frame work was performed using R - sdm\(^8\) and Maxent.

RESULTS

- Maxent (AUC = 0.83) and GAM (AUC = 0.80) produced the best models over GLM (AUC = 0.69).\(^8\)
- GAM is the regression method that showed a better capability to discriminate presence from absence.\(^9\)
- Regression methods based on presence-absence records overpredicted the potential distribution of P. cinnamomi, and produced more errors (false positives). However, we cannot ensure the accuracy of absence data records (not detectable).\(^10\)
- The response curves show how each environmental variable affects the Maxent prediction. The presence of P. cinnamomi is more related to soil, climate and water conditions.\(^10\)

CONCLUSIONS

- Phytophthora cinnamomi has a large potential distribution area in Andalusia, from one-third to one-half of the region.
- According to models, the potential distribution of P. cinnamomi shows connected areas.
- In general, the models are moderately predictive. Overprediction may be caused by the uncertain nature of absences.
- There is a need to improve the sampling network of soil pathogens beyond the Andalusian Forest Monitoring Network.
- The results can help to understand the potential distribution of P. cinnamomi and guide future sampling strategies.
- Based on the preliminary results, ENMs can help to predict the potential (or probable) distribution of Phytophthora cinnamomi.

REFERENCES


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