

The Contribution of Epistasis to the Evolution of Natural Populations

A Case Study of an Annual Plant

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Quantifying the contribution of epistasis in the adaptation of natural populations to their environment is central to our understanding of the evolutionary process and to other evolutionary phenomena, including the maintenance of genetic variation, the evolution of sex and selfing, and speciation (Whitlock et al. 1995; Fenster et al. 1997). In historical context, epistasis plays its most significant role in the differentiation of the theories of Fisher (1930) and Wright (1931, 1932). Because Fisher believed species to be essentially panmictic, genes under selection would be tested in all genetic backgrounds. As a consequence, their additive effects (or, in a statistical sense, their main effects) would determine their evolutionary fate. Wright, however, believed that population genetic structure was an important feature of evolution. Genetic structure implies that the genetic background of alleles under selection will differ among populations. Between-population differences in the genetic background influence the evolutionary fate of nonneutral alleles by locally altering their main or average effects (Goodnight, chap. 8, this volume). As a result, Wright's models of adaptive evolution reflect interactions among genes or, in other words, epistasis. Epistasis also generates the fitness peaks and valleys of Wright's adaptive landscape that are fundamental to his shifting-balance theory (Wright 1932; Wade 1992b; Brodie, chap. 1, this volume). While all the components of shifting balance have not been demonstrated, particularly whether populations drift through fitness valleys to higher adaptive peaks and whether coadapted genes successfully spread (Coyne et al. 1997), we hope to demonstrate that two components, drift and epistasis, have an important impact on evolution in natural populations.

Since the 1960s, empirical work has demonstrated that species exhibit significant population genetic structure. In particular, limited dispersal and some degree of inbreeding—characteristics of structured populations—are demonstrated by F_1 heterosis in the progeny of interpopulation crosses (e.g., Levin 1984; Fenster 1991b, and references therein) and population differentiation for neutral single-locus molecular markers (Hamrick and Godt 1989). The presence of population genetic structure implies the opportunity for genetic background effects to play a role in evolution as populations are likely to differ in gene frequencies and allelic combinations. However, our understanding of the role of epistasis in evolution lags far behind our understanding of population structure. This is surprising, because, while drift may influence first-order genetic parameters such as levels of genetic variation, and so on, it also provides variation in genetic background between populations, which enhances the possibility of the evolution of second-order gene interactions specific to individual populations. So we are left with the fundamental question, "How common is epistasis?"

The lack of empirical work on epistasis, in part, reflects the difficulty in quantification of epistasis (Whitlock et al. 1995; Fenster et al. 1997). However, epistasis has not gone completely unstudied; some of the earliest *Drosophila* studies led to the coining of the term "genetic coadaptation" (Wallace 1953; Dobzhansky 1955; Wallace and Vetukhiv 1955). More recently, studies that used marker-assisted techniques have demonstrated the contribution of epistasis to the adaptation of experimental populations of cultivated barley (Clegg et al. 1978), to reproductive isolation among sibling species of *Drosophila* (Palapoli and Wu 1994), to introgressive hybridization in *Helianthus* (Rieseberg et al. 1996), and to genetic differentiation among cultivars for traits correlated to yield (Doebley et al. 1995; Lark et al. 1995; Li et al. 1997a). Furthermore, the role of epistasis in adaptive evolution has been investigated by the quantification of epistasis in laboratory environments that simulate natural conditions, and the investigation of the contribution of epistasis to the divergence of characters that reflect adaptive evolution. Examples include the evolution of alcohol tolerance in the laboratory in populations of *Drosophila melanogaster* (Cavener and Clegg 1981), population differentiation of photoperiod requirements for diapause in the pitcher-plant mosquito (Hard et al. 1992; Bradshaw and Holzapfel, chap. 15, this volume), osmoregulation of the tidepool copepod *Tigropous californicus* (Burton 1987, 1990b), gill raker length differences between sympatric species of stickleback (Hatfield, 1997), and among-line differences for morphological and behavioral traits of houseflies subjected to bottlenecks (Meffert, chap. 11, this volume).

