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INBREEDING DEPRESSION AND ITS EVOLUTIONARY CONSEQUENCES

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INTRODUCTION

The harmful effects of close inbreeding have been noticed for many centuries (34, 35, 165). With the rise of Mendelian genetics, it was realized that the main genetic consequence of inbreeding is homozygosis (165, Ch. 2). Two main theories were early proposed to account for inbreeding depression and its converse, heterosis (the increase in vigor observed in an F_1 between two inbred lines). These are the overdominance and partial dominance hypotheses, discussed in more detail below. Research into this question has continued up to the present, and this is one of the topics that we discuss.

Darwin (35, 36) was the first to point out that the evident adaptations of many plants for ensuring outcrossing could be understood in terms of the selective advantage of avoiding inbreeding depression. We review the evidence that the evolution of breeding systems of animals and plants has been significantly influenced by the occurrence of inbreeding depression. In order to do this, we consider the contemporary genetic theory of inbreeding depression and heterosis, and the experimental data concerning the strength of inbreeding depression. We emphasize data and theory relevant to natural, rather than domesticated, populations as we are chiefly concerned to evaluate the evolutionary significance of inbreeding depression. We do not attempt to give a complete bibliography of this very extensive field but try to concentrate on what seem to be the most significant findings in relation to this aim.

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GENETIC THEORIES OF INBREEDING DEPRESSION

The standard measure of the degree of inbreeding of an individual is Wright's (164) coefficient of inbreeding, f. Originally expressed as the correlation of additive genetic values between two uniting gametes, it is now usually interpreted as the probability of identity-by descent of two alleles at a locus in an individual (29, 30, 95.) A variety of methods of computing inbreeding coefficients from pedigrees are available (15); these asssume neutrality with respect to selection, so that the transmission probabilities of alleles can be calculated from Mendelian ratios. The quantitative effects of inbreeding on a measurable trait can be expressed in terms of the functional dependence of the mean (and higher order moments) of the trait on f.

In order to understand the causes of inbreeding depression in fitness components, it is necessary to formulate models relating genetic parameters of the base population to the behavior of a trait in a set of lines derived from it by inbreeding. A classic theoretical result is that the mean of a character controlled by a single locus i with two alleles A_{i1} and A_{i2} is only affected by the value of f if there is some degree of dominance (40, p. 226). Assume that the trait is scaled such that the values for the genotypes $A_{i1}A_{i1}$, $A_{i1}A_{i2}$, and $A_{i2}A_{i2}$ are $-a_i$, d_i, and a_i respectively. The quantities a_i and d_i measure the effect of the locus on the character and the degree of dominance of the locus, respectively. With two alleles, there is a linear decline in the mean of a trait with increasing f either with overdominance ($d_i > a_i$) or if the allele associated with an increased value of the trait is dominant or partially dominant ($a_i \geq d_i > 0$). With additive joint effects of different loci on the trait, this conclusion can be extended to a polygenic character; inbreeding decline occurs if the average value of d_i over all i is positive (40, p. 227).

These simple results underlie the two classical rival theories of inbreeding depression and heterosis, the overdominance and partial dominance hypotheses (165). On the former hypothesis, inbreeding depression is due to the superiority of heterozygotes over homozygotes at individual loci affecting the trait in question. F_1s between inbred lines fixed for different alleles are superior because of their heterozygosity at these loci. On the latter hypothesis, inbreeding decline results from the fact that inbred lines become fixed for recessive or partially recessive deleterious alleles; crosses between inbred lines fixed for deleterious alleles at different loci produce genotypes which are superior to the parents because the deleterious effects are partly covered up in the F_1s. Of course, complications arise if there are epistatic interactions between loci affecting a polygenic trait (71, 97), but (assuming linkage equilibrium and a random-mating initial population) the conclusion that dominance is necessary for inbreeding decline still holds (13, p. 106).

