Evolution, 39(1), 1985, pp. 24–40

THE EVOLUTION OF SELF-FERTILIZATION AND INBREEDING DEPRESSION IN PLANTS. I. GENETIC MODELS

RUSSELL LANDE AND DOUGLAS W. SCHEMSKE
Department of Biology, University of Chicago, Chicago, IL 60637

Summary.—The amounts of inbreeding depression upon selfing and of heterosis upon outcrossing determine the strength of selection on the selfing rate in a population when this evolves polygenically by small steps. Genetic models are constructed which allow inbreeding depression to change with the mean selfing rate in a population by incorporating both mutation to recessive and partially dominant lethal and sublethal alleles at many loci and mutation in quantitative characters under stabilizing selection. The models help to explain observations of high inbreeding depression (>50%) upon selfing in primarily outcrossing populations, as well as considerable heterosis upon outcrossing in primarily selfing populations. Predominant selfing and predominant outcrossing are found to be alternative stable states of the mating system in most plant populations. Which of these stable states a species approaches depends on the history of its population structure and the magnitude of effect of genes influencing the selfing rate.

Received December 7, 1983. Revised June 22, 1984

Many species of monoecious or hermaphroditic plants have mechanisms which prevent self-fertilization and promote outcrossing, such as self-incompatibility systems, heterostyly, and dichogamy. A major selective force maintaining outcrossing appears to be substantial inbreeding depression in the fitness of selfed progeny due to the expression of largely recessive deleterious mutations in homozygotes. However, in a variety of plant taxa, predominantly self-fertilizing species which are closely related to primarily outcrossing species exist (Stebbins, 1957; Jain, 1976; Charlesworth and Charlesworth, 1979*a*; Schemske and Lande, 1985).

In this paper we present models of mutation and selection to analyze the joint evolution of inbreeding depression and self-fertilization in natural populations. The models demonstrate that in many situations the two extremes of predominant outcrossing and predominant self-fertilization represent alternative stable states of the mating system. By which of these mechanisms a species is selected to reproduce depends largely on the history of its population structure. Species with a long history of occasional population bottlenecks and/or pollinator failure are expected to show relatively little inbreeding depression and to be selected for self-fertilization, whereas species with historically large, outcrossing populations are expected to have substantial inbreeding depression and to be selected for mechanisms to prevent inbreeding. We summarize data which support these generalizations, and which also indicate that there is a bimodal distribution of selfing rates among plant species, corresponding to the two evolutionarily stable reproductive modes of predominant outcrossing and predominant selfing (Schemske and Lande, 1985).

In the absence of inbreeding depression, a gene causing a plant to self-fertilize its seed without reducing pollen dispersal would have an advantage of 50% in an initially outbreeding population and would rapidly spread until the entire population became completely self-fertilizing, as first shown by Fisher (1941) for a semidominant gene, and under more general conditions by Nagylaki (1976) and Wells (1979). In addition to the cost of outcrossing there are several other selective factors which could promote the evolution of selfing, such as lack of pollinators, repeated colonization of new areas by single individuals, and selection

for local adaptation (Stebbins, 1957; Antonovics, 1968; Jain, 1976; Lloyd, 1979). Temporal and spatial variation in environments can select for outcrossing and recombination, but it is doubtful whether this alone could produce a 50% advantage for outcrossing (Maynard Smith, 1978 Ch. 6).

Inbreeding depression is the only general factor in large outcrossing populations which appears to be strong enough to prevent the evolution of self-fertilization in most species (Charlesworth and Charlesworth, 1979*a*). Previous models of the evolution of plant mating systems do not allow inbreeding depression to evolve with changes in the mating system of a population (reviewed by Charlesworth and Charlesworth, 1979*a*). Our model for the joint evolution of inbreeding depression and self-fertilization does not provide a complete dynamical description of the process but it does permit us to make qualitative predictions concerning the evolutionary stable states of a population by assessing the strength of selection on the selfing rate. It also suggests that the evolution of the mating system may depend on whether the genetic change in the selfing rate occurs in a polygenic fashion by small steps, or by a major change at a single locus as in Fisher's model.

Selection on the Selfing Rate

Construction of an exact multilocus model of the evolution of self-fertilization is difficult because partial selfing generates departures from random combination of diploid genotypes at different loci in zygotes (Haldane, 1949; Weir and Cockerham, 1973). Nevertheless, some insight into the process can be gained by examining a simple measure of the intensity of selection on genetic variation in the selfing rate. As argued below, this approach is likely to be valid for the evolution of selfing by small steps—that is, for genes with small effect on the selfing rate—but does not apply to genes which produce a large change in the selfing rate, such as complete self-fertilization.

Consider a large hermaphroditic population which is partially self-fertilizing, or inbreeding due to limited dispersal. A gene with a small effect on the selfing rate but no direct effect on fitness will nevertheless evolve through the cost of outcrossing and by indirect selection through its association with deleterious homozygous mutations at other loci. Provided that linkage between the selfing locus and the selected loci is loose and the mean selfing rate in the population is not very high, most of the association between genotypes at the selfing locus and those at the selected loci will be created anew each generation by selection on selfed and outcrossed progeny. An approximate measure of the strength of selection on the selfing rate can therefore be obtained by comparing the expected fitness of progeny produced by plants with different selfing rates, weighting the selfed progeny twice as much as the outcrossed progeny.

Let the mean selfing rate in the population be $\bar{r}$ and let $\bar{w}_0$ and $\bar{w}_1$ be, respectively, the mean fitnesses of outcrossed and selfed progeny in the population. Assuming that all genotypes produce the same amount of pollen, and that any seeds which are not outcrossed are self-fertilized, the expected fitness of genotypes with the selfing rate r is approximately

$$w = r\bar{w}_1 + \frac{1}{2}(1 - r)\bar{w}_0 + \frac{1}{2}(1 - \bar{r})\bar{w}_0$$

in which the first two terms are components of fitness from selfed and outcrossed seed, and the last term is that from pollen fertilizing ovules of other plants. It is important to recall that $\bar{w}_0$ and $\bar{w}_1$ are functions of the mean selfing rate (or inbreeding coefficient) in the population.

The intensity of selection on genotypes with a small effect on the selfing rate is approximately proportional to the magnitude of their effect on the selfing rate and to the differential coefficient $\partial w/\partial r$, which from the previous expression is

$$\partial w/\partial r = \bar{w}_1 - \frac{1}{2}\bar{w}_0.$$

Thus if the expected fitness of selfed progeny is greater than ½ that of outcrossed progeny, there is selection to increase the selfing rate in the population. A convenient measure of inbreeding depression is the proportional decrement in expected fitness of selfed progeny compared to the expected fitness of outcrossed progeny,

$$\begin{aligned}\delta &= (\bar{w}_0 - \bar{w}_1)/\bar{w}_0 \\ &= 1 - \bar{w}_1/\bar{w}_0. \qquad (1)\end{aligned}$$

The condition for evolution of increased selfing rate in the population is $\delta < ½$. In other words, there is selection for increased selfing if the inbreeding depression is less than 50%, and there is selection for increased outcrossing if the inbreeding depression is greater than 50%.

This condition applies to the mode of reproduction in which any seed not outcrossed is selfed. Lloyd (1979) examined this and other modes of reproduction to derive analogous conditions for selection to favor selfing. For example, in species where selfing occurs prior to outcrossing and only a fraction c of ovules not selfed are successfully cross-fertilized, the condition for selection to increase the selfing rate, $\delta < 1 - c/2$, is less stringent than the previous condition (cf. Maynard Smith, 1978; Lloyd, 1979). Similarly, if outcrossing precedes selfing, but only a fraction c of ovules not outcrossed are successfully self-fertilized, the condition for selection to favor selfing is $\delta < 1 - 1/(2c)$. Finally if the more highly selfing genotypes disperse less pollen, a reduction of pollen output of cr for plants with the selfing rate r produces selection in favor of increased selfing when $\delta < (1 - c)/2$ (cf. Lloyd, 1979; Charlesworth, 1980). Thus each of these complicating factors changes the threshold value of inbreeding depression in a population, above which there is selection for increased outcrossing and below which there is selection for increased self-fertilization.