We know less about the role of epistasis *in situ*, under natural conditions. Although the above studies have provided us with information about the potential role of epistasis in population differentiation, they may not provide a complete understanding of the genetic architecture responsible for population differentiation in nature. The few studies that have quantified epistatic contributions to population differentiation in the native environment have examined only the F_1 generation (Fenster 1991b; Waser 1993), and have therefore provided only a partial assessment of the relevance of epistasis. Determination of the mode of gene expression that underlies the evolution of fitness in nature is necessary since it is how natural selection "perceives" epistatic interactions that will determine their

role in the evolution of natural populations. Thus, a reasonable question is, "To what extent would the epistasis documented in the above studies be expressed in the wild?" "If epistasis is expressed under native conditions, is it strong, or weak?" In addition, we have little knowledge of the variation of expression of epistasis owing to genetic variation or environmental factors, or the frequency with which epistasis contributes to population differentiation. If frequent, then epistasis plays a fundamental role in evolution.

Here, we present the results of experiments designed to quantify the contribution of epistasis to population differentiation. The results are derived from three experiments that address the following questions: (1) "Does epistasis among nuclear, biparentally inherited genes contribute to population differentiation for fitness?" (2) "Does epistasis between maternally inherited cytoplasmic genomes and the biparentally inherited nuclear genome contribute to population differentiation for fitness?" Because epistatic interactions that enhance fitness are likely to have been fixed within populations (Whitlock et al. 1995), we examined the role of epistasis in population differentiation by creating interpopulation hybrids. In brief, we chose to test the effect of placing genes in alternative genetic backgrounds: that is, to test for hybrid breakdown that results from the mixing of differentiated gene pools (Dobzhansky 1970; Lynch 1991). While F_1 hybrids have a full complement of genes from both populations, epistatic combinations may be disrupted in later generation hybrids (F_2 , F_3 , etc.) because of recombination (Mather and Jinks 1982; Lynch 1991). Therefore, we quantified the contribution of epistasis to population differentiation of the native annual legume *Chamaecrista fasciculata* by following the performance of progeny of interpopulation crosses. Since additive processes of allele substitution may result in epistatic differentiation among populations or species (Dobzhansky 1970; Maynard Smith 1989), genetic architecture measured by these methods will not necessarily reflect selection on polymorphic gene interactions. However, the epistasis measured by the quantification of performance among segregating progeny of interpopulation crosses may influence a species' or population's potential for future evolutionary change, and may contribute to the initial stages of postzygotic reproductive isolation (Whitlock et al. 1995). We discuss our results in terms of their implication for the evolutionary process.

Study Organism

Chamaecrista fasciculata Michx., partridge pea (= *Cassia fasciculata*) (Irwin and Barneby 1982), is a self-compatible, mostly outcrossing (Fenster 1991a, 1995) annual legume of eastern North America. It is found in open woodlands, old fields, roadsides, dunes, savanna, and prairie. Seedlings emerge from mid-April to mid-May. Flowering of this species begins in mid to late July and continues until first frost (late September to early November for the study populations). *Chamaecrista fasciculata* falls into the "buzz" pollination syndrome (Faegri and Van der Pijl 1979; Fenster 1995). The large, yellow caesalpinoid flowers provide no nectar rewards and the pollen is released through terminal pores in the anthers after vibrations caused by large bees (Fenster 1991a). Seed dispersal is through explosive pod

dehiscence and begins in early September. Because *C. fasciculata* is an annual with a limited seed bank (Baskin and Baskin 1988; Fenster 1991b), total lifetime fitness can be assessed by determining germination, survivorship to flowering, and total fruit production. There are no sterility barriers between populations separated by up to 2000 km.

The size of *C. fasciculata*'s genetic neighborhood is small (radius < 5 m) and corresponds to a density of approximately 100 individuals (Fenster 1991a, 1991b). Proximity-dependent inbreeding depression (Fenster 1991b), suggests that most mating events within the neighborhood are between close relatives. Heterosis in the progeny increases rapidly with interparent distance and then plateaus, with little increase of fitness following crosses between parents in different neighborhoods. Additional work (Fenster and Galloway 2000a) demonstrates that progeny of crosses between populations from 100 m to 2000 km apart also express F_1 heterosis. Since the expression of heterosis in the progeny depends on genetic differentiation between the parents (Falconer 1981), these results demonstrate some degree of population differentiation in *C. fasciculata*. The spatial pattern of genetic variation, determined by an extensive isozyme survey (Fenster and Dudash, 1994), support this conclusion. Three thousand individuals from northern Illinois and Indiana were mapped to the nearest 10 cm and genotyped. Individuals within the neighborhood and in different populations from 40 m to hundreds of kilometers apart were genotyped. The genetic relatedness between all pairs of individuals was inferred by using Rogers' similarity index (Rogers 1972). The relationship between genetic similarity and interplant distance correspond strikingly to the level of inbreeding depression and heterosis observed after crosses of individuals with different interparent distances. In sum, small neighborhood sizes, rapid increase of progeny fitness that results from increasing interparent distance, and rapid decrease of genetic similarity among individuals indicates that genetic relatedness falls off quickly with increasing distance, which corresponds to a model of limited gene flow (Malecot 1969).

