

紫茎泽兰 *Eupatorium adenophorum* Spreng 在中国入侵分布预测

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摘要: 原产于墨西哥的紫茎泽兰 *Eupatorium adenophorum* Spreng 作为一个有害的外来物种在印度、新西兰和澳大利亚生长已有很长时间。在中国,尤其是在南方和西南地区其蔓延速度之快,带来了不可忽视的经济和社会后果。我们采用了生态位模拟新方法来预测紫茎泽兰可能入侵的范围。据此,预测的潜在分布区包括该植物在中国境内已分布的省份及未来华中、华东易受入侵的区域。

关键词: 生态位模拟; GARP; 紫茎泽兰; 入侵物种

中图分类号: Q 949.783.5

文献标识码: A

文章编号: 1000-470X (2003) 02-0137-06

Predicting the Potential Invasive Distribution for *Eupatorium adenophorum* Spreng in China

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Abstract: Originating in Mexico, *Eupatorium adenophorum* Spreng, is a noxious weed long present as a non-native species in India, New Zealand, and Australia. In China, it is spreading rapidly, particularly in the southern and southwestern parts of the country, with serious economic and social consequences. A new method, ecological niche modeling, was applied for predicting its potential geographic range of invasion. Predicted potential distributional areas included the Chinese provinces where the plant is known to occur, as well as additional areas in central and eastern China that appear susceptible to further spread of this species.

Key words: Ecological niche modeling; GARP; *Eupatorium adenophorum*; Invasive species

Crofton weed (*Eupatorium adenophorum* Spreng) is native to Mexico, where it is a common weedy shrub. Its introduction in India, New Zealand, and Australia had serious economic consequences for local agriculture^[1]. It was introduced in Yunnan Province, China, around 1940. It has spread rapidly throughout southwestern China, and presently can be found in Guizhou, Xizang (Tibet), Guangxi, Yunnan, and Sichuan provinces^[2]. Because it invades mainly grasslands, economic im-

plications are significant. This plant may cause chronic pulmonary disease in horses, or even death in livestock^[1]. Such consequences led us to investigate further the potential distribution of this species in China.

Peterson and Vieglais^[3] presented a methodology for application of ecological niche modeling techniques in prediction of the geographic potential of species' invasions. The essence of the approach is development of an ecological niche model based

Received date: 2002-06-05, Accepted date: 2002-12-09

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on the ecological characteristics of known occurrences on the native distribution of a species. This technique, originally developed for predicting species' distributions on native geographic distributional areas^[4,5], was modified^[3] to include projection of the niche model to potentially invaded regions to predict geographic potential on the invaded distribution.

We applied this methodology to reconstruct the native distribution of *Eupatorium* in Mexico and to predict the invasive range of this species in China. We then compared our results with the available information concerning the native and invasive distribution of this plant.

1 Methods

Ecological niche models were developed based on georeferenced occurrence points taken from diverse sources, including herbarium specimen records, scientific literature including floras and systematic treatments, etc. In all, 45 occurrence points were obtained within the native range of the species. The seemingly low numbers of occurrence points obtained after months of searching literature and contacting museum curators emphasizes the critical need for computerization of natural history museum holdings, and integration of such data sets via the Internet to provide efficient access to biodiversity data.

Ecological niches were modeled using the Genetic Algorithm for Rule-set Prediction (GARP)^[4-6]. In general, the procedure focuses on modeling ecological niches (the conjunction of ecological conditions within which a species is able to maintain populations without immigration)^[7]. Specifically, GARP relates the ecological characteristics of known occurrence points to those of points randomly sampled from the rest of the study region, seeking to develop a series of decision rules that best summarize those factors associated with the species' presence

Occurrence points are divided twice evenly into training and test data sets—that is, an initial 50% of the data points are set aside for a completely independent test of model quality (extrinsic test data); of the remaining points, 50% are used for developing models (training data) and 50% are used for tests of model quality internal to GARP (intrinsic test data). GARP works in an iterative process of rule selection, evaluation, testing, and incorporation or rejection: a method is chosen from a set of possibilities (e.g., logistic regression, bioclimatic rules), applied to the training data, and a rule is developed or evolved. Predictive accuracy is then evaluated based on 1 250 points resampled from the intrinsic test data and 1 250 points sampled randomly from the study region as a whole. Rules may evolve by a number of means that mimic DNA evolution: point mutations, deletions, crossing over, etc. The change in predictive accuracy from one iteration to the next, measured via the intrinsic data, is used to evaluate whether a particular rule should be incorporated into the model, and the algorithm runs either 1 000 iterations or until convergence.*

All modeling in this study was carried out on a desktop implementation of GARP now available for public, free download¹⁾. This implementation offers much-improved flexibility in choice of predictive environmental/ecological GIS (Geographic Information Systems) data coverages: in this case, initially, we used 12 data layers summarizing elevation; slope; aspect (all from the U. S. Geological Survey's²⁾ Hydro-1K data set); aspects of climate including diurnal temperature range; frost days; mean annual precipitation; solar radiation; maximum, minimum, and mean annual temperatures; vapor pressure; and wet days (annual means 1961-1990; from the Intergovernmental Panel on Climate Change³⁾. The area of analysis included Mexico, where *Eupatorium* is native, and sur-

1) <http://beta.lifemapper.org/desktopgarp/>.