Observations on Inbreeding Depression

In predominantly outcrossing species with historically large population sizes, substantial inbreeding depression is generally manifest after self-fertilization by a high frequency of embryonic lethals, and by decreases in the mean values of other major components of fitness such as germination, growth rate, survival, and reproduction (e.g., Sorensen et al., 1976; Schemske, 1983; Schoen, 1983).

The total inbreeding depression due to selfing is often quite large in outcrossing species, frequently greater than 50%, and the average individual typically is heterozygous for one or more recessive lethal factors (Crumpacker, 1967; Sorensen, 1969; Franklin, 1972; Lloyd, 1974; Wright, 1977 Ch. 2; Klekowski, 1982, 1984; Schemske, 1983; Schoen, 1983). Considerable inbreeding depression occurs even in domesticated populations started from crosses between inbred lines which have been purged of recessive lethal mutations (Wright, 1977 Ch. 2; Mayo, 1980 Ch. 9; Frankel, 1983). The most detailed data on inbreeding depression, from various species of *Drosophila,* indicates that in historically large outcrossing populations most of the inbreeding depression is due to rare, largely recessive, lethal and sublethal mutations at many loci, while the remainder of the inbreeding depression is caused by genes with small, more nearly additive effects on fitness (Simmons and Crow, 1977; Frankham, 1982).

Habitually self-fertilizing plant populations usually have much smaller inbreeding depression than obligate outcrossers, although considerable hybrid vigor or heterosis may still occur upon crossing different inbred strains (Griffing and Langridge, 1963; Wright, 1977 Ch. 2; Brown, 1979). It is often difficult to distinguish whether heterosis in inbred populations is caused by partly recessive deleterious mutations, or by a general heterozygote advantage at many loci, or both. However, artificial production of inbred lines which perform as well as hybrids argues strongly against a general

heterozygote advantage (reviewed by Wright, 1977; Gardner, 1978; Sprague, 1983; Jinks, 1983).

In view of these observations, the equilibrium of selection and mutation will be analyzed for two types of genes contributing to inbreeding depression in populations with different amounts of self-fertilization or other inbreeding. First we model mutation to lethal and sublethal alleles at many loci; then we investigate a model of quantitative variation which does not depend on heterozygote advantage, but which explains observations of heterosis in predominantly inbreeding populations, as well as the substantial proportion of quantitative genetic variance in fitness traits due to epistatic interactions.

Equilibrium Models of Inbreeding Depression

Lethal and Sublethal Mutations.—In large obligately outcrossing populations the equilibrium genetic load produced by recurrent mutation at a rate μ to deleterious alleles at a given locus is between μ, for completely recessive mutations, and 2μ, for partially or fully dominant mutations (Haldane, 1937; Muller, 1950). Most lethal and sublethal mutations segregating in natural populations are not completely recessive (Simmons and Crow, 1977). The total spontaneous mutation rate to lethals at all loci in *Drosophila melanogaster* is about 1×10^{-2} per gamete per generation, which results from mutations at about 5,000 loci, giving an average per locus mutation rate to lethals of about 2×10^{-6} per gamete per generation (Crow and Simmons, 1983). A recent study of ferns suggests a similar magnitude for the total mutation rate to recessive lethals (Klekowski, 1984). The total genetic load from lethal mutations is thus rather small, less than a few percent (Fisher, 1949; Crow, 1952; Simmons and Crow, 1977). Therefore, although typical individuals in large outbreeding populations are heterozygous for one or more nearly recessive lethal (or sublethal) genes, it is quite unlikely for zygotes to be homozygous for more than one lethal mutation.

Because a small amount of inbreeding can greatly increase the expression of rare recessive traits, the equilibrium frequency of lethals should be much lower under partial selfing than in a randomly mating population. Even in a population with a low level of selfing, the inbreeding depression due to recessive lethal and sublethal mutations is expected to be greatly reduced in comparison to that in a completely outcrossing population.

Although partial selfing creates an association between homozygotes at different loci in a population as a whole, it does not produce any association of genes or genotypes at unlinked loci within subgroups of the population composed of individuals with the same coefficient of inbreeding (Haldane, 1949). The randomly outcrossed progeny evidently form a uniform group with no inbreeding, and, with respect to lethal and sublethal alleles, the inbreeding coefficient of selfed progeny is nearly uniform since mutant homozygotes are eliminated each generation.

Partial selfing does produce an association between homozygous genotypes at linked loci within subgroups of the population with the same inbreeding coefficient (Haldane, 1949), but a given chromosome is unlikely to carry more than one recessive lethal or sublethal mutation, even in predominantly outcrossing populations. This justifies ignoring departures from random combination of diploid genotypes at different loci producing lethal and sublethal mutations within selfed and outcrossed subgroups of the population. Thus the mean fitnesses of selfed and outcrossed progeny subgroups can be calculated using the approximation of random combination of diploid genotypes at different loci within these subgroups.

Assuming that selection acts independently on each lethal and sublethal locus, fitness effects are multiplicative across loci. With nearly random combination among genotypes at different loci within

subpopulations of selfed or outcrossed progeny, the mean fitness in the selfed (or outcrossed) group is nearly equal to the product of the mean fitnesses at each locus. Since rare lethal and sublethal alleles at any given locus contribute only a small amount to the inbreeding depression, the ratio of the mean fitnesses of selfed and outcrossed progeny is approximately

$$\bar{w}_1/\bar{w}_0 = \prod_{i=1}^{n} [\bar{w}_1(i)/\bar{w}_0(i)] = \exp\left\{-\sum_{i=1}^{n} \delta(i)\right\} \qquad (2)$$

where $\delta(i) = 1 - \bar{w}_1(i)/\bar{w}_0(i)$ is the inbreeding depression contributed by the ith locus (Crow, 1970).

For simplicity and concreteness, we initially analyze completely recessive lethal and sublethal mutations in a large population with mixed selfing and random mating. We then generalize this to partially dominant mutations under an arbitrary system of inbreeding.

Completely Recessive Lethals.—Let μ be the mutation rate from "wild type" allele A to the recessive lethal or sublethal allele a at a particular locus. Since the deleterious allele is kept rare by selection, reverse mutation can be neglected in comparison with forward mutation. The frequencies of the wild homozygote, the heterozygote, and the mutant homozygotes before selection are denoted as D, $2H$, and R, respectively, so that $D + 2H + R = 1$. The frequency of allele A in zygotes before selection is $p = D + H$, and that of the mutant allele a is $q = H + R$. The fitness of the recessive mutant homozygote is $1 - s$ in comparison with unity for the other genotypes.

Regardless of the mating system, the frequency of allele A after one generation of selection and mutation is

$$p' = (1 - \mu)p/(1 - sR).$$

At equilibrium $p' = p$ and the frequency of the recessive homozygote is

$$R = \mu/s. \qquad (3a)$$

At equilibrium between selection and mutation to recessive lethal and sublethal alleles, the mean fitness of genotypes at this locus, $1 - sR = 1 - \mu$, depends only on the mutation rate and not on the system of mating (Haldane, 1937).