Methods

Contribution of Nuclear \times Nuclear Epistasis to Population Differentiation

Field

To evaluate epistatic differentiation for nuclear genes between *C. fasciculata* populations, we crossed populations over six spatial distances, ranging from 100 m to 2000 km. For each population pair, we created three generations of hybrids (F_1 , F_2 , F_3) and used within-population crosses to produce parental seed under greenhouse conditions. We replicated this design across three regions of the United States (Maryland, Illinois, and Kansas). In each region, a single target population was chosen and crossed to other populations over the six distances. The two longest distance crosses, 1000 km and 2000 km, reflect crosses between target populations. As a consequence, there are two replicates of the 1000-km cross

(Maryland–Illinois and Kansas–Illinois) and one replicate of the 2000-km cross (Maryland–Kansas). To evaluate whether epistatic interactions between genes contribute to fitness in nature, we established a field plot at the location of the target population in each region and planted hybrid and parental seed for all crosses in it for 2 years. For each generation and crossing distance, at least 360 seeds were planted each year for a total of at least 8000 seeds/site/year. We estimated fitness as the number of fruit produced per seed planted. The genetic basis of between-population differences for components of fitness is presented elsewhere (Fenster and Galloway 2000a).

We quantified the contribution of epistasis to population differentiation by statistically comparing the recombinant hybrid generations (F_2 and F_3) to the average of the mid-parent and the F_1 generation (Mather and Jinks 1982; Lynch 1991; Lynch and Walsh 1998). In the absence of epistasis, the performance of the F_2 and F_3 generations should be equal to the average of the parents and the F_1 . However, performance of the recombinant hybrid generations may be less than expected if there are groups of genes that interact to enhance fitness but that are disrupted during meiosis via recombination and independent assortment. The reduction in performance of recombinant hybrid generations compared with the expected value reveals the presence of different groups of epistatically interacting genes between populations (Box 15.1 in Bradshaw and Holzapfel, chap. 15, this volume).

Common Garden

We also evaluated the genetic architecture of the divergence between populations in more detail by focusing on one of the crosses in the between-population study above. For the cross between the Maryland and Illinois target populations, we created additional backcross hybrid generations. The F_1 hybrids were backcrossed to each parental population to create two new generations: backcrosses to Maryland (BCM) and backcrosses to Illinois (BCI). We planted both parental populations (M, I), two hybrid generations (F_1 , F_2), and the two backcrosses (BCM, BCI) into a garden plot in Maryland. We used joint-scaling tests (Mather and Jinks 1982; Lynch and Walsh 1998; Bradshaw and Holzapfel, chap. 15, this volume) to evaluate the genetic architecture of fruit production. Joint-scaling tests use least-square regression techniques on generation means to test for the contribution of additivity, dominance, and epistasis to phenotypic character expression (see Box 15.1 in Bradshaw and Holzapfel, chap. 15, this volume). In this common garden study, we examined the genetic architecture of our fitness correlate, fruit production, and a number of floral and vegetative traits that differ between the populations (not reported here: Galloway and Fenster, submitted).

Cytonuclear Interactions

Our last approach to understanding the prevalence of epistasis for fitness in natural populations was to quantify the contribution of interactions between

nuclear and cytoplasmic genes to local adaptation (Galloway and Fenster 1999). We did this by creating second-generation backcross hybrids between the Maryland and Illinois target populations and planting them for 2 years into the sites native to each population. Cytoplasmic genes are presumed to be maternally inherited in *C. fasciculata* (Galloway and Fenster 1999), and therefore reflect the maternal population of an F_1 hybrid. We reciprocally crossed the parental populations to create F_1 seeds with similar nuclear genes but different cytoplasmic genes. We then separately backcrossed the Maryland and Illinois parental populations (male) onto each of the reciprocal F_1 hybrids (female) to create four types of seed: *MD* cytoplasm and nuclear genes (*mM*), *MD* cytoplasm and *IL* nuclear genes (*mI*), *IL* cytoplasm and *MD* nuclear genes (*iM*), and *IL* cytoplasm and nuclear genes (*iI*). Because backcrossing was conducted for two generations, on average 87.5% of the nuclear genes are from the paternal population. More simply, this experimental design uses backcrossing to create seeds in which the nuclear and cytoplasmic genomes “match” (*iI, mM*) and seeds where the two genomes are mismatched (*iM, mI*). If the fitness of individuals with matched genomes is greater than or less than the expected value based on the independent combinations of nuclear and cytoplasmic genes (i.e., marginal values), epistatic interactions between cytoplasmic and nuclear genes contribute to fitness. Epistatic interactions between the genomes contribute to local adaptation if individuals with matched genomes that represent the home population have greater fitness than individuals with transplanted genes (cytoplasmic and nuclear).

