EFFECTS OF DIOECY ON POPULATION GENETIC STRUCTURE IN *CAREX SCIRPOIDEA* MICHAUX ssp. *SCIRPOIDEA*

by

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Effects of Dioecy on Population Genetic Structure in *Carex scirpoidea* Michaux ssp. *scirpoidea* (Cyperaceae)

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ABSTRACT

A strictly dioecious breeding system results in obligate outcrossing in angiosperms. Supporting this, the population genetic literature reveals that dioecious species tend to maintain relatively high genetic diversity ($P = 65\%$, $A = 2.49$, $H_e = 0.297$) apportioned within, rather than among populations ($G_{ST} = 0.204$). Allozyme analysis conducted on five Colorado populations of the dioecious sedge, *Carex scirpoidea* ssp. *scirpoidea* (Cyperaceae), revealed only modest levels of diversity ($P = 20\%$, $A = 1.33$, $A_p = 2.17$, $H_e = 0.068$), presumably due to the isolation of these disjunct populations from the primarily boreal distribution of the species. However, as expected, genetic diversity was apportioned among individuals within populations ($G_{ST} = 0.123$), with all populations in Hardy-Weinberg Equilibrium, but slight heterozygous excess. Population differentiation in *C. scirpoidea* ssp. *scirpoidea* was comparable to other dioecious species, as well as outcrossing, rhizomatous carices ($G_{ST} = 0.159$), and wind-pollinated, outcrossing species ($G_{ST} = 0.099$). Dioecy may effectively maintain population genetic structure in these disjunct Colorado populations of *C. scirpoidea* ssp. *scirpoidea* despite the reduction of genetic diversity driven by biogeographic isolation.

This abstract accurately represents the content of the candidate's thesis. I recommend its publication.

Signed [redacted]

Leo P. Bruederle, Ph. D.

DEDICATION

This research is dedicated to my wife and children who have provided me with the inspiration and perseverance to complete this work.

ACKNOWLEDGMENTS

I would like to thank my advisor, Dr. Leo P. Bruederle, for giving so much of his own time and expertise to this effort. His instruction and guidance were instrumental in completing this research. I wish to thank Dr. Diana Tomback for her excellent instruction in graduate classes and her critical review and input on this thesis. I also wish to thank the University of Colorado at Denver for providing excellent facilities and resources with which to conduct the research.

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1. Introduction

Since 1986, a large body of data describing population genetic diversity and structure in the genus *Carex* (Cyperaceae) has accumulated. Starch gel electrophoresis and allozyme analysis have been used primarily to assess systematic relationships and elucidate genetic structure within and among populations of closely related species of *Carex*, such as the *C. crinita* Lam. complex (Bruederle and Fairbrothers, 1986). More recently, these data have also been used to study population genetic variation in rare species, such as *C. mitchelliana* M. A. Curtis (Bruederle et al., 1989); hybrid origins of taxa, such as *C. membranaceae* Hook. × *utriculata*, *C.* × *physocarpoides*, and *C.* × *mainensis* (Ford et al., 1993); and finally, to test hypotheses regarding population genetic structure and breeding system in clonal species, such as *C. bigelowii* Torr (Jonsson, 1995; Jonsson et al., 1996).

All of the aforementioned research has considered population genetic variation in monoecious carices. Monoecy, the condition in which each plant of a species bears both unisexual male and unisexual female flowers, is the dominant breeding system in this large genus. However, dioecy has been reported from three sections of the genus: *Scirpinae*, *Dioicae*, and *Pictae* (Martens, 1939). Dioecy is predicted to have a significant influence on genetic structure in *C. scirpoidea* ssp. *scirpoidea*, particularly as effected by gene flow.

The primary objective of this research was to study the effect of dioecy on population genetic structure in a perennial herb. The dioecious sedge, *C. scirpoidea* Michaux ssp. *scirpoidea*, was used as the model system. Although this has not been previously addressed in *Carex*, a modest number of investigations have utilized

allozyme or RAPD data to study genetic diversity and structure in other dioecious taxa; these include *Populus* (Jelinski and Cheliak, 1992), *Cecropia* (Alvarez-Buylla and Garay, 1994), *Eurya* (Chung and Kang, 1994), *Buchloë* (Peakall et al., 1995), *Schiedea* and *Alsinidendron* (Weller et al., 1996), and *Schizopepon* (Akimoto et al., 1999). This research has revealed relatively high levels of genetic diversity, e.g., percentage of polymorphic loci (P) = 65%, with the majority of this (approximately 80%) due to differences among individuals within populations. Generally speaking, populations are poorly differentiated genetically, e.g., mean G_{ST}.

Five populations of *C. scirpoidea* ssp. *scirpoidea*, representing a disjunct distribution of this species, were sampled in Park County, Colorado, USA. Starch gel electrophoresis and allozyme analysis were utilized to gather genotypic data. These data were then utilized to make comparisons of genetic diversity and apportionment between *C. scirpoidea* ssp. *scirpoidea* and several other taxa of interest.

1.1 Taxonomy

The Canadian single-spike sedge, *C. scirpoidea* ssp. *scirpoidea*, is a member of *Carex* section *Scirpinae* Tuckerman, which is comprised of only two species (Dunlop, 1990): *C. curatorum* Stacey and *C. scirpoidea*. Dunlop (1990) further recognized four subspecies comprising *C. scirpoidea*: *C. scirpoidea* ssp. *scirpoidea*, *C. scirpoidea* ssp. *pseudoscirpoidea* (Rydberg) Dunlop, *C. scirpoidea* ssp. *stenochlaena* (Holm) Mack., and *C. scirpoidea* ssp. *convoluta* Kükenthal.

Section *Scirpinae* is discriminated from other sections in the genus *Carex* by the presence of solitary spikes, unisexual inflorescences, pubescent peryginia, and

tristigmatic pistils. Within section *Scirpinae*, *C. scirpoidea* is discriminated from *C. curatorum* by achenes that fill the peryginia, glabrous adaxial leaf surfaces, and a primarily arctic and/or alpine distribution. *Carex scirpoidea* ssp. *scirpoidea* may be differentiated from the other three subspecies of *C. scirpoidea* by relatively ovate to obovate peryginia, anthocyanic scale leaves at the base of the culms (i.e., aphyllopodic culms), and flat to widely V-shaped leaves. Plants average two to three decimeters tall.

In *Carex*, the production of monopodial and sympodial rhizomes, coupled with variable rhizome length and aerial culm production, results in different growth forms, i.e., tussock, tufted, caespitose, and rhizomatous (Jermy et al., 1982). *Carex scirpoidea* ssp. *scirpoidea* is a loosely caespitose plant, with short rhizomes present (Fig.1.1).

Fig. 1.1. Line drawing of *Carex scirpoidea* (Cyperaceae). Adapted from Hermann (1970).

1.2 Biogeography

Carex scirpoidea ssp. *scirpoidea* is generally widespread and contiguous in the northern latitudes of North America, from the arctic and subarctic, south through the New England states and much of western Canada. It also occurs in several disjunct pockets in the Great Lakes region and throughout the Rocky Mountains of the Western United States (Fig. 1.2). Dunlop (1990) proposed three hypotheses for the current distribution of *C. scirpoidea* ssp. *scirpoidea*. The first hypothesis states that *C. scirpoidea* ssp. *scirpoidea* may have survived glaciation in refugia in the Beringian area of Alaska, and subsequently migrated south and east. The second hypothesis states that it survived south of the ice sheets in the Rocky Mountains and subsequently migrated eastward and north; however, the species is currently poorly represented in the southern Rocky Mountains compared with Beringia. The third hypothesis states that the species survived periglacially, having a presence in eastern North America and elsewhere. In any case, the Colorado populations of *C. scirpoidea* ssp. *scirpoidea* are currently disjunct from other populations of the species, with presumably little possibility of gene flow among them.

Accessions maintained at the University of Colorado Museum Herbarium (Herbarium COLO) at Boulder, Colorado, revealed only eight discrete populations of *C. scirpoidea* ssp. *scirpoidea* in Colorado (Ranker, 1997): Mt. Sheridan (Park County, CO), Horseshoe Mountain Cirque (Park County, CO), High Creek Fen (Park County, CO), Silverheels Ranch, Fairplay (Park County, CO), Geneva Creek (Park County, CO), Beaver Creek (Park County, CO), and along the Middle Fork of the South Platte (Park County, CO).

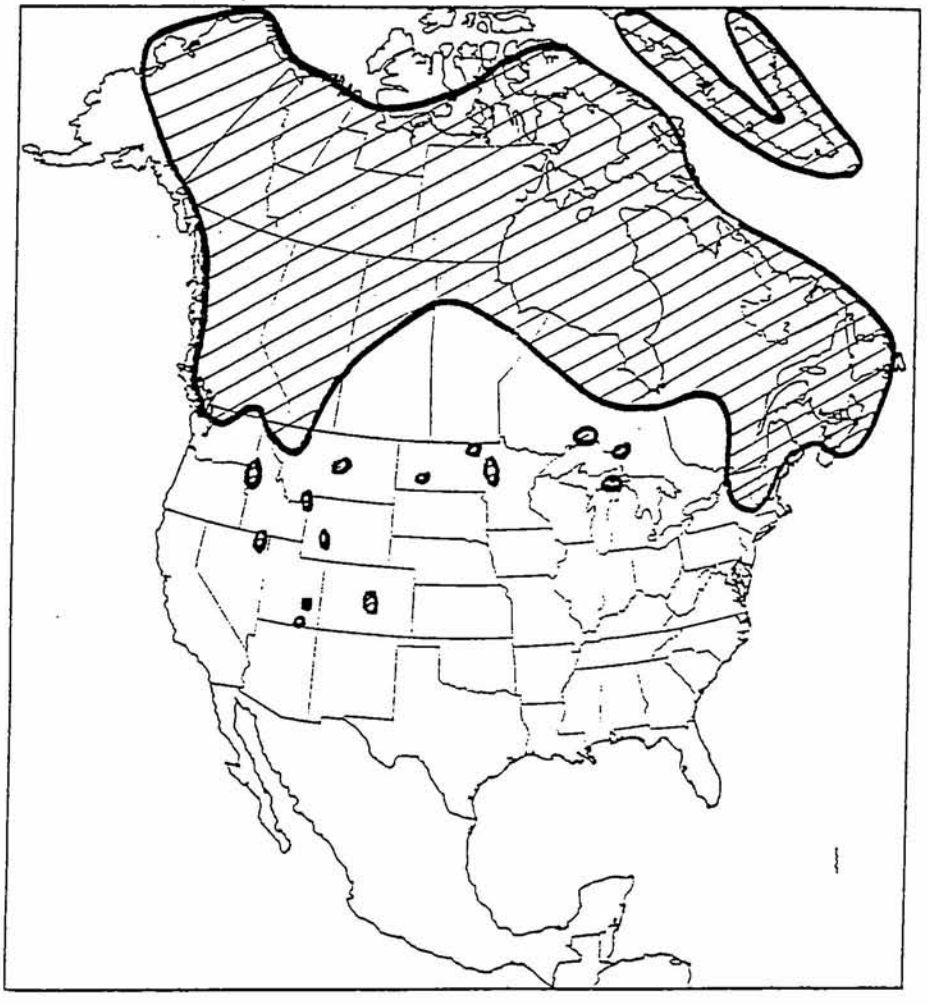


Fig. 1.2. North American range of *Carex scirpoidea* ssp. *scirpoidea* (Cyperaceae). Adapted from Dunlop (1990).

Colorado populations of *C. scirpoidea* ssp. *scripoidea* are principally found covering peaty hummocks at the edge of rich to extreme rich fens. These habitats are found in the upper montane through alpine lifezones, and exist in areas with groundwater discharge over or through calcareous bedrock or alluvium. In this environment, *C. scirpoidea* ssp. *scripoidea* acts as a calciphile, tolerating high concentrations of calcium, sodium, and magnesium salts in the peat hummocks. Dunlop (1990) noted that *C. scirpoidea* ssp. *scripoidea* typically occurs on substrates with calcium concentrations ranging between 2,058 parts per million (ppm) to 2.52%. The extreme rich calcareous fens of South Park represent the very southern end of the North American range for this habitat type (Cooper, 1996).

Cooper (1996) suggested that the characteristic flora of South Park's extreme rich fens is controlled primarily by the peat substrate in which the plants grow. Only 0.3% of Colorado's landscape are peatlands, which may explain the restricted distribution of the species in Colorado. Biogeographically, dioecious species typically comprise less than 10% of continental floras and temperate island floras (Bawa, 1980). Locations rich in dioecious species include tropical islands, such as Hawaii (27.7% of the flora) and New Zealand (>12% of the flora).

1.3 Reproductive Biology

Only seven percent of all genera of flowering plants have one or more dioecious species, and only an estimated 14,260 of all 240,000 flowering plants species (6%) are dioecious (Renner and Ricklefs, 1995). In contrast to the small overall numbers of genera and species exhibiting the dioecious breeding system, Yampolsky and Yampolsky (1922) reported 37 of 51 plant orders had some dioecious species.

Dioecy is very uncommon in the genus *Carex*, occurring in only three divergent sections (Martens, 1939). It is thus likely, that dioecy has evolved independently in these three sections of the genus. Dunlop (1990) found members of section *Scirpinae* to be strictly dioecious (obligate outcrossers), with sex expression fixed, and the ratio of male to female plants approximately 1:1 in most populations.

While strictly dioecious species possess male and female flowers on separate, unisexual plants, there are other less strict forms of dioecy, including gynodioecy, androdioecy, subdioecy, and cryptic dioecy. Gynodioecious plants bear either all female flowers or all bisexual flowers; androdioecious plants bear either all male flowers or all bisexual flowers; and subdioecious species may have all male or all female flowered plants, as well as plants with a combination of bisexual and unisexual flowers. Cryptic dioecy occurs when a species appears to have perfect flowered (hermaphroditic) plants, but only a single sex is functional. These various forms of dioecy contrast with monoecy, in which each plant of a species bears unisexual male flowers and unisexual female flowers; and hermaphroditism, the most common breeding system, in which all plants of a species bear only bisexual (perfect) flowers (Yampolsky and Yampolsky, 1922; Lloyd, 1982).

A comprehensive study of the evolution of plant breeding systems began when Darwin (1877) sought to catalog and evaluate the different systems he had observed. Darwin remarked that, "There is much difficulty in understanding why hermaphrodite plants should ever have been rendered dioecious." In the intervening years since Darwin's statement, much effort has been applied to understand this breeding system. It is generally accepted that dioecy evolves in response to selection pressures that

favor outcrossing (Baker, 1959; Bawa and Opler, 1975; Charlesworth and Charlesworth, 1978 and 1979; Grant, 1951; Lloyd, 1975 and 1976; Mather, 1940 and 1973; Smith, 1978; Ross, 1978 and 1980). Studies by Lewis (1942) and Westergaard (1958) supported the concept that dioecy evolved in several independent taxa, from hermaphroditic or monoecious ancestors. Charlesworth and Charlesworth (1978) remarked that it takes two mutations (one causing male sterility and one causing female sterility) to transform a hermaphrodite or monoecious species into a dioecious species. The likelihood of these two mutations arising simultaneously appeared remote to the authors, who therefore assumed dioecy had evolved from the intermediate condition of gynodioecy. Bawa (1980), who studied evolutionary pathways leading to dioecy from hermaphroditism, gynodioecy, androdioecy, monoecy, and heterostyly, argued that the evolution of dioecy should not be viewed solely as driven by selection pressure for increased outcrossing. Other factors such as sexual selection, optimization of seed dispersal, role of pollination, and predation may all be important considerations in the evolution of the dioecious breeding system.