In a large population reproducing by partial self-fertilization at the rate r, and outcrossing (by random mating) at a rate $1 - r$, the frequency of the dominant homozygote after one generation of selection and mutation is

$$D' = (1 - \mu)^2[r(D + H/2) + (1 - r)(D + H)^2/(1 - sR)]/(1 - sR).$$

At equilibrium $D' = D = 1 - 2H - R$ and using (3a) this yields a quadratic equation for H, which has the approximate solution

$$H = (1 - r)^{-1}\left\{-r/4 + \sqrt{(r/4)^2 + (1 - r)[r + (1 - r)/s]\mu}\right\}. \qquad (3b)$$

Under completely random mating ($r = 0$) this reduces to $H = \sqrt{\mu/s}$. Expression (3b) is quite accurate for any value of the selfing rate, but if r is greater than a few percent ($r \gg 4\sqrt{\mu/s}$) the following formula can be used.

$$H = 2\mu[1 + (1 - r)/rs]. \qquad (3c)$$

The mean fitness of genotypes at this locus among selfed progeny, weighted by the frequencies of parental genotypes after selection (neglecting new mutations), is

$$\bar{w}_1 = \{D + (1 - s/4)2H + (1 - s)^2R\}/(1 - sR),$$

which simplifies, using (3a), to approximately $1 - sH/2 - (1 - s)\mu$. In a randomly mating population at equilibrium, this gives

$$\bar{w}_1 = 1 - \sqrt{\mu s}/2 + O(\mu) \qquad (4a)$$

and for selfing rates greater than a few percent ($r \gg 4\sqrt{\mu/s}$) employing (3c) yields

$$\bar{w}_1 = 1 - \mu/r + O(\mu^2) \qquad (4b)$$

where the term $O(\cdot)$ gives the order of magnitude of the error in the expression.

Outcrossed progeny produced by random mating have genotypic frequencies in Hardy-Weinberg proportions, with a mean fitness at a particular locus of

$$\bar{w}_0 = 1 - sq^2 = 1 - s(H + R)^2.$$

At equilibrium under random mating $\bar{w}_0 = 1 - \mu$, whereas in a population with appreciable selfing ($r \gg 4\sqrt{\mu/s}$) at equilibrium

$$\bar{w}_0 = 1 + O(\mu^2). \qquad (5)$$

These formulae confirm that a small amount of selfing greatly reduces the equilibrium frequency of recessive lethal and sublethal mutations, and eliminates most of the inbreeding depression due to this cause. For example, with the per locus mutation rate $\mu = 2 \times 10^{-6}$ to recessive lethal mutations at 5,000 loci, the equilibrium inbreeding depression produced only by lethals in a randomly mating population is $\delta = .97$, whereas with partial selfing at the rate of 1% at equilibrium $\delta = .61$, with 5% selfing $\delta = .18$, with 10% selfing $\delta = .095$, and at equilibrium under complete selfing the amount of heterosis upon outcrossing is $\delta = .01$. The total inbreeding depression may be considerably larger than these values, particularly at the higher selfing rates, when the contributions of many genes with small effects on fitness are included.

Partially Dominant Lethals.—In contrast to completely recessive mutations in habitually outcrossing populations, partial dominance of homozygous lethal and sublethal mutations greatly decreases their equilibrium frequency, and also decreases the equilibrium inbreeding depression (Crow, 1970; Crow and Simmons, 1983). In this situation, lethal and sublethal homozygotes at each locus are so rare that most of the selective elimination of the mutant alleles occurs in heterozygotes.

The degree of dominance of a mutation affecting fitness is measured by the coefficient h, which gives the proportional expression of the mutant gene in heterozygotes in comparison with mutant homozygotes. The average degree of dominance of spontaneous lethal and sublethal mutations in populations of *Drosophila melanogaster* is about $h = .05$, and that for lethal and sublethal mutations segregating in natural populations is somewhat lower, about $h = .02$ due to stronger selection against the more dominant mutations (Crow and Simmons, 1983).

The amount of inbreeding in a population, caused by partial self-fertilization, mating between close relatives, and limited dispersal, can be measured by Wright's inbreeding coefficient, f, which gives the proportional reduction in heterozygosity in comparison with a random mating population with the same gene frequency (Wright, 1969 Ch. 7).

Genotype	Frequency	Fitness
AA	$D = fp + (1 - f)p^2$	1
Aa	$2H = 2(1 - f)pq$	$1 - hs$
aa	$R = fq + (1 - f)q^2$	$1 - s$

In outcrossing populations slightly dominant lethal and sublethal mutations are maintained at much lower frequencies than completely recessive mutations. Therefore, a small amount of inbreeding is not expected to have a drastic effect on decreasing the mutant gene frequency, or the inbreeding depression, until inbreeding is sufficiently common so that most of the mutant alleles are eliminated as homozygotes. This condition, $sR > hsH$, can be simply approximated for a rare mutant using the inbreeding formulae above as $f > h$. Thus a small amount of inbreeding should greatly decrease the equilibrium inbreeding depression due to slightly dominant lethal and sublethal mutations.

The frequency of the nearly dominant

wild type allele at a locus after one generation of selection and mutation is

$$p' = (1 - \mu)[D + (1 - sh)H]/(1 - 2hsH - sR).$$

Substituting the inbreeding formulae produces a quadratic equation for the equilibrium frequency of the mutant allele (Crow, 1970), which gives very nearly

$$q = [-\beta + \sqrt{\beta^2 + 4\alpha\mu/s}]/2 \quad (6a)$$

where $\beta = f + (1 - f)h$ and $\alpha = (1 - f)(1 - 2h)$. When there is appreciable dominance or inbreeding, $h + f \gg 2\sqrt{\mu/s}$, this becomes

$$q \cong \mu/\{s[f + (1 - f)h]\}. \quad (6b)$$

The mean fitness of genotypes at a locus among outcrossed progeny, assuming $h \gg 2\sqrt{\mu/s}$, approximates

$$\bar{w}_0 = 1 - 2hspq - sq^2 \cong 1 - 2hsq. \quad (7)$$

The mean fitness of genotypes at this locus among selfed progeny, weighted by the fitness of the parental genotypes (and neglecting new mutations) is

$$\bar{w}_1 = \frac{\left\{\begin{array}{c} D + [\frac{1}{4} + \frac{1}{2}(1 - sh) + \frac{1}{4}(1 - s)] \\ \cdot(1 - sh)2H + (1 - s)^2R \end{array}\right\}}{1 - 2hsH - sR}.$$

For a rare mutation, $H = (1 - f)q$ approximately, and

$$\bar{w}_1 \cong 1 - (1 + 2h)\cdot(1 - sh)sH/2 \cong 1 - (1 + 2h)\cdot(1 - sh)(1 - f)q/2. \quad (8)$$

Some caution is necessary in applying Wright's inbreeding coefficient, f, to lethal and sublethal mutations. This can be illustrated in the case of completely recessive mutations, under mixed selfing and random mating, where Wright's formula for the heterozygote frequency, with (3a) and (3c), yields the approximation

$$f = 1 - H/pq = R/(H + R) - H/(1 - H - R) \cong r/(2 - r + 2rs). \quad (9)$$

Under weak selection ($s \ll 1$) this formula for the inbreeding coefficient approximates that for a neutral gene, $f = r/(2 - r)$ (Wright, 1921, 1969 Ch. 7), but for recessive lethal mutations $f = r/(2 + r)$ which has a maximum value under complete selfing of $f = \frac{1}{3}$.

In populations with a low level of selfing, $r < .2$, the inbreeding coefficient is nearly $f = r/2$, regardless of the form of selection. In highly self-fertilizing populations, most of the selection on slightly dominant deleterious mutations occurs on homozygotes (if $f > h$); thus f should be nearly the same as for completely recessive mutations. For a deleterious mutation with slight dominance in a totally self-fertilizing population, with $f = 1/(1 + 2s)$, formulae (6b), (7) and (8) yield the approximations $\bar{w}_0 = 1 - 2(1 + 2s)h\mu/(1 + 2hs)$ and $\bar{w}_1 = 1 - \mu(1 - hs)\cdot(1 + 2h)/(1 + 2hs)$.

