



Predicting the impacts of climate change, soils and vegetation types on the geographic distribution of *Polyporus umbellatus* in China



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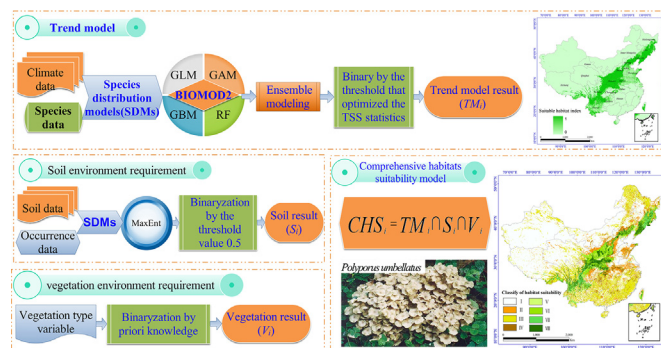
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HIGHLIGHTS

- We built a comprehensive habitat suitability model for a medicinal fungus *Polyporus umbellatus*.
- We separately consider the climate, soil and vegetation environmental demands for fungus species.
- In northeastern and southwestern China suitable habitats of *P. umbellatus* will continue to spread.
- In central China, the original *P. umbellatus* production area will continue to decrease.
- Not having enough forestland is the main limiting factor, but the limiting effect of soil will increase.

GRAPHICAL ABSTRACT



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ABSTRACT

Polyporus umbellatus is a fungus that has been used medically as a diuretic for thousands of years in China. To evaluate the impacts of climatic change on the distribution of *P. umbellatus*, we selected the annual mean air temperature, isothermality, minimum temperature of the coldest month, annual temperature range, annual precipitation and precipitation seasonality and used observations from the 2000s and simulated values from two future periods (2041 to 2060 and 2061 to 2080) to build an ensemble model (EM); then, we developed a comprehensive habitat suitability model by integrating soil and vegetation conditions into the EM to assess the distribution of suitable *P. umbellatus* habitats across China in the 2000s and the two future periods. Our results show that annual precipitation and annual mean air temperature together largely determine the distribution of *P. umbellatus* and those suitable *P. umbellatus* habitats generally occur in areas with an optimal annual precipitation of approximately 1000 mm and an optimal annual mean air temperature of approximately 13 °C. In other words, *P. umbellatus* requires a humid and cool environment for growth. In addition, brown soils with a granular structure and low acidity are more suitable for *P. umbellatus*. Furthermore, we have observed that the distribution of *P. umbellatus* is usually associated with the presence of coniferous, mixed coniferous, and broad-leaved forests,

Abbreviations: SDM, species distribution model; GLM, generalized linear model; GAM, generalized additive model; GBM, generalized boosting model; RF, random forest; MaxEnt, maximal entropy; PCA, principal component analysis; EM, ensemble model; TSS, true skill statistic; AUC, area under the receiver operating characteristic curve; CHS, comprehensive habitat suitability; Bio1, annual mean air temperature; Bio3, isothermality; Bio6, min temperature of the coldest month; Bio7, annual temperature range; Bio12, annual precipitation; Bio15, precipitation seasonality.

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suggesting that these vegetation types are suitable habitats for *P. umbellatus*. In the future, annual precipitation and annual mean air temperature will continue to increase, consequently increasing the availability of habitats suitable for *P. umbellatus* in northeastern and southwestern China but likely leading to a degradation of suitable *P. umbellatus* habitats in central China.

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1. Introduction

It is widely accepted that global climate changes will have significant effects on the natural distribution of species (Bertrand et al., 2011; Despland and Houle, 1997; Guo et al., 2017; Lenoir et al., 2008). Many studies have indicated that climate change is a significant driver of biodiversity loss, habitat fragmentation, and changes in the spatial patterns of species and can increase the risk of extinction for endangered species (Bálint et al., 2011; Boddy et al., 2014; Costion et al., 2015; Li et al., 2013). Detailed knowledge about the distribution of target species and their potential habitats is essential for rehabilitation (Adhikari et al., 2012; Lu et al., 2012). Moreover, understanding the impacts of climate change on species distribution has long-term implications for their protection and sustainable utilization (Forester et al., 2013; Summers et al., 2012). In recent decades, research concerns regarding the effects of climate change on species distribution have led to the widespread use of species distribution models (SDMs) (Anderson, 2013; Elith and Leathwick, 2009). However, due to the idiosyncratic life cycles and growth forms of fungi, few studies have focused on the distribution of fungi at large spatial and temporal scales (Guo et al., 2017; Suz et al., 2015; Yuan et al., 2015).