Results

Contribution of Nuclear \times Nuclear Epistasis to Population Differentiation

Field

There was substantial loss of fitness in the F_3 generation for both years and all crossing distances relative to the F_2 , and to the expected average (average of mid-parents and F_1) in the absence of epistasis (Fig. 14.1, Fenster and Galloway 2000a). These results reveal that epistatic gene complexes differ between populations and that the contribution of interacting genes to fitness is widespread. Fitness of the F_2 generation did not differ from the expected value, except in a few short-distance crosses that were equally divided between negative and positive epistasis. Because hybrid breakdown was largely observed in the F_3 generation and not the F_2 , epistatic interactions appear to be due to linked genes that are disrupted in the additional round of recombination between the generations. The magnitude of hybrid breakdown did not scale with distance; coadapted gene complexes are equally differentiated for populations that are hundreds of meters apart and those that are thousands of kilometers apart. However, the degree of hybrid breakdown was environment-specific, varying with site and year, which implied that contribution of gene interactions to fitness varies with the local environment.

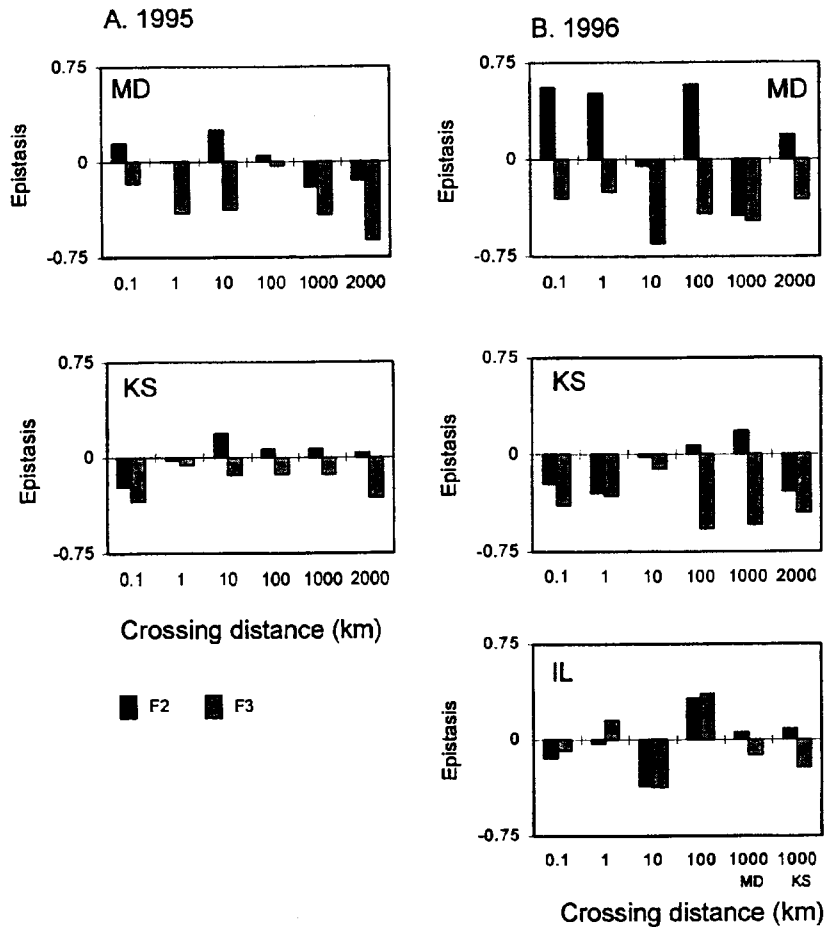


Figure 14.1 Contribution of epistasis to genetic differences among populations of *Chamaecrista fasciculata*. Deviation of fruit production per seed planted of F₂ and F₃ hybrids from the average of the F₁ and mid-parent generations is presented. This average ($\mu=0$) represents the null expectation that populations do not differ for epistatically interacting groups of alleles. Means of F₂ and F₃ generation that differ significantly from the null expectation (see graphs) reveal that epistasis contributes to population differentiation. Deviations of <zero indicate the disruption of coadapted genes, while values significantly >zero indicate that recombinants of the interpopulation crosses exhibit positive epistasis. The F₃ fitness was less than expected in MD and KS for both years and was not different from that expected in IL 1996. The F₂ fitness was not different from the expected value for all states and years except MD 1996, where it was greater than expected (see Fenster and Galloway 2000a, for full analysis).

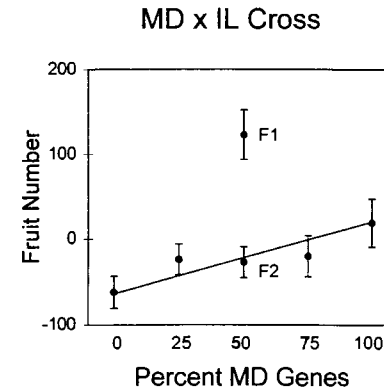