These approximations for a totally selfing population can be checked against the more accurate recursion equations for slightly dominant deleterious mutations in Ohta and Cockerham (1974), which, however, are accurate only for populations with a high selfing rate. In a totally selfing population the equilibrium values are $H = 2\mu/(1 + hs)$ and $R = (\mu/s)(1 - hs)/(1 + hs)$. Substituting $q = H + R$ into (7) and calculating the mean fitness in the population reveals that, for slightly dominant deleterious mutations ($h \ll 1$) in a totally selfing population, the two methods of approximation are in close agreement:

$$\bar{w}_0 = 1 - 2(1 + 2s)h\mu + O(\mu h^2) \quad (10a)$$

$$\bar{w}_1 = 1 - (1 + 2hs)\mu + O(\mu h^2) \quad (10b)$$

For a numerical example, consider a population under mixed selfing and random mating with 5,000 loci mutating to

slightly dominant lethal alleles at the rate of 2×10^{-6} per locus per generation with $h = .02$. In a randomly mating population, the inbreeding depression at equilibrium is $\delta = .21$, whereas with partial selfing at the rate of 1% the equilibrium inbreeding depression is $\delta = .17$, with 5% selfing $\delta = .10$, with 10% selfing $\delta = .06$, and at equilibrium under complete selfing the heterosis upon outcrossing is roughly $\delta = .01$.

In comparison with the previous numerical example of completely recessive mutations, partial dominance of deleterious mutations in a random mating population greatly decreases the equilibrium inbreeding depression. This example also confirms that with slightly dominant lethals, inbreeding has little effect in reducing the equilibrium inbreeding depression until the inbreeding coefficient exceeds the dominance of the mutant alleles.

Even a small amount of variation in the level of dominance among different lethal-producing loci can substantially increase the inbreeding depression in a large outcrossing population. From the preceding equations (1), (2), (6b) and (7), at equilibrium under random mating, the total inbreeding depression due to slightly dominant lethals depends on the average value of μ/h, and, if the mutation rate is the same for all n loci we have approximately $\delta = 1 - \exp\{-n\mu/2\tilde{h}\}$ where $\tilde{h}$ is the harmonic mean of h, which is always less than or equal to the arithmetic mean, $\bar{h}$. For example, with 5,000 loci mutating to slightly dominant lethals at a per locus rate of $\mu = 2 \times 10^{-6}$ with $\bar{h} = .02$ and enough variation in the level of dominance so that $\tilde{h} = .01$, in a randomly mating population the equilibrium inbreeding depression is approximately $\delta = .39$. This can be compared with value of $\delta = .21$ previously calculated for the same parameters except with no variance in h. Therefore, allowing for variation in the level of dominance of lethal and sublethal mutations, in addition to the influence of quantitative variation caused by mutation at numerous loci with small effects on fitness, the total inbreeding depression may often exceed 50% in large, historically outcrossing populations. Including all mutations with major or minor effects on fitness, the equilibrium level of the total inbreeding depression may not fall below the critical value of about 50% until the selfing rate in a population exceeds several percent.

Quantitative Variation in Fitness.—We next investigate a simple model of inbreeding depression and heterosis produced by stabilizing selection on quantitative characters, such as growth form, leaf shape, and floral morphology. On the primary character scale, all of the genetic variation is assumed to be additive and to be maintained by polygenic mutation and recombination. In a model of this type for a single character, Wright (1935) showed that on the fitness scale substantial dominance and epistatic genetic interactions are produced by the nonlinear relation of the character with fitness.

Weak stabilizing selection on a quantitative character, z, toward an optimal phenotype, θ, can be approximated by the quadratic fitness function

$$w(z) = 1 - k(z - \theta)^2, \qquad (11a)$$

in which k is a constant measuring the strength of selection. The mean fitness with regard to this character in a population (or subpopulation) is given by Wright (1935) as

$$\bar{w} = 1 - k[G + E + (\bar{z} - \theta)^2] \qquad (11b)$$

where G and E are, respectively, the additive genetic and environmental components of the total phenotypic variance in the character. The mean phenotypes are the same in the selfed and outcrossed progeny groups, since all of the genetic variance is additive. Assuming that the environmental variances are equal in the two groups, the relative fitnesses of selfed and outcrossed progeny, with respect to this character, depend only on the strength of stabilizing selection and on the differ-

ence in additive genetic variance in the two groups,

$$\delta = 1 - \bar{w}_1/\bar{w}_0 \cong k(G_1 - G_0). \quad (12)$$

This expression also holds if the optimum phenotype fluctuates in time. The heterosis or inbreeding depression produced by many independent characters is approximately $\delta = 1 - \exp\{-\sum_j \delta(j)\}$, where $\delta(j)$ is the inbreeding depression due to the jth character.

In a population with an inbreeding coefficient f, there is a correlation of f between effects of uniting gametes on any character (Wright, 1921, 1969 Ch. 7). Therefore the component of the genetic variance within both gametes is $G/(1 + f)$, and that between gametes is $Gf/(1 + f)$, which sum to G. The additive genetic variance in the character among randomly outcrossed progeny is

$$G_0 = G/(1 + f).$$

Under weak selection, the inbreeding coefficient of selfed progeny is approximately $f' = (1 + f)/2$ (Wright, 1921, 1969 Ch. 7), and the additive genetic variance among them is

$$G_1 = (1 + f')G/(1 + f).$$

The difference in additive genetic variance of the character in selfed and outcrossed progeny is

$$G_1 - G_0 = f'G/(1 + f) = G/2. \quad (13)$$

In a model of mutation with a wide range of possible allelic effects on a quantitative trait at each locus and a constant input of additive genetic variance each generation, the genetic variance in the character maintained under stabilizing selection, G, is independent of the mating system, which only redistributes the total expressed genetic variance within and between uniting gametes (Lande, 1977).

For this model of selection on quantitative traits, (12) and (13) show that the inbreeding depression caused by selfing in an habitually outcrossing population is approximately equal to the heterosis upon outcrossing in an habitually selfing population. Data from *Drosophila* indicate that the inbreeding depression due to quantitative variation among genotypes with quasinormal fitnesses is often in the range of 20% to 30% or more (Simmons and Crow, 1977). This property of the model helps to explain the persistence of considerable heterosis in predominantly self-fertilizing populations, without the need for invoking a general heterozygote advantage, for which there is little evidence (Lewontin, 1974). In this context, it is worth noting that one-locus polymorphisms maintained by heterozygote advantage in outcrossing populations cannot be maintained in predominantly self-fertilizing populations except in the improbable situation where the fitnesses of the homozygous genotypes are nearly equal (Nagylaki, 1977 p. 56–58).

If multivariate selection acts to correlate different characters (Lande and Arnold, 1983), continued inbreeding can increase the magnitude of their genetic correlation, increasing the mean fitness and decreasing the inbreeding depression in the population (Lande, 1984). But this would not alter the conclusion that substantial quantitative genetic variation and inbreeding depression (or heterosis) can be maintained even in a highly selfing population. This theoretical result is supported by evidence of a great deal of heritable variation in quantitative traits within populations in primarily selfing species (Allard et al., 1968).

