Taxonomic patterns in the naturalisation rate of plant species in New Zealand

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Summary New plant invasions are largely unpredictable and species with no cultivation history present a particularly difficult problem for weed-risk assessment. Rules identifying species most likely to naturalise, based purely on grounds of probability determined from the historical behaviour of the taxonomic group to which the species belongs, would assist in predicting potential invaders. Becoming naturalised involves escaping from cultivation and establishing a self-sustaining wild population. This is a critical step for an invasive species while their eventual impact will be revealed only after some time. We used a list of 24,732 seed plant species (i.e. gymnosperms and angiosperms) introduced into New Zealand, along with whether those species naturalised or not, to test three hypotheses concerning naturalisation. First we found naturalisation rate was significantly clumped in certain families. Second, within 12 of 13 large families, naturalisation rate was significantly clumped within genera. Third, naturalisation rate was highest in species with native congeners. Some families therefore pose significantly greater risk than others, and in general, this risk is higher for some genera than others within those families. In New Zealand, introduced species with native congeners are a higher risk than those without native congeners.

Keywords Naturalisation rate, weeds, risk assessment.

INTRODUCTION

However good our biological knowledge of new invaders, in many cases we may do no better than get a probability of an impact (Williamson 2001). Naturalisation is the first step towards an introduced plant species having sufficient impact to become classified as a weed. The proportion of plants that naturalise from among all those introduced into a country can be very low if the whole flora is considered (Williamson 1996). One factor that may provide information about the probability that a plant species will naturalise is the taxonomic classification of the species. Closely related species tend to share traits in common. If certain shared traits influence the probability that a plant species will naturalise, then we might expect higher naturalisation rates in some groups of closely related species (those that share traits promoting naturalisation) and lower naturalisation rates in others (related species lacking those traits). For example, tropical grasses are known to have high naturalisation rates in Australia (Lonsdale 1994), and such groups tend to be specifically identified in weed-risk assessment models (Pheloung *et al.* 1999). To assist in providing a basis for weed risk assessments, we determined, from a list of all the seed plant species known to have been introduced to New Zealand, whether naturalised species were clustered in certain families, and within certain genera within families. We also assessed whether species were more likely to naturalise if they had congeneric native relatives.

METHODS

We obtained a list of all exotic angiosperm and gymnosperm species that have been introduced for cultivation to New Zealand, compiled using lists obtained from commercial seed plant catalogues, national agricultural research organisations, national herbaria records, botanic gardens, Government departments and many private and commercial collections. Only valid plant names were used and the species were classified to family. The list comprised 24,774 species in 3863 genera and 262 families. Of these, 1769 species in 749 genera have fully naturalised in New Zealand. That is, they form populations self-maintained by seed or vegetative reproduction, or occur repeatedly in the wild or urban environments. We also compiled a list of 1511 native plant species that occur in genera with at least one introduced species.

Among families We determined whether naturalisation success rate was evenly spread among families or clumped within certain families. To test this, we fitted a generalised linear mixed model using PROC NLMIXED in SAS version 8, with naturalisation success rate per genus (number of naturalised species in a genus as a proportion of the total number of introduced species in a genus) as the response variable, and a variable coding for family as a random effect. We fit a model using a logit link function and binomial error distribution. By including family as a random effect in the model we are treating the families

introduced to New Zealand as a random sample of all the world's plant families, so that inferences drawn from the analysis apply to this larger population and not just to those families introduced to New Zealand. A significant variance component for the random effect, family, would indicate there was significant variation in naturalisation success rate in New Zealand among families. We tested the significance of adding family as a random effect to the model using a likelihood ratio test by calculating the change in deviance associated with adding the variable family to the model and comparing the change in deviance to a chi-square distribution with the appropriate degrees of freedom.

Among genera We used a similar approach to test whether, within families, naturalisation success rate was evenly spread among genera or clumped within certain genera. We identified families that had 50 or more introduced genera (but excluded the families Orchidaceae, Arecaceae, Cactaceae and Asclepiadaceae, which had 50 or more introduced genera but none or very few naturalised species). For each family, we included all introduced species, with the response variable being whether a species was naturalised or not, and with genus included as a random effect in the model. A significant variance component for the random effect genus (assessed using a likelihood ratio test) would indicate there was significant variation in naturalisation success rate among genera within a family.

RESULTS

Among families The likelihood ratio test for the addition of family as a random effect to the model containing all introduced species was highly significant (chi-square = 2211.1, P<0.0001), showing that there are significant differences among families in naturalisation rate, and therefore that species in some families are more likely to naturalise than species in other families.

For families with more than 100 species introduced to New Zealand, the ten families with the highest naturalisation rate and the ten families with the lowest naturalisation rate are shown in Table 1.