Figure 14.2 Common garden experiment to determine the genetic basis of differentiation of fruit production between two distant populations of *Chamaecrista fasciculata*. Observed means and standard errors for fruit production measured in each of the six generations are shown. Data represent the residuals after removal of block effects. A priori expectations of additive genetic effects are represented by the line that connects the parental means.

Common Garden

A joint-scaling test found that additive, dominance, and epistatic gene action contribute to the divergence in fruit production between Maryland and Illinois populations of *C. fasciculata*. A model that included only additivity and dominance was a poor fit ($\chi^2 = 13.7$, $df = 3$, $p < .005$; also Galloway and Fenster, submitted). This result is illustrated in Fig. 14.2. If differences between populations were additive, hybrid means would fall on the line that connects the two parental populations. If dominance contributed to gene expression, the hybrid generations would resemble one parent more than the other, and if overdominance, associated with heterosis, is expressed, the F₁ will have a value greater than either parent. Epistatic interactions between genes are present if neither additivity nor dominance fully explains the hybrid generation means. As can be seen from Fig. 14.2, the F₁ is significantly above the line, thereby indicating heterosis, while the low performance of the F₂, less than half the distance between the line and the F₁, indicates epistasis.

Cytonuclear Interactions

Interactions between cytoplasmic and nuclear genes contributed to fitness (fruit produced/seed planted) in *C. fasciculata*, but this result was not consistent across sites or years. In 1996, individuals planted in Illinois with *il* cytoplasm performed equally well with both *MD* and *IL* nuclear genes (Fig. 14.3a), while those with *md* cytoplasm outperformed other seed types when combined with *MD* nuclear genes, but they performed the most poorly when combined with *IL* nuclear genes (Fig. 14.3a, Galloway and Fenster 1999). Therefore, individuals with matching cytoplasmic and nuclear genes within a nuclear type had greater fitness than those with mismatching genomes. No nuclear \times cytoplasmic interactions were detected in *MD* for either year or in *IL* in 1997. However, strong nuclear effects were observed as *MD* nuclear genes outperformed *IL* nuclear genes in both *MD* and *IL*. The discovery of an interaction between cytoplasmic and nuclear genomes that is

