



# Predicting current and future disease outbreaks of *Diplodia sapinea* shoot blight in Italy: species distribution models as a tool for forest management planning



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## ABSTRACT

Species distribution models (SDMs) provide realistic scenarios to explain the influence of bioclimatic variables on plant pathogen distribution. *Diplodia sapinea* is most harmful to plantations of both exotic and native pine species in Italy, causing economic consequences especially to edible seed production. In this study, we developed maximum entropy models for *D. sapinea* in Italy to reach the following goals: (i) to carry out the pathogen's first geographical distribution analysis in Italy and determine which eco-geographical variables (EGVs) may influence its outbreaks; (ii) to detect the effect of climate change on the potential occurrence of disease outbreaks by 2050 and 2070. We used Maxent ver. 3.4.0 to develop SDMs. We used six global climate models (BCC-CSM1-1, CCSM4, GISS-E2-R, MIROC5, HadGEM2-ES and MPI-ESM-LR) for two representative concentration pathways (4.5 and 8.5) and two time projections (2050 and 2070) to detect future climate projections of *D. sapinea*. The most important EGVs influencing outbreaks were land cover, altitude, mean temperature of driest and wettest quarter, precipitation of wettest quarter, precipitation seasonality and minimum temperature of coldest month. The distribution of *D. sapinea* mostly expanded in central and southern Italy and shifted in altitude upwards on average by ca. 93m a.s.l. Moreover the fungus expanded the range where disease outbreaks may be recorded in response to an increase in the mean temperature of wettest and driest quarter by ca. 1.9 °C and 5.8 °C, respectively in all climate change scenarios. Precipitation of wettest quarter did not differ between current and any of future models. Under different climate change scenarios *D. sapinea*'s disease outbreaks will be likely to affect larger areas of pine forests in the country, probably causing heavy effects on the dynamics and evolution of these stands or perhaps constraining their survival.

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## 1. Introduction

Climate change is one of the principal factors that influence plant disease emergence (Garrett et al., 2006; Lindner et al., 2010; Chakraborty and Newton, 2011). It affects host–pathogen interactions by: (i) increasing pathogen multiplication or survival during the vegetation season (Woods et al., 2005, 2010); and (ii) changing the host resistance and susceptibility (Desprez-Loustau et al., 2006). Under climate change, pathogens, just like plants,

may be unable to migrate or adapt as rapidly as would be needed to keep the pace with changing environmental conditions. Most pathogens, however, will be advantaged over plants thanks to their shorter generation times and, in many cases, their ability to move readily by wind dispersal (Garrett et al., 2006). Climate change may bring about significant consequences for plant pathogens with strong implications for agricultural and forest ecosystems. For instance, climate change may alter frequencies of pest outbreaks and sporulation and colonization success of fungal pathogens, and may induce changes (shifts, expansions or contraction) in their geographical ranges (Garrett et al., 2006; Lindner et al., 2010; Chakraborty and Newton, 2011).

Species Distribution Models (SDMs) are commonly used to detect potential distribution at current and future projections in

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the geographic ranges of plant pathogens (Václavík et al., 2010; Elith et al., 2013; Shabani et al., 2014; Narouei-Khandan et al., 2015, 2017; Bosso et al., 2016a, 2016b). However, while SDMs may be appropriate to assess habitat suitability at the current time, they may not always be the best way to summarize projected habitat ranges in the future due to the influence of differences in global climate models' (GCMs) range and emission scenarios. GCMs and emission scenarios represent a range of plausible futures (Ruosteenoja et al., 2003; Rosentrater, 2010). They are not intended to provide accurate predictions regarding the future state of the climate system at any given point in time, but to establish the envelope that future climate could conceivably occupy. For this reason, it is very important to use several GCMs, considering the variability represented by different climate models and/or emission scenarios, and analyze them all (Porfirio et al., 2014; Trnka et al., 2014).

The *Diplodia* shoot blight, caused by a pathogen recently renamed as *Diplodia sapinea* (Fr.) Fuckel (Phillips et al., 2013; Slippers et al., 2013) (= *Diplodia pinea* and *Sphaeropsis sapinea*), is a good example of an emerging disease whose incidence may have been promoted by several environmental factors. The pathogen causes serious damage to pine trees (*Pinus* spp.) worldwide (Burgess et al., 2004; Phillips et al., 2013) and was recorded to affect several *Pinus* species, such as *Pinus nigra*, *P. sylvestris*, *P. halepensis*, *P. radiata* and *P. pinea* (Luchi et al., 2014). In *P. pinea*, especially serious damages are recorded, such as cone abortion, with direct economic consequences on edible seed production (Vagniluca et al., 1995; Santini et al., 2008). *Diplodia* species are opportunistic agents that affect hosts subjected to predisposing stress factors, such as hail, drought or heat waves (Paoletti et al., 2001; Stanosz et al., 2001; van Staden et al., 2004). de Kam (1985) suggested that several factors could concur to cause *Diplodia* shoot blight emergences in Europe, among which climate change: this may influence both host susceptibility and pathogen presence especially through changes in temperatures and precipitations (Fabre et al., 2011). The reported increase in temperature and drought associated with climate change would thus potentially increase the frequency of *D. sapinea*'s disease outbreaks in some regions (Keen and Smits, 1989; Desprez-Loustau et al., 2007). A rise in the temperature could strongly increase water stress in pines, making them more susceptible to *D. sapinea* (Blodgett and Stanosz, 1997). In South Africa, areas at high risk of *D. sapinea* diebacks coincide with the summer rainfall hail belt, so planting resistant *Pinus* spp. in these regions would be an important strategy to prevent damage (van Staden et al., 2004). In France, a climate-based model showed that the main factors influencing *D. sapinea* presence were the occurrence of certain host species (essentially *P. nigra* and *P. sylvestris*) and winter temperature and summer rain, both positively correlated with cone colonization.