Inbreeding Decline as Determined by Conditions in the Initial Population

Morton et al (104) proposed a general model to relate inbreeding decline to mechanisms for maintaining variation in natural populations. This has since been extended by many workers (84, pp. 74–80). The model assumes independent effects of different environmental and genetic factors on probabilities of survival or reproduction, such that multiplicative effects of different factors result. Fitness effects are thus assumed to be additive on a logarithmic scale. The model is most clearly expressed in terms of survival from egg to adulthood in a discrete generation model; it can readily be extended to other fitness components. The mean fitness of a random-mating population is written as

$$w_O = \mathrm{C}\ \exp -\mathrm{A}, \qquad 1.$$

where C is a constant representing the effects of environmental factors in reducing survival below the maximum possible value (one, in the case of probability of survival), and A measures the net effect of all genetic factors in reducing survival below the value for the optimum genotype.

The fitness of an inbred population with inbreeding coefficient f is written as

$$w_I = \mathrm{C}\ \exp\ -(A + Bf), \qquad 2.$$

where B is the regression coefficient of minus the natural logarithm of fitness on f, and $A - \log_e \mathrm{C}$ is the intercept at zero f.

Values for A and B can be calculated from models for the maintenance of genetic variability. We shall consider in detail only two such models here, mutation-selection balance and heterozygote advantage (corresponding to the partial dominance and overdominance hypotheses described above). Consider the standard model of mutation at single locus at rate u from wild-type allele A_1 to deleterious allele A_2, with the relative fitnesses of the genotypes A_1A_1, A_1A_2 and A_2A_2 being 1, 1-hs, and 1-s respectively (s is the selection coefficient and h measures the degree of dominance of A_2). For a random-mating population in equilibrium, the mean fitness with respect to this locus is approximately 1-2u [provided that $h > 0$, as is suggested by the data from *Drosophila* (133)], and the fitness of a population with inbreeding coefficient f derived from this population without change in allele frequency is $1-2u-2u\{1/(2h)-1\}$. The net effect of all loci on fitness is obtained from Equation 2, such that

$$A = 2U \qquad 3a.$$

and

$$B = U\{1/(h-2\}, \qquad 3b.$$

where U is the per-genome mutation rate (i.e. the sum of the values of u over all loci), and h is the harmonic mean of the values of h across loci, weighted by mutation rate (104). Clearly, the closer the value of h to zero, the larger the regression coefficient B for a given U value. The ratio B/A is equal to $\{1/(2h)-1\}$.

For heterozygote advantage at a single locus with two alleles, with the fitnesses of the A_1A_1, A_1A_2 and A_2A_2 genotypes being 1-s, 1, and 1-t respectively, we have

$$A = B = st/(s + t), \qquad 4.$$

so that $B/A = 1$. Multiple alleles maintained by heterozygote advantage will increase the B/A ratio in proportion to the number of alleles. This may easily be extended to many loci by replacing $st/(s + t)$ with its sum over loci. (30, p. 308).

Other selective mechanisms for the maintenance of genetic variation are of course possible (30, 84) and may have somewhat different consequences for inbreeding depression. Frequency-dependent selection, for example, can maintain variation in the absence of any selective advantage to heterozygotes and may therefore contribute little to inbreeding depression. Environmental heterogeneity in selection pressure is another mechanism for maintaining variation and has been intensively studied theoretically (51, 63). Gillespie (50, 51) has shown that inbreeding depression and the associated lower developmental stability of inbred individuals is consistent with his *SAS/CFF* model for the maintenance of genetic variation by means of environmental variation in enzyme activity. Since this model effectively results in heterozygote advantage at the level of fitness, due to the assumed concave relationship between activity and fitness, the prediction of inbreeding decline is not surprising intuitively. Results quantitatively similar to those obtained with the model of constant fitnesses with heterozygote advantage would be expected.