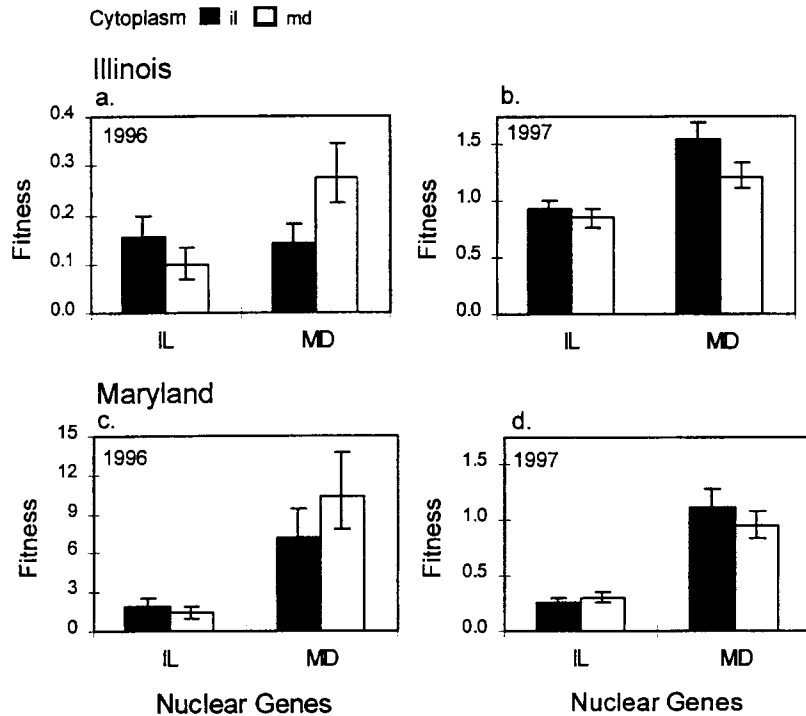


Figure 14.3 Mean (\pm SE) cumulative fitness (fruit/seed planted) of *Chamaecrista fasciculata* plants with either Illinois or Maryland cytoplasmic genes and 87% Illinois or Maryland nuclear genes grown in Maryland and Illinois for 2 years. Note: scales on the y-axis vary. (Figure follows Galloway and Fenster 1999).

expressed only in Illinois demonstrates that the expression of cytonuclear interactions is environment dependent. However, this epistatic interaction does not contribute to local adaptation in *C. fasciculata*, as individuals with matching MD genomes had greater fitness than those with matching IL genomes.

Discussion

The results from our experiments indicate that epistasis contributes consistently and substantially to population differentiation. Results from both the common garden and field experiments demonstrate that combining genes from different populations leads to a uniform decrease in fitness beyond that expected due to loss of heterozygosity. Because negative epistasis is mostly observed in the F_3 generation, and less consistently in the F_2 generation, an additional round of recombination appears to be necessary to disrupt putatively linked epistatically interacting genes. These results conform to theoretical predictions that the evolution of

interacting gene systems is facilitated where recombination is limited either through limited gene flow, previously documented for *C. fasciculata*, or through linkage (reviewed in Fenster et al. 1997). Our results also indicate that a gene likely to increase fitness in the genetic background of the source population may decrease fitness when placed in a different genetic background. As a consequence, evolution in *C. fasciculata* appears to be contingent on the frequency of particular alleles within a population. Our results corroborate earlier work that documents inbreeding and genetic coadaptation in *Drosophila* and other species tested in laboratory conditions (reviewed in Whitlock et al. 1995; Fenster et al. 1997), but they are in contrast to the outcome of a large-scale agricultural field study with maize where no epistatic interactions were detected (Moll et al. 1965), perhaps because epistasis was quantified only through the F_2 generation.

We were also able to detect epistasis between nuclear and cytoplasmic genes in *C. fasciculata*. A number of studies have demonstrated interactions between cytoplasmic and nuclear genes by the use of individuals created with mismatched genomes within a species (Clark and Lyckegaard 1988; MacRae and Anderson 1988; Fos et al. 1990; Nigro 1994; Palmer and Minor 1994) and between-species (Grant 1975; Robertson and Frey 1984; Beavis and Frey 1987; Pollak 1991; Jan 1992; Inai et al. 1993; Breeuwer and Werren 1995; Hutter and Rand 1995). In animals, there is no evidence for cytonuclear interactions within populations (Clark and Lyckegaard 1988), which perhaps reflects a lack of variation in the cytoplasmic genome at this scale. However, a number of studies on plants at the intraspecific level, particularly those studies that are used to investigate cytoplasmic male sterility, have documented cytoplasmic genetic variation (e.g., Belhassen et al. 1993; Saumitou-Laprade et al. 1993; McCauley 1995; Ronfort et al. 1995) and cytonuclear interactions within populations (Belhassen et al. 1991). Our experimental design did not allow us to detect scale effects. However, seed dispersal, the most likely vector of cytoplasmic genes, is limited relative to pollen dispersal [quantified in *C. fasciculata* (Fenster 1991a) and elsewhere (McCauley 1994, 1995, 1998)], which suggests that, as found in the above studies, coadaptation between nuclear and cytoplasmic genes might also exist at smaller spatial scales.