Population genetic investigations of dioecious species are surprisingly limited. Jelinski and Cheliak (1992) studied genetic diversity in the clonal pioneer tree species *Populus tremuloides* Michx.(Salicaceae). All populations were found to maintain high levels of genetic diversity ($P = 89.1\%$, $A = 2.14$, $H = 0.319$), but deviated somewhat from Hardy-Weinberg expectations with heterozygote excess ($F = -0.102$). Alvarez-Buylla and Garay (1994) investigated the anemophilous tree species *Cecropia obtusifolia* Bertol. (Moraceae), documenting a trend toward heterozygous deficiency, but genetic diversity maintained within, rather than among populations.

Chung and Kang (1994) studied the Asian evergreen *Eurya japonica* Thunb. (Theaceae). Genetic diversity in this species was also very high (P = 90 - 100%, A = 3.79, H_e = 0.462), with less than 7% of the genetic variation found among populations. Peakall et al. (1995) evaluated two diploid races of the dioecious shortgrass *Buchloë dactyloides* Engelmann (Poaceae). This study used allozyme analysis and RAPD analysis to document a slight trend toward outcrossing (F_{IS} = -0.08). Weller et al. (1996) studied the Hawaiian genera *Schiedea* and *Alsinidendron* (Caryophyllaceae: Alsinoideae), of which some species are hermaphrodites, some are gynodioecious, and others are strictly dioecious. In general, selfing species had lower genetic diversity than outcrossers. The very rare breeding system of androdioecy was investigated by Akimoto et al. (1999) in *Schizopepon bryoniaefolius Maxim.* (Cucurbitaceae), revealing a high degree of population differentiation (G_{ST} = 0.688). Male plants had an inbreeding coefficient of nearly zero, while hermaphroditic plants showed significant heterozygous deficiency.

In addition to population genetic research on dioecious species, a number of investigations have been conducted on obligate outcrossing species, including *Liatris cylindricea* Michx. (Asteraceae) (Schaal, 1975), *Stepanomeria exigua* ssp. *carotifera* (Compositae) (Gottlieb, 1975), *Gaura longiflora* Spach and *G. demareei* Raven & Gregory (Onagraceae) (Gottlieb and Pilz, 1976), *Oenothera* L. (Onagraceae) (Ellstrand and Levin, 1980), *Phlox* spp. L. (Polemoniaceae) (Schwaegerle et al., 1986; Levin, 1978), *Heuchera* spp. L. (Saxifragaceae) (Soltis,1985), *Lasthenia* spp. (Asteraceae) (Crawford and Ornduff, 1989), and *Vaccinium* L. sect. *Cyanococcus* Gray (Ericaceae) (Bruederle et al., 1991). In each case, the proportion of genetic diversity among populations was lower than that reported by Hamrick (1983) for

outcrossing species (G_{ST} = 0.221). These data reveal a strong trend toward apportionment of genetic diversity (80% or more) among individuals within populations in outcrossing species.

1.4 Research Hypotheses

A dioecious breeding system results in obligate outcrossing in *C. scirpoidea* ssp. *scirpoidea*. It is therefore hypothesized, that genetic diversity will be apportioned differently in *C. scirpoidea* ssp. *scirpoidea* in comparison to monoecious carices, as well as other monoecious flowering plants.

Other factors, such as habit, can also be expected to affect genetic structure with regard to gene flow in *Carex*. While confounded by a number of other factors, carices with a caespitose habit have been shown to be predominantly inbred, presumably due to selfing. Genetic evidence supporting this phenomenon was first reported by Bruederle (1987), and subsequently by others, including Bruederle and Jensen (1991). In contrast, rhizomatous carices tend to outcross due to genet intermingling, yielding higher levels of genetic variation and lower population differentiation in comparison to those species with the caespitose growth forms. It is hypothesized that *C. scirpoidea* ssp. *scirpoidea*, despite its caespitose habit, will apportion its genetic diversity within rather than among populations (consistent with rhizomatous carices) due to the effects of obligate outcrossing.

Many traits may variously affect the amount of genetic diversity maintained by plant species, e.g., breeding system and life form (Hamrick and Godt, 1990). Notable among these traits is biogeography. As noted previously, *Carex scirpoidea*

ssp. *scirpoidea* occurs in widespread, boreal populations; however, Colorado populations are disjunct from these populations. Thus, it is further hypothesized that biogeographic isolation will result in lower genetic diversity in Colorado populations than would be expected for boreal populations.

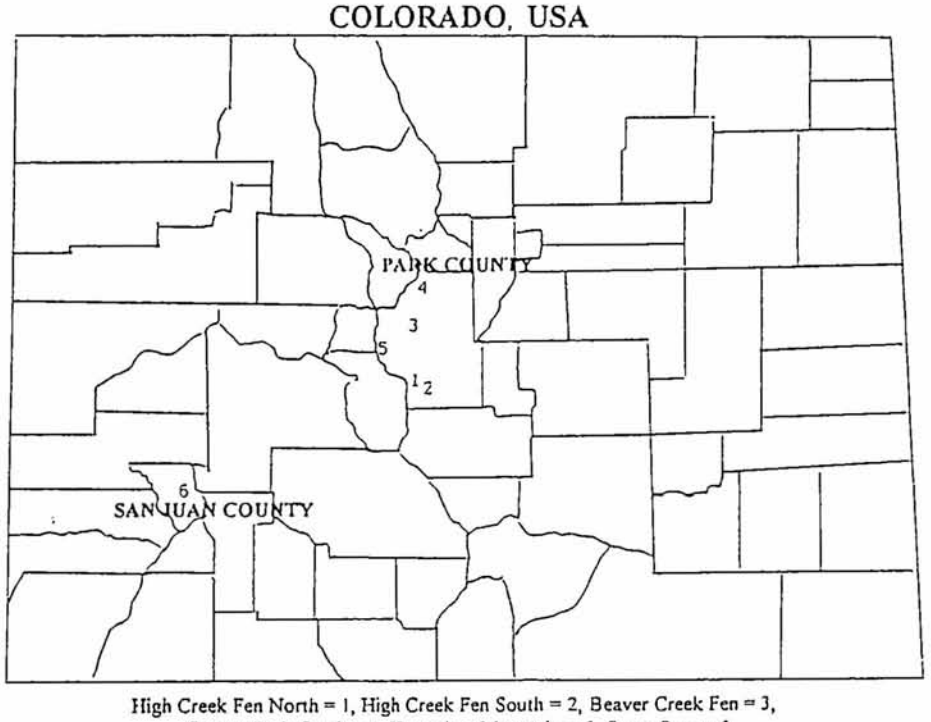
2. Materials and Methods

2.1 Field Methods

Soluble enzymatic proteins were extracted from leaf tissue harvested from individual plants of *Carex scirpoidea* ssp. *scirpoidea* representing five distinct populations in Colorado (Fig. 2.1, Table 2.1). Samples were collected from plants that were at least one meter apart, with samples limited to one flowering culm per plant. A minimum of 50 plants per population were sampled, with roughly equal numbers of male and female plants collected. Samples were individually bagged and maintained at approximately 4°C until protein extraction.

The five populations of *C. scirpoidea* ssp. *scirpoidea* sampled were designated High Creek Fen North (Park County, CO), High Creek Fen South (Park County, CO), Beaver Creek Fen (Park County, CO), Geneva Park Creek (Park County, CO) and Horseshoe Mountain (Park County, CO). The two High Creek Fen populations represent the upper montane lifezone, Beaver Creek Fen and Geneva Park Creek are both from the subalpine lifezone, and the Horseshoe Mountain population represents the alpine lifezone. Additionally, a population of *C. scirpoidea* ssp. *pseudoscirpoidea* was collected at Stony Pass, in the San Juan Mountains of Colorado, but was not analyzed as part of this thesis effort (Fig. 2.1).

Voucher specimens for each population were deposited at Herbarium COLO and at Denver Botanic Garden herbarium (DBG). A Garmin model 38 global positioning system (GPS) was utilized to determine approximate coordinates of each population sampled. Field data were recorded in logbooks.



High Creek Fen North = 1, High Creek Fen South = 2, Beaver Creek Fen = 3,
Geneva Park Creek = 4, Horseshoe Mountain = 5, Stony Pass = 6

Fig. 2.1 Park County, Colorado collection sites for *Carex scirpoidea* ssp. *scirpoidea* and San Juan County, Colorado collection site for *Carex scirpoidea* ssp. *pseudoscirpoidea* (Cyperaceae).

TABLE 2.1. *Carex scirpoidea* ssp. *scirpoidea* (Cyperaceae) sites in Park County, Colorado, sampled for allozyme analysis. Note: Stony Pass samples (San Juan County) of *Carex scirpoidea* ssp. *pseudoscirpoidea* have not been analyzed.

Population	N	Latitude - Longitude	Legal Description	Elevation	Lifezone
High Creek Fen North (1)	50	N39°5'53", W 105°58'7"	T11S, R77 W, Sec. 14	2826 m	upper montane
High Creek Fen South (2)	50	N39°5'48", W 105°57'51 "	T11S, R77W, Sec. 14	2822 m	upper montane
Beaver Creek Fen (3)	50	N39°18'33", W 106°1'28"	T8S, R77W, Sec. 31	3389 m	subalpine
Geneva Park Creek (4)	50	N39°31'9", W 105°43'23"	T6S, R75W, Sec. 13	2949 m	subalpine
Horseshoe Mountain (5)	50	N39°11'35", W 106°9'13"	T10S, R79W	3666 m	alpine
Stony Pass (6)	100	N37°47'42", W107°32'57"	T41N, R6W, Sec.20	3837 m	alpine

2.2 Laboratory Methods

Methods and materials for allozyme extraction and starch gel electrophoresis followed Bruederle and Fairbrothers (1986) and Bruederle and Jensen (1991). Allozymes were extracted from each sample by grinding ~1 cm^2 of leaf tissue with sea sand in an extraction buffer of 0.25 mL of a 0.1 M Tris-HCl extract buffer, pH 7.5 (Gottlieb,1981), 20% (w/v) PVP-40, and 0.1% 2-mercaptoethanol. Extracts were absorbed onto 12 x 3 mm wicks cut from chromatography paper (Whatman No. 17) and stored in a -70°C freezer until electrophoresis.

Starch gel electrophoresis of allozymes utilized 10.5% gels prepared for each of four gel and electrode buffer systems using hydrolyzed potato starch (Sigma Chemical Company). The four starch gel and electrode buffer systems utilized were: lithium-borate pH 7.6/8.0 (Soltis et al., 1983), run at 275 V; histidine-HCl pH 7.0 (Gottlieb, 1981), run at 100 mA; histidine-citrate pH 6.5 (Shields et al., 1983), run at 30 ma; and tris-citrate pH 7.5 (Soltis et al., 1983), run at 50 mA. Gels were prepared approximately 12 hours prior to use, allowed to stand covered at room temperature, and refrigerated (4°C) thirty minutes prior to sample application. Sample wicks were applied to a slit at the cathodal end of the gel, with a bromophenol blue marker (0.1%) used to monitor progress of the electrophoretic run. Electrophoresis was conducted at 4°C and constant current, with the exception of the lithium borate gel, which was run at constant voltage, until the dye front had migrated anodally 9-13 cm. Each gel was sliced horizontally into seven slices, approximately 1.5 mm thick. End slices were discarded with the remaining slices stained using substrate-specific stains.

Fifteen substrate-specific stains were evaluated for effectiveness in identifying polymorphic loci (Appendix A). Lithium-borate (pH 7.6/8.0) system gels were stained for alcohol dehydrogenase (*ADH*), diaphorase (*DIA*), malic enzyme (*ME*), superoxidase dismutase (*SOD*), and triose-phosphate isomerase (*TPI*); histidine-citrate (pH 6.3) system gels for aldolase (*ALD*) and phosphoglucomutase (*PGM*); tris-citrate (pH 7.5) system gels for acid phosphatase (*ACP*), aminotransferase (*AAT*), glyceraldehyde-3-phosphate dehydrogenase (*G3PDH*), and shikimate dehydrogenase (*SDH*); and histidine-HCl (pH 7.0) system gels for malate dehydrogenase (*MDH*), menadione reductase (*MNR*), 6-phosphogluconate dehydrogenase (*PGD*), and phosphogluco-isomerase (*PGI*). Enzyme nomenclature generally follows that of the International Union of Biochemistry (1984). Data were collected as individual genotypes for each population.

2.3 Statistical Methods

Statistical analyses were performed on the genotypic data at both the species and population level. At the population level, percentage of loci polymorphic (*P*), mean number of alleles per locus (*A*), mean number of alleles per polymorphic locus (*Ap*), observed heterozygosity (H_o), and expected heterozygosity (H_e) were calculated. Chi-square tests were used to evaluate deviations from Hardy-Weinberg Equilibrium. Mean and standard error values were calculated over all populations for each of the aforementioned statistics.

At the species level, percentage of polymorphic loci (P_s), mean number of alleles per locus (A_s), mean number of alleles per polymorphic locus (A_{ps}), observed heterozygosity (H_{os}), and expected heterozygosity (H_{es}) were calculated, following

Hamrick and Godt (1990).

Apportionment of genetic diversity was also determined within and among populations. Statistical measures of genetic diversity included: average observed heterozygosity across individual populations (H_I), average expected heterozygosity across individual populations (H_S), average expected heterozygosity for all populations (H_T), proportion of genetic diversity within populations (D_{ST}), and proportion of genetic diversity between populations (G_{ST}). Nei's (1978) genetic identity coefficient (I) and genetic distance coefficient (D) were calculated to describe similarity between populations. Fixation indices (F) were calculated for each polymorphic locus. Values for this statistic may range from -1 to 1, with negative F values documenting a tendency toward outcrossing and heterozygous excess, while positive values reveal inbreeding populations with heterozygous deficiencies. Summary F-statistics include the measure for reduction of heterozygosity due to non-random mating in subpopulations (F_{IS}), the measure of reduction of heterozygosity due to genetic drift and inbreeding in individuals relative to the total population (F_{IT}), and the measure of reduction of heterozygosity due to genetic drift or population differentiation (F_{ST}). Population genetics statistics were calculated using *BIOSYS* -1 (Swofford and Selander, 1981) software (Appendix B) and GENESTAT-PC (Appendix C) software.

Statistical analyses were also performed to compare measures of genetic diversity and population differentiation among various plant taxa important to this study. Comparisons of genetic diversity were made between the following groups: monoecious vs. dioecious flowering plants, monoecious species vs. *C. scirpoidea*

ssp. *scirpoidea* populations, monoecious carices vs. *C. scirpoidea* ssp. *scirpoidea* populations, dioecious species vs. *C. scirpoidea* ssp. *scirpoidea* populations, caespitose carices vs. *C. scirpoidea* ssp. *scirpoidea* populations, and rhizomatous carices vs. *C. scirpoidea* ssp. *scirpoidea* populations. Comparisons of population differentiation were made between the following groups: monoecious vs. dioecious species, and caespitose vs. rhizomatous carices. Anderson-Darling normality tests were conducted on genetic diversity data from all of these groups and several were revealed to be nonparametric in their distribution. Therefore, Mann-Whitney *U*-tests (a nonparametric test) were selected to reveal differences in pairwise comparisons of the data (Appendix I). Minitab® statistical software was utilized to perform both the normality and *U*-tests.