Inbreeding Depression in Polyploid Species.—In many families of higher plants, a large proportion of the species are polyploid, having usually arisen by doubling of the chromosomes (Stebbins, 1950; Burnham, 1962). To assess the relative likelihood that polyploid species are selected for self-fertilization, we compare the theoretical inbreeding depression maintained in predominantly outcrossing diploid and tetraploid species. The Appendix shows that tetraploidy substantially reduces the inbreeding depression due to largely recessive lethal and sublethal mutations, assuming the spon-

taneous mutation rates are the same as in the ancestral diploid(s). Judging from the *Drosophila* data, where most of the inbreeding depression is produced by lethal and sublethal mutations, it appears that, contrary to a statement by Bennett (1976), tetraploidy generally reduces the total inbreeding depression at equilibrium and hence increases the likelihood of selection for self-fertilization. Because self-compatibility is necessary for the evolution of self-fertilization it is of interest to note that tetraploidy usually results in the physiological breakdown of gametophytic self-incompatibility in dicots, but not in monocots (de Nettancourt, 1977 p. 113–115), and allopolyploids originating from a single plant must initially have been self-compatible, if not self-fertilizing to a considerable degree (Burnham, 1962).

Nonequilibrium Models of Inbreeding Depression

Evolution of a Gene for Complete Selfing.—In the absence of inbreeding depression, Fisher (1941) showed that a single semidominant gene causing complete self-fertilization without diminishing pollen dispersal would rapidly sweep through a population. Nagylaki (1976) generalized this result by proving that a partially dominant gene for increased selfing, which does not entirely eliminate pollen output, would eventually be fixed if there is no inbreeding depression. However, virtually every natural population displays the complementary effects of inbreeding depression and heterosis (Wright, 1977). As we have seen above, in an initially outcrossing population the evolution of selfing by small genetic steps is prevented by an inbreeding depression of 50% or more. In contrast with the prevailing view (e.g., Maynard Smith, 1978 p. 125–130), we will now argue that a single gene which causes complete selfing when homozygous, without eliminating pollen dispersal, will increase in frequency in an initially outcrossing population, regardless of the amount of inbreeding depression.

A single gene causing complete self-fertilization when homozygous creates a subpopulation composed of purely selfing lineages. In an initially outcrossing population with a large inbreeding depression, the majority of completely selfing lines may become extinct, but if the gene for total selfing is continually reintroduced into the population by spontaneous mutation at a low rate, eventually a line of selfers will be established which has purified itself of most of the inbreeding depression due to recurrent lethal and sublethal mutations.

A completely selfing lineage is closed to gene flow from the outside, although it may continue to disperse pollen which can fertilize the ovules of outcrossers in the same population. To determine whether a rare line of complete selfers will increase in frequency in an initially outcrossing population, it is therefore sufficient to demonstrate that the mean fitness in a closed population of selfers is at least as large as that in a totally outcrossing population at equilibrium under mutation and selection.

For a locus mutating to fully recessive deleterious alleles at a rate μ, the mean fitness of genotypes at equilibrium is $1 - \mu$ independent of the system of mating in a population (Haldane, 1937). If the deleterious alleles have appreciable dominance, the mean fitness of genotypes in an outcrossing population at equilibrium is approximately $1 - 2\mu$ (Muller, 1950; Crow, 1970), which is clearly less than the value of $1 - (1 + 2hs)\mu$ for a completely selfing population (10b). With respect to quantitative variation, in the one-character model described above the mean fitness in a population at mutation-selection equilibrium is nearly independent of the mating system, and when selection acts to correlate characters inbreeding can increase the mean fitness. Qualitatively similar arguments apply to the evolution of selfing in tetraploid populations.

Thus the eventual fitness from seed in a completely selfing lineage is greater than or equal to the total fitness from seed and

pollen in an habitually outcrossing population. A rare selfing genotype in an outcrossing population will gain an additional advantage from the dispersal of pollen that may be accepted by outcrossers, which will then segregate more selfing genotypes. A rare major gene for complete self-fertilization will therefore eventually increase in frequency in an initially outcrossing population, regardless of the amount of inbreeding depression. It also seems likely that such a gene would proceed to fixation, although this has not been demonstrated.

In view of the above conclusion, the existence of many plant species which are predominantly outcrossing implies that (1) single genes causing complete selfing do not arise in most species, or (2) if they do occur they have a strong intrinsic disadvantage beyond that produced by increasing homozygosity at other loci, or (3) predominantly selfing lineages speciate less often or become extinct more rapidly on average than outcrossing species. This last possibility is consistent with evidence that selfing species are usually evolved from outcrossers (Stebbins, 1957).

Jain (1976) has reviewed the genetic basis of variation in plant breeding systems. In species with gametophytic self-incompatibility mechanisms, single gene mutations conferring self-compatibility do occur (Jain, 1976; Charlesworth and Charlesworth, 1979*b*), although self-compatibility does not necessarily imply a high rate of self-fertilization. Polygenic influences on the selfing rate have been reported in several species (Jain, 1976). In self-compatible species, the selfing rate is usually subject to modification by mutations in quantitative characters such as the degree of protandry (Arroyo, 1973; Schoen, 1982) and floral traits which influence pollen dispersal by physical agencies and pollinators (e.g., Rick et al., 1977; Ennos, 1981).

Rate of Accumulation of Inbreeding Depression.—Many species are subject to sporadic environmental perturbations which can substantially alter the level of inbreeding and the amount of inbreeding depression. Extreme reduction in population size can sharply increase homozygosity, selecting against deleterious recessive mutations and reducing inbreeding depression in subsequent generations. In plant species where any ovules not outcrossed tend to be selfed, partial failure of physical or biotic pollinating agents could have a similar effect. After such an episode, a large outcrossing population may require many generations to accumulate the equilibrium level of inbreeding depression by mutation. If extreme population crashes or substantial failure of pollinators tend to recur on a time scale shorter than that necessary for the achievement of an equilibrium between mutation and selection, the average inbreeding depression may be reduced sufficiently to favor the evolution of a highly self-fertilizing mode of reproduction.

In a large outcrossing population, partial failure of pollinating agents, such that a proportion r of the ovules are self-fertilized during one generation, reduces the frequency of completely or nearly recessive lethal and sublethal mutations, and hence the corresponding component of inbreeding depression, by a fraction $r/2$. Reduction of population size to a few breeding individuals increases homozygosity, selecting against largely recessive deleterious lethal and sublethal mutations and reducing their frequency by a fraction of about $1/2N_e$, where N_e is the effective number of breeding individuals in the population (Wright, 1969 Ch. 8). Thus a single generation of pollinator failure, or an extreme population crash, can substantially reduce the inbreeding depression due to largely recessive lethal and sublethal mutations.

For quantitative (polygenic) characters under stabilizing selection, a single generation of pollinator failure would have relatively little effect on the amount of additive genetic variance maintained or on the associated component of inbreeding depression (cf. Lande, 1977 and above). One generation of reduced population size would reduce the additive genetic variance of a quantitative trait,

and the associated inbreeding depression, by a fraction of $1/2N_e$ (Lande, 1980 and above).

After a rapid depletion of inbreeding depression due to a partial failure of pollinating agents or a severe population crash, the restoration of a large outcrossing population structure will lead to the accumulation of different types of mutations contributing to inbreeding depression. The time scales for equilibration of the different components of inbreeding depression in a large outcrossing population can be derived as follows.

For a locus mutating to completely recessive lethal or sublethal alleles at a rate $\mu \ll s$, in a large randomly mating population the frequency of the rare mutant allele, $q \ll 1$, obeys the approximate equation $dq/dt = -sq^2 + \mu$. Starting from a monomorphic population of nonmutants the frequency of the mutant allele at generation t is given by

$$q(t) = \sqrt{\mu/s}[1 - 2/(1 + \exp\{2\sqrt{\mu s}\, t\})].$$

The time scale for this process is a few times $1/(2\sqrt{\mu s})$ generations, as shown by Nagylaki (1977 p. 94). Using typical mutation rates to recessive lethal and sublethal alleles, $\mu = 2 \times 10^{-6}$ and $s = 1$, the equilibration time is on the order of several hundred generations.