Our results indicate that gene interaction is a fundamental feature of the evolution of natural populations, since even populations separated by hundreds of meters are epistatically differentiated from one another. Each of the populations of *C. fasciculata* represents a different adaptive combination of alleles, relative to the target populations. Therefore, similar selection pressures on different populations may result in equivalent phenotypes, but may represent very different genetic responses (Cohan 1984; Goodnight, chap. 8, this volume). The occurrence of unique and independent genetic solutions imposed by selection is known as genetic redundancy (Futuyma 1998). The coadaptation that we have documented, and which gives rise to genetic redundancy, may reflect the action of drift that creates different genetic backgrounds, as well as the incorporation of novel mutations that will be random across populations. Order of incorporation can be an important factor if subsequent evolution depends on incorporation of mutations with epistatic effects (Mani and Clarke 1990).

Our results appear to match the predictions of a simulation study by Goldstein and Holsinger (1992): namely, that genetic redundancy is an outcome of limited

gene flow and stabilizing selection. Stabilizing selection makes the expression of alleles at each locus dependent on the genetic composition at other loci (Wright 1935; Barton 1986, 1989a; Whitlock et al. 1995; Brodie, chap. 1, this volume). If limited gene flow leads to different combinations of genes in different populations (which arise through drift and independent mutation), then similar selection pressures on different populations may result in different genes that reproduce similar phenotypes. The epistasis that we have documented therefore need not reflect selection on polymorphic segregating variation, but may be an outcome of limited gene flow that causes populations to differentiate through the combined effects of drift and accumulation of independent mutations. Consequently, the selective value of alleles will differ among populations, according to their particular genetic background. Our results thus confirm that epistasis and limited gene flow may be important factors in the maintenance of between-population genetic variation (Gimelfarb 1989; Goldstein and Holsinger 1992).

There is much evidence that adaptations in different populations, or at higher taxonomic levels, reflect genetic redundancy. Replicate lines or populations diverge from one another when subjected to the same strong selection pressures (Cohan 1984), thus demonstrating that drift or the incorporation of novel mutations into different lines may constrain populations to evolve different genetic responses (Cohan and Hoffmann 1986; Cohan et al. 1989; Korona et al. 1994; Travisano et al. 1995). Constraint is used here to describe limitation of the types of genetic responses that a population can make to selection. The breakdown of presumably adaptive characters in progeny of crosses among natural populations also demonstrates independent genetic solutions at the intraspecific level. Examples include F_1 progeny with larger retina size in crosses between different populations of the blind cave fish, *Anoptichthys antrobius* (Wilkens 1971), the breakdown of pesticide resistance following crosses among populations of houseflies, *Musca domestica* (King 1955), and the recovery of the wild-type outcrossing mid-styled morph in the F_1 of crosses between selfing modified mid-morphs from different populations in *Eichhornia paniculata* (Fenster and Barrett 1994). However, these different responses need not represent the evolution of interacting coadapted gene complexes. Rather, they may represent the fixation of alleles at different loci with additive effect (e.g., the independent evolution of alcohol tolerance in replicate selected lines; Cohan et al. 1989), or the fixation of recessive alleles at different loci (complementary genes; e.g., Fenster and Barrett 1994). The breakdown in fitness quantified for the F_3 generation *C. fasciculata* in the field demonstrates that genetic redundancy in the ability of populations to be adapted to the environment is widespread. Our results differ from the above examples because we have explicitly demonstrated that epistasis, or genetic background effects, contribute to the variety of genetic solutions to selection pressures imposed by the environment.

Although data reported here and elsewhere provide evidence for two important features of Wright's shifting-balance theory—genetic drift (Fenster 1991a, 1991b; Fenster and Galloway 2000a; Galloway and Fenster 2000) and epistasis for fitness—they do not prove that population differences have evolved by the crossing of a fitness valley (Maynard Smith 1989). With intermediate environments or gene frequencies, it is just as possible that simple selection on the individual effects of genes as opposed to selection on gene interactions may have resulted in

populations becoming differentiated for epistatic interactions (Dobzhansky 1937; Gavrillets and Hastings 1996). Ridges may connect the peaks and it may not be necessary to invoke populations crossing through a fitness valley. We observed a large environmental effect on the expression of epistasis, heterosis, and parental performance (Fenster and Galloway 2000a; Galloway and Fenster 2000), which suggest that the fitness surface is fluid. A fitness valley in one year may be a peak in another, and viceversa. Therefore, our results may be concordant with both Fisher's (1930) and Wright's (1931) vision of the evolutionary process in that populations may always evolve by increasing fitness, but that different populations have different genetic starting points because of limited gene flow and epistasis.