3. Results

3.1 Genetic Diversity

Allozyme analysis for the combined five populations of *C. scirpoidea* ssp. *scirpoidea* resolved seventeen putative genetic loci: alcohol dehydrogenase (*ADH*), aldolase (*ALD*), diaphorase (*DIA*-1, *DIA*-2, *DIA*-3), glyceraldehyde-3-phosphate dehydrogenase (*G3PDH*-1), malate dehydrogenase (*MDH*-2, *MDH*-3, *MDH*-4), malic enzyme (*ME*), 6-phosphogluconate dehydrogenase (*PGD*), phosphogluco-isomerase (*PGI*-2), phosphoglucomutase (*PGM*-3), shikimate dehydrogenase (*SDH*), superoxidase dismutase (*SOD*-2), and triose-phosphate isomerase (*TPI*-1, and *TPI*–2). Ten of the loci were monomorphic (using no criterion) and, thus, uninformative for description of genetic structure (*ADH*, *ALD*, *DIA*-1, *DIA*-3, *G3PDH*-1, *MDH*-2, *MDH*-4, *ME*, *PGD*, and *SOD*-2). The remaining seven loci were found to be polymorphic (Table 3.1.1). Five of the seven loci (*DIA*-2, *MDH*-3, *PGM*-3, *TPI*-1 and *TPI*-2) maintained two alleles, while the remaining two polymorphic loci maintained three alleles each (*PGI*-2 and *SDH*).

TABLE 3.1.1. Allele frequencies at seven polymorphic loci in five populations of *Carex scirpoidea* ssp. *scirpoidea* (Cyperaceae) sampled in Park County, Colorado. N = number of samples.

Population/ Locus - Allele	High Creek Fen South	High Creek Fen North	Beaver Creek Fen	Geneva Park Creek	Horseshoe Mountain
DIA-2	N = 50	N = 46	N = 41	N = 50	N = 50
a	0.090	0.196	0.317	0.390	0.350
b	0.910	0.804	0.683	0.610	0.650
MDH-3	N = 46	N = 50	N = 50	N = 36	N = 50
a	0.011	0.040	0.000	0.194	0.000
b	0.989	0.960	1.000	0.806	1.000
PGI-2	N = 49	N = 49	N = 49	N = 49	N = 50
a	0.173	0.122	0.102	0.163	0.000
b	0.745	0.735	0.816	0.806	0.620
PGM-3	N = 49	N = 50	N = 50	N = 49	N = 50
a	0.939	0.980	0.940	0.929	0.990
b	0.061	0.020	0.060	0.071	0.010
SDH	N = 46	N = 48	N = 50	N = 47	N = 50
a	0.109	0.000	0.000	0.181	0.000
b	0.891	1.000	1.000	0.819	0.500
TPI-1	N = 50	N = 44	N = 50	N = 50	N = 50
a	0.030	0.011	0.000	0.000	0.000
b	0.970	0.989	1.000	1.000	1.000
TPI-2	N = 50	N = 44	N = 50	N = 50	N = 50
a	1.000	0.977	1.000	1.000	1.000
b	0.000	0.023	0.000	0.000	0.000

Overall levels of genetic diversity within populations of *C. scirpoidea* ssp. *scirpoidea* were moderate to low, with respect to percentage of polymorphic loci, mean number of alleles per locus, and mean heterozygosity per locus (Table 3.1.2). Percentage of loci polymorphic (*P*) using the 0.05 criterion ranged from 11.76% for the High Creek Fen North population to 29.41% for the Geneva Park Creek population, with an overall population mean of 20%. Utilizing no criterion for *P*, values ranged from 35.29% in the High Creek Fen North and South populations to a low of 17.65% for the Beaver Creek Fen population. Average number of alleles per locus (*A*) varied from 1.24 in the Horseshoe Mountain and Beaver Creek Fen populations to a high of 1.41 in High Creek Fen North and South populations, with a mean value of 1.33 (SE 0.04). The mean value for average number of alleles per polymorphic locus (A_p) was 2.17 (SE 0.05). Mean expected heterozygosity per locus (H_e) ranged from a low of 0.05 for the Beaver Creek Fen population to 0.09 in the Geneva Park Creek population, with an overall mean H_e of 0.07 (SE 0.01) or 7%.

TABLE 3.1.2. Genetic diversity in five populations of *Carex scirpoidea* ssp. *scirpoidea* (Cyperaceae) sampled in Park County, Colorado. $P_{(.05)}$ = percentage of polymorphic loci using 0.05 criterion, $P_{(no)}$ = percentage of polymorphic loci using no criterion, A = average number of alleles per locus, A_P = average number of alleles per polymorphic locus, H_e = expected heterozygosity.

Population	$P_{(.05)}$	$P_{(no)}$	A	A_P	H_e
High Creek Fen North	11.76	35.29	1.41 (SE.15)	2.17 (SE.17)	0.06 (SE .03)
High Creek Fen South	23.53	35.29	1.41 (SE.15)	2.17 (SE.17)	0.07 (SE .03)
Beaver Creek Fen	17.65	17.65	1.24 (SE .14)	2.33 (SE .33)	0.05 (SE .03)
Geneva Park Creek	29.41	29.41	1.35 (SE .15)	2.20 (SE .20)	0.09 (SE.05)
Horseshoe Mountain	17.65	23.53	1.24 (SE .11)	2.00 (SE .00)	0.09 (SE .05)
Population Mean	20.00	28.23	1.33 (SE .04)	2.17 (SE .05)	0.07 (SE .01)
Species	29.41	41.18	1.53	2.29	0.08

Species-level statistics revealed a proportion of polymorphic loci of 29.41% and 41.18% in *C. scirpoidea* ssp. *scirpoidea,* using the .05 and no criterion, respectively. This represents an increase of approximately 1.5 times the population mean values. Similarly, the species-level values for A_s (1.53) and A_{ps} (2.29) were larger than comparable statistics at the population level. Expected heterozygosity at the species level (H_{es}) was 0.08 or 8%.

3.2 Population Genetic Structure

An evaluation of apportionment of genetic diversity across all polymorphic loci revealed 12.3% to be among populations ($G_{ST} = 0.123$). That is, approximately 88% of genetic diversity is attributable to differences among individuals within populations of *C. scirpoidea* ssp. *scirpoidea*. Mean observed heterozygosity across populations (H_I) was .074 (SE .013), or 7.4%. Expected heterozygosity averaged over all populations (H_S) was .068 with a standard error of 0.008 (Table 3.2.1). Total expected heterozygosity (H_T) for all populations was 0.078. These statistics are very similar, deviating by no more than 1%. This similarity indicates that these populations are panmictic or randomly breeding ($H_I = H_S = H_T$), supporting the expectation of Hardy-Weinberg Equilibrium (HWE).

TABLE 3.2.1. Genetic structure in five populations of *Carex scirpoidea* ssp. *scirpoidea* (Cyperaceae) sampled in Park County, Colorado. H_o = observed heterozygosity, H_e = expected heterozygosity.

Population	Observed Heterozygosity	Expected Heterozygosity
High Creek Fen North	0.055 (SE 0.030)	0.055 (SE 0.030)
High Creek Fen South	0.058 (SE 0.027)	0.057 (SE 0.027)
Beaver Creek Fen	0.053 (SE 0.032)	0.051 (SE 0.031)
Geneva Park Creek	0.119 (SE 0.053)	0.092 (SE 0.038)
Horseshoe Mountain	0.085 (SE 0.046)	0.086 (SE 0.046)
Population Mean	0.074 (SE 0.013)	0.068 (SE 0.008)

However, 15 significant deviations from HWE were revealed for five polymorphic loci across all five populations using Chi-square tests (X^2). The *DIA*-2 locus differed significantly ($p > 0.05$) from HWE expectations, with slight heterozygous excess in the High Creek Fen South, Beaver Creek Fen, Geneva Park Creek, and Horseshoe Mountain populations. The *MDH*-3 locus differed significantly from expectations ($p > 0.05$) in only the Geneva Park Creek population, with slight heterozygous excess reported. The *PGI*-2 locus differed significantly from expectations ($p > 0.05$) in each of the five populations tested. Interestingly, this locus accounted for slight heterozygous excess in the High Creek Fen North and Geneva Park Creek populations, but slight heterozygous deficiency in the High Creek Fen South, Beaver Creek Fen, and Horseshoe Mountain populations. The *PGM*-3 locus revealed significant ($p > 0.05$) heterozygous excesses in the High Creek Fen South, Beaver Creek Fen, and Geneva Park Creek populations. Heterozygosity at the *SDH* locus was significantly different than expectations ($p > 0.05$) in the High Creek Fen South and the Geneva Park Creek populations, with slight heterozygous excess observed in both populations. The fixation indices revealed that overall, the five populations of *Carex scripoidea* ssp. *scirpoidea* deviated only slightly from Hardy-Weinberg expectations, with a trend toward heterozygous excess in these populations (Table 3.2.2).

TABLE 3.2.2. Wright's fixation indices for polymorphic loci resolved in five populations of *Carex scirpoidea* ssp. *scripoidea* (Cyperaceae) sampled in Park County, Colorado. An asterisk indicates that the corresponding fixation index value deviated significantly ($p > 0.05$) from Hardy-Weinberg expectations.

Population/ Locus	High Creek Fen South	High Creek Fen North	Beaver Creek Fen	Geneva Park Creek	Horseshoe Mountain
DIA-2	-0.099*	0.033	-0.126*	-0.555*	-0.187*
MDH-3	-0.011	-0.042	---	-0.241*	---
PGI-2	0.050*	-0.057*	0.097*	-0.202*	0.236*
PGM-3	-0.065*	-0.020	-0.064*	-0.077*	-0.010
SDH	-0.122*	---	---	-0.221*	-0.040
TPI-1	-0.031	-0.011	---	---	---
TPI-2	---	-0.023	---	---	---
Mean/ (SE)	-0.046 (0.026)	-0.020 (0.013)	-0.031 (0.066)	-0.259 (0.079)	0.000 (0.088)

Summary F-statistics for *C. scirpoidea* ssp. *scirpoidea* (Table 3.2.3) revealed a trend (five of the seven polymorphic loci) toward slight outcrossing (F_{IS} and F_{IT} values slightly less than 1). Exceptions are the *SDH* and *PGI*-2 loci, with slightly positive F_{IT} values. This is possibly indicative of genetic drift and/or inbreeding at these loci. Overall population means revealed a slight increase in heterozygosity due to non-random mating (F_{IS} of -0.097), but a very slight trend for overall inbreeding (F_{IT} = 0.023), due to variation at the SDH locus. Population subdivision (F_{ST}) was 10.9%.

TABLE 3.2.3. Summary of *F*-statistics at all polymorphic loci resolved in five populations of *Carex scirpoidea* ssp. *scirpoidea* (Cyperaceae) sampled in Park County, Colorado. F_{IS} = reduction in heterozygosity due to non-random mating, F_{IT} = overall inbreeding coefficient, and F_{ST} = population differentiation.

	F-statistic		
Locus	F_{IS}	F_{IT}	F_{ST}
DIA-2	-0.222	-0.147	0.062
MDH-3	-0.192	-0.052	0.118
PGI-2	0.038	0.094	0.058
PGM-3	-0.062	-0.047	0.014
SDH	-0.110	0.208	0.287
TPI-1	-0.026	-0.008	0.017
TPI-2	-0.023	-0.005	0.018
Mean	-0.097	0.023	0.109

Nei's genetic identity (*I*) and genetic distance (*D*) were evaluated to determine proportion of alleles shared by descent between populations. It is clear that all five populations are very similar genetically. Identities ranged from 0.979 to 0.999, with a mean identity of 0.990, while distances ranged from 0.001 to 0.021. All five populations clearly conform to a single subspecies (i.e., *C. scirpoidea* ssp. *scirpoidea*).

4. Discussion

A summary of the plant population genetic literature by Hamrick and Godt (1990) found an average of 34.2% of a populations' loci to be polymorphic, average number of alleles per locus was 1.53, average genetic diversity was 11.3%, and population differentiation averaged 22.4% (Table 4.0). It is clear that Colorado populations of *C. scirpoidea* ssp. *scirpoidea* harbor less genetic diversity than that found in an average plant population ($P_{.05}$ = 20%, A = 1.33; H_e = 6.8%); furthermore, this species apportions approximately half as much of that diversity among its populations as compared to other flowering plants.

Several authors, including Jelinski and Cheliak (1992), Alvarez-Buylla and Garay (1994), Chung and Kang (1994), Peakall et al. (1995), Weller et al. (1996), and Akimoto et al. (1999), have reported genetic diversity statistics for dioecious species. These data reveal an average value for P of 64.7%, A of 2.49, and H_e of 29.7% (Appendix D). In contrast, genetic diversity statistics for monoecious species reveal an average value for P of 39.3%, an average A of 1.72, and an average H_e of 10.4% (Appendix E). Dioecious species average 1.5 times more polymorphic loci, 1.4 times the average alleles per locus, and 2.8 times the average expected heterozygosity compared with monoecious species. The difference in genetic diversity between dioecious and monoecious flowering plants was tested using nonparametric Mann-Whitney U-tests. Statistically significant differences ($p < 0.05$) were found between dioecious and monoecious plant species for all genetic diversity parameters tested.

Genetic diversity in Colorado populations of *C. scirpoidea* ssp. *scirpoidea* was revealed to be generally less than that found in other dioecious flowering plants.

Dioecious flowering plants average more than three times higher P than that found in *C. scirpoidea* ssp. *scirpoidea*. Likewise, A in dioecious species was nearly twice as high as that found in Colorado populations of *C. scirpoidea* ssp. *scirpoidea*. Expected heterozygosity in dioecious species is more than four times higher than *C. scirpoidea* ssp. *scirpoidea*. Mann-Whitney *U*-tests revealed that *C. scirpoidea* ssp. *scirpoidea* populations are significantly different ($p < 0.05$) for the parameters P, A, H_o, and H_e compared with other dioecious flowering plants.

Genetic diversity in Colorado populations of *C. scirpoidea* ssp. *scirpoidea* was generally less than the average for monoecious flowering plants. Percentage of polymorphic loci was almost 20% higher in monoecious species (39.3%) versus *C. scirpoidea* ssp. *scirpoidea* populations (20%). Monoecious species had a mean value for A of 1.72 versus 1.33 in *C. scirpoidea* ssp. *scirpoidea* populations. Average expected heterozygosity was 0.104 (10.4%) in monoecious species versus 0.068 (6.8%) in *C. scirpoidea* ssp. *scirpoidea* populations. Mann-Whitney *U*-tests found no significant difference ($p > 0.05$) in any of the genetic diversity parameters (P, A, H_o, and H_e) tested.

Comparisons of genetic diversity between *C. scirpoidea* ssp. *scirpoidea* populations and other carices, all of which are monoecious, (Appendix F) found average values for P, A, H_o, and H_e to be very similar. Both taxa had approximately 20% of their loci polymorphic, 1.3 alleles per locus, 7% observed heterozygosity, and 7% expected heterozygosity. Mann-Whitney *U*-tests found no significant differences

($p > 0.05$) for any of the genetic diversity parameters tested between *C. scirpoidea* ssp. *scirpoidea* and monoecious carices.

Comparisons of genetic diversity were made between caespitose and rhizomatous carices, and between each of these taxa and *C. scirpoidea* ssp. *scirpoidea* populations. Mean genetic diversity values for caespitose carices included P of 14.4%, A of 1.2, H_o of 0.033, and H_e of 0.040. In contrast, rhizomatous carices average a P of 44.5%, A of 1.6, H_o of 0.174, and H_e of 0.171. Comparing these data, the rhizomatous carices averaged three times more polymorphic loci, 1.33 times more alleles per locus, 5.27 times more observed heterozygosity, and 4.27 times more expected heterozygosity. The Mann-Whitney U-test found significant statistical difference ($p < 0.05$) between caespitose and rhizomatous carices for each of the genetic diversity parameters evaluated.

Colorado populations of *C. scirpoidea* ssp. *scirpoidea* maintained a greater proportion of polymorphic loci (20%) than caespitose carices (14%), but substantially less than rhizomatous carices (44%). *Carex scirpoidea* ssp. *scirpoidea* populations averaged 1.33 alleles per locus, versus 1.2 for caespitose carices and 1.6 for rhizomatous carices. *Carex scirpoidea* ssp. *scirpoidea* was determined to have more than twice as much observed heterozygosity in comparison to caespitose carices (7.4% vs. 3.3%, respectively), but substantially less than rhizomatous carices (7.4% vs. 17.4%). The Mann-Whitney U-tests found *C. scirpoidea* ssp. *scirpoidea* populations to be significantly different ($p < 0.05$) in terms of genetic diversity compared to both caespitose and rhizomatous carices.

