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Genetic change following fire in populations of a seed-banking perennial plant

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41 Abstract

42 Disturbances such as fire have the potential to remove genetic variation, but seed banks 43 may counter this loss by restoring alleles through a reservoir effect. We used allozyme 44 analysis to characterize genetic change in two populations of the perennial *Hypericum* 45 *cumulicola*, an endemic of the fire-prone Florida scrub. We assessed genetic variation 46 before and one, two, and three years after fire that killed nearly all aboveground plants. 47 Populations increased in size following fire, with most seedlings likely recruited from a 48 persistent seed bank. Four of five loci were variable. Most alleles were present in low 49 frequencies, but our large sample sizes allowed detection of significant trends. Expected 50 heterozygosity increased, and allele presence and allele frequencies showed marked shifts 51 following fire. The post-fire seedling cohort contained new alleles to the study and one 52 new allele to the species. Population differentiation between the two study sites did not 53 change. Our study is the first to directly documents genetic changes following fire, a 54 dominant ecological disturbance worldwide, and is also one of the few to consider shifts 55 in a naturally recruiting post-disturbance seedling cohort. We demonstrate the potential 56 of seed banks to restore genetic variation lost between disturbances. Our study 57 demonstrates that rapid genetic change can occur with disturbance and that fire can have 58 positive effects on the genetics of rare species.

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- 61

62 Keywords

63 allozymes, fire, Florida scrub, genetic variation, *Hypericum cumulicola*

64 Introduction

Rapid shifts in the genetic structure of populations are increasingly recognized as important responses of wild plants and animals to environmental changes such as global warming (Bradshaw and Holzapfel 2001), alterations in soil chemistry (Snaydon and Davies 1982), or invasion of exotic species (Groman and Pellmyr 2000). Ecological disturbances, by causing mass mortality and allowing prodigious recruitment, should also be capable of causing rapid genetic changes. However, this process remains virtually unstudied.

72

73 Fire is probably the predominant ecological disturbance worldwide, controlling much 74 variation in vegetation, carbon, and nutrient dynamics (Bond and Keeley 2005). 75 However, no studies have investigated the effects of fire as a driver of genetic change. 76 For plant species that are generally killed by fire and recover via a persistent seed bank, 77 there is great potential for such change. Seed banks can be genetically distinct from 78 aboveground plants, and can serve as genetic reservoirs, harboring and replenishing 79 variation that has been lost aboveground (Del Castillo 1994). They have the potential to 80 affect the evolutionary potential of plant populations (McCue and Holtsford 1998; Mahy 81 et al. 1999) by dispersing genes through time (Tonsor et al. 1993). If built up over many 82 years, seed banks can store genetic memory of variation lost in aboveground plants 83 (Templeton and Levin 1979; Cabin 1996) due to inbreeding and drift. Yet, field studies of 84 seed bank genetics (Baskin and Baskin 1978; Tonsor 1993; Peroni and Armstrong 2001; 85 Mandák et al. 2006) and the genetics of naturally occurring seedling cohorts (Epperson 86 and Alvarez-Buylla 1997) are rare.

88	Florida scrub is a fire-prone, disturbance mediated habitat (Menges 2007). Fire reduces
89	aboveground biomass and releases herbaceous species from competition (Quintana-
90	Ascencio and Morales-Hernández 1997). Many of these herbaceous plants are killed by
91	fire, but populations are rapidly restored by recruitment from seeds in a persistent seed
92	bank (Menges and Kohfeldt 1995). Post-fire seeders are particularly well-represented
93	among rare plants of Florida scrub, which is itself a hotspot for endemism (Christman
94	and Judd 1990; Estill and Cruzan 2001).
95	
96	Although the effects of fire on the demography of several Florida scrub endemics have
97	been documented (e.g., Quintana-Ascencio et al. 2003; Menges and Quintana-Ascencio
98	2004; Menges et al. 2006), no previous study has examined the effects of fire on genetic
99	change in a Florida scrub plant. We used allozyme markers to study genetic changes
100	following fire in the federally-endangered Hypericum cumulicola (Small) P. Adams
101	(Clusiaceae) at two sites on the Lake Wales Ridge in central Florida. Complete censuses
102	were conducted pre-fire at both sites. Fires the following year killed almost all
103	aboveground plants. We then sampled all seedlings emerging each of the next three
104	years. These seedlings were assumed to have derived from the seed bank based on the
105	extremely limited seed dispersal documented for this species (Quintana-Ascencio et al.
106	1998). Congruent spatial patterns within populations pre-fire vs. post-fire (Quintana-
107	Ascencio et al. in preparation) also suggest limited dispersal. Thus, we were able to track
108	genetic changes occurring post-fire by comparing genetic variation in pre-burn
109	aboveground populations with that in cohorts of emerging post-fire seedlings.