Medicinal fungi play an important role in healthcare and have been employed for millennia for the improvement of health and longevity (Phan et al., 2017). *Polyporus umbellatus*, a species of saprophytic fungus belonging to the Polyporaceae family, is one of the traditional Chinese medicinal fungi (He et al., 2017; Zhao, 2013). Sclerotia constitute the main component of *P. umbellatus* fungi and are commonly used to treat edema and promote diuretic processes (Bandara et al., 2015; Zhao, 2013). Modern pharmacology has confirmed that different compounds extracted from *P. umbellatus* have diuretic, anti-tumor, hepatoprotective, nephroprotective, and antioxidative properties (Bandara et al., 2015; He et al., 2017; Song et al., 2014; Zhao, 2013). Over the past two decades, the popularity of *P. umbellatus* in drug markets has increased due to its good clinical performance, which has led to shortages of this wild species (Xing et al., 2013). Climate change has impacted the environmental conditions in the original production area of *P. umbellatus*, which will increase the risk of resource shortages (Guo et al., 2017; Liu et al., 2015a; Tian, 2015; Zhang, 2014). Hence, the mapping of suitable *P. umbellatus* habitats and predictions of the impacts of climate change are vital for habitat protection and the sustainable development of this species.

SDMs have been widely employed to predict the potential distribution of species, particularly at large spatial and temporal scales (Anderson, 2013; Elith and Leathwick, 2009; Guo et al., 2017). SDMs relate species occurrence data to environmental predictor variables to simulate a species niche, and when combined with statistical or theoretical methods, SDMs can be used to map the potential distribution of species across landscapes and extrapolate these distribution over space and time (Elith and Leathwick, 2009; Guo et al., 2016). With technological advancements, numerous statistical methods and software applications have become widely available for describing patterns and performing predictions (Marmion et al., 2009; Naimi and Araújo, 2016; Zhao et al., 2017). Among these models, a generalized linear model (GLM) is a traditional regression algorithm that allows response variables to exhibit an error distribution other than a normal distribution. GLMs are common algorithms for SDMs (Guisan et al., 2002). Generalized additive models (GAMs) are semi-parametric extensions of GLMs that can

address highly non-linear and non-monotonic relationships between a species distribution response and a set of explanatory environmental variables. GAMs are useful algorithms for species distribution research (Leathwick et al., 2006). Generalized boosting models (GBMs) combine the strengths of regression trees and boosting in an additive regression model in which the dividable terms are simple trees fitted in a forward, stage-wise manner (Moisen et al., 2006). Random forest (RF) algorithms are a common type of machine learning algorithm developed from classification and regression trees and bagging approaches. In species distribution research, the high precision of RF algorithms has been well established (Bradter et al., 2013; Mi et al., 2017). Maximal entropy (MaxEnt) models are currently the most popular SDMs because of various benefits such as being freely available and presenting a user-friendly operational interface (Merow et al., 2013; Phillips et al., 2006; Yuan et al., 2015). In addition, in MaxEnt models, both continuous and categorical data can be employed as environmental variable inputs (Guo et al., 2017; Merow et al., 2013). Various niche patterns cause differences in suitable habitat characteristics among species. The selection of optimal SDMs for particular species under designated space-time backgrounds is restricted by many factors, such as species niche characteristics, environment complexity, data availability, and data resolution. Hence, the ensemble model (EM) strategy, which combines the information from individual models fitted with different modeling techniques, has been proposed to solve this problem (Strubbe et al., 2015; Thuiller et al., 2009). Ensemble modeling avoids the selection of a single best model, thus eliminating (or at least limiting) model selection bias, but this approach also provides relative measures of the importance of each predictor across all candidate models (Burnham and Anderson, 2002; Guisan et al., 2017).

In this study, we collected species presence data from 80 locations and data on 32 environmental variables and used the EM strategy to simulate the migration trend of the *P. umbellatus* distribution under climate change scenarios. We then built a comprehensive habitat suitability model to predict the potential future geographic distribution of *P. umbellatus* in China. The objectives of this study were to predict the impacts of climate change on the potential habitats of *P. umbellatus* and to identify the key environmental variables limiting the distribution of *P. umbellatus*. This study provides an example of modeling the distribution of fungi and valuable insights for the protection of *P. umbellatus* resources.

2. Methods

2.1. Species occurrence data

P. umbellatus occurrence data were obtained from field survey reports from the last 10 years (Tian, 2015; Liu et al., 2015a; Xing et al., 2012; Liu et al., 2015b). Records with precise latitude and longitude information were selected to ensure geographic accuracy, and priority was given to records from the traditional *P. umbellatus* production area. Reasonable sampling sites were selected based on the following principles: First, only one record was retained for replicate site data, and based on the resolution of the environmental variables, we deleted some sampling points in the distribution point data aggregation area to ensure that the distance between two sampling points was always >10 km. Second, the sampling sites were selected based on different environmental conditions to ensure independence of the species

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