Conservation genetics of *Euphorbia telephioides* (Euphorbiaceae), a threatened species from the Florida Panhandle: Implications for Recovery

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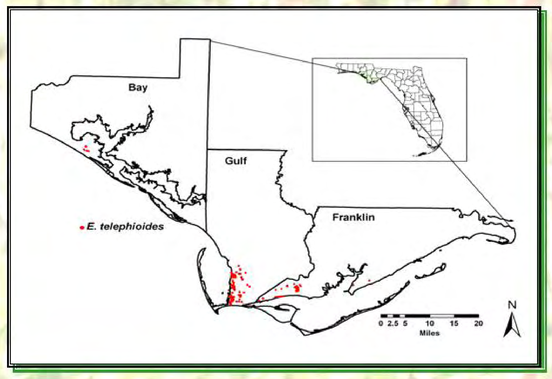
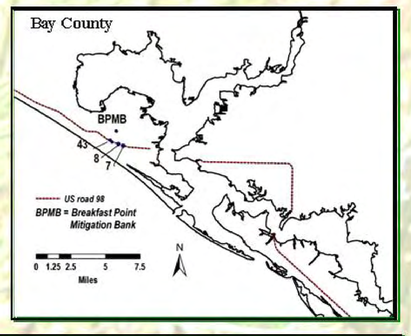
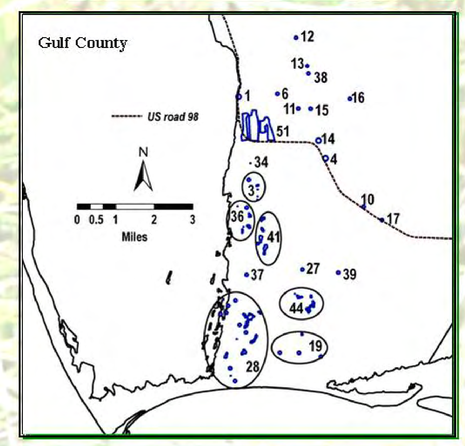


Euphorbia telephioides Chapman (telephus spurge), a member of the spurge family (Euphorbiaceae) is adapted to recurrent natural fires. It is found from xeric to mesic pine flatwoods and in scrubby pinelands dominated by wiregrass and/or *Pinus palustris* or *P. elliottii,* and on sandy outer coastal plain ridges of Pleistocene, Pliocene, or Miocene age. The plant reaches 30-40 cm in height, possesses a long, deep taproot, and is functionally dioecious with staminate (male) and pistillate (female) plants.

Telephus spurge is endemic to the Florida Panhandle, restricted to Bay, Gulf, and Franklin Counties, where it has been observed in approximately 38 locations, all within 4 miles of the coast of the Gulf of Mexico. Nearly half of the populations occur on public lands, however, many populations are on private timberland and utility rights-of-way. Development has extirpated several populations and has left other sites highly fragmented.

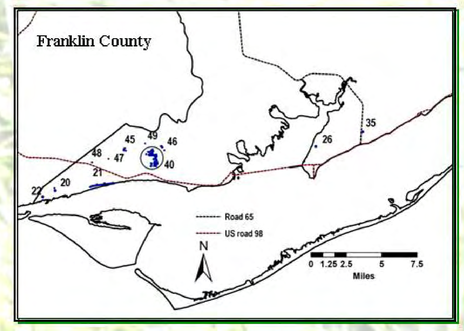


Genetic diversity plays a role in the survival and adaptability of a population. Greater genetic diversity means a population is more likely to include individuals that can tolerate a new stress or that are well-suited to a changed environment (e.g., climate change).



Objectives

Estimate the levels and distribution of genetic diversity within and among populations of *E. telephioides* using allozymes to recommend management plans to contribute to recovery, i.e., determine which populations should be priorities for conservation



Summary of genetic diversity within populations of *E. telephioides*

Population	N	P (%)	AP	Na	Ho
3	49	86.4	3.16	66	0.294
4	10	78.3	2.56	51	0.325
6	12	78.3	2.50	50	0.299
19	17	82.6	2.84	58	0.324
21	49	87.0	3.15	66	0.279
28	51	73.9	3.35	63	0.266
36 (subp.1)	27	87.0	2.80	59	0.284
36 (subp.2)	28	82.6	3.00	61	0.308
40	48	78.3	2.94	58	0.303
41	25	82.6	3.11	63	0.315
44	31	78.3	2.83	56	0.316
51	40	78.3	3.11	54	0.332
22	45	81.8	3.11	63	0.312
43	22	82.6	2.95	60	0.374
45	15	78.3	2.83	56	0.358
BPMB	23	78.3	3.11	61	0.297
7	49	78.3	3.22	63	0.284
MEANS	***31.8***	***80.7***	***2.98***	***59.5***	***0.310***

- 23 allozyme loci were resolved & 82 alleles were observed
- 21 of the 23 loci (91.3%) were polymorphic, thus levels of genetic diversity were quite high
- within populations, the mean percentage of polymorphic loci (P) was 80.7% (range 73.9% - 86.4%)
- the highest number of alleles occurred in populations #3 (66) and # 21 (66)
- the lowest number of alleles observed occurred in two of the smaller populations [#6 (50) and # 4 (51)]
- Nei's genetic identity values (mean $\bar{I}$ = 0.932) indicated that populations *45 ($\bar{I}$ = 0.884), BPMP ($\bar{I}$ = 0.899)* and *6 ($\bar{I}$ = 0.912)* had the lowest mean genetic identities.

Implications for Recovery

Priority populations for conservation

- Highest number of alleles
  - populations *3* and *21*
- Most genetically distinct
  - populations *45, BPMB*, and *6*

(1) *Euphorbia telephioides* maintains a very high level of allozyme genetic diversity relative to other plant species. Genetic diversity values for *E. telephioides* rank it among the highest 10% of all plant species that have been analyzed. It is possible that *E. telephioides* may be a recent polyploid species.

(2) Genetic differentiation (GST = 0.106) found among populations of this species are much lower than that observed for other herbaceous outcrossing perennial plant species (GST > 0.200). This indicates that relatively high rates of gene flow have historically occurred between populations of this species. This is probably due to the relatively short spatial distances between its populations.

allele = an alternative form of a gene; allozyme = different molecular forms of enzymes found at the same locus; locus (plural loci) = a fixed position on a chromosome; N = number of individuals analyzed; P = percent of polymorphic loci; AP = number of alleles per polymorphic locus; Na = total number of alleles observed; Ho = observed heterozygosity; genetic identity (*I*) = estimates the proportion of genes that are identical in two populations