111	Seed banks are notoriously difficult to study, but can be very important life stages when
112	considering metapopulation dynamics and genetic structure. This is especially true in
113	rare plants with few populations, where the seed bank may represent a significant
114	proportion of the gene pool. Prior genetic studies of seed banks relied on meticulously
115	recovering seeds from soil cores and germinating them in greenhouses under artificial
116	conditions (e.g., McGraw 1993; Cabin 1996; McCue and Holtsford 1998; Mandák et al.
117	2006). Our study system overcomes several shortcomings of this approach: 1) seed
118	banks can be large and aggregated, making it hard to know where to collect samples at a
119	site (Cabin 1998); 2) recovery of seeds from seed cores often results in few available
120	seeds to grow into seedlings, so previous studies looked at few seed genotypes and
121	therefore lacked statistical power to detect low frequency alleles (e.g., Mahy et al. 1999).
122	Our <i>in situ</i> system and large sample sizes make our study one of the most comprehensive
123	studies of genetic change in a wild plant species yet conducted.

124 Materials and Methods

125 Study species

126 *Hypericum cumulicola*, the Highlands scrub hypericum, is a short-lived perennial herb. It 127 is a federally listed endangered plant endemic to the Lake Wales Ridge in central Florida 128 (Christman and Judd 1990). It grows in xeric, open areas of well-drained white sand in 129 Florida scrub dominated by Florida rosemary (Ceratiola ericoides) and scrub oaks 130 (Quercus spp.) (Menges 1999). Populations tend to occur in discrete patches that are 131 separated by large patches of unsuitable habitat (Quintana-Ascencio and Menges 1996). 132 Plants are self-compatible and have high rates of inbreeding (Dolan et al. 1999) 133 Pollinators of *H. cumulicola* are bees that forage locally in a trap-line fashion and are 134 unlikely to travel between patches of occupied habitat (Boyle and Menges 2001). Seeds 135 and fruits disperse on average less than a meter (Menges et al. 1998). Consequently, most 136 seedlings are found in the vicinity of fruiting plants (Quintana-Ascencio et al. 1998, 137 Quintana-Ascencio et al. in preparation). Interpopulation gene flow, via either pollen or 138 seeds, is therefore quite unlikely. As a consequence, F_{ST} , the proportion of genetic 139 variation found among populations, at patch level, is extremely large (0.72; Dolan et al... 140 1999; this study included 34 populations including the two populations included in this 141 study). No populations were in Hardy-Weinberg equilibrium. 142

143 Florida rosemary scrub probably burns infrequently, about every 15-30 (Menges 2007) or

144 20-80 years (Menges and Hawkes 1998). Fire kills aboveground *H. cumulicola* plants

145 (Menges and Kohfeldt 1995) as well as the dominant Florida rosemary (Johnson 1982).

