Improving the agent selection, release and evaluation process: the role of bioclimatic modelling

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Summary Climate models are frequently used to evaluate the potential distribution of introduced species. However, despite their potential value, their use in biological control remains limited. Using a number of weed biocontrol programs as case studies, we assessed the value of CLIMEX models to inform biocontrol programs, including predicting the potential distribution of biocontrol agents and their subsequent population dynamics. Bioclimatic models for the weed *Parkinsonia aculeata*, two *Lantana camara* biocontrol agents, and five *Mimosa pigra* biocontrol agents were examined, encompassing a variety of life histories, climatic zones and quality of data for model development and evaluation. The results show the contribution of data types to CLIMEX models and the capacity of these models to inform and improve the selection, release and post release evaluation of biocontrol agents. Foremost among these is the quality of spatial and temporal information as well as the extent to which overseas range data samples the species' climatic envelope. *Post hoc* evaluation and refinement of these models requires improved long-term monitoring of introduced agents and their dynamics at well selected study sites. We describe the findings of these case studies, highlight their implications, and consider how to effectively incorporate them into biocontrol programs.

Keywords CLIMEX, model evaluation, seasonal phenology, spatial dynamics.

INTRODUCTION

Bioclimatic models are increasingly being used to assess the likely climatic suitability of Australia for potential weed biocontrol agents (Zalucki and van Klinken 2006). CLIMEX is one such modelling program that enables the user to estimate the potential geographic distribution and seasonal abundance of a species in relation to climate (Sutherst *et al.* 2004), and is widely used in biological control. The CLIMEX program incorporates both growth (temperature and soil moisture) and stress (hot, cold, wet, and dry) parameters into an Ecoclimatic Index (EI) which predicts the relative climatic suitability of a site for a particular species.

The predictive capacity of these models is influenced by many factors, including the type (e.g. distribution, phenology, abundance), quality and quantity of data available on the species, yet research on their effects remains scant. We assessed the effects of data type, quality and quantity using case studies of a weed and several weed biocontrol agents. Our objective was to provide the information needed to underpin more accurate CLIMEX models for biocontrol agents, and to allow better judgments on the likely predictive success of current and future models.

MATERIALS AND METHODS

CLIMEX Version 2.0 (Sutherst *et al.* 2004) was used to develop predictive models of the potential distribution of biocontrol agents in Australia. Initially, CLIMEX climate-envelope models were developed for each species using available non-Australian distributional and phenological data to parameterise the model.

The woody weed, *Parkinsonia aculeata* L., was used to examine the sensitivity of CLIMEX model parameters and whether these disproportionately affect the native vs predicted range. A baseline model for the species was constructed using native range presence-absence data. Model parameters (e.g. soil moisture, heat stress) that were difficult to fit were identified, and the extent to which each could be altered without a noticeable change in the fitted species climate envelope was determined. The relative change in the extent and predicted growth between the native and predicted Australian range was then examined.

For the two *Lantana camara* L. agents, *Teleonemia scrupulosa* Stål and *Octotoma scabripennis* Guérin-Méneville, three models were constructed for each species based upon overseas distribution only, seasonal phenology descriptions only, and a combined distribution-phenology model. The aim was to examine the contribution of different data types to bioclimatic model predictions, and to understand the effects of high (*T. scrupulosa*) and low (*O. scabripennis*) quantity and quality of data on model predictions.

Models for five *Mimosa pigra* L. agents representing different post-release outcomes were examined, two being very abundant species (*Carmenta mimosa*

Eichlin & Passoa and *Neurostrota gunniella* Busck), one abundant species (*Acanthoscelides* complex Johnson & Schaeffer) and two species failing to establish (*Chalcodermus serripes* Fåhraeus and *Sibinia fastigiata* Clark). CLIMEX climate envelope models were constructed from limited distributional and abundance data, and compared to predictions from the simplified 'match climates' function of CLIMEX using the native range locality adjudged by experts to have the highest abundance of the species. Temporal predictions of each species' climate envelope model were compared to recorded temporal abundance of the species to ascertain the model's capacity to predict temporal dynamics.

RESULTS

***Parkinsonia aculeate* model sensitivity** Analysis of the sensitivity of a *Parkinsonia* model to altered parameters revealed that changed parameters had a minimal impact on the native range distribution. In contrast, the Australian distribution showed that two parameters (lower temperature and high moisture), and a combination of these, resulted in substantial variations in the predicted range. The model was not sensitive to variations in stress parameters (Table 1).

***Lantana camara* biocontrol agents** Models for *T. scrupulosa* constructed from higher quality (detailed seasonal phenology descriptions) and quantity of data (76 records in 33 countries) than its *O. scabripennis* counterpart (general seasonal phenology descriptions; nine localities in five countries), presented a much more accurate representation of the species' Australian distribution, as indicated by a higher proportion of records intersecting with higher EI bands (Figure 1). The *T. scrupulosa* models showed an increase in the proportion of species records intersecting with higher EI bands with the shift from 'seasonal phenology' to 'overseas distribution' to the 'combined' model. In contrast, there was no noticeable trend between the corresponding *O. scabripennis* models, and much lower proportion of record intersection with upper EI bands.

***Mimosa pigra* biocontrol agents** Climate-envelope models developed from very few native range records (6–12) had no greater spatial predictive qualities than the simpler match climates based model (see Figure 2). Neither modelling approach was able to predict the likely success or failure of establishment of the five agents. Where high quality observational data

Table 1. Effects of CLIMEX parameter variations on the fitted Americas distribution and the predicted Australian distribution compared to the baseline *Parkinsonia aculeata* model. Low R^2 values (in **bold**) indicate the model types where predictions varied substantially.

