Patterns of genetic variation among rare, widespread and invasive *Cirsium* congeners

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INTRODUCTION

Conservation biology has long sought to understand the genetic underpinning that distinguishes rare, widespread and invasive species (3). Although genetic variation is often perceived to be lower in rare species and higher in those that are widespread, reviews of the literature on rare and common plant congeners has shown that this generalization cannot be made (3).

As previous reviews have compared only single rare–widespread species pairs among different genera, the purpose of this study was to provide a more extensive examination within a single genus, through comparing genetic diversity between a larger number of congeners. Genetic diversity was thus assessed among several rare, widespread, as well as invasive species within the genus *Cirsium* (Asteraceae). The *Cirsium* genus is an ideal study system as it contains species that are highly noxious weeds (*C. arvense, C. vulgare*), species that have widespread distributions (*C. heterophyllum, C. acaule, C. occidentale, C. quercetorum*), as well as species that are considered rare (*C. pitcheri, C. hillii,* and *C. andrewsii*).

The main question addressed in this study was: can the invasiveness or rarity of *Cirsium* congeners be explained by differing patterns in genetic diversity?

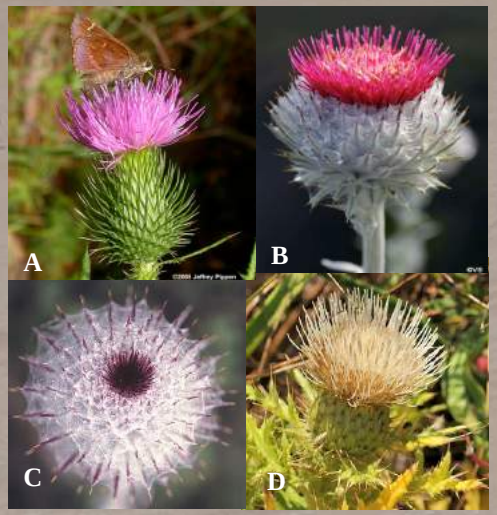
MATERIALS and METHODS

Plant material/DNA Extraction

Ten individuals were sampled from eight different *Cirsium* populations in Point Reyes National Seashore, California – two populations representing each of the four species under study (*C. quercetorum, C. andrewsii, C. vulgare,* and *C. occidentale*). Genomic DNA was extracted from a 4 cm^2 sample of mature leaf tissue, following the protocol outlined in the DNEasy kit (QIAGEN). The other species used in this study were taken from published data from Jump *et al.* (2003) as well as unpublished data from J. Fant on *C. pitcheri* and *C. hillii*.

Genotyping/Analysis

The eighty individuals were genotyped at four microsatellite loci, previously isolated in *C. acaule* by Jump *et al.* (2002). The loci used included CaCo4A, CaCo5, CaCo8, and CaCo10, all of which displayed polymorphism in the four *Cirsium* species used. PCR reactions were carried out under the Cirsium50 program and products were analyzed on the CEQ 8000 Genetic Analysis System. Observed heterozygosity (H_E), mean number of alleles per locus at the population and species level (A_{pop}; A_{sp}), and coefficient of inbreeding (F_{IS}) were calculated using the software program FSTAT in all species, except those provided by Jump *et al.* (2003).



Above - **(A)** *C. vulgare* (Bull Thistle) **(B)** *C. occidentale* (Cobwebby Thistle) **(C)** *C. andrewsii* (Franciscan Thistle) **(D)** *C. quercetorum* (Brownie Thistle). Photos taken from: http://calphotos.berkeley.edu/

Table 1. Summary of population-level genetic diversity statistics for 9 Cirsium congeners.

	A_{pop}	H_O	F_{IS}
RARE			
C. andrewsii			
Population #1	4.25	0.625	0.131
Population #2	4.5	0.722	0.219
C. pitcheri			
Population #1	1.7	0.201	0.251
Population #2	3	0.252	-0.08
C. hillii			
Population #1	3.7	0.386	-0.285
Population #2	5	0.682	-0.008
WIDESPREAD			
C. occidentale			
Population #1	4.25	0.653	0.103
Population #2	3.25	0.556	0.108
C. quercetorum			
Population #1	4	0.67	0.24
Population #2	3.75	0.613	0.491
INVASIVE			
C. vulgare			
Population #1	5	0.725	0.584
Population #2	3	0.703	-0.193

Abbreviations: A_{pop}=average number of alleles per locus at the species level; H_o = Observed heterozygosity ; F_{IS} = coefficient of inbreeding

Table 2. Summary of species-level genetic diversity statistics for 9 *Cirsium* congeners.

	A_{SP}	$\%A_{sp}$	H_O	F_{IS}
RARE				
C. andrewsii	5.5	68.80%	0.73	0.24
C. pitcheri	2.75	34.40%	0.37	0.51
*C. hillii**	5.67	70.90%	0.67	0.08
WIDESPREAD				
C. occidentale	5	62.50%	0.69	0.22
C. quercetorum	4.75	59.40%	0.71	0.39
*C. acaule**	3	37.50%	0.52	-0.08
*C. heterophyllum**	2.5	31.25%	0.49	0.05
INVASIVE				
C. vulgare	5.75	71.90%	0.76	0.272
*C. arvense**	6	75%	0.67	-0.106

*=asexual species; Abbreviations: A_{sp}=average number of alleles per locus at the species level; H_o = Observed heterozygosity ; F_{IS} = coefficient of inbreeding

DISCUSSION/CONCLUSIONS

- No general trend was observed with respect to genetic diversity among rare, widespread, and invasive *Cirsium* congeners (Table 1). Invasive species *C. vulgare* and *C. arvense* yielded A_{sp} values on the higher end of the spectrum, as did rare species *C. andrewsii* and *C. hillii*.
- The lowest A_{sp} values are observed for two widespread species (*C. acaule and C. heterophyllum*), as well as for the rare species *C. pitcheri*. The low diversity in *C. pitcheri* is the result of its relatively recent speciation from its progenitor *C. canescens*, in an environment (the newly created sand dunes post-Wisconsin glaciation) where it endured repeated population bottlenecks (4).
- Inbreeding coefficients are lowest for clonal species – while this may not seem intuitive, it may be that viable seed that does develop into adult organisms must be competitive enough to out-compete surrounding clones, and thus is likely manifesting heterozygote advantage. Demographic characteristics, therefore, not only inherent genetic diversity, are an important consideration for understanding rarity and invasiveness.
- Different attributes cause different species to be rare – rarity is not a single entity but rather may be the result of a number of factors including population size, habitat specificity, and geographic range (3). As seen with *C. pitcheri* and *C. hilli* (Table 2), larger populations (Population #1) exhibit more diversity than smaller populations (Population #2) within the same rare species.
- Understanding differences in rare, widespread and invasive *Cirsium* congeners should be understood as a function of differences in available habitat type, population size and other species-specific factors, rather than over-generalizing all rare species to be genetically depauperate.

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