For slightly dominant mutations which are lethal or sublethal as homozygotes but selected against mainly as heterozygotes, with $\mu \ll hs$, in a random mating population the frequency of the rare mutant allele changes approximately as $dq/dt = -hsq + \mu$. In an initially monomorphic population the solution

$$q(t) = (\mu/hs)[1 - \exp\{-hst\}]$$

shows that the time scale for equilibration, a few times $1/hs$ generations, is independent of the mutation rate. With typical values of partial dominance of lethal and sublethal mutations, $h = .02$, this time scale is on the order of 100 generations. This is equivalent to the mean "persistence time" or average number of generations that new lethal mutations survive before they are eliminated by selection (Muller, 1950; Crow and Simmons, 1983).

Rates of production of additive genetic variance per generation in quantitative characters are typically about 10^{-3} times as large as the environmental variance which would be expressed among individuals of the same genotype (Lande, 1975). With weak stabilizing selection, involving selective mortality of a few percent per character per generation, normal levels of heritable variation can be accumulated within a few hundred to a thousand generations in a predominantly outcrossing population (Lande, 1977, 1980).

Therefore if a population which is usually large and habitually outcrossing experiences a severe failure of pollinating agents, or undergoes a drastic reduction in population size, more often than about once every 100 generations, the inbreeding depression will often be substantially lower than the equilibrium level achieved in a continuously large outcrossing population. Sporadic pollinator failure and/or population bottlenecks on a time scale of less than roughly 100 generations therefore will tend to promote selection for a highly self-fertilizing mode of reproduction.

Discussion

Genetic models of inbreeding depression produced by the accumulation of nearly recessive lethal and sublethal mutations, in addition to mutation in quantitative characters, can explain most of the classical observations on inbreeding depression and heterosis. These include potentially very large amounts of inbreeding depression in historically large outcrossing populations, due in large part to (nearly) recessive lethals, as well as considerable heterosis in predominantly self-fertilizing populations. The models indicate that continued selfing at a rate of a few to several percent eliminates most of the inbreeding depression produced by recessive lethal and semilethal mutations; this could also occur through sporadic failure of pollinating agents or ex-

treme population bottlenecks occurring more often than once every 100 generations. However, even under high levels of selfing, considerable heterosis upon outcrossing can be created by stabilizing selection on quantitative traits in which genetic variation is maintained by polygenic mutation.

Other mechanisms which could theoretically contribute to inbreeding depression either have received alternative explanations or are conspicuously lacking in empirical support. For example, the developmental instability of inbred lines compared with their F_1 hybrids, advocated by Lerner (1954) as a major cause of heterosis, has been explained in part as a statistical artifact resulting from zones of phenotypic canalization around an optimum phenotype, for which there is considerable evidence (Lande, 1980). The association within populations between homozygosity at electrophoretic marker loci and increased variance in quantitative traits (and decreased fitness) observed by Mitton (1978), Eanes (1978), Zouros et al. (1980), and Fleischer et al. (1983), could be attributable to partial inbreeding which simultaneously increases genotypic variance (as in eq. 13) and decreases fitness of the most homozygous subgroup in a population. There is little evidence for a general heterozygote advantage at a single loci (Lewontin, 1974), and observed amounts of polygenic mutation appear capable of maintaining much of the heritable variation in quantitative characters, even in highly selfing populations (Lande, 1975, 1977, 1984; Turelli, 1984).

The present genetic models of inbreeding depression suggest that, when the selfing rate in a population is under polygenic control and evolves by small steps, there are two possible stable states for the mating system: predominantly outcrossing or highly self-fertilizing. In some cases, single gene mutations causing nearly complete selfing may have been fixed in outcrossing populations despite an initially high inbreeding depression (e.g., Gottlieb, 1973). Thus the models predict that among species where the selfing rate is largely under genetic control and is not subject to tremendous environmental variation, there should be a bimodal distribution of selfing rates. To test this prediction we compiled data from the literature on estimates of outcrossing rates ($t = 1 - r$) in natural populations obtained using genetic markers (Schemske and Lande, 1985). These data show a strongly bimodal distribution of outcrossing rates estimated from 55 plant species. Despite several possible sources of error in the estimates, the data indicate that most species are either primarily outcrossing ($t > .8$) or primarily selfing ($t < .2$). Detailed examination of these data also disclosed that the bimodality of outcrossing rates is apparent within plant families, and even within certain genera.

The present genetic models of inbreeding depression further suggest that highly self-fertilizing species can evolve much more readily from predominantly outcrossing species than vice versa. This follows from the fact that predominantly outcrossing species are susceptible to failure of pollinating agents and to population crashes, which can directly increase the level of selfing (and other inbreeding) or select for a breakdown of self-incompatibility mechanisms; such events occurring on a time scale of once every hundred generations or less would purify a population of most of the inbreeding depression due to (nearly) recessive lethal and semilethal mutations, which could then lead to selection for a high rate of selfing. In contrast, a population with a history of predominant self-fertilization and a relatively low inbreeding depression can not accumulate recessive lethal and semilethal mutations to restore a high level of inbreeding depression and to select for a high rate of outcrossing, even if the population achieves and maintains a large size. Thus predominant outcrossing is subject to environmental conditions which can cause the evolution of selfing, and a highly selfing population can not readily revert to outcrossing. This conclusion agrees with the finding of

Stebbins (1957) that highly selfing species have generally evolved from predominant outcrossers. Since self-fertilization is an effective barrier to gene flow, the evolution of highly selfing populations may promote speciation in some plant taxa. However, the present theory does not support the notion that predominant selfing is necessarily an evolutionary dead end, since the amount of quantitative genetic variation maintained in a large population, and which is available for adaptive evolution, is expected to be substantial even in a highly selfing population.

Our survey of the literature also revealed six plant species with extremely variable estimates of outcrossing rates in different populations (Schemske and Lande, 1985). In part, the extreme variation in selfing rates in these species may reflect a greater effort made in studying them in a range of localities, but this is unlikely to be the entire explanation. The most important factor apparently is an extreme susceptibility to environmental influences on the selfing rate, due to wide variation in the ratio of pollinator and plant densities among populations (Horovitz and Harding, 1972). Other factors which may be involved are sampling error in estimates based on a small number of parent plants per population, insufficient time for closely related populations to evolve to alternative equilibria, and gene flow between populations preventing the achievement of these equilibria.

There are two additional mechanisms, not incorporated in the models, which help to explain why all species are not either completely selfing or completely outcrossing, i.e., group selection (Stebbins and Jain, pers. comm.) and reproductive compensation. In a predominantly selfing species, with a total inbreeding depression less than about 50%, individual selection within local populations favors complete selfing, but with repeated colonization of new areas, the more heterotic (outbred) individuals may gain an advantage in the founding of new populations. Partially outcrossing populations may also be more adaptable to changing environmental conditions, by generating a greater diversity of genotypes through segregation and recombination, especially if the effective size of local populations is small. In predominantly outcrossing populations, reproductive compensation can occur by seed or fruit abortion, or by sibling competition at or before the seedling stage, which selectively eliminates most of the selfed progeny without decreasing total productivity. The capacity for reproductive compensation in most species is limited, such that plants with a low selfing rate may almost perfectly compensate for zygotic wastage, but plants with relatively high selfing rates can not and suffer substantial inbreeding depression (>50% for exclusively selfed plants). In this situation a high total frequency of nearly recessive lethal mutations can be maintained in large populations and selection will preserve the predominantly outcrossing mode of reproduction. Limited reproductive compensation of this type has been described for conifers by Sorensen (1982), and for ferns by Klekowski (1982, 1984).

Acknowledgments

We thank B. and D. Charlesworth, J. F. Crow, D. G. Lloyd, and T. Nagylaki for discussions and criticisms of the manuscript. This work was supported by U.S. Public Health Service grant GM27120 to R. Lande and National Science Foundation grant DEB822186 to D. W. Schemske.