Among genera For 12 of the 13 families with more than 50 introduced genera, genus was a highly significant predictor of naturalisation probability, showing that there are significant differences among genera in naturalisation rate within these 12 families (Table 2). The only exception was the family Myrtaceae, which showed no significant clumping of success rate by genus.

Table 1. The ten families with the highest naturalisation rate and the ten families with the lowest naturalisation rate, for families with more than 100 species introduced to New Zealand.

Family	No. of introduced species	No. of naturalised species	% naturalised
Poaceae	563	270	48
Cyperaceae	105	42	40
Solanaceae	188	48	26
Polygonaceae	123	30	24
Salicaceae	106	25	24
Apiaceae	162	31	19
Brassicaceae	386	67	17
Malvaceae	116	20	17
Boraginaceae	139	22	16
Caryophyllaceae	294	46	16
Ericaceae	655	12	2
Rutaceae	144	1	<1
Saxifragaceae	180	1	<1
Arecaceae	601	3	<1
Asclepiadaceae	484	2	<1
Cactaceae	1837	2	<1
Bromeliaceae	824	0	0
Gesneriaceae	124	0	0
Orchidaceae	1758	0	0
Zamiaceae	115	0	0

Examples of genera with more than 10 introduced species that have high naturalisation rates for five of the families shown in Table 2 are (with the percent of naturalised species in the genus shown in brackets):

Asteraceae:	*Hieracium*	(59)
	Crepis	(40)
	Cirsium	(33)
Fabaceae:	*Racosperma*	(65)
	Vicia	(53)
	Medicago	(47)
Liliaceae:	*Asparagus*	(22)
	Bomarea	(20)
	Narcissus	(17)
Poaceae:	*Rytidosperma*	(90)
	Panicum	(80)
	Hordeum	(73)
Lamiaceae:	*Mentha*	(50)
	Stachys	(21)
	Phlomis	(18)

A cross-classification of introduced genera according to whether they contained at least one naturalised species or not, and whether they contained at least one native species or not (Table 3), showed that introduced genera containing at least one native species had a significantly higher rate of naturalisation than introduced genera lacking native species (Duncan

and Williams 2002). Furthermore, for the 218 introduced genera with at least one native species, the naturalisation rate per genus (the number of naturalised species as a proportion of the total number of introduced species) was significantly higher in genera containing a greater number of native species (Duncan and Williams 2002).

CONCLUSIONS

Our results show significant taxonomic clumping in naturalisation rate. Members of some families are significantly more likely to naturalise than others and, within most families, members of some genera are significantly more likely to naturalise than others. A likely explanation for these patterns is that the species in certain families or genera tend to share traits that increase their chances of naturalisation, relative to species in other families and genera. The finding that naturalisation rate is also higher for species in introduced genera with native species further supports this. Introduced species in these genera may share traits with their native relatives that pre-adapt them to the New Zealand environment (Duncan and Williams 2002).

These findings show that the chance of a novel introduced species becoming naturalised can be predicted from the naturalisation success of its relatives, and the presence of closely related native species. Both of these results suggest that there are certain traits, shared by closely related species that enhance the probability of naturalisation. From the historical behaviour of species in different taxonomic groups it is therefore possible to identify certain families and genera that pose a greater risk of naturalisation and to incorporate this information into week risk assessments.

Table 2. Selected families with more than 50 genera introduced to New Zealand, showing whether or not there is a significant clumping of naturalisation success among genera within that family. The likelihood ratio chi-square (and associated P value) tests whether inclusion of the variable genus significantly predicts the probability of naturalisation within each family.

Family	No. of introduced genera	No. of introduced species	No. of naturalised species	Likelihood ratio chi-square	P
Asteraceae	308	1335	180	74.5	<0.0001
Fabaceae	205	1090	114	112.1	<0.0001
Liliaceae	201	1725	47	20.2	<0.0001
Poaceae	155	563	270	70.5	<0.0001
Lamiaceae	78	567	57	12.5	0.0004
Scrophulariaceae	77	466	43	25.0	<0.0001
Aizoaceae	76	384	8	6.3	0.0121
Brassicaceae	75	386	67	72.3	<0.0001
Apiaceae	74	162	31	5.1	0.0239
Iridaceae	72	739	39	8.7	0.0032
Rosaceae	71	671	81	34.6	<0.0001
Myrtaceae	60	554	26	2.0	0.1573
Rubiaceae	53	119	10	40.8	<0.0001

Table 3. Cross-classification of the 3863 seed plant genera introduced to New Zealand according to whether or not the genus contained at least one fully naturalised species, and whether or not the genus contained at least one native species (from Duncan and Williams 2002).

		Genus contains native species	
		No	Yes
Genus contains naturalised species	No	2995	119
	Yes	650	99
	% naturalised genera	18	45

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