Few studies have recorded population differentiation data for dioecious flowering plants. Mean G_{ST} value for those taxa that have been studied was 0.204 or 20.4%. These data indicate that dioecious species tend to apportion genetic diversity within rather than among populations, supporting expectations. Values for G_{ST} ranged from a low of 0.029 to a maximum value of 0.688. Because the standard deviation for dioecious G_{ST} values is large and the data set is small (N = 4), statistical comparisons using these taxa are problematic. Hamrick and Godt (1990) report a mean G_{ST} for wind-pollinated, outcrossing species of 0.099, or 9.9%. The mean G_{ST} for wind-pollinated, outcrossing species may be more instructive for comparative purposes due to the greater number of taxa (N = 134) used to arrive at the mean. Population differentiation data are much more common for monoecious flowering plants. Mean G_{ST} for a select group of monoecious species (31.2%) revealed a higher degree of genetic diversity apportioned among populations, as compared to both dioecious and to wind-pollinated, outcrossing species. The Mann-Whitney *U*-test was not able to find a statistically significant difference between dioecious and monoecious species for G_{ST} ($p > 0.05$).

A review of population genetic structure data for caespitose carices reveals an average G_{ST} of 0.462 (Appendix G). This value represents a nearly equal apportionment of genetic diversity among and within populations of caespitose carices. Rhizomatous carices, in contrast, have a mean G_{ST} of 0.159, indicating that nearly 84% of genetic diversity is apportioned among individuals within populations (Appendix H). The Mann-Whitney *U*-test found caespitose and rhizomatous species to differ significantly in terms of G_{ST} ($p < 0.05$).

Population genetic structure in Colorado populations of *C. scirpoidea* ssp. *scirpoidea* is characterized by maintenance of Hardy-Weinberg Equilibrium and apportionment of genetic diversity (G_{ST} = 12.3%) within populations rather than among them. The G_{ST} value for *C. scirpoidea* ssp. *scirpoidea* is less than that for monoecious species (G_{ST} = 31.2%), monoecious carices (G_{ST} = 38.9%), and other dioecious species (G_{ST} = 20.4%). The G_{ST} for *C. scirpoidea* ssp. *scirpoidea* does, however, correspond well with the mean G_{ST} for wind-pollinated, outcrossing species (12.3% versus 9.9%). Population genetic structure in *C. scirpoidea* ssp. *scirpoidea* reveals a pattern similar to rhizomatous carices (G_{ST} = 15.9%), with genetic diversity apportioned within rather than among populations. Caespitose carices maintain more of their genetic diversity among populations (G_{ST} = 46.2%). These data highlight the confounding aspect of the correlation of growth form and breeding system in the genus *Carex*. Population genetic structure in *C. scirpoidea* ssp. *scirpoidea* appears to be influenced by the obligate outcrossing nature of its breeding system. Not surprisingly, its caespitose growth form appears to be less important in population differentiation.

TABLE 4.0. Comparison of population-level genetic diversity between *Carex scirpoidea* ssp. *scirpoidea* (Cyperaceae) sampled in Park County, Colorado, USA and other dioecious, wind-pollinated/outcrossing, monoecious, caespitose, and rhizomatous flowering plants. * Data summarized by Yarbrough from studies by Jelinski and Cheliak (1992); Alvarez-Buylla and Garay (1994); Chung and Kang (1994); Peakall, et al. (1995); Weller, et al. (1996); and Akimoto, et al. (1999). ** Data summarized by Yarbrough from studies of 87 separate monoecious species ***Data summarized by Kuchel (1999). **** Data summarized by Hamrick and Godt, 1990. P = percent polymorphic loci, A = average number of alleles per locus, H_e = expected heterozygosity, G_{ST}/F_{ST} = population differentiation.

Taxa	P	A	H_o	H_e	G_{ST}/F_{ST}
C. scirpoidea ssp. *scirpoidea*	20.0	1.33	0.074	0.068	0.123
Dioecious species*	64.7	2.49	0.281	0.297	0.204
Wind-pollinated, outcrossing species****	49.7	1.79	---	0.148	0.099
Monoecious species**	39.3	1.72	0.106	0.104	0.312
Monoecious carices***	23.6	1.30	0.070	0.073	0.389
Rhizomatous carices***	44.5	1.6	0.174	0.171	0.159
Caespitose carices***	14.4	1.2	0.033	0.044	0.462
All Plant Taxa****	34.2	1.53	---	0.113	0.224

Low levels of genetic diversity in Colorado populations of *C. scirpoidea* ssp. *scirpoidea* may be attributable to several factors, including disjunct biogeography and the presumed recent evolutionary history of the species. Although no molecular data are available from the main boreal populations, it is reasonable to assume that genetic diversity in the biogeographic center for the species is greater, and potentially much greater, than that found in the disjunct Colorado populations.

The disjunct distribution and caespitose growth form are expected to result in decreased gene flow and increased inbreeding in plant species. However, populations of *C. scirpoidea* ssp. *scirpoidea* in Colorado maintain a modest level of genetic diversity, with most of that variation apportioned within populations. Furthermore, these populations are maintaining Hardy-Weinberg Equilibrium. This obviously is a result of the dioecious breeding system imparting obligate outcrossing and promoting the gene flow that prevents these populations from experiencing inbreeding. Dioecy in this sense, may be a stabilizing force helping to maintain genetic diversity in populations of *C. scirpoidea* ssp. *scirpoidea.*

While this research was not designed to test hypotheses regarding the biogeographic and recent evolutionary history of *C. scirpoidea* ssp. *scirpoidea*, the significantly lower than expected levels of genetic diversity reported herein do not support Dunlop's (1990) proposed hypothesis of a Southern Rocky Mountain glacial refugium for this species. Additional research examining genetic diversity in the *C. scirpoidea* species complex should be designed to include Beringian and periglacial populations in order to better test hypotheses concerning this species' distribution.

Appendix A Gel and Electrode Buffer Systems and Substrate-Specific Stains

lithium-borate pH 7.6/8.0

alcohol dehydrogenase (*ADH*)

diaphorase (*DIA*)

malic enzyme (*ME*)

superoxidase dismutase (*SOD*)

triose-phosphate isomerase (*TPI*)

histidine-citrate pH 6.3

aldolase (*ALD*)

phosphoglucomutase (*PGM*)

tris-citrate pH 7.5

acid phosphatase (*ACP*)

aminotransferase (*AAT*)

glyceraldehyde-3-phosphate dehydrogenase (*G3PDH*)

shikimate dehydrogenase (*SDH*)

histidine-HCl pH 7.0

malate dehydrogenase (*MDH*)

menadione reductase (*MNR*)

6-phosphogluconate dehydrogenase (*PGD*)

phosphogluco-isomerase (*PGI*)

Appendix B BIOSYS Data

```
BBBBBBBB   IIIIIII   OOOOOOO   SSSSSSSS YYY     YYY  SSSSSSSS        111
  BBBBBBBBB  IIIIIII  OOOOOOOOO  SSSSSSSSS  YYY   YYY  SSSSSSSSS      1111
  BBB   BBB    III    OOO   OOO  SSS         YYY YYY   SSS            11111
  BBB   BBB    III    OOO   OOO  SSS          YYYYY    SSS              111
  BBBBBBBB     III    OOO   OOO  SSSSSSSS      YYY     SSSSSSSS  XXXXX  111
  BBBBBBBB     III    OOO   OOO   SSSSSSSS     YYY      SSSSSSSS XXXXX  111
  BBB   BBB    III    OOO   OOO        SSS     YYY           SSS        111
  BBB   BBB    III    OOO   OOO        SSS     YYY           SSS        111
  BBBBBBBBB  IIIIIII  OOOOOOOOO  SSSSSSSSS     YYY     SSSSSSSSS      1111111
  BBBBBBBB   IIIIIII   OOOOOOO   SSSSSSSS      YYY     SSSSSSSS       1111111

Release 1.7       University of Illinois        21:06:1999       04:02:01

Title: SINGLE INDIVIDUAL GENOTYPE INPUT (ALPHABETIC ALLELIC DESIGNATIONS)

 Number of populations (OTU's) =    5
 Number of loci =   17
 Maximum number of alleles per locus =    3

 Output restricted to width of 80 columns

*******************************************************************************
*                                                                             *
*  SINGLE INDIVIDUAL GENOTYPE INPUT (ALPHABETIC ALLELIC DESIGNATIONS)         *
*                                                                             *
*  Initial Data Step                                                          *
*                                                                             *
*  BIOSYS-1   Release 1.7   21:06:1999     04:02:01                           *
*                                                                             *
*******************************************************************************

Input data: Single-individual genotypes

 Allelic designations: Alphabetic

Allele frequencies in populations  1 thru  5
 ********************************************

-----------------------------------------------
                    Population
          ------------------------------------
Locus       1        2        3        4        5
-----------------------------------------------

ADH
  (N)      50       47       49       50       48
   A    1.000    1.000    1.000    1.000    1.000

ALD
  (N)      49       41       25       30       50
   A    1.000    1.000    1.000    1.000    1.000

DIA-1
  (N)      48       45       44       50       50
   A    1.000    1.000    1.000    1.000    1.000

DIA-2
```

(N)	50	46	41	50	50
A	.090	.196	.317	.390	.350
B	.910	.804	.683	.610	.650
DIA-3					
(N)	48	46	50	50	50
A	1.000	1.000	1.000	1.000	1.000
GPD-1					
(N)	25	50	50	50	49
A	1.000	1.000	1.000	1.000	1.000
MDH-2					
(N)	46	50	50	50	50
A	1.000	1.000	1.000	1.000	1.000
MDH-3					
(N)	46	50	50	36	50
A	.011	.040	.000	.194	.000
B	.989	.960	1.000	.806	1.000
MDH-4					
(N)	24	50	49	26	48
A	1.000	1.000	1.000	1.000	1.000
ME					
(N)	47	44	46	49	50
A	1.000	1.000	1.000	1.000	1.000
PGD					
(N)	49	48	48	48	50
A	1.000	1.000	1.000	1.000	1.000
PGI-2					
(N)	49	49	49	49	50
A	.173	.122	.102	.163	.000
B	.745	.735	.816	.806	.620
C	.082	.143	.082	.031	.380
PGM-3					
(N)	49	50	50	49	50
A	.939	.980	.940	.929	.990
B	.061	.020	.060	.071	.010
SDH					
(N)	46	48	50	47	50
A	.109	.000	.000	.181	.000
B	.891	1.000	1.000	.819	.500
C	.000	.000	.000	.000	.500
SOD-2					
(N)	50	45	49	50	50
A	1.000	1.000	1.000	1.000	1.000
TPI-1					
(N)	50	44	50	50	50
A	.030	.011	.000	.000	.000

B	.970	.989	1.000	1.000	1.000
TPI-2					
(N)	50	44	50	50	50
A	1.000	.977	1.000	1.000	1.000
B	.000	.023	.000	.000	.000

Key to populations

Original pop. no.	Pop. no. on printout	Population name
HCFS	1	HIGH CREEK SOUTH
HCFN	2	HIGH CREEK NORTH
BCF	3	BEAVER CREEK FEN
GPC	4	GENEVA PARK CREE
HSM	5	HORSESHOE MOUNTA

SINGLE INDIVIDUAL GENOTYPE INPUT (ALPHABETIC ALLELIC DESIGNATIONS)

Genetic variability analysis

BIOSYS-1 Release 1.7 21:06:1999 04:02:01

Allele frequencies and genetic variability measures

Population: HIGH CREEK SOUTH (HCFS)

	Locus and sample size								
Allele	ADH 50	ALD 49	DIA-1 48	DIA-2 50	DIA-3 48	GPD-1 25	MDH-2 46	MDH-3 46	MDH-4 24
A	1.000	1.000	1.000	.090	1.000	1.000	1.000	.011	1.000
B	.000	.000	.000	.910	.000	.000	.000	.989	.000
C	.000	.000	.000	.000	.000	.000	.000	.000	.000
H	.000	.000	.000	.164	.000	.000	.000	.022	.000
H(unb)	.000	.000	.000	.165	.000	.000	.000	.022	.000
H(D.C.)	.000	.000	.000	.180	.000	.000	.000	.022	.000

	Locus and sample size							
Allele	ME 47	PGD 49	PGI-2 49	PGM-3 49	SDH 46	SOD-2 50	TPI-1 50	TPI-2 50
A	1.000	1.000	.173	.939	.109	1.000	.030	1.000
B	.000	.000	.745	.061	.891	.000	.970	.000
C	.000	.000	.082	.000	.000	.000	.000	.000
H	.000	.000	.408	.115	.194	.000	.058	.000
H(unb)	.000	.000	.413	.116	.196	.000	.059	.000
H(D.C.)	.000	.000	.388	.122	.217	.000	.060	.000

Mean heterozygosity per locus (biased estimate) = .057 (S.E. .027)

Mean heterozygosity per locus (unbiased estimate) = .057 (S.E. .027)

Mean heterozygosity per locus (direct-count estimate) = .058 (S.E. .027)

Mean number of alleles per locus = 1.41 (S.E. .15)

Percentage of loci polymorphic (0.95 criterion) = 23.53

Percentage of loci polymorphic (0.99 criterion) = 35.29

Percentage of loci polymorphic (no criterion) = 35.29

Allele frequencies and genetic variability measures

****

Population: HIGH CREEK NORTH (HCFN)

	Locus and sample size								
Allele	ADH 47	ALD 41	DIA-1 45	DIA-2 46	DIA-3 46	GPD-1 50	MDH-2 50	MDH-3 50	MDH-4 50
A	1.000	1.000	1.000	.196	1.000	1.000	1.000	.040	1.000
B	.000	.000	.000	.804	.000	.000	.000	.960	.000
C	.000	.000	.000	.000	.000	.000	.000	.000	.000
H	.000	.000	.000	.315	.000	.000	.000	.077	.000
H(unb)	.000	.000	.000	.318	.000	.000	.000	.078	.000
H(D.C.)	.000	.000	.000	.304	.000	.000	.000	.080	.000

	Locus and sample size							
Allele	ME 44	PGD 48	PGI-2 49	PGM-3 50	SDH 48	SOD-2 45	TPI-1 44	TPI-2 44

A	1.000	1.000	.122	.980	.000	1.000	.011	.977
B	.000	.000	.735	.020	1.000	.000	.989	.023
C	.000	.000	.143	.000	.000	.000	.000	.000
H	.000	.000	.425	.039	.000	.000	.022	.044
H(unb)	.000	.000	.429	.040	.000	.000	.023	.045
H(D.C.)	.000	.000	.449	.040	.000	.000	.023	.045

Mean heterozygosity per locus (biased estimate) = .054 (S.E. .030)

Mean heterozygosity per locus (unbiased estimate) = .055 (S.E. .030)

Mean heterozygosity per locus (direct-count estimate) = .055 (S.E. .030)

Mean number of alleles per locus = 1.41 (S.E. .15)

Percentage of loci polymorphic (0.95 criterion) = 11.76

Percentage of loci polymorphic (0.99 criterion) = 35.29

Percentage of loci polymorphic (no criterion) = 35.29

Allele frequencies and genetic variability measures

****

Population: BEAVER CREEK FEN (BCF)

	Locus and sample size								
Allele	ADH 49	ALD 25	DIA-1 44	DIA-2 41	DIA-3 50	GPD-1 50	MDH-2 50	MDH-3 50	MDH-4 49
A	1.000	1.000	1.000	.317	1.000	1.000	1.000	.000	1.000
B	.000	.000	.000	.683	.000	.000	.000	1.000	.000
C	.000	.000	.000	.000	.000	.000	.000	.000	.000
H	.000	.000	.000	.433	.000	.000	.000	.000	.000
H(unb)	.000	.000	.000	.438	.000	.000	.000	.000	.000
H(D.C.)	.000	.000	.000	.488	.000	.000	.000	.000	.000