Literature Cited

Allard, R. W., S. K. Jain, and P. L. Workman. 1968. The genetics of inbreeding populations. Adv. Genet. 14:55–131.

Antonovics, J. 1968. Evolution in closely adjacent plant populations. V. Evolution of self-fertility. Heredity 23:219–238.

Arroyo, M. T. K. 1973. Chiasma frequency evidence on the evolution of autogamy in *Limnanthes floccosa* (Limnanthaceae). Evolution 27:679–688.

Bennett, J. H. 1976. Expectations for inbreeding depression on self-fertilization of tetraploids. Biometrics 32:449–452.

Brown, A. H. D. 1979. Enzyme polymorphism

in plant populations. Theoret. Pop. Biol. 15:1–42.

BURNHAM, C. R. 1962. Discussions in Cytogenetics. Burgess, Minneapolis.

CHARLESWORTH, B. 1980. The cost of sex in relation to mating system. J. Theoret. Biol. 84: 655–671.

CHARLESWORTH, B., AND D. CHARLESWORTH. 1979a. The evolutionary genetics of sexual systems in flowering plants. Proc. Roy. Soc. London B 205:513–530.

CHARLESWORTH, D., AND B. CHARLESWORTH. 1979b. The evolution and breakdown of S-allele systems. Heredity 43:41–55.

CHRISTIANSEN, F. B., AND O. FRYDENBERG. 1977. Selection-mutation balance for two nonallelic recessives producing an inferior double homozygote. Amer. J. Hum. Genet. 29:195–207.

CROW, J. F. 1952. Dominance and overdominance, p. 282–297. *In* J. W. Gowen (ed.), Heterosis. Iowa State College Press, Ames.

———. 1970. Genetic loads and the cost of natural selection, p. 128–177. *In* K. Kojima (ed.), Mathematical Topics in Population Genetics. Springer-Verlag, N.Y.

CROW, J. F., AND M. J. SIMMONS. 1983. The mutation load in *Drosophila,* p. 1–35. *In* M. Ashburner et al. (eds.), The Genetics and Biology of *Drosophila,* Vol. 3c. Academic Press, N.Y.

CRUMPACKER, D. W. 1967. Genetic loads in maize (*Zea mays* L.) and other cross-fertilized plants and animals. Evol. Biol. 1:1–131.

EANES, W. 1978. Morphological variance and enzyme heterozygosity in the monarch butterfly. Nature 276:263–264.

ENNOS, R. A. 1981. Quantitative studies of the mating system in two sympatric species of *Ipomoea* (Convolvulaceae). Genetica 57:93–98.

FISHER, R. A. 1935. The sheltering of lethals. Amer. Natur. 69:446–455.

———. 1941. Average excess and average effect of a gene substitution. Ann. Eugen. 11:53–63.

———. 1949. The Theory of Inbreeding. Oliver and Boyd, London.

FLEISHER, R. C., R. F. JOHNSTON, AND W. J. KLITZ. 1983. Allozymic heterozygosity and morphological variation in house sparrows. Nature 304: 628–630.

FRANKEL, R. (ed.). 1983. Heterosis: Reappraisal of Theory and Practice. Springer-Verlag, N.Y.

FRANKHAM, R. 1982. Contributions of *Drosophila* research to quantitative genetics and animal breeding. Proc. 2nd World Congress on Genetics Applied to Livestock Production 5:43–56.

FRANKLIN, E. C. 1972. Genetic load in loblolly pine. Amer. Natur. 106:262–265.

GARDNER, C. O. 1978. Population improvement in maize, p. 207–228. *In* D. B. Walden (ed.), Maize Breeding and Genetics. Wiley, N.Y.

GOTTLIEB, L. D. 1973. Genetic differentiation, sympatric speciation, and the origin of diploid species of *Stephanomeria.* Amer. J. Bot. 60:545–553.

GRIFFING, B., AND J. LANGRIDGE. 1963. Phenotypic stability of growth in the self-fertilized species, *Arabidopsis thaliana,* p. 363–394. *In* W. F. Hanson and H. F. Robinson (eds.), Statistical Genetics and Plant Breeding. Nat. Acad. Sci.—Nat. Res. Council, Wash., D.C.

HALDANE, J. B. S. 1937. The effect of variation on fitness. Amer. Natur. 71:337–349.

———. 1949. The association of characters as a result of inbreeding and linkage. Ann. Eugen. 15:15–23.

HOROVITZ, A., AND J. HARDING. 1972. Genetics of *Lupinus.* V. Intraspecific variability for reproductive traits in *Lupinus nanus.* Bot. Gaz. 133:155–165.

JAIN, S. K. 1976. The evolution of inbreeding in plants. Ann. Rev. Ecol. Syst. 7:469–495.

JINKS, J. L. 1983. Biometrical genetics of heterosis, p. 1–46. *In* R. Frankel (ed.), Heterosis: Reappraisal of Theory and Practice. Springer-Verlag, N.Y.

KLEKOWSKI, E. J., JR. 1982. Genetic load and soft selection in ferns. Heredity 49:191–197.

———. 1984. Mutational load in clonal plants: a study of two fern species. Evolution 38:417–426.

LANDE, R. 1975. The maintenance of genetic variability by mutation in a polygenic character with linked loci. Genet. Res. 26:221–235.

———. 1977. The influence of the mating system on the maintenance of genetic variability in polygenic characters. Genetics 86:485–498.

———. 1980. Genetic variation and phenotypic evolution during allopatric speciation. Amer. Natur. 116:463–479.

———. 1984. The genetic correlation between characters maintained by selection, linkage, and inbreeding. Genet. Res. *In press.*

LANDE, R., AND S. J. ARNOLD. 1983. The measurement of selection on correlated characters. Evolution 37:1210–1226.

LERNER, I. M. 1954. Genetic Homeostasis. Oliver and Boyd, London.

LEWONTIN, R. C. 1974. The Genetic Basis of Evolutionary Change. Columbia Univ. Press, N.Y.

LLOYD, R. M. 1974. Mating systems and genetic load in pioneer and non-pioneer Hawaiian Pteridophyta. Bot. J. Linn. Soc. 69:23–35.

LLOYD, D. G. 1979. Some reproductive factors affecting the selection of self-fertilization in plants. Amer. Natur. 113:67–97.

MAYNARD SMITH, J. 1978. The Evolution of Sex. Cambridge Univ. Press, Cambridge.

MAYO, O. 1971. Rates of change in gene frequency in tetrasomic organisms. Genetica 42:329–337.

———. 1980. The Theory of Plant Breeding. Oxford Univ. Press, Oxford.