The net decline in log fitness produced by complete inbreeding to $f = 1$ is given by B, which is clearly dependent on the number of loci as well as their effects on fitness for both models of inbreeding decline. A related measure is the *number of lethal equivalents* carried by a gamete or zygote (104). A lethal equivalent is a group of genes which would on average cause one death if

dispersed in different individuals and made homozygous. This is strictly speaking equal to $A + B$ for a gamete, or 2 $(A + B)$ for a zygote, but is frequently estimated simply as B or $2B$, owing to the difficulty of estimating A (see below). If data are only available for an outbred population and for a single inbreeding coefficient, B can be estimated by $\log_e(w_O/w_I)$, divided by the f value in question. It therefore provides a useful measure of the magnitude of inbreeding depression, although the validity of the extrapolation procedure involved is dependent on the adequacy of the assumption of independent effects of different factors. This is examined below. In what follows, we usually measure the magnitude of inbreeding depression by B (which is called the *inbreeding load*) or the corresponding ratio of totally inbred to outbred fitnesses. In discussing the effects of selfing in plant populations, however, we simply use the ratio of the fitnesses of selfed to outcrossed progeny as the measure of inbreeding depression.

The parameter A cannot be estimated directly, since the log mean fitness of an outbred population is equal to $\log_e C - A$. The convention in studies of inbreeding decline has been to assume that the fitness of the optimal genotype, C, is ≤ 1, so that the intercept of the graph of minus log fitness at $f = 0$ provides an overestimate of A (84, 104). For traits other than survival probability, the value of C could could be greater than one, and this creates difficulties (84, pp. 77–80).

Inbreeding Decline in Partially Self-Fertilizing Populations

We have so far assumed that the initial population from which inbred lines are extracted is random-mating. Many species of plants are, however, partially self-fertilizing, and the extent of inbreeding depression in such species is an important parameter of models of the evolution of breeding systems in such species (reviewed below). It is frequently suggested that selfing will purge populations of deleterious alleles, so that only low levels of inbreeding depression are to be expected in partially self-fertilizing species (e.g. 132, pp. 55–56; 144, p. 165). The only quantitative theoretical analysis of inbreeding depression in selfing species is that of Lande & Schemske (82), who considered the mutation-selection balance model for a single locus and extended it to multiple loci by assuming independence of genotype frequencies between loci with multiplicative fitness effects. They showed that even a moderate degree of selfing (10%) in the initial population greatly reduces the level of inbreeding depression contributed by recessive or nearly recessive mutations. While the evidence from *Drosophila* suggests that lethal mutations from natural populations have an average h of 0.02 (31, 133), the value used by Lande & Schemske (82, p. 31), a large component of the inbreeding load is contributed by detrimental genes of small effect (Table 1), which have much higher coefficients of dominance (31, 133).

Table 1 *Drosophila* data on fitness components of chromosomal homozygotes

Species and Chromosome	Egg-to-adult viability: Ratio of Inbred to Outbred Viability		Loads		References
	Detrimental	Lethal	Detrimental	Lethal	
D. melanogaster					
Chromosome 1	>0.046	1	<0.047	0	38
Chromosome 2	0.790	0.780	0.236	0.247	133
Chromosome 3	0.753	0.666	0.284	0.407	133
D. pseudoobscura					
Chromosome 2	0.782	0.815	0.246	0.830	133
Chromosome 3	0.739	0.798	0.352	0.226	133
D. subobscura					
Chromosome O	0.850	0.833	0.163	0.183	142
D. willistoni					
Chromosome 2	0.684	0.680	0.380	0.386	133
Chromosome 3	0.603	0.832	0.506	0.184	133

Species and Chromosome	Net fitness (All autosomal data from 133, table 4): Ratio of inbred to outbred fitness	References
D. melanogaster		
Chromosome 1	0.62	163
Chromosome 2	0.16	
Chromosome 3	0.21	
D. pseudoobscura		
Chromosome 2	0.36	
D. willistoni		
Chromosome 2	0.34	

The inbreeding depression caused by such partially recessive mutations can be studied using the equations of Ohta & Cockerham (109) for equilibrium at a single locus with mutation at rate u from the wild-type allele A_1 to the deleterious allele A_2, which assumes that the equilibrium mutant allele frequency is sufficiently low and h is sufficiently high that selective elimination of A_2A_2 homozygotes produced by outcrossing can be neglected (the statement by Lande & Schemske that this is valid only for high selfing is incorrect). If the frequencies of zygotes produced by self-fertilization and random mating are S and $1-S$,

duced by self-fertilization and outcrossing random individuals (w_I and w_O) are given by

$$w_I \approx 1-s\{\tfrac{1}{2}H_1(h+\tfrac{1}{2})+H_2\} \qquad 5a.$$

and

$$w_O \approx 1 - hs(H_1 + 2H_2), \qquad 5b.$$

where H_1 and H_2 are the equilibrium frequencies of A_1A_2 and A_2A_2 given by Ohta & Cockerham (109) and are functions of the mutation rate and S, as well as s and h.