	Locus and sample size							
Allele	ME 46	PGD 48	PGI-2 49	PGM-3 50	SDH 50	SOD-2 49	TPI-1 50	TPI-2 50
A	1.000	1.000	.102	.940	.000	1.000	.000	1.000
B	.000	.000	.816	.060	1.000	.000	1.000	.000
C	.000	.000	.082	.000	.000	.000	.000	.000

H	.000	.000	.317	.113	.000	.000	.000	.000
H(unb)	.000	.000	.320	.114	.000	.000	.000	.000
H(D.C.)	.000	.000	.286	.120	.000	.000	.000	.000

Mean heterozygosity per locus (biased estimate) = .051 (S.E. .031)

Mean heterozygosity per locus (unbiased estimate) = .051 (S.E. .031)

Mean heterozygosity per locus (direct-count estimate) = .053 (S.E. .032)

Mean number of alleles per locus = 1.24 (S.E. .14)

Percentage of loci polymorphic (0.95 criterion) = 17.65

Percentage of loci polymorphic (0.99 criterion) = 17.65

Percentage of loci polymorphic (no criterion) = 17.65

Allele frequencies and genetic variability measures

****

Population: GENEVA PARK CREE (GPC)

	Locus and sample size								
Allele	ADH 50	ALD 30	DIA-1 50	DIA-2 50	DIA-3 50	GPD-1 50	MDH-2 50	MDH-3 36	MDH-4 26
A	1.000	1.000	1.000	.390	1.000	1.000	1.000	.194	1.000
B	.000	.000	.000	.610	.000	.000	.000	.806	.000
C	.000	.000	.000	.000	.000	.000	.000	.000	.000
H	.000	.000	.000	.476	.000	.000	.000	.313	.000
H(unb)	.000	.000	.000	.481	.000	.000	.000	.318	.000
H(D.C.)	.000	.000	.000	.740	.000	.000	.000	.389	.000

	Locus and sample size							
Allele	ME 49	PGD 48	PGI-2 49	PGM-3 49	SDH 47	SOD-2 50	TPI-1 50	TPI-2 50
A	1.000	1.000	.163	.929	.181	1.000	.000	1.000
B	.000	.000	.806	.071	.819	.000	1.000	.000
C	.000	.000	.031	.000	.000	.000	.000	.000
H	.000	.000	.323	.133	.296	.000	.000	.000
H(unb)	.000	.000	.326	.134	.299	.000	.000	.000
H(D.C.)	.000	.000	.388	.143	.362	.000	.000	.000

Mean heterozygosity per locus (biased estimate) = .091 (S.E. .038)

Mean heterozygosity per locus (unbiased estimate) = .092 (S.E. .038)

Mean heterozygosity per locus (direct-count estimate) = .119 (S.E. .053)

Mean number of alleles per locus = 1.35 (S.E. .15)

Percentage of loci polymorphic (0.95 criterion) = 29.41

Percentage of loci polymorphic (0.99 criterion) = 29.41

Percentage of loci polymorphic (no criterion) = 29.41

Allele frequencies and genetic variability measures

****

Population: HORSESHOE MOUNTA (HSM)

	Locus and sample size								
Allele	ADH 48	ALD 50	DIA-1 50	DIA-2 50	DIA-3 50	GPD-1 49	MDH-2 50	MDH-3 50	MDH-4 48
A	1.000	1.000	1.000	.350	1.000	1.000	1.000	.000	1.000
B	.000	.000	.000	.650	.000	.000	.000	1.000	.000
C	.000	.000	.000	.000	.000	.000	.000	.000	.000
H	.000	.000	.000	.455	.000	.000	.000	.000	.000
H(unb)	.000	.000	.000	.460	.000	.000	.000	.000	.000
H(D.C.)	.000	.000	.000	.540	.000	.000	.000	.000	.000

	Locus and sample size							
Allele	ME 50	PGD 50	PGI-2 50	PGM-3 50	SDH 50	SOD-2 50	TPI-1 50	TPI-2 50
A	1.000	1.000	.000	.990	.000	1.000	.000	1.000
B	.000	.000	.620	.010	.500	.000	1.000	.000
C	.000	.000	.380	.000	.500	.000	.000	.000
H	.000	.000	.471	.020	.500	.000	.000	.000
H(unb)	.000	.000	.476	.020	.505	.000	.000	.000
H(D.C.)	.000	.000	.360	.020	.520	.000	.000	.000

Mean heterozygosity per locus (biased estimate) = .085 (S.E. .045)

Mean heterozygosity per locus (unbiased estimate) = .086 (S.E. .046)

Mean heterozygosity per locus (direct-count estimate) = .085 (S.E. .046)

Mean number of alleles per locus = 1.24 (S.E. .11)

Percentage of loci polymorphic (0.95 criterion) = 17.65

Percentage of loci polymorphic (0.99 criterion) = 23.53

Percentage of loci polymorphic (no criterion) = 23.53

Genetic variability at 17 loci in all populations

(standard errors in parentheses)

Population	Mean sample size per Locus	Mean no. of alleles per locus	Percentage of loci polymorphic*	Mean heterozygosity: Direct-count	Mean heterozygosity: HdyWbg expected**
1. HIGH CREEK SOUTH	45.6 (2.0)	1.4 (.1)	23.5	.058 (.027)	.057 (.027)
2. HIGH CREEK NORTH	46.9 (.7)	1.4 (.1)	11.8	.055 (.030)	.055 (.030)
3. BEAVER CREEK FEN	47.1 (1.5)	1.2 (.1)	17.6	.053 (.032)	.051 (.031)
4. GENEVA PARK CREE	46.1 (1.9)	1.4 (.1)	29.4	.119 (.053)	.092 (.038)
5. HORSESHOE MOUNTA	49.7 (.2)	1.2 (.1)	17.6	.085 (.046)	.086 (.046)

* A locus is considered polymorphic if the frequency of the most common allele does not exceed .95

** Unbiased estimate (see Nei, 1978)

SINGLE INDIVIDUAL GENOTYPE INPUT (ALPHABETIC ALLELIC DESIGNATIONS)

Test for conformance to Hardy-Weinberg equilibrium

BIOSYS-1 Release 1.7 21:06:1999 04:02:01

Levene (1949) correction for small sample size employed in chi-square analyses

Chi-square test for deviation from Hardy-Weinberg equilibrium

Population: HIGH CREEK SOUTH (HCFS)

Locus	Class	Observed frequency	Expected frequency	Chi-square	DF	P
DIA-2						
	A-A	0	.364			
	A-B	9	8.273			
	B-B	41	41.364			
				.431	1	.512
MDH-3						
	A-A	0	.000			
	A-B	1	1.000			
	B-B	45	45.000			
				.000	1	1.000
PGI-2						
	A-A	3	1.402			
	A-B	11	12.794			
	A-C	0	1.402			
	B-B	27	27.093			
	B-C	8	6.021			
	C-C	0	.289			
				4.414	3	.220
PGM-3						
	A-A	43	43.155			
	A-B	6	5.691			
	B-B	0	.155			
				.172	1	.678
SDH						
	A-A	0	.495			
	A-B	10	9.011			
	B-B	36	36.495			
				.610	1	.435
TPI-1						
	A-A	0	.030			
	A-B	3	2.939			
	B-B	47	47.030			
				.032	1	.859

Chi-square test with pooling
****

Population: HIGH CREEK SOUTH (HCFS)

Locus	Class	Observed frequency	Expected frequency	Chi-square	DF	P
PGI-2	Homozygotes for					

most common allele	27	27.093			
Common/rare heterozygotes	19	18.814			
Rare homozygotes and other heterozygotes	3	3.093	.005	1	.944

Significance test using exact probabilities

Population: HIGH CREEK SOUTH (HCFS)

Locus	R1	R2	R3	P
DIA-2	41	9	0	1.000
MDH-3	45	1	0	1.000
PGI-2	27	19	3	1.000
PGM-3	43	6	0	1.000
SDH	36	10	0	1.000
TPI-1	47	3	0	1.000

Coefficients for heterozygote deficiency or excess

Population: HIGH CREEK SOUTH (HCFS)

Locus	Observed heterozygotes	Expected heterozygotes	Fixation index (F)	D
DIA-2	9	8.273	-.099	.088
MDH-3	1	1.000	-.011	.000
PGI-2	19	20.216	.050	-.060
PGM-3	6	5.691	-.065	.054
SDH	10	9.011	-.122	.110
TPI-1	3	2.939	-.031	.021

Chi-square test for deviation from Hardy-Weinberg equilibrium

Population: HIGH CREEK NORTH (HCFN)

Locus	Class	Observed frequency	Expected frequency	Chi-square	DF	P
DIA-2						

	A-A	2	1.681			
	A-B	14	14.637			
	B-B	30	29.681			
				.092	1	.762
MDH-3						
	A-A	0	.061			
	A-B	4	3.879			
	B-B	46	46.061			
				.064	1	.800
PGI-2						
	A-A	2	.680			
	A-B	8	8.907			
	A-C	0	1.732			
	B-B	25	26.351			
	B-C	14	10.392			
	C-C	0	.938			
				6.644	3	.084
PGM-3						
	A-A	48	48.010			
	A-B	2	1.980			
	B-B	0	.010			
				.010	1	.919
TPI-1						
	A-A	0	.000			
	A-B	1	1.000			
	B-B	43	43.000			
				.000	1	1.000
TPI-2						
	A-A	42	42.011			
	A-B	2	1.977			
	B-B	0	.011			
				.012	1	.914

Chi-square test with pooling

Population: HIGH CREEK NORTH (HCFN)

Locus	Class	Observed frequency	Expected frequency	Chi-square	DF	P
PGI-2	Homozygotes for most common allele	25	26.351			
	Common/rare heterozygotes	22	19.299			
	Rare homozygotes and other heterozygotes	2	3.351	.992	1	.319

Significance test using exact probabilities

Population: HIGH CREEK NORTH (HCFN)

Locus	R1	R2	R3	P
DIA-2	30	14	2	1.000
MDH-3	46	4	0	1.000
PGI-2	25	22	2	.467
PGM-3	48	2	0	1.000
TPI-1	43	1	0	1.000
TPI-2	42	2	0	1.000

Coefficients for heterozygote deficiency or excess

Population: HIGH CREEK NORTH (HCFN)

Locus	Observed heterozygotes	Expected heterozygotes	Fixation index (F)	D
DIA-2	14	14.637	.033	-.044
MDH-3	4	3.879	-.042	.031
PGI-2	22	21.031	-.057	.046
PGM-3	2	1.980	-.020	.010
TPI-1	1	1.000	-.011	.000
TPI-2	2	1.977	-.023	.012

Chi-square test for deviation from Hardy-Weinberg equilibrium

Population: BEAVER CREEK FEN (BCF)

Locus	Class	Observed frequency	Expected frequency	Chi-square	DF	P
DIA-2						
	A-A	3	4.012			
	A-B	20	17.975			
	B-B	18	19.012			
				.537	1	.464
PGI-2						
	A-A	2	.464			

	A-B	6	8.247		
	A-C	0	.825		
	B-B	33	32.577		
	B-C	8	6.598		
	C-C	0	.289		
			7.115	3	.068
PGM-3					
	A-A	44	44.152		
	A-B	6	5.697		
	B-B	0	.152		
			.168	1	.682

Chi-square test with pooling

****

Population: BEAVER CREEK FEN (BCF)

Locus	Class	Observed frequency	Expected frequency	Chi-square	DF	P
PGI-2	Homozygotes for most common allele	33	32.577			
	Common/rare heterozygotes	14	14.845			
	Rare homozygotes and other heterozygotes	2	1.577	.167	1	.683

Significance test using exact probabilities

****

Population: BEAVER CREEK FEN (BCF)

Locus	R1	R2	R3	P
DIA-2	18	20	3	.717
PGI-2	33	14	2	.648
PGM-3	44	6	0	1.000

Coefficients for heterozygote deficiency or excess

****

Population: BEAVER CREEK FEN (BCF)

Locus	Observed heterozygotes	Expected heterozygotes	Fixation index (F)	D
DIA-2	20	17.975	-.126	.113

PGI-2	14	15.670	.097	-.107
PGM-3	6	5.697	-.064	.053

Chi-square test for deviation from Hardy-Weinberg equilibrium

Population: GENEVA PARK CREE (GPC)

Locus	Class	Observed frequency	Expected frequency	Chi-square	DF	P
DIA-2						
	A-A	1	7.485			
	A-B	37	24.030			
	B-B	12	18.485			
				14.894	1	.000
MDH-3						
	A-A	0	1.282			
	A-B	14	11.437			
	B-B	22	23.282			
				1.927	1	.165
PGI-2						
	A-A	0	1.237			
	A-B	16	13.031			
	A-C	0	.495			
	B-B	30	31.763			
	B-C	3	2.443			
	C-C	0	.031			
				2.664	3	.446
PGM-3						
	A-A	42	42.216			
	A-B	7	6.567			
	B-B	0	.216			
				.246	1	.620
SDH						
	A-A	0	1.462			
	A-B	17	14.075			
	B-B	30	31.462			
				2.138	1	.144

Chi-square test with pooling

Population: GENEVA PARK CREE (GPC)

Locus	Class	Observed frequency	Expected frequency	Chi-square	DF	P

PGI-2	Homozygotes for most common allele	30	31.763			
	Common/rare heterozygotes	19	15.474			
	Rare homozygotes and other heterozygotes	0	1.763	2.664	1	.103

Significance test using exact probabilities

Population: GENEVA PARK CREE (GPC)

Locus	R1	R2	R3	P
DIA-2	12	37	1	.000
MDH-3	22	14	0	.305
PGI-2	30	19	0	.174
PGM-3	42	7	0	1.000
SDH	30	17	0	.319

Coefficients for heterozygote deficiency or excess

Population: GENEVA PARK CREE (GPC)

Locus	Observed heterozygotes	Expected heterozygotes	Fixation index (F)	D
DIA-2	37	24.030	-.555	.540
MDH-3	14	11.437	-.241	.224
PGI-2	19	15.969	-.202	.190
PGM-3	7	6.567	-.077	.066
SDH	17	14.075	-.221	.208

Chi-square test for deviation from Hardy-Weinberg equilibrium

Population: HORSESHOE MOUNTA (HSM)

Locus	Class	Observed frequency	Expected frequency	Chi-square	DF	P
DIA-2						

	A-A	4	6.010			
	A-B	27	22.980			
	B-B	19	21.010			
				1.568	1	.211
PGI-2						
	B-B	22	19.101			
	B-C	18	23.798			
	C-C	10	7.101			
				3.036	1	.081
PGM-3						
	A-A	49	49.000			
	A-B	1	1.000			
	B-B	0	.000			
				.000	1	1.000
SDH						
	B-B	12	12.374			
	B-C	26	25.253			
	C-C	12	12.374			
				.045	1	.833

Significance test using exact probabilities

Population: HORSESHOE MOUNTA (HSM)

Locus	R1	R2	R3	P
DIA-2	19	27	4	.348
PGI-2	22	18	10	.130
PGM-3	49	1	0	1.000
SDH	12	26	12	1.000

Coefficients for heterozygote deficiency or excess

Population: HORSESHOE MOUNTA (HSM)