2) <http://edcdaac.usgs.gov/gtopo30/hydro/>.

* 3) <http://ipcc.ch/>.

rounding areas GARP's predictive abilities have been tested under diverse circumstances^[3, 8-15].

To reduce environmental coverage sets to just those coverages that provide highest predictive accuracy, we used a variety of jackknife manipulations. In general, we ran multiple iterations (1-20) of models omitting each coverage, or suites of coverages, systematically. We then examined the correlation between inclusion or exclusion of each coverage (coded as 1s and 0s) and omission error (percent of extrinsic test data not predicted as present). Positive correlations were considered indicative of detrimental contribution of a particular coverage to model quality, and those coverages were removed from further analysis. It is important to note that the jackknife manipulations were done solely on the native distribution, and so do not detract from the independent nature of the invaded-range predictions presented herein.

To optimize model performance, we developed 100 replicate models of species' ecological niche based on random 50-50 splits of available occurrence points. Unlike previous applications, which either used single models to predict species' distributions^[12, 14] or summed multiple models to incorporate model-to-model variation^[3], we used a new procedure (Anderson *et al.* submitted) for choosing best subsets of models. The procedure is based on the observations that (1) models vary in quality, (2) variation among models involves an inverse relationship between errors of omission (leaving out true distributional area) and commission (including areas not actually inhabited), and (3) best models (as judged by experts blind to error statistics in the original derivation of the methodology) are clustered in a region of minimum omission of independent test points and moderate area predicted (an axis related directly to commission error). The relative position of the cloud of points relative to the two error axes provides an assessment of the relative accuracy of each model. Hence, to choose best subsets of models, we (1) eliminated all models that had non-zero omission error based on independent test points, (2) calcu-

lated the average area predicted present among these zero-omission points, and (3) identified models that were within 1% of the overall average. Out of 342 models with no omission error we summed the 14 models which confined to the 1% threshold. Model quality was tested via the extrinsic test data: a χ^2 test was used to compare observed success in predicting the distribution of test points with that expected under a random model (proportional area predicted present provides an estimate of occurrence points correctly predicted were the prediction to be random with respect to the distribution of the test points). Projection of the rule-sets for these models onto maps of southern and eastern Asia provided predictions of potentially invaded distributions.

2 Results

The jackknife manipulations identified coverages that detracted from the predictive abilities of the algorithm. The first round of jackknife manipulations detected 6 coverages positively correlated with omission error (ground frost frequency, $r = 0.02$; annual mean minimum temperature, $r = 0.05$; annual mean temperature, $r = 0.11$; annual mean maximum temperature, $r = 0.03$; vapor pressure, $r = 0.01$; and aspect, $r = 0.02$). These coverages were eliminated from further analysis. The remaining six layers (diurnal temperature range, elevation, slope, precipitation, solar radiation, and wet day frequency) were examined in jackknife manipulations in which all possible combinations of the 6 coverages were tested. The best prediction of the native distribution of *Eupatorium* (i.e., zero omission) was obtained using four layers: diurnal temperature range, wet days, elevation, and slope.

All subsets models were highly statistically significant. The χ^2 tests based on the independent extrinsic test data sets, which included 22 points of known occurrence, all indicated predictive ability far better than random models (all $P < 2.14 \times 10^{-20}$). Hence, all best subsets models were highly predictive for the native distribution, and, for that

reason, we proceeded to explore their predictions for invaded distributional areas in China

Four of the five provinces where *Eupatorium* is known to occur in China were predicted as highly

suitable in our prediction of the invasive distribution (Fig. 1). One additional province from which the species is known, Xizang (Tibet), was