146 Reestablishment of both species occurs primarily from a persistent seed bank (Quintana-

147	Ascencio et al. 1998), with Hypericum cumulicola establishment enhanced during wet
148	winters (Quintana-Ascencio et al. 2007). Survival and growth are greatest in recently
149	burned patches (Quintana-Ascencio 1997), where there is less competition due to the
150	temporary removal of aboveground shrub biomass and ground lichens (Quintana-
151	Ascencio and Morales-Hernández (1997).
152	
153	Study sites
154	We studied genetic shifts in <i>H. cumulicola</i> with fire at two sites: Archbold Biological
155	Station (ABS) and Lake Placid Scrub (LPS). At each site, H. cumulicola occurs
156	primarily in rosemary scrub, and periodic fires have been part of the recent history of
157	each site. The patch at Archbold extends for <i>ca</i> . 400 m from north to south and is 80 m at
158	its widest. The patch at Lake Placid Scrub extends for ca. 90 m from northwest to
159	southeast and is 35 m at its widest. Sites are 6 km apart and suitable habitat is
160	discontinuous between the sites due to wetlands and human-caused habitat fragmentation.
161	For both sites, complete pre-fire censuses for <i>H. cumulicola</i> were conducted in
162	preparation for planned prescribed fires.
163	
164	At ABS, an accidental fire ignited by a passing train burned over the study site in
165	February, 2001. This was a high intensity fire burning during an extreme drought
166	(Weekley et al. 2007). Unlike most landscape fires over the years, this fire burned
167	completely through seasonal ponds (that were bone dry) In addition, it produced
168	unusually little variation in fire intensity in xeric uplands such as rosemary scrub (ABS
169	fire data and Menges, personal observations). In particular, this fire burned >99% of the

area in the patch, killing most standing *H. cumulicola*. Fewer than 1 % (8 of 842) of all
plants survived through 2002; only three of them survived to 2003. The surviving plants
were unburned and located in a single gap at the south end of the patch. Because of the
large scale and homogeneity of this fire, along with the poor dispersal of *H. cumulicola*fruits, we believe the vast majority of post-fire seedlings derived from on-site seeds in the
persistent seed bank.

176

At LPS, the prescribed fire occurred as planned in July, 2001, just after the 2001 drought
(Weekley et al. 2007). Because of higher humidity, this prescribed fire resulted in a
patchy burn. Nevertheless, most standing *H. cumulicola* plants in this patch were also
killed. Fourteen plants (7.5 % of 186 total plants in the patch) in 6 gaps that did not burn
on the eastern part of the Lake Placid patch survived through 2002; 4 of them survived
through 2004.

183

Recruitment of new seedlings began during the winter of 2001-2002. We located, marked and mapped with a laser (Impulse, Laser Technology Inc., Englewood, Colorado, USA, 1 cm accuracy) every new recruit between July and September of 2002, 2003 and 2004 within all gaps at Archbold and Lake Placid scrub patches (a total of over 1700 seedlings) Sites were visited 2-3 times every other week during peak germination time to increase chances of finding seedlings.

190

191 Allozyme analysis

192 Small samples of leaf and stem or flower buds were collected from each plant larger than 193 2 cm at both study sites (ABS and LPS) during the summer of 2000 (pre-fire) and 2002 194 (post-fire) Additionally, during 2003 and 2004, samples from newly established 195 seedlings were collected. Almost all plants were large enough to be sampled (Table 1). 196 197 Material was sent to Butler University via overnight mail, where standard procedures for 198 starch gel electrophoresis for allozymes were conducted with recipes following Dolan et 199 al. (1999). Gels were stained for the five variable loci identified in our previous, 200 extensive, species-wide survey of *H. cumulicola* (Dolan et al. 1999): isocitrate 201 dehydrogenase (IDH), malate dehydrogenase 1 (MDH1), malate dehydrogenase 3 202 (MDH3), menadione reductase (MNR), and 6-phosphoglucomutase (6PGD) We used 203 the GDA software of Lewis and Zaykin (1999) for genetic analysis. Because sample 204 sizes were large (at least 699 at ABS and 172 at LPS for each year) and nearly complete 205 we applied no cut-off criterion for considering a locus polymorphic, including all alleles 206 detected in our analyses. The few plants that survived the fire at either site were included 207 in pre-fire genetic analyses but not the post-fire analyses. 208

209 Statistical Analyses

210 Expected heterozygosity was calculated for each study site pre-fire (2000) and post-fire

211 (2002, 2003, 2004). We used contingency chi-square tests (recommended by Ryman and

212 Jorde 2001 over other tests) generated by Systat software (Academic Distributing, Inc.,

213 Dewey, AZ, USA) to compare allele frequencies between pre-fire plants and 2002 post-

214 fire plants derived from the seed bank. Alpha levels are adjusted via Bonferroni

 sites was analyzed using θp, a measure of the extent to which populations are differentiated (Weir 1996). 218 219 220 	215	correction to reduce the likelihood of type I errors. Genetic structure between the two
 217 differentiated (Weir 1996). 218 219 220 	216	sites was analyzed using θ p, a measure of the extent to which populations are
218 219 220	217	differentiated (Weir 1996).
219 220	218	
220	219	
	220	