Locus	Observed heterozygotes	Expected heterozygotes	Fixation index (F)	D
DIA-2	27	22.980	-.187	.175
PGI-2	18	23.798	.236	-.244
PGM-3	1	1.000	-.010	.000
SDH	26	25.253	-.040	.030

```
**************************************************************************
*                                                                        *
*  SINGLE INDIVIDUAL GENOTYPE INPUT (ALPHABETIC ALLELIC DESIGNATIONS)    *
*                                                                        *
*  F-Statistics                                                          *
*                                                                        *
*  BIOSYS-1   Release 1.7   21:06:1999     04:02:01                      *
*                                                                        *
**************************************************************************

Full output requested

FIS(IK) values
 **************

     Locus: DIA-2

-----------------------------------------
                  Subpopulation
          -------------------------------
 Allele      1       2       3       4       5
 -----------------------------------------------
   A      -.099    .033   -.126   -.555   -.187
   B      -.099    .033   -.126   -.555   -.187
 -----------------------------------------------
 Mean     -.099    .033   -.126   -.555   -.187
 -----------------------------------------------

F-statistics for individual alleles
 ***********************************

     LOCUS: DIA-2

-------------------------------------
 Allele      F(IS)      F(IT)      F(ST)
 -------------------------------------
   A         -.222      -.147       .062
   B         -.222      -.147       .062
 -------------------------------------
 Mean        -.222      -.147       .062
 -------------------------------------

FIS(IK) values
 **************

     Locus: MDH-3

-------------------------------------------
                  Subpopulation
          -------------------------------
 Allele      1       2       3       4       5
 -----------------------------------------------
   A      -.011   -.042      ...   -.241      ...
   B      -.011   -.042      ...   -.241      ...
 -----------------------------------------------
 Mean     -.011   -.042      ...   -.241      ...
 -----------------------------------------------
```

F-statistics for individual alleles

LOCUS: MDH-3

Allele	F(IS)	F(IT)	F(ST)
A	-.192	-.052	.118
B	-.192	-.052	.118
Mean	-.192	-.052	.118

FIS(IK) values

Locus: PGI-2

	Subpopulation				
Allele	1	2	3	4	5
A	.217	.240	.332	-.195	...
B	-.020	-.152	.047	-.241	.236
C	-.089	-.167	-.089	-.032	.236
Mean	.050	-.057	.097	-.202	.236

F-statistics for individual alleles

LOCUS: PGI-2

Allele	F(IS)	F(IT)	F(ST)
A	.127	.160	.038
B	-.009	.017	.026
C	.039	.158	.124
Mean	.038	.094	.058

FIS(IK) values

Locus: PGM-3

	Subpopulation				
Allele	1	2	3	4	5

	Subpopulation				
Allele	1	2	3	4	5
A	-.031	-.011	...	...	...
B	-.031	-.011	...	...	...
Mean	-.031	-.011	...	...	...

F-statistics for individual alleles

LOCUS: TPI-1

Allele	F(IS)	F(IT)	F(ST)
A	-.026	-.008	.017
B	-.026	-.008	.017
Mean	-.026	-.008	.017

FIS(IK) values

Locus: TPI-2

	Subpopulation				
Allele	1	2	3	4	5
A	...	-.023	...	...	...
B	...	-.023	...	...	...
Mean	...	-.023	...	...	...

F-statistics for individual alleles

LOCUS: TPI-2

Allele	F(IS)	F(IT)	F(ST)
A	-.023	-.005	.018
B	-.023	-.005	.018
Mean	-.023	-.005	.018

Summary of F-statistics at all loci

A	-.065	-.020	-.064	-.077	-.010
B	-.065	-.020	-.064	-.077	-.010
Mean	-.065	-.020	-.064	-.077	-.010

F-statistics for individual alleles

****

LOCUS: PGM-3

Allele	F(IS)	F(IT)	F(ST)
A	-.062	-.047	.014
B	-.062	-.047	.014
Mean	-.062	-.047	.014

FIS(IK) values

****

Locus: SDH

	Subpopulation				
Allele	1	2	3	4	5
A	-.122	...	...	-.221	...
B	-.122	...	...	-.221	-.040
C	...	...	...	...	-.040
Mean	-.122	...	...	-.221	-.040

F-statistics for individual alleles

****

LOCUS: SDH

Allele	F(IS)	F(IT)	F(ST)
A	-.182	-.061	.102
B	-.110	.173	.255
C	-.040	.422	.444
Mean	-.110	.208	.287

FIS(IK) values

****

Locus: TPI-1

Locus	F(IS)	F(IT)	F(ST)
DIA-2	-.222	-.147	.062
MDH-3	-.192	-.052	.118
PGI-2	.038	.094	.058
PGM-3	-.062	-.047	.014
SDH	-.110	.208	.287
TPI-1	-.026	-.008	.017
TPI-2	-.023	-.005	.018
Mean	-.097	.023	.109

Appendix C GENESTAT Data

```
CALC WAS CHOSEN
NOGROUPS WAS CHOSEN


Number of loci = 17
Number of populations = 5


   LOCUS      ALLELES
--------     --------
     ADH       A
     ALD       A
   DIA-1       A
   DIA-2       A  B
   DIA-3       A
   GPD-1       A
   MDH-2       A
   MDH-3       A  B
   MDH-4       A
      ME       A
     PGD       A
   PGI-2       A  B  C
   PGM-3       A  B
     SDH       A  B  C
   SOD-2       A
   TPI-1       A  B
   TPI-2       A  B

TABLE OF ALLELE FREQUENCIES
LOCUS-                HCFS      HCFN       BCF       GPC       HSM
  ALLELE                 N         N         N         N         N

     ADH                50        47        49        50        48

       A             1.000     1.000     1.000     1.000     1.000

     ALD                49        41        25        30        50

       A             1.000     1.000     1.000     1.000     1.000

   DIA-1                48        45        44        50        50

       A             1.000     1.000     1.000     1.000     1.000

   DIA-2                50        46        41        50        50

       A             0.090     0.196     0.317     0.390     0.350
       B             0.910     0.804     0.683     0.610     0.650

   DIA-3                48        46        50        50        50
```

A	1.000	1.000	1.000	1.000	1.000
GPD-1	25	50	50	50	49
A	1.000	1.000	1.000	1.000	1.000
MDH-2	46	50	50	50	50
A	1.000	1.000	1.000	1.000	1.000
MDH-3	46	50	50	36	50
A	0.011	0.040	0.000	0.194	0.000
B	0.989	0.960	1.000	0.806	1.000
MDH-4	24	50	49	26	48
A	1.000	1.000	1.000	1.000	1.000
ME	47	44	46	49	50
A	1.000	1.000	1.000	1.000	1.000
PGD	49	48	48	48	50
A	1.000	1.000	1.000	1.000	1.000
PGI-2	49	49	49	49	50
A	0.173	0.122	0.102	0.163	0.000
B	0.745	0.735	0.816	0.806	0.620
C	0.082	0.143	0.082	0.031	0.380
PGM-3	49	50	50	49	50
A	0.939	0.980	0.940	0.929	0.990
B	0.061	0.020	0.060	0.071	0.010
SDH	46	48	50	47	50
A	0.109	0.000	0.000	0.181	0.000
B	0.891	1.000	1.000	0.819	0.500
C	0.000	0.000	0.000	0.000	0.500
SOD-2	50	45	49	50	50
A	1.000	1.000	1.000	1.000	1.000
TPI-1	50	44	50	50	50
A	0.030	0.011	0.000	0.000	0.000
B	0.970	0.989	1.000	1.000	1.000
TPI-2	50	44	50	50	50
A	1.000	0.977	1.000	1.000	1.000

B	0.000	0.023	0.000	0.000	0.000

GENETIC IDENTITIES (ABOVE) AND GENETIC DISTANCES (BELOW)

	HCFS	HCFN	BCF	GPC	HSM
HCFS		0.999	0.996	0.993	0.979
HCFN	0.001		0.999	0.994	0.981
BCF	0.004	0.001		0.996	0.981
GPC	0.007	0.006	0.004		0.980
HSM	0.021	0.019	0.020	0.020	

MATRIX OF GENE IDENTITIES

	ADH	ALD	DIA-1	DIA-2	DIA-3	GPD-1	MDH-2	MDH-3
HCFS	1.000	1.000	1.000	0.836	1.000	1.000	1.000	0.978
HCFN	1.000	1.000	1.000	0.685	1.000	1.000	1.000	0.923
BCF	1.000	1.000	1.000	0.567	1.000	1.000	1.000	1.000
GPC	1.000	1.000	1.000	0.524	1.000	1.000	1.000	0.687
HSM	1.000	1.000	1.000	0.545	1.000	1.000	1.000	1.000

	MDH-4	ME	PGD	PGI-2	PGM-3	SDH	SOD-2	TPI-1
HCFS	1.000	1.000	1.000	0.592	0.885	0.806	1.000	0.942
HCFN	1.000	1.000	1.000	0.576	0.961	1.000	1.000	0.978
BCF	1.000	1.000	1.000	0.683	0.887	1.000	1.000	1.000
GPC	1.000	1.000	1.000	0.677	0.868	0.704	1.000	1.000
HSM	1.000	1.000	1.000	0.529	0.930	0.500	1.000	1.000

	TPI-2
HCFS	1.000
HCFN	0.955
BCF	1.000
GPC	1.000
HSM	1.000

GENE DIVERSITY STATISTICS, UNBIASED FOR SAMPLE SIZE

	Hs	Js	Ht	Jt	Dst	CDst	Gst	CGst
ADH	0.000	1.000	0.000	1.000	0.000	0.000	0.000	0.000
ALD	0.000	1.000	0.000	1.000	0.000	0.000	0.000	0.000
DIA-1	0.000	1.000	0.000	1.000	0.000	0.000	0.000	0.000

DIA-2	0.373	0.627	0.394	0.606	0.021	0.034	0.054	0.069
DIA-3	0.000	1.000	0.000	1.000	0.000	0.000	0.000	0.000
GPD-1	0.000	1.000	0.000	1.000	0.000	0.000	0.000	0.000
MDH-2	0.000	1.000	0.000	1.000	0.000	0.000	0.000	0.000
MDH-3	0.083	0.917	0.093	0.907	0.010	0.011	0.109	0.114
MDH-4	0.000	1.000	0.000	1.000	0.000	0.000	0.000	0.000
ME	0.000	1.000	0.000	1.000	0.000	0.000	0.000	0.000
PGD	0.000	1.000	0.000	1.000	0.000	0.000	0.000	0.000
PGI-2	0.393	0.607	0.414	0.586	0.021	0.035	0.050	0.065
PGM-3	0.085	0.915	0.085	0.915	0.001	0.001	0.006	0.006
SDH	0.200	0.800	0.278	0.722	0.078	0.102	0.280	0.314
SOD-2	0.000	1.000	0.000	1.000	0.000	0.000	0.000	0.000
TPI-1	0.016	0.984	0.016	0.984	0.000	0.000	0.009	0.009
TPI-2	0.009	0.991	0.009	0.991	0.000	0.000	0.000	0.000

GENE DIVERSITY STATISTICS OVER ALL LOCI,
UNBIASED FOR SAMPLE SIZE

Hs	Js	Ht	Jt	Dst	CDst	Gst	CGst
0.068	0.932	0.076	0.924	0.008	0.008	0.101	0.105

GENE DIVERSITY STATISTICS, UNBIASED FOR
SAMPLE SIZE AND POPULATION NUMBER

	Hs	Js	Ht	Jt	Dst	CDst	Gst	CGst
ADH	0.000	1.000	0.000	1.000	0.000	0.000	0.000	0.000
ALD	0.000	1.000	0.000	1.000	0.000	0.000	0.000	0.000
DIA-1	0.000	1.000	0.000	1.000	0.000	0.000	0.000	0.000
DIA-2	0.373	0.627	0.399	0.601	0.026	0.043	0.066	0.084
DIA-3	0.000	1.000	0.000	1.000	0.000	0.000	0.000	0.000
GPD-1	0.000	1.000	0.000	1.000	0.000	0.000	0.000	0.000
MDH-2	0.000	1.000	0.000	1.000	0.000	0.000	0.000	0.000
MDH-3	0.083	0.917	0.096	0.904	0.012	0.014	0.131	0.137
MDH-4	0.000	1.000	0.000	1.000	0.000	0.000	0.000	0.000
ME	0.000	1.000	0.000	1.000	0.000	0.000	0.000	0.000
PGD	0.000	1.000	0.000	1.000	0.000	0.000	0.000	0.000
PGI-2	0.393	0.607	0.419	0.581	0.026	0.044	0.063	0.081
PGM-3	0.085	0.915	0.085	0.915	0.000	0.000	0.000	0.000
SDH	0.200	0.800	0.298	0.702	0.098	0.130	0.328	0.368
SOD-2	0.000	1.000	0.000	1.000	0.000	0.000	0.000	0.000
TPI-1	0.016	0.984	0.016	0.984	0.000	0.000	0.000	0.000
TPI-2	0.009	0.991	0.009	0.991	0.000	0.000	0.000	0.000

GENE DIVERSITY STATISTICS OVER ALL LOCI,
UNBIASED FOR SAMPLE SIZE AND POPULATION NUMBER

Hs	Js	Ht	Jt	Dst	CDst	Gst	CGst
0.068	0.932	0.078	0.922	0.010	0.010	0.123	0.128

Appendix D Genetic Diversity and Structure in Dioecious Flowering Plants

Taxa	P	A	H_o	H_e	H_T	G_{ST}/F_{ST}	Source
Buchloe	54.54	2.92	–	0.14	–	–	Peakall et al., 1995
Eurya japonica***	94.17	3.79	0.425	0.462	0.496	0.069	Chung & Kang
Schiedea adamantis**	22	1.56	0.077	–	–	–	Weller et al., 1996
Schiedea globosa*	46.66	1.78	0.192	–	–	–	Weller et al., 1996
Schiedea kealiae*	66.7	2.78	0.322	–	–	–	Weller et al., 1996
Schiedea salicaria**	72.25	2.22	0.304	–	–	–	Weller et al., 1996
Schiedea sarmentosa**	77.8	2.56	0.31	–	–	–	Weller et al., 1996
Schiedea ligustrina***	66.7	2.44	0.294	–	–	–	Weller et al., 1996
Populus	81.3	2.4	0.32	0.29	0.31	0.03	Jelinski & Cheliak
Cecropia obtusifolia	–	–	–	–	–	0.029	Alvarez-Buylla &
Schizopepon	–	–	–	–	0.358	0.688	Akimoto et al.,
No. of Data Points	9	9	8	3	3	4	Yarbrough
MEAN	64.68	2.49	0.281	0.297	0.388	0.204	Yarbrough
Standard Deviation	21.31	0.653	0.104	0.161	0.097	0.323	Yarbrough

* = subdioecy, ** = gynodioecy, *** = dioecy, ND = no data, P = percent polymorphic loci, A = avg. # of alleles per locus, H_o = observed heterozygosity, H_e = expected heterozygosity, H_T = total heterozygosity, G_{ST} = population differentiation, F_{ST} = population subdivision.