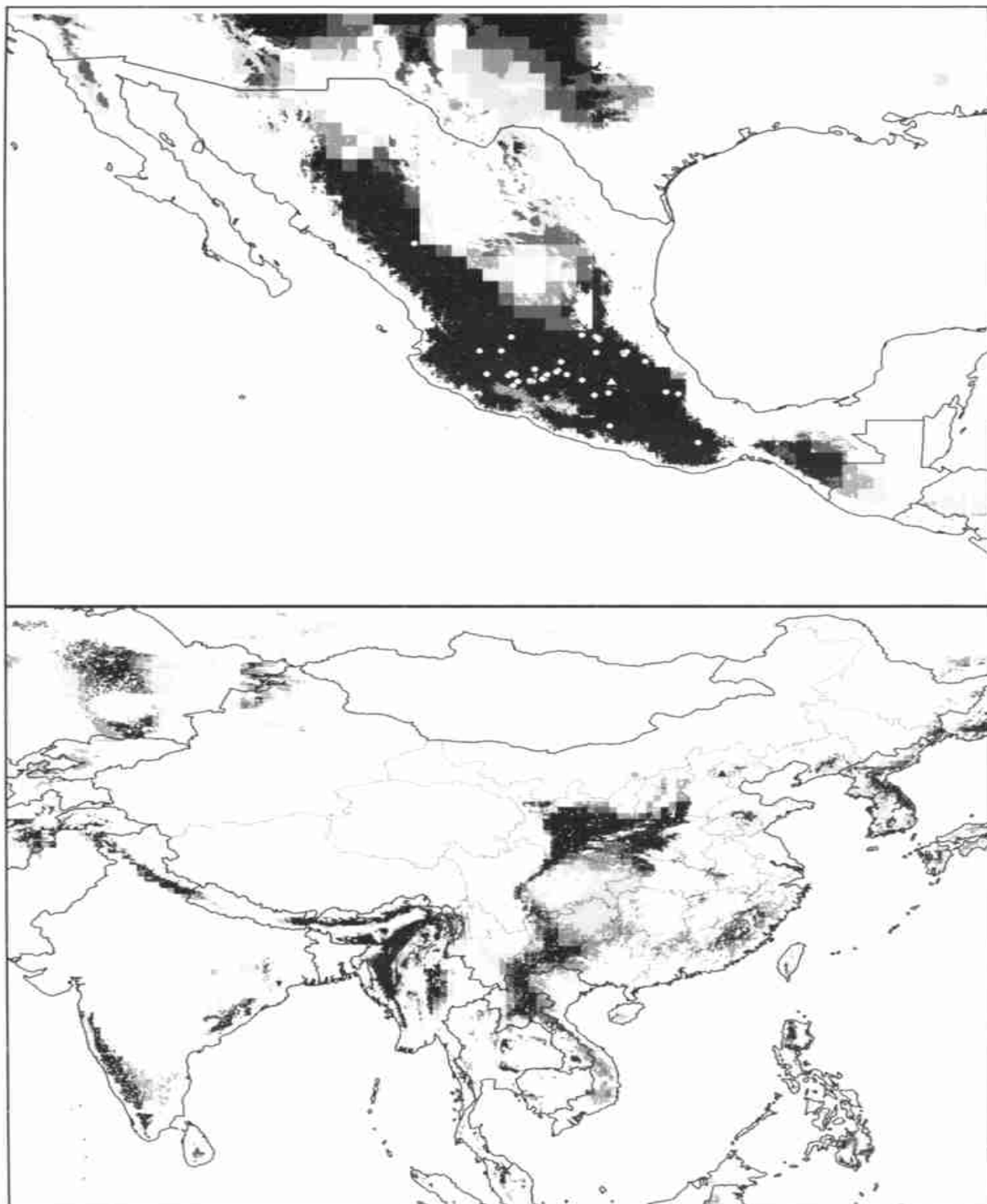


Fig. 1 Modeled predictions for *Eupatorium adenophorum* on its native geographic distribution (top) and projection to potentially invaded range in eastern Asia (bottom). Increasingly dark shades of gray indicate greater confidence in predictions of presence (white-zero models predicted present, and black-14 models predicted present; white circles-points of native occurrence; white triangle-Mexico City; black triangle-Beijing)

marginally included in our predictions. However, in each case, the lack of more precise distributional data from within China limits our abilities to assess the predictive nature of our models. GARP models indicated additional potential areas of invasion, mainly in central and eastern China.

3 Discussion

One of the most important threats to native communities is represented by the invasive exotic species^[16]. They often displace native dominants, altering community function and composition^[17], and can have serious economic consequences. Predicting the geographic potential species' invasions using ecological niche modeling techniques seems to be the most suitable approach to this problem^[3]. It can be applied no matter where the geographical region of interest is, as long as data on the native distribution of the species are available.

Our prediction concerning the possible areas of invasion of *Eupatorium* in China provinces where this weed is known to be included the four established^[2]. Native to Mexico and Central America, this plant species is clearly not yet in equilibrium distributionally, and for that reason does not yet inhabit its entire potential distributional area in Asia. However, lack of precise occurrence data for the plant in China limited our ability to test the accuracy of our models. Indeed, such was the motivation for publication of this paper: we present our model predictions in the hope that they stimulate the presentation of precise distributional information in the future.

This study detected other potential areas of invasion in China. The eastern part of the country was in general predicted as more suitable for invasion than the western part. More or less continuous with the areas currently occupied, to the north, are six provinces that appear to be directly vulnerable: Gansu, Ningxia, Shaanxi, Shanxi, Henan, and Hubei. Our model also detected two potential distributional areas that are disjunct from

the present distribution, in the northeast and southeast, in which this species could likely establish if introduced. These potential distributional areas include Liaoning and Heilongjiang provinces in the northeast and Fujian and Zhejiang provinces in the southeast.

Acknowledgments: Data were kindly provided by James C. Solomon from Missouri Botanical Garden, Marjorie Knowles from the Smithsonian Institute, and by the Red Mundial de Información sobre Biodiversidad (REMB⁴⁾) for data from the Herbario del Instituto de Ecología, A. C. Guojun Chen kindly assisted with translation of critical bibliographic references and review of the Chinese abstract. This study was funded by the U. S. National Science Foundation and the U. S. Environmental Protection Agency. *

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