Our results also demonstrate a possible microevolutionary basis for speciation that includes the generation of genome-wide negative epistasis among loci expressed in species hybrids (Dobzhansky 1937; Gavrillets and Hastings 1996). The very same patterns of hybrid breakdown in species hybrids that are caused by negative epistasis among genes mixed from different species are also exhibited in our *intraspecific*, interpopulation crosses. There has been a long tradition, mainly among botanists, of also viewing hybridization as having a creative role in evolution, with the formation of chance novel recombinants with high-fitness following interspecific crosses (Stebbins 1950; Grant 1981; Rieseberg 1997). Our results also demonstrate that selectively advantageous recombinants can occur since crosses between some populations exhibited enhanced fitness and mirror results from between-species crosses (Rieseberg 1997; Burke et al. 1998). Thus, hybrids, whether derived from interpopulation or interspecific crosses, may sometimes result in the expression of favorable gene interactions that may provide the basis for further adaptation. The cytonuclear interaction effects on fitness that we observed have also been documented for hybrids of interspecies crosses. For example, in a case that mirrors our asymmetrical results, Louisiana iris hybrids showed distortion from expected Mendelian ratios in the F_2 generation for only one of the two nonparental combinations of nuclear and cytoplasmic markers (Burke et al. 1998). If our results are found to be common, then epistatic differentiation at the population level suggests that the evolution of postzygotic reproductive isolation may be relatively rapid, as has been predicted by theory (Orr 1995).

In a conservation context, our results demonstrate that the use of composite populations, or the bolstering of population size by the addition of individuals from other populations, may have only short-term benefits as combining genes from different populations may ultimately lead to a decrease in mean fitness in the F_3 and perhaps later segregating generations. Although the F_3 generation in our study expressed outbreeding depression, it is important to note that their fitness was often greater than or equal to that of one of the parents, which suggests that heterosis may offset the decrease in fitness associated with the disruption of epistatically interacting genes (Fenster and Galloway 2000b). How quickly the fitness of the hybrid population recovers will depend on how rapidly the selectively advantageous recombinants are generated, and whether more epistatic interactions would be revealed by further bouts of recombination.

Evolution in populations of *C. fasciculata* is contextual. To paraphrase Lewontin (1974), it is this context of genetic background effects that is so essential in the determination of the subsequent evolution of these populations.

Consequently, the evolutionary process is complex for populations of *C. fasciculata*, and generalizations concerning evolutionary trajectories may not be extrapolated from studies of a limited number of populations. Elsewhere (Fenster and Galloway 2000a; Galloway and Fenster 2000), we demonstrate that while populations are differentiated from one another, we could find only limited evidence of home-site advantage or local adaptation. The home-site advantage that was observed was mostly found in comparisons between home populations and populations transplanted ≥ 1000 km. This result, along with the results presented here, suggests that evolution of *C. fasciculata* populations to their environments represents a myriad of genetic solutions that reflect the evolution of gene interactions particular to each population.

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The Evolution of Genetic Architectures and the Divergence of Natural Populations

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In this chapter, we are concerned with the evolution of genetic architectures in natural populations and the role that genic interactions play in this evolution. The genetic architecture of a population refers to the number of loci and the number and frequency of alleles at those loci that affect a particular trait, their allelic (dominance) and genic (epistatic) interactions, and their relationship to other traits (pleiotropy). Since most traits that affect fitness result from the expression of multiple loci, each of varying effect, our understanding of the genetics of fitness-related traits and the evolution of life histories has required the application of quantitative genetics. Much of the attention of quantitative genetic studies of life-history evolution has focused on genetic tradeoffs, or antagonistic pleiotropy, both as a constraint to the independent evolution of genetically correlated traits, and as an explanation for standing additive genetic variation for fitness traits within populations.

Studies of tradeoffs have dealt primarily with additive genetic variation and correlation within and among fitness traits of laboratory populations (Roff 1992; Stearns 1992). Two problems arise as a result of these biases. First, interactions among loci (epistasis) “greatly complicate quantitative genetic theory and, hence, they are generally assumed to be absent” (Roff 1997, p. 31), despite the fact that the extent and consequences of epistasis constitute a major source of the differences between Fisher and Wright in their fundamental view of evolution in natural populations (Wade and Goodnight 1998; Brodie, chap. 1, this volume). Second, the genetic variance–covariance structure of a population depends to a great extent upon the environment that the population experiences. When populations encounter a novel environment, such as an unnatural laboratory setting,