222 Results

223 We found several changes in allele presence during our study. A total of 12 alleles were 224 detected for the 5 loci assayed (Table 1). MDH1, surveyed because it was variable at 225 some sites in our previous work (Dolan et al. 1999) was not variable in either site in any 226 vear. The population at ABS had greater allelic richness, with alleles for *IDH* and *6PGD* 227 that were not present during any sample years at LPS. The very low frequency *IDH*-b 228 allele was lost from ABS following the fire. Three alleles were detected in our study sites 229 only after the fire: MDH3-c and 6PGD-a at ABS and MNR-c at LPS. 6PGD-a is a 230 globally new allele; not being found in our previous species-wide survey (Dolan et al 231 1999).

232

233 Quantitative shifts in allele frequencies following fire were often marked, were present in 234 seedlings recruited the first year post-fire, and persisted throughout our study. At ABS, 235 three of the four variable loci had significant allele frequency shifts in 2002, the first year 236 seedlings were present following the burn (Table 1). MDH3-a increased almost five-fold 237 while 6PGD-b decreased by about one-third. 6PGD-d, present at 0.4% frequency prefire, was not detected in the first survey year post-fire, but was found the next two years. 238 239 At LPS, one of the two variable loci had significant allele frequency differences 240 following the burn compared to pre-fire. There was a 42% reduction in frequency of 241 *MDH3*-b in the first sample year post-burn. All significant allele frequency shifts were 242 robust enough that they continued to be significant (p < 0.05) even when alpha levels are 243 adjusted via Bonferroni correction to reduce the likelihood of type I errors. 244

245	Population size at ABS increased 75% after the fire, increasing for at least three years,
246	through 2004 (Fig. 1). Similarly, population size at LPS increased 95% after the fire,
247	peaking two years post-fire in 2003 (Fig. 1). Both sites experienced increases in expected
248	heterozygosity (that mostly paralleled population size increases) by the end of the study
249	period (50% at ASB, 62.5% at LPS), following slight drops in the first post-fire census
250	year, 2002 (Fig. 1).
251	
252	Populations at ABS and LPS were significantly differentiated genetically in all sample
253	years (95% confidence intervals of θ p did not overlap zero; Fig. 2). The magnitude of

the differentiation was similar in all sample years(95% confidence intervals overlap).

256 **Discussion**

257 The seed bank of *Hypericum cumulicola* has the potential to serve as a genetic reservoir,

storing and accumulating genes of the fittest plants over many years and under a range of

environmental conditions. The formation of a persistent seed bank allows *H. cumulicola*

260 to reverse population declines that occur between fires in Florida scrub (Quintana-

Ascencio et al. 2003, 2007). The moderate (15-30 years) fire return frequency proposed

262 for rosemary scrub (Menges 2007) allows sufficient time for a fecund species such as *H*.

263 *cumulicola* to build up a very large seed bank. Although the longevity of its seed bank is

not known (it is at least two years; Quintana-Ascencio et al. 1998), other species found in

rosemary scrub may have seeds that can persist for at least 7 years (Menges and

266 Quintana-Ascencio 2004).

267

268 Recruitment in *H. cumulicola* is highest just after fire, although some germination occurs 269 every year (Quintana-Ascencio et al. 2003). Although the initial flush of plants must have 270 come from the persistent seed bank, some seedlings may have subsequently been 271 produced from early-flowering post-fire plants. Therefore, we do not know how many of 272 seedlings we analyzed arose from the seed bank. Therefore, continued seedling 273 recruitment may dilute the seed bank reservoir effect. Nonetheless, even these additional 274 seedlings may harbor alleles that owe their post-fire existence to prior storage in the soil 275 seed bank.