Model types	Comparison with baseline model (R^2)	
	Americas	Australia
Temperature		
Low	0.91	**0.58**
High	0.91	0.99
Moisture		
Low	1.00	0.99
High	0.91	**0.55**
Dry Stress		
Tolerant	1.00	1.00
Sensitive	1.00	1.00
Heat Stress		
Tolerant	1.00	1.00
Sensitive	0.99	0.99
Combined		
Low temp, High moist	0.83	**0.29**

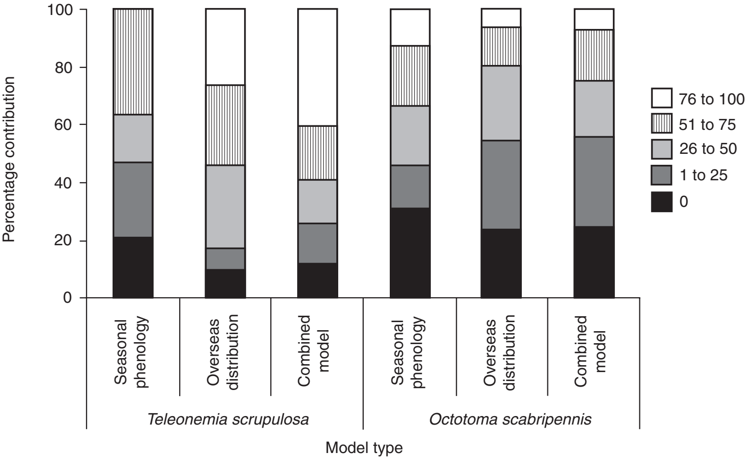

Figure 1. The relative proportion of *Lantana camara* biocontrol agent presence among EI categories of models constructed from different data types.

on *N. gunniella* seasonal phenology was available, a reasonably strong correlation was shown between the predicted and observed population dynamics. Little to no correlation was evident for catchment-aggregated monthly and yearly observation data and predictions of population dynamics for the five agents examined.

DISCUSSION

Sensitivity analysis of a model for *Parkinsonia* revealed that parameter selection can disproportionately affect the predicted range distribution as compared to the native range distribution. Additionally, where native range records for an agent adequately sample the extent of the native range, stress parameters are easily defined. As a result, only growth indices are sensitive to variation in parameter values and need alternative means of confirming appropriate values.

The *Lantana* agent results suggest that CLIMEX models based on low quality seasonal phenology data and/or a small quantity of distributional data are of minimal value in predicting the spatial extent of an introduced species. However, temporal predictions were not so adversely affected.

Predictions for *Mimosa* agents suggest that where only a small quantity of data exists with which to construct a model, the 'match climates' function of CLIMEX is quicker than, and of similar accuracy to, the more time-consuming climate envelope models in making spatial predictions. However, the latter is to be preferred if the data available is considered to reasonably approximate the species' overseas range, and preferably contains some documented phenological responses.

Temporal predictions, which are only available with climate envelope models, were highly variable and inconsistent predictors of monthly and yearly variation. Of these, the only consistent correlation in the predicted range occurred with the one comparison with high quality observational data from a single site of the agent *N. gunniella*.

CONCLUSIONS

Bioclimatic models are an important tool in weed biocontrol programs, yet their value and limitations remain poorly documented. Our research demonstrates the need for adequate native range data. Spatially adequate distributional data is required to ensure that stress parameters do not underestimate the predicted introduced range, and reduces the number of parameters that are sensitive to variation. Seasonal phenology data broadens the information base on which to construct predictive models and limits the number of parameters that need to be iteratively determined (Zalucki and van Klinken 2006). To maximise the accuracy of predictions from such bioclimatic models, model development should be based upon presence-absence data across the agent's native climatic range and two or more climatically differing localities at which the agent's seasonal phenology has been described in detail for at least 12 months. In addition, the use of sensitivity analyses to determine the parameters that cause the largest variance in a model can allow the strategic data needs from the native range to be identified.

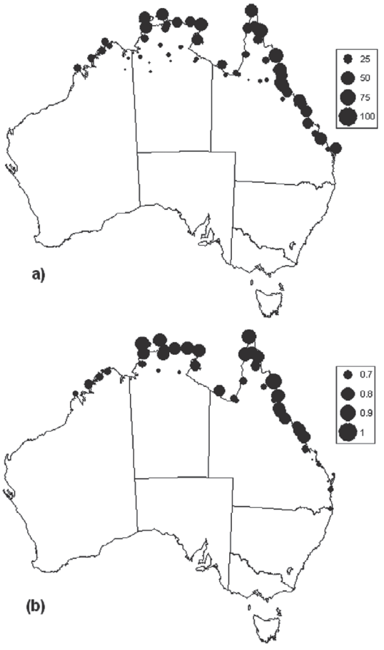

Figure 2. Predicted distribution of *Carmenta mimosa* in Australia using CLIMEX models developed using (a) climatic envelope and (b) match climates with Veracruz, Mexico.

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REFERENCES

Sutherst, R.W., Maywald, G.F., Bottomley, W. and Bourne, A. (2004). 'CLIMEX user's guide, Version 2' (Hearne Scientific Software, Melbourne).

Zalucki, M.P. and van Klinken, R. (2006). Predicting population dynamics and abundance of introduced biological agents: science or gazing into crystal balls? *Australian Journal of Entomology* 45, 330-43.