Appendix E Genetic Diversity and Structure in Monoecious Flowering Plants

TAXON	P	A	Ap	Ho	He	Ht	Gst	SOURCE
Carex bigelowii	46.7	1.8	2.4	0.163	0.167		0.055	Jonsson et al. 1998
Carex lasiocarpa	48	1.8	2.2	0.21	0.22	0.288	0.151	McClintock and Waterway 1993
Carex membranacea	44.4	1.8		0.153	0.162	0.199	0.183	Ford et al. 1991
Carex pellita	44	1.8	2.2	0.22	0.21	0.248	0.161	McClintock and Waterway 1993
Carex rotunda	37.2	1.5		0.163	0.12	0.148	0.184	Ford et al. 1991
Carex saxatilis	44.5	1.8		0.135	0.146	0.162	0.198	Ford et al. 1991
Carex abrupta	25.8	1.3	2	0	0.064	0.17	0.5	Whitlaus 1992
Carex aurea	22.1	1.2	2.1	0.023	0.053	0.173	0.282	Unknown
Carex basiantha	40.2	1.5		0.189	0.138	0.156	0.114	Ford et al. 1998
Carex crinita	2.3	1	2	0	0.007	0.256	0.656	Bruederle and Fairbrothers 1986*
Carex crinita var. brevicrinis	1.6	1	2	0.003	0.006	0.258	0.656	Bruederle and Fairbrothers 1988
Carex cryptolepis	3.5	1		0.004	0.011			Unknown
Carex flava	9.6	1.1	2	0.003	0.018	0.038	0.416	Bruederle and Jansen 1991
Carex gynandra	10.2	1.1	2	0.006	0.032	0.256	0.658	Bruederle and Fairbrothers 1986
Carex gynodynama	3.5	1.1	2	0	0.095			Waterway 1990
Carex hartfordii	4.8	1.1	2	0	0.016	0.052	0.712	Whitlaus 1992
Carex hirtissima	14.7	1.2	2	0.007	0.036		0.361	Waterway 1998
Carex integra	19.5	1.2	2.1	0.019	0.047	0.169	0.426	Whitlaus 1992
Carex macloviana	0	1		0	0	0		Whitlaus 1992
Carex mendocinensis	27.5	1.3	2.1	0.056	0.06	0.097	0.15	Waterway 1990
Carex misera	34.8	1.4	2.3	0.082	0.082	0.349	0.161	Godt et al. 1998
Carex misera	9.7	1.1	2.2	0.008	0.019	0.043	0.551	Schell and Waterwey 1992
Carex mitchelliana	10	1.1	2	0.01	0.037	0.147	0.369	Bruederle and Fairbrothers 1986
Carex pacystachya	8.4	1.1	2	0.001	0.025	0.127	0.803	Whitlaus 1992
Carex preslii	10	1.1	2	0	0.04	0.041		Whitlaus 1992
Carex subbracteata	8	1.1	2.2	0	0.006	0.009		Whitlaus 1992
Carex subfusca	5.5	1.1	2	0	0.008	0.15	0.967	Whitlaus 1992
Carex superata	21.6	1.3		0.114	0.071	0.072	0.011	Ford et al. 1998
Carex vindula	13.3	1.1	2	0.02	0.041	0.212	0.806	Bruederle and Jansen 1991
Carex wildenowii	40	1.5		0.237	0.148	0.177	0.167	Ford et al. 1998
Vaccinium elliotii	45	2.08	2.9	0.096		0.151	0.126	Breuderle et al. 1991
Vaccinium myrtilloides	45	2.2	2.72	0.14		0.196	0.133	Breuderle et al. 1991
Vaccinium tenellum	54	2.28	2.86	0.176		0.212	0.127	Breuderle et al. 1991
Vaccinium antrococcum	77.28		2.5	0.28	0.287			Bruederle & Vorsa 1994
Vaccinium boreale	75.76		2.6	0.25	0.264			Bruederle & Vorsa 1994
Vaccinium caesariense	72.73		2.8	0.244	0.276			Bruederle & Vorsa 1994
Vaccinium darrowii	84.09		2.8	0.304	0.321			Bruederle & Vorsa 1994
Vaccinium vacillans	84.85		3.2	0.318	0.353			Bruederle & Vorsa 1994
Pedicularis dasyantha	3	1.03		0	0.016		0.718	Odasz & Savolainen 1998
Plantago major	13.4				0.03			Wolff 1991
Plantago lanceolata	17.5				0.051			Wolff 1991
Plantago coronopus	29.5				0.11			Wolff 1991
Schiedea diffusa	0	1		0				Weller et al. 1998
Schiedea hookeri	66.7	2.11		0.311				Weller et al. 1998
Schiedea kaalae	11.1	1.11		0.041				Weller et al. 1998
Schiedea ligustrina	66.7	2.44		0.294				Weller et al. 1998
Schiedea lydgatei	88.9	2.67		0.322				Weller et al. 1998
Schiedea membranacea	66.7	3		0.366				Weller et al. 1998
Schiedea menziesii	77.8	2.67		0.34				Weller et al. 1998
Schiedea nuttallii	22.2	1.44		0.103				Weller et al. 1998
Schiedea pubescens	22.2	1.22		0.114				Weller et al. 1998
Schiedea stellarioides	22.2	1.33		0.098				Weller et al. 1998
Schiedea verticillata	88.9	2.67		0.371				Weller et al. 1998
Alsinidendron lychnoides	11.1	1.11		0.056				Weller et al. 1998
Alsinidendron obovatum	0	1.11		0.004				Weller et al. 1998
Alsinidendron trinerve	0	1		0				Weller et al. 1998
Alsinidendron viscosum	0	1		0				Weller et al. 1998
Trifolium amoenum	22.5	1.25		0.034	0.087			Knapp and Connors 1999
Trifolium albopureum	32.5	1.35		0.048	0.086			Knapp and Connors 1999
Trifolium macraei	18.33	1.23		0.0005	0.0696			Knapp and Connors 1999
Tricyrtis flava	64.7	2.05	2.88		0.168		0.409	Maki et al. 1999
Tricyrtis nana	23.5	1.24	2.33		0.026		0.483	Maki et al. 1999
Abronia macrocarpa	66.7	2.4			0.269		0.272	Williamson and Worth 1999
Wyethia reticulata	75	2.25	2.55				0.25	Ayers and Ryan 1999
Achillea millefolium megacephala	42	1.74	2.75				0.08	Purdy and Bayer 1996
Achillea millefolium lanulosa	47	2.05	3.22				0.3	Purdy and Bayer 1996
Aletes humilus	81	3.33	3.8				0.2	Linhart and Premoli 1993
Aletes acaulis	81	3.5	4.1				0.28	Linhart and Premoli 1993
Asclepias texana	93	3					0.07	Edwards and Wyatt 1994
Asclepias perennis	100	3.6					0.08	Edwards and Wyatt 1994
Dalea aspera	94	4.3					0.12	Baskauf et al. 1994
Dalea mimosoides	94	4.3					0.11	Baskauf et al. 1994
Echinacea tennesseensis	28	1.5					0.09	Young and Brown 1996
Echinacea angustifolia	44	2.5					0.07	Young and Brown 1996
Erythronium propullans	24	1.8	2.3				0.33	Pleasants and Wendel 1989
Erythronium albidum	36	3	3.1				0.02	Pleasants and Wendel 1989
Rhus michauxii	47		2.38				0.34	Sherman-Broyles et al. 1992
Rhus glabra	88		2.87				0.2	Sherman-Broyles et al. 1992
Rhus copalina	88		3.21				0.3	Sherman-Broyles et al. 1992
Stellaria arenicola	30	1.41	2.23				0.3	Purdy et al. 1994
Stellaria longipes	34	1.48	2.36					Purdy et al. 1994
Agave victoriae-reginae	83	2.2			0.335		0.238	Martinez-Palacious et al. 1999
Asclepias exaltata	84.5		2.38	0.202	0.182			Lipow et al. 1999
Goodyera procera	33.33						0.523	Wong and Sun 1999
Eryngium cunneifolium	42.8	1.61		0.041	0.054			Dolan et al. 1999
Hypericum cumulicola	28	1.25		0.008	0.023			Dolan et al. 1999
Liatris ohlingerae	50	1.93						Dolan et al. 1999
Number of data points (n)	87	74	45	60	49	29	51	S. Yarbrough
MEAN	39.27	1.72	2.45	0.106	0.104	0.157	0.312	S. Yarbrough
STANDARD DEVIATION	29.27	0.791	0.496	0.118	0.099	0.085	0.232	S. Yarbrough

Note: Carex data collected and summarized by S. Kuchel. Grey shading = no data available.

Appendix F Genetic Diversity and Structure in Monoecious Carices

Taxon	P	A	H_o	H_e	H_T	G_{ST}	Source
Carex bigelowii	49	1.8	0.16	0.17	ND	0.06	Jonsson et al., 1996
Carex lasiocarpa	48	1.6	0.21	0.22	0.27	0.15	McClintock and Waterway 1993
Carex membranacea	44	1.6	0.15	0.16	0.20	0.18	Ford et al., 1991
Carex pellita	44	1.6	0.22	0.21	0.25	0.18	McClintock and Waterway 1993
Carex rotunda	37	1.5	0.16	0.12	0.15	0.18	Ford et al., 1991
Carex saxatilis	45	1.6	0.14	0.15	0.18	0.20	Ford et al., 1991
Carex abrupta	26	1.3	0	0.06	0.17	0.5	Whitkus 1992
Carex aurea	22	1.2	0.02	0.05	0.17	0.28	Unknown
Carex basiantha	40	1.5	0.19	0.14	0.16	0.11	Ford et al., 1998
Carex crinita	2.3	1	0	0.01	0.26	0.66	Bruederle and Fairbrothers 1986*
Carex crinita var.	1.6	1	0	0.01	0.26	0.66	Bruederle and Fairbrothers 1986
Carex flava	9.6	1.1	0	0.02	0.04	0.42	Bruederle and Jensen 1991
Carex gynandra	10	1.1	0.01	0.03	0.26	0.66	Bruederle and Fairbrothers 1986
Carex harfordii	4.8	1.1	0	0.02	0.05	0.71	Whitkus 1992
Carex hirtissima	15	1.2	0.01	0.04	ND	0.36	Waterway 1996
Carex integra	20	1.2	0.02	0.05	0.17	0.43	Whikus 1992
Carex mendocinensis	28	1.3	0.06	0.06	0.10	0.15	Waterway 1990
Carex misera	35	1.4	0.08	0.08	0.35	0.16	Godt et al., 1996
Carex misera	9.7	1.1	0.01	0.02	0.04	0.55	Schell and Waterway 1992
Carex mitchelliana	10	1.1	0.01	0.04	0.15	0.37	Bruederle and Fairbrothers 1986
Carex pacystachya	8.4	1.1	0	0.03	0.13	0.80	Whitkus 1992
Carex subfusca	5.5	1.1	0	0.01	0.15	0.97	Whitkus 1992
Carex superata	22	1.3	0.11	0.07	0.07	0.01	Ford et al., 1998
Carex viridula	13	1.1	0.02	0.04	0.21	0.81	Bruederle and Jensen 1991
Carex willdenowii	40	1.5	0.24	0.15	0.18	0.17	Ford et al., 1998
No. of Data Points.	25	25	25	25	23	25	Yarbrough
Mean	23.60	1.30	0.07	0.073	0.172	0.389	Yarbrough
Standard Deviation	16.09	0.23	0.084	0.065	0.080	0.272	Yarbrough

Appendix G Genetic Diversity and Structure in Caespitose Carices

TAXON	*P*%	*A*	*Ap*	*Ho*	H_e	H_T	G_{ST}	Reference
Carex abrupta	25.8	1.3	2	0	0.064	0.17	0.5	Whitkus, 1992
Carex aurea**	22.1	1.2	2.1	0.023	0.053	0.173	0.282	Unknown
Carex basiantha	40.2	1.5	No data	0.189	0.138	0.158	0.114	Ford et al., 1998
Carex crinita	2.3	1	2	0.003	0.007	0.256	0.658	Bruederle & Fairbrothers, 1986***
Carex crinita var. brevicrinis	1.8	1	2	0	0.006	0.256	0.658	Bruederle & Fairbrothers, 1986
Carex cryptolepis	3.5	1	No data	0.004	0.011	No data	No data	Unknown
Carex flava	9.6	1.1	2	0.003	0.018	0.036	0.416	Bruederle & Jensen, 1991
Carex gynandra	10.2	1.1	2	0.008	0.032	0.256	0.658	Bruederle & Fairbrothers, 1986
Carex gynodynama	3.5	1.1	2	0	0.095	No data	No data	Waterway, 1990
Carex harfordii	4.8	1.1	2	0	0.016	0.052	0.712	Whitkus, 1992
Carex hirtissima	14.7	1.2	2	0.007	0.036	No data	0.361	Waterway, 1996
Carex integra	19.5	1.2	2.1	0.019	0.047	0.169	0.426	Whitkus, 1992
Carex macloviana	0	1	No data	0	0	0	No data	Whitkus, 1992
Carex mendocinensis	27.5	1.3	2.1	0.056	0.06	0.097	0.15	Waterway, 1990
Carex misera	34.8	1.4	2.3	0.082	0.082	0.349	0.161	Godt, et al., 1996
Carex misera	9.7	1.1	2.2	0.008	0.019	0.043	0.551	Scheil and Waterway, 1992
Carex mitchelliana	10	1.1	2	0.01	0.037	0.147	0.369	Bruederle & Fairbrothers, 1986
Carex pacystachya	8.4	1.1	2	0.001	0.025	0.127	0.803	Whitkus, 1992
Carex preslii	10	1.1	2	0	0.04	0.041	No data	Whitkus, 1992
Carex subbracteata	6	1.1	2.2	0	0.006	0.009	No data	Whitkus, 1992
Carex subfusca	5.5	1.1	2	0	0.008	0.15	0.967	Whitkus, 1992
Carex superata	21.6	1.3	No data	0.114	0.071	0.072	0.011	Ford, et al., 1998
Carex viridula	13.3	1.1	2	0.02	0.041	0.212	0.806	Bruederle & Jensen, 1991
Carex willdenowii	40	1.5	No data	0.237	0.148	0.177	0.167	Ford, et al., 1998
MEAN	14.4	1.2	2.1	0.033	0.044	0.14	0.462	
Standard Deviation	12	0.15	0.09	0.063	0.04	0.094	0.272	

*Data for this table compiled by S.D. Kuchel, 1999

*** GST value is over all polymorphic loci in complex

P% = percent polymorphic loci

A = Avg. # of alleles per locus

A_p = Avg. # of alleles per polymorphic locus

H_o = observed heterozygosity

H_e = expected heterozygosity

H_T = total heterozygosity

G_{ST} = population differentiation

Appendix H Genetic Diversity and Structure in Rhizomatous Carices

TAXON	P%	A	A_p	H_o	H_e	H_T	G_{ST}	Reference
Carex bigelowii	48.7	1.8	2.4	0.163	0.167	No data	0.055	Jonsson et al., 1996
Carex lasiocarpa	48	1.6	2.2	0.21	0.22	0.266	0.151	McClintock & Waterway, 1993
Carex membranaceae	44.4	1.6	No data	0.153	0.162	0.199	0.183	Ford et al., 1991
Carex pellita	44	1.6	2.2	0.22	0.21	0.248	0.181	McClintock & Waterway, 1993
Carex rotunda	37.2	1.5	No data	0.163	0.12	0.148	0.184	Ford et al., 1991
Carex saxatilis	44.5	1.6	No data	0.135	0.146	0.182	0.198	Ford et al., 1991
Mean	44.5	1.6	2.3	0.174	0.171	0.209	0.159	
Standard Deviation	4.08	0.1	0.12	0.034	0.038	0.048	0.053	