MITTON, J. B. 1978. Relationship between heterozygosity for enzyme loci and variation of

morphological characters in natural populations. Nature 273:661–662.
MULLER, H. J. 1950. Our load of mutations. Amer. J. Hum. Genet. 2:111–176.
NAGYLAKI, T. 1976. A model for the evolution of self-fertilization and vegetative reproduction. J. Theoret. Biol. 58:55–58.
———. 1977. Selection in One- and Two-Locus Systems. Springer-Verlag, N.Y.
DE NETTANCOURT, D. 1977. Incompatibility in Angiosperms. Springer-Verlag, N.Y.
OHTA, T., AND C. C. COCKERHAM. 1974. Detrimental genes with partial selfing and effects on a neutral locus. Genet. Res. 23:191–200.
RICK, C. M., J. F. FOBES, AND M. HOLLE. 1977. Genetic variation in *Lycopersion pimpinellifolium*: evidence for evolutionary change in mating systems. Plant Syst. Evol. 127:139–170.
SCHEMSKE, D. W. 1983. Breeding system and habitat effects on fitness components in three neotropical *Costus* (Zingiberaceae). Evolution 37: 523–539.
SCHEMSKE, D. W., AND R. LANDE. 1985. The evolution of self-fertilization and inbreeding depression in plants. II. Empirical observations. Evolution 39:41–52.
SCHOEN, D. J. 1982. The breeding system of *Gilia achilleifolia*: variation in floral characteristics and outcrossing rate. Evolution 36:352–360.
———. 1983. Relative fitness of selfed and outcrossed progeny in *Gilia achilleifolia* (Polemoniaceae). Evolution 37:292–301.
SIMMONS, M. J., AND J. F. CROW. 1977. Mutations affecting fitness in *Drosophila* populations. Ann. Rev. Genet. 11:49–78.
SORENSEN, F. 1969. Embryonic genetic load in coastal Douglas-fir, *Pseudotsuga menziesii* var. *menziesii*. Amer. Natur. 103:389–398.
———. 1982. The roles of polyembryony and embryo vitality in the genetic system of conifers. Evolution 36:725–733.
SORENSEN, F., J. F. FRANKLIN, AND R. WOOLLARD. 1976. Self-pollination effects on seed and seedling traits in noble fir. Forest Sci. 22:155–159.
SPRAGUE, G. F. 1983. Heterosis in maize: theory and practice, p. 47–70. *In* R. Frankel (ed.), Heterosis: Reappraisal of Theory and Practice. Springer-Verlag, N.Y.
STEBBINS, L. G. 1950. Variation and Evolution in Plants. Columbia Univ. Press, N.Y.
———. 1957. Self fertilization and population variability in the higher plants. Amer. Natur. 91:337–354.
TURELLI, M. 1984. Heritable genetic variation via mutation selection balance: Lerch's zeta meets the abdominal bristle. Theoret. Pop. Biol. 25: 138–193.
WEIR, B. S., AND C. C. COCKERHAM. 1973. Mixed self and random mating at two loci. Genet. Res. 21:247–262.
WELLS, H. 1979. Self-fertilization: advantageous or deleterious? Evolution 33:252–255.
WRIGHT, S. 1921. Systems of mating. II. The effects of inbreeding on the genetic composition of a population. Genetics 6:124–143.
———. 1935. The analysis of variance and the correlations between relatives with respect to deviations from an optimum. J. Genet. 30:243–256.
———. 1969. Evolution and the Genetics of Populations, Vol. 2. The Theory of Gene Frequencies. Univ. Chicago Press, Chicago.
———. 1977. Evolution and the Genetics of Populations, Vol. 3. Experimental Results and Evolutionary Deductions. Univ. Chicago Press, Chicago.
ZOUROS, E., S. M. SINGH, AND H. E. MILES. 1980. Growth rate in oysters: an overdominant phenotype and its possible explanations. Evolution 34:856–867.

Corresponding Editor: S. G. Weller

APPENDIX

Consider first an allotetraploid species with duplicate loci having wild type alleles A_1 and A_2 mutating to deleterious alleles a_1 and a_2 which are recessive and epistatic such that only the double mutant homozygote $a_1a_1a_2a_2$ is selected against. Letting the fitness of this genotype be $1 - s$ in comparison to a fitness of unity for the other genotypes and assuming that the loci are unlinked, in a randomly mating population there is approximate linkage equilibrium, and the frequencies of the wild type alleles at the two loci obey the equations

$$p_i' = (1 - \mu_i)p_i[1 - sq_1^2q_2^2]^{-1} \qquad \text{for } i = 1, 2$$

(Fisher, 1935; Christiansen and Frydenberg, 1977). Because the term in brackets is the same for both loci, the ratio of the gene frequencies p_1/p_2 changes by the factor $(1 - \mu_1)/(1 - \mu_2)$ each generation. Any difference in mutation rates at the two loci will eventually lead to fixation of the mutant allele at the locus with the higher mutation rate, and the system will revert in effect to diploidy. In the case of equal mutation rates at the two loci, $\mu_1 = \mu_2 = \mu$, an equilibrium of mutation and selection can occur at any combination of gene frequencies such that $q_1^2q_1^2 = \mu/s$. A new allotetraploid population is most likely to have arisen from a single plant with the genotype $A_1A_1A_2A_2$ since the mutant alleles at each locus in the diploid parental species are kept rare by selection. If in addition a large population size is attained before many mutations have occurred, the mutant alleles will be nearly equal in frequency at both loci, and at equilibrium

$$q_1 = q_2 = (\mu/s)^{1/4}$$

(Fisher, 1935; Christiansen and Frydenberg, 1977). At equilibrium the mean fitness (of outcrossed progeny) is $\bar{w}_0 = 1 - \mu$. Among selfed progeny the

great majority of double mutant homozygotes are produced by doubly heterozygous parents, hence $\bar{w}_1 = 1 - \sqrt{\mu s}/4$. The equilibrium inbreeding depression due to lethal and sublethal mutations at duplicate loci is about half that for completely recessive deleterious mutations at a single locus (4a).

For incompletely recessive deleterious mutations at duplicate loci, the fitnesses of the genotypes can be represented as

	A_1A_1	A_1a_1	a_1a_1
A_2A_2	1	$1 - h_1s$	$1 - 2h_1s$
A_2a_2	$1 - h_2s$	$1 - (h_1 + h_2)s$	$1 - (2h_1 + h_2)s$
a_2a_2	$1 - 2h_2s$	$1 - (h_1 + 2h_2)s$	$1 - s$.

If most of the mutant alleles are eliminated as heterozygotes, their equilibrium frequencies are approximately $q_1 = \mu_1/h_1s$ and $q_2 = \mu_2/h_2s$. The mean fitness of outcrossed progeny is nearly $\bar{w}_0 = 1 - 2(\mu_1 + \mu_2)$ and that of selfed progeny is

$$\begin{aligned}\bar{w}_1 &= 1 - 2(\mu_1 + \mu_2) \\ &\quad - (1 - 2h_1 - 2h_2)\mu_1\mu_2/4sh_1h_2 \\ &= \bar{w}_0 + O(\mu_1\mu_2).\end{aligned}$$

Therefore the inbreeding depression due to partially dominant delterious mutations at duplicate loci in an allotetraploid population is negligible.

In an autotetraploid population under random mating the equilibrium frequency of a completely recessive lethal or sublethal mutation at a locus close to the centromere is approximately $q = (\mu/s)^{1/4}$ (Mayo, 1971) and the inbreeding depression is essentially the same as with allotetraploidy. Loci which are not tightly linked to the centromere in autotetraploids undergo a significant fraction of double reduction, such that the genotype *AAAa* produces some aa gametes in addition to *AA* and *Aa*. This somewhat reduces the equilibrium frequency of the deleterious allele *a* and also diminishes the inbreeding depression in comparison to that due to loci close to the centromere. Double reduction also reduces the inbreeding depression due to loci with incompletely recessive deleterious mutations.

The influence of allotetraploidy on the component of inbreeding depression caused by quantitative variation differs from that produced by lethal and sublethal mutations. Assume that there is dosage compensation such that the mean values of the characters are unchanged, and each allele has half the effect in the allotetraploid as in the diploid. If the mutation rates of alleles are independent of ploidy the total genetic variance created by mutation in a particular character, σ_m^2, is half as large in an allotetraploid as in a diploid, but the effective number of loci influencing the character, n_E, is twice as large in the allotetraploid. The amount of additive genetic variance maintained in a character under weak stabilizing selection is nearly proportional to $\sqrt{n_E\sigma_m^2}$ (Lande, 1977), which would then be about equal in an allotetraploid and in a diploid population. The component of inbreeding depression due to quantitative variation is therefore approximately the same in an allotetraploid species as in its diploid progenitors.