276

277 Qualitative and quantitative differences in alleles between aboveground plants and their

associated seed banks have been found in several other studies. Cases of both alleles

present aboveground and missing belowground and vice-versa have been reported (Cabin
et al. 1998; McCue and Holtsford 1998; Tonsor 1993; Mahy et al. 1999; Mandák et al.
2006). Alleles involved were rare and usually found in very low frequency, as were the
one lost aboveground and three gained in our study (mean frequency = 0.4%). Alleles
with frequencies this low would likely have been missed in studies with smaller sample
sizes.

285

286 Long-term seed banks play an important role in *H. cumulicola* demography, being critical 287 to reduce risks of decline or extinction during unfavorable years in fire-suppressed 288 habitats (Quintana-Ascencio et al. 2003) For H. cumulicola, environmental conditions 289 decline between fires as growing shrubs become more competitive neighbors (Quintana-290 Ascencio and Morales-Hernandez 1997; Quintana-Ascencio et al. 1998). Seedling 291 recruitment declines greatly with time since fire (Quintana-Ascencio et al. in 292 preparation.). Emigration from unfavorable patches is unlikely because dispersal 293 distances are small and suitable patches usually too far away. 294 295 Matrix models of *H. cumulicola* indicate that seeds constitute 90-99 % of population 296 stable stage distributions in most habitats (particularly long unburned habitats; Picó et al. 297 2003), and that seed transitions have large influences on population growth (Quintana-298 Ascencio et al. 2003). Since seeds are the dominant stage both in terms of numbers and 299 in terms of their impact on population growth, small evolutionary changes in seed 300 survival and seed dormancy can have profound consequences for *H. cumulicola* 301 persistence.

303	Our study demonstrates that rapid and significant genetic change can occur with
304	disturbance. Fire, the principal disturbance responsible for shaping community structure
305	in rosemary scrub vegetation, can also significantly influence genetic patterns in
306	individual species. Fire both kills all (aboveground) H. cumulicola plants and triggers a
307	flush of germination from a persistent seed bank. In so doing, it also triggers rapid
308	genetic change and allows genetic material stored in the soil seed bank to once again be
309	expressed in growing plants.

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Table 1. Allele frequencies for the four polymorphic loci, for entire aboveground populations by site and year. Pre-fire = 2000. The fires occurred in 2001, but no plants emerged that year. N = number of plants sampled. % = percent of total population. Contingency analysis Chi-square (X^2) values are given for loci that differed significantly in allele frequencies between pre-fire and 2002. Allele frequencies in subsequent years were not significantly different from those present in 2002. X^2 results are not included for *IDH* at ASB and *MNR* at LPS due to the presence of sparse cells.

		ABS					LPS				
		Pre-	2002	X ²	2003	2004	Pre-	2002	X^2	2003	2004
		fire					fire				
Ν		816	699		1430	1454	 172	182		337	309
%		100	86.6		88.9	99.7	 100	95.7		92.3	99.7
Locus	Allele										
IDH	a	0.995	1.000		1.000	1.000	1.000	1.000		1.000	1.000
	b	0.005	-		-	-	-	-		-	-
MDH3	а	0.016	0.076	66.6***	0.084	0.084	0.018	0.092	97.3***	0.071	0.074
	b	0.984	0.924		0.910	0.910	0.836	0.483		0.564	0.570
	c	-	-		0.006	0.006	0.146	0.424		0.365	0.356
MNR	b	0.807	0.862	15.9***	0.815	0.816	1.000	0.995		0.977	0.977

	с	0.193	0.138		0.185	0.184	-	0.005	0.023	0.023
6PGD	а	-	-		0.001	0.001	-	-	-	-
	b	0.169	0.055	107.0***	0.076	0.098	-	-	-	-
	c	0.823	0.945		0.908	0.886	1.000	1.000	1.000	1.000
	d	0.009	-		0.015	0.015	-	-	-	-

*** = p < 0.001





Figure 1 Population size (closed circles and solid lines) and expected heterozygosity (open circles and dashed lines) for study populations ABS and LPS pre-fire (2000), the year of the fire (2001) and the three sample years post-fire. Expected heterozygosity was not calculated in the fire year.

ABS



Figure 2 Degree of population differentiation (θ p), with 95% confidence intervals indicated, between study populations ABS and LPS, pre-fire (2000) and the three sample years post-fire. θ p values greater than zero indicate significant differentiation.