*Data for this table compiled by S.D. Kuchel, 1999

P% = percent polymorphic loci

A = Avg. # of alleles per locus

A_p = Avg. # of alleles per polymorphic locus

H_o = observed heterozygosity

H_e = expected heterozygosit

H_T = total heterozygosity

G_{ST} = population differentiati

Appendix I Mann-Whitney *U*-test Statistical Results

```
Worksheet size: 3500 cells

MTB > Retrieve  'C:\THESIS\SCIRP.MTW'.
Retrieving worksheet from file: C:\THESIS\SCIRP.MTW
Worksheet was saved on  4/16/2000
MTB > Mann-Whitney 95.0 'DioP' 'MOspP';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

DioP        N =  10     Median =       66.70
MOspP       N =  81     Median =       32.50
Point estimate for ETA1-ETA2 is        27.47
95.0 Percent C.I. for ETA1-ETA2 is (5.50,45.29)
W = 650.5
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.0159
The test is significant at 0.0159 (adjusted for ties)

MTB > Mann-Whitney 95.0 'DioA' 'MOspA';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

DioA        N =  10     Median =      2.4200
MOspA       N =  70     Median =      1.4050
Point estimate for ETA1-ETA2 is       0.7700
95.1 Percent C.I. for ETA1-ETA2 is (0.2998,1.2901)
W = 605.0
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.0037
The test is significant at 0.0036 (adjusted for ties)

MTB > Mann-Whitney 95.0 'DIspHo' 'MOspHo';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

DIspHo      N =   9     Median =      0.3040
MOspHo      N =  57     Median =      0.0560
```

```
Point estimate for ETA1-ETA2 is      0.1720
95.0 Percent C.I. for ETA1-ETA2 is (0.0690,0.2880)
W = 462.5
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.0027
The test is significant at 0.0026 (adjusted for ties)

MTB > Mann-Whitney 95.0 'DioHe' 'MOspHe';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

DioHe       N =   4     Median =      0.2150
MOspHe      N =  45     Median =      0.0640
Point estimate for ETA1-ETA2 is      0.1215
95.3 Percent C.I. for ETA1-ETA2 is (0.0020,0.2950)
W = 155.0
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.0466
The test is significant at 0.0466 (adjusted for ties)

MTB > Mann-Whitney 95.0 'DioP' 'MoCrxP';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

DioP        N =  10     Median =       66.70
MoCrxP      N =  25     Median =       22.00
Point estimate for ETA1-ETA2 is       39.21
95.3 Percent C.I. for ETA1-ETA2 is (24.26,56.71)
W = 286.0
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.0001
The test is significant at 0.0001 (adjusted for ties)

MTB > Mann-Whitney 95.0 'DioA' 'MoCrxA';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test
```

```
DioA        N =  10     Median =      2.4200
MoCrxA      N =  25     Median =      1.2000
Point estimate for ETA1-ETA2 is       1.1200
95.3 Percent C.I. for ETA1-ETA2 is (0.6200,1.4199)
W = 294.0
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.0000
The test is significant at 0.0000 (adjusted for ties)

MTB > Mann-Whitney 95.0 'DIspHo' 'MOcrxHo';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

DIspHo      N =   9     Median =      0.3040
MOcrxHo     N =  25     Median =      0.0200
Point estimate for ETA1-ETA2 is       0.1920
95.4 Percent C.I. for ETA1-ETA2 is (0.0770,0.3000)
W = 247.0
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.0005
The test is significant at 0.0005 (adjusted for ties)

MTB > Mann-Whitney 95.0 'DioHe' 'MoCrxHe';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

DioHe       N =   4     Median =      0.2150
MoCrxHe     N =  25     Median =      0.0500
Point estimate for ETA1-ETA2 is       0.1250
95.4 Percent C.I. for ETA1-ETA2 is (0.0200,0.3220)
W = 95.0
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.0291
The test is significant at 0.0288 (adjusted for ties)

MTB > Mann-Whitney 95.0 'CaesCrxP' 'RhizCrxP';
SUBC>   Alternative 0.
```

```
Mann-Whitney Confidence Interval and Test

CaesCrxP   N =  24     Median =       10.00
RhizCrxP   N =   6     Median =       44.45
Point estimate for ETA1-ETA2 is      -34.10
95.4 Percent C.I. for ETA1-ETA2 is (-39.60,-22.30)
W = 302.0
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.0003
The test is significant at 0.0003 (adjusted for ties)

MTB > Mann-Whitney 95.0 'CaeCrxA' 'RhizCrxA';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

CaeCrxA    N =  24     Median =      1.1000
RhizCrxA   N =   6     Median =      1.6000
Point estimate for ETA1-ETA2 is     -0.5000
95.4 Percent C.I. for ETA1-ETA2 is (-0.6000,-0.3000)
W = 301.0
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.0003
The test is significant at 0.0002 (adjusted for ties)

MTB > Mann-Whitney 95.0 'CaespHo' 'RhizHo';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

CaespHo    N =  24     Median =     0.00550
RhizHo     N =   6     Median =     0.16300
Point estimate for ETA1-ETA2 is    -0.15300
95.4 Percent C.I. for ETA1-ETA2 is (-0.19999,-0.12802)
W = 310.0
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.0014
The test is significant at 0.0013 (adjusted for ties)

MTB > Mann-Whitney 95.0 'CaeCrxHe' 'RhiCrxHe';
```

```
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

CaeCrxHe    N =  24     Median =     0.03650
RhiCrxHe    N =   6     Median =     0.16450
Point estimate for ETA1-ETA2 is    -0.12900
95.4 Percent C.I. for ETA1-ETA2 is (-0.16300,-0.09100)
W = 303.0
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.0004
The test is significant at 0.0004 (adjusted for ties)

MTB > Mann-Whitney 95.0 'ScirpP' 'DioP';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

ScirpP      N =   5     Median =      17.65
DioP        N =  10     Median =      66.70
Point estimate for ETA1-ETA2 is      -45.78
95.7 Percent C.I. for ETA1-ETA2 is (-63.65,-23.13)
W = 17.0
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.0059
The test is significant at 0.0058 (adjusted for ties)

MTB > Mann-Whitney 95.0 'ScirpA' 'DioA';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

ScirpA      N =   5     Median =      1.3500
DioA        N =  10     Median =      2.4200
Point estimate for ETA1-ETA2 is     -1.0700
95.7 Percent C.I. for ETA1-ETA2 is (-1.5401,-0.3200)
W = 15.0
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.0027
The test is significant at 0.0026 (adjusted for ties)
```

```
MTB > Mann-Whitney 95.0 'ScirpHo' 'DIspHo';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

ScirpHo    N =   5     Median =      0.0580
DIspHo     N =   9     Median =      0.3040
Point estimate for ETA1-ETA2 is     -0.2250
95.4 Percent C.I. for ETA1-ETA2 is (-0.2670,-0.0210)
W = 19.0
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.0164

MTB > Mann-Whitney 95.0 'ScirpHe' 'DioHe';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

ScirpHe    N =   5     Median =      0.0700
DioHe      N =   4     Median =      0.2150
Point estimate for ETA1-ETA2 is     -0.1450
96.3 Percent C.I. for ETA1-ETA2 is (-0.4019,0.0100)
W = 17.0
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.0662
The test is significant at 0.0651 (adjusted for ties)

Cannot reject at alpha = 0.05

MTB > Mann-Whitney 95.0 'ScirpP' 'MOspP';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

ScirpP     N =   5     Median =      17.65
MOspP      N =  81     Median =      32.50
Point estimate for ETA1-ETA2 is     -12.24
95.2 Percent C.I. for ETA1-ETA2 is (-47.05,7.65)
W = 158.0
```

```
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.2762
The test is significant at 0.2761 (adjusted for ties)

Cannot reject at alpha = 0.05

MTB > Mann-Whitney 95.0 'ScirpA' 'MOspA';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

ScirpA      N =   5     Median =      1.3500
MOspA       N =  70     Median =      1.4050
Point estimate for ETA1-ETA2 is     -0.0700
95.1 Percent C.I. for ETA1-ETA2 is (-0.8499,0.2099)
W = 174.5
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.7500
The test is significant at 0.7495 (adjusted for ties)

Cannot reject at alpha = 0.05

MTB > Mann-Whitney 95.0 'ScirpHo' 'MOspHo';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

ScirpHo     N =   5     Median =     0.05800
MOspHo      N =  57     Median =     0.05600
Point estimate for ETA1-ETA2 is      0.01600
95.1 Percent C.I. for ETA1-ETA2 is (-0.13101,0.05799)
W = 168.0
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.7960
The test is significant at 0.7953 (adjusted for ties)

Cannot reject at alpha = 0.05

MTB > Mann-Whitney 95.0 'ScirpHe' 'MOspHe';
SUBC>   Alternative 0.
```

```
Mann-Whitney Confidence Interval and Test

ScirpHe     N =    5     Median =      0.07000
MOspHe      N =   45     Median =      0.06400
Point estimate for ETA1-ETA2 is       0.00700
95.1 Percent C.I. for ETA1-ETA2 is (-0.08800,0.04900)
W = 135.5
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.8084
The test is significant at 0.8083 (adjusted for ties)

Cannot reject at alpha = 0.05

MTB > Mann-Whitney 95.0 'ScirpP' 'MoCrxP';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

ScirpP      N =    5     Median =       17.65
MoCrxP      N =   25     Median =       22.00
Point estimate for ETA1-ETA2 is       -2.35
95.5 Percent C.I. for ETA1-ETA2 is (-20.47,12.14)
W = 76.0
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.9556
The test is significant at 0.9556 (adjusted for ties)

Cannot reject at alpha = 0.05

MTB > Mann-Whitney 95.0 'ScirpA' 'MoCrxA';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

ScirpA      N =    5     Median =      1.3500
MoCrxA      N =   25     Median =      1.2000
Point estimate for ETA1-ETA2 is       0.1100
95.5 Percent C.I. for ETA1-ETA2 is (-0.1901,0.2501)
W = 91.0
```

```
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.4694
The test is significant at 0.4639 (adjusted for ties)

Cannot reject at alpha = 0.05

MTB > Mann-Whitney 95.0 'ScirpHo' 'MOcrxHo';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

ScirpHo     N =   5     Median =     0.05800
MOcrxHo     N =  25     Median =     0.02000
Point estimate for ETA1-ETA2 is      0.03900
95.5 Percent C.I. for ETA1-ETA2 is (-0.09202,0.06498)
W = 90.0
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.5043
The test is significant at 0.5009 (adjusted for ties)

Cannot reject at alpha = 0.05

MTB > Mann-Whitney 95.0 'ScirpHe' 'MoCrxHe';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

ScirpHe     N =   5     Median =     0.07000
MoCrxHe     N =  25     Median =     0.05000
Point estimate for ETA1-ETA2 is      0.02000
95.5 Percent C.I. for ETA1-ETA2 is (-0.06999,0.05001)
W = 90.5
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.4867
The test is significant at 0.4855 (adjusted for ties)

Cannot reject at alpha = 0.05

MTB > Mann-Whitney 95.0 'ScirpP' 'CaesCrxP';
SUBC>   Alternative 0.
```

```
Mann-Whitney Confidence Interval and Test

ScirpP      N =   5     Median =       17.65
CaesCrxP    N =  24     Median =       10.00
Point estimate for ETA1-ETA2 is         7.88
95.4 Percent C.I. for ETA1-ETA2 is (-4.46,16.05)
W = 101.0
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.1410
The test is significant at 0.1408 (adjusted for ties)

Cannot reject at alpha = 0.05

MTB > Mann-Whitney 95.0 'ScirpA' 'CaeCrxA';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

ScirpA      N =   5     Median =      1.3500
CaeCrxA     N =  24     Median =      1.1000
Point estimate for ETA1-ETA2 is       0.1500
95.4 Percent C.I. for ETA1-ETA2 is (0.0400,0.3100)
W = 116.0
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.0194
The test is significant at 0.0159 (adjusted for ties)

MTB > Mann-Whitney 95.0 'ScirpHo' 'CaespHo';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

ScirpHo     N =   5     Median =     0.05800
CaespHo     N =  24     Median =     0.00550
Point estimate for ETA1-ETA2 is      0.05350
95.4 Percent C.I. for ETA1-ETA2 is (0.03300,0.08500)
W = 116.0
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.0194
```

```
The test is significant at 0.0181 (adjusted for ties)

MTB > Mann-Whitney 95.0 'ScirpHe' 'CaeCrxHe';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

ScirpHe     N =   5     Median =     0.07000
CaeCrxHe    N =  24     Median =     0.03650
Point estimate for ETA1-ETA2 is      0.03600
95.4 Percent C.I. for ETA1-ETA2 is (-0.00001,0.06000)
W = 109.5
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.0496
The test is significant at 0.0495 (adjusted for ties)

MTB > Mann-Whitney 95.0 'ScirpP' 'RhizCrxP';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

ScirpP      N =   5     Median =       17.65
RhizCrxP    N =   6     Median =       44.45
Point estimate for ETA1-ETA2 is      -25.89
96.4 Percent C.I. for ETA1-ETA2 is (-32.64,-14.99)
W = 15.0
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.0081
The test is significant at 0.0080 (adjusted for ties)

MTB > Mann-Whitney 95.0 'ScirpA' 'RhizCrxA';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

ScirpA      N =   5     Median =      1.3500
RhizCrxA    N =   6     Median =      1.6000
Point estimate for ETA1-ETA2 is     -0.2550
96.4 Percent C.I. for ETA1-ETA2 is (-0.3900,-0.1900)
W = 15.0
```

```
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.0081
The test is significant at 0.0065 (adjusted for ties)

MTB > Mann-Whitney 95.0 'ScirpHo' 'RhizHo';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

ScirpHo    N =   5     Median =     0.05800
RhizHo     N =   6     Median =     0.16300
Point estimate for ETA1-ETA2 is    -0.10050
96.4 Percent C.I. for ETA1-ETA2 is (-0.15701,-0.04399)
W = 15.0
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.0081
The test is significant at 0.0080 (adjusted for ties)

MTB > Mann-Whitney 95.0 'ScirpHe' 'RhiCrxHe';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

ScirpHe    N =   5     Median =     0.07000
RhiCrxHe   N =   6     Median =     0.16450
Point estimate for ETA1-ETA2 is    -0.09650
96.4 Percent C.I. for ETA1-ETA2 is (-0.15002,-0.05600)
W = 15.0
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.0081
The test is significant at 0.0080 (adjusted for ties)

MTB > Mann-Whitney 95.0 'DIspGst' 'MOspGst';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

DIspGst    N =   4     Median =      0.0495
MOspGst    N =  49     Median =      0.2000
Point estimate for ETA1-ETA2 is     -0.1150
```

```
95.1 Percent C.I. for ETA1-ETA2 is (-0.3571,0.1879)
W = 61.0
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.1174
The test is significant at 0.1174 (adjusted for ties)

Cannot reject at alpha = 0.05

MTB > Mann-Whitney 95.0 'DIspGst' 'MOcrxGst';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

DIspGst    N =   4     Median =      0.0495
MOcrxGst   N =  25     Median =      0.3600
Point estimate for ETA1-ETA2 is     -0.1500
95.4 Percent C.I. for ETA1-ETA2 is (-0.5910,0.0592)
W = 35.0
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.1213
The test is significant at 0.1208 (adjusted for ties)

Cannot reject at alpha = 0.05

MTB > Mann-Whitney 95.0 'DIspGst' 'CaespGst';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

DIspGst    N =   4     Median =      0.0495
CaespGst   N =  19     Median =      0.4260
Point estimate for ETA1-ETA2 is     -0.2960
95.3 Percent C.I. for ETA1-ETA2 is (-0.6288,0.0300)
W = 28.0
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.1137
The test is significant at 0.1134 (adjusted for ties)

Cannot reject at alpha = 0.05
```

```
MTB > Mann-Whitney 95.0 'DIspGst' 'RhizGst';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

DIspGst    N =   4     Median =      0.0495
RhizGst    N =   6     Median =      0.1820
Point estimate for ETA1-ETA2 is     -0.1145
95.7 Percent C.I. for ETA1-ETA2 is (-0.1550,0.5069)
W = 17.0
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.3374

Cannot reject at alpha = 0.05

MTB > Mann-Whitney 95.0 'CaespGst' 'RhizGst';
SUBC>   Alternative 0.

Mann-Whitney Confidence Interval and Test

CaespGst   N =  19     Median =      0.4260
RhizGst    N =   6     Median =      0.1820
Point estimate for ETA1-ETA2 is      0.3040
95.5 Percent C.I. for ETA1-ETA2 is (0.0159,0.5280)
W = 280.0
Test of ETA1 = ETA2  vs.  ETA1 ~= ETA2 is significant a
t 0.0386
The test is significant at 0.0385 (adjusted for ties)

MTB >
```

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