In Italy *D. sapinea* has been so far studied through conventional field and laboratory approaches, mainly based on classical and molecular techniques (Maresi et al., 2002; Luchi et al., 2005a, 2005b, 2014; Maresi et al., 2007; Mancini et al., 2010; Luchi et al., 2014). However, no studies have addressed the ecological requirements of the pathogen on a broader scale.

In this study, we use maximum entropy (Maxent; Phillips et al., 2006) SDMs for *D. sapinea* in Italy to: (i) carry out the first analysis of potential geographical distribution in the country and determine which eco-geographical variables (EGVs) may affect disease outbreaks; and (ii) forecast the effects of climate change on the potential occurrence of disease outbreaks by 2050 and 2070. Specifically, we predict that since the species is favored by warm temperatures, climate change will lead to a considerable range increase in the pathogen's outbreaks.

## 2. Materials and methods

### 2.1. Study area and data collection

We considered the entire Italian territory comprised ca. between latitudes 45°N–36°N and longitudes 6°E–18°E (corresponding to a total surface area ca. 301,000 km<sup>2</sup>, elevation range = 0–4810 m a.s.l.).

Presence records for *D. sapinea* (n = 78) originated from the collection of infected plant tissues in pine forests at various geographical locations throughout Italy, in both urban and natural areas characterized by different altitudes and climatic conditions (Luchi et al., 2014). This pine shoot pathogen can be found in both symptomatic and asymptomatic shoots, i.e. where *D. sapinea* may have been present in latent phase (Luchi et al., 2014). We considered only presence records of isolates collected from symptomatic pine samples that after genetic analysis based on internal transcribed spacer (ITS) sequences, were identified as *D. sapinea* (Luchi et al., 2014). Because we only refer to *D. sapinea* symptomatic pine samples, the probability of presence, habitat suitability, the potential distribution and occurrence of *D. sapinea* all refer to disease outbreaks of the fungal pathogen. Records were screened in ArcGis (version 9.2) for spatial autocorrelation using average nearest neighbour analyses and Moran's I measure of spatial autocorrelation to remove spatially correlated data points and guarantee independence (Dormann et al., 2007; Russo et al., 2014; Kwon et al., 2016; Smeraldo et al., 2017; Bosso et al., in press). After this selection, 35 occurrence records were used to generate current and future SDMs of *D. sapinea*.

### 2.2. Selection of EGVs to detect current distribution of *D. sapinea*

To produce current SDMs for *D. sapinea* in Italy, we considered initially a set of 21 EGVs. We included altitude, 19 bioclimatic variables and land cover. Altitude and the 19 bioclimatic variables were obtained from WorldClim database ([www.worldclim.org/current](http://www.worldclim.org/current)) (Hijmans et al., 2005). Land cover was obtained from the IV-level Corine Land Cover (available from <http://www.sinanet.isprambiente.it/it/sia-ispra/download-mais/corine-land-cover>). In order to remove any variables that were highly correlated before generating the models, we calculated a correlation matrix using Pearson's technique and selected only the variables for which  $r < 0.80$  (Hernandez et al., 2006; Lobo et al., 2010; Russo et al., 2015; Bosso et al., 2016c). From this first set of predictors, we selected only the variables that were most representative of the species' ecological requirements (van Staden et al., 2004; Fabre et al., 2011) and this led to the final set of EGVs shown in Table 1. All final EGVs were converted in ASCII files with a 30-arc second resolution ( $0.93 \times 0.93 \text{ km} = 0.86 \text{ km}^2$  at the equator) and

**Table 1**

List of Ecogeographical Variables (type and measurement unit) used to predict current and future potential distribution of *D. sapinea* outbreaks in Italy.

Type	Ecogeographical Variable	Unit
Topographical	Altitude	m
Habitat	Corine Land cover	–
Bioclimatic	Annual Mean Temperature	°C
	Mean Temperature of Wettest Quarter	°C
	Mean Temperature of Driest Quarter	°C
	Mean Temperature of Warmest Quarter	°C
	Min Temperature of Coldest Quarter	°C
	Precipitation of Wettest Month	mm
	Precipitation of Driest Month	mm
	Precipitation of Warmest Quarter	mm
	Precipitation of Coldest Quarter	mm

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