The inbreeding depression due to selfing can be measured by $\delta = (w_O - w_I)/w_O$. It is easily shown that for $h < \frac{1}{2}$, as is reasonable to assume, δ is a decreasing function of the selfing rate S, as would be expected intuitively. The extent to which inbreeding depression is reduced by the level of selfing in the base population is conveniently represented by $k(S)$, the ratio of δ for a given value of S to the value for a random-mating population. Figure 1A shows the graph of $k(S)$ against S for a mutation rate of 10^{-5} [numerical studies show that k(S) is very insensitive to mutation rate], for various values of s and h. The case when $s = 1$ and h = 0.02 is realistic for recessive lethal mutations, as mentioned above, and the results are consistent with those of Lande & Schemske (82). The value $s = 0.02$ has been chosen because the results of Mukai and collaborators suggest this value for newly arisen, mildly deleterious viability mutations in *Drosophila* (31, 133). The dominance coefficients 0.35 and 0.20 are values estimated for newly arisen, mildly deleterious *Drosophila* viability mutations and for such alleles in random-mating populations, respectively. The lower value presumably reflects the differential elimination of more dominant alleles from populations (31, 133); since selection on heterozygous effects of deleterious mutations plays a less important role in selfing populations, the mean value of h for mildly deleterious mutations for selfing populations will presumably lie between these values, if the *Drosophila* viability data are any guide. It will be seen that even populations with very high levels of selfing retain a substantial fraction of the inbreeding depression found with random mating, as far as mutations of small effect are concerned.

Of course, the amount of inbreeding depression contributed by a single locus on this model is extremely small. Lande & Schemske (82) proposed that it is reasonable to assume independence of genotype frequencies at different loci and to combine fitness effects at different loci according to the multiplicative scheme used above. If this is done with the model just described, the ratio $w_I(S)/w_O(S)$ for a given S, taking account of all loci, can be written as $\exp - \frac{1}{2}Bk(S)$, where B is the inbreeding load parameter for a random-mating population introduced above. Figure 1B shows the graph of w_I/w_O for various values of $k(S)$ against the value for a random-mating population, $w_I(0)/w_O(0) = \exp - \frac{1}{2}B$.

A similar analysis of inbreeding depression in a partial selfer can be carried out for the case of heterozygote advantage at a single locus with two alleles,

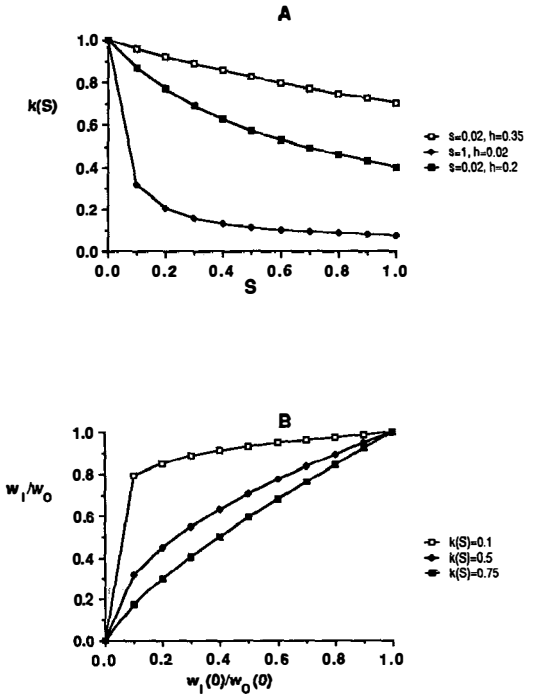

Figure 1 Inbreeding depression with mutation-selection balance in a partially self-fertilizing population. A: relation of $k(S)$ (see text) to S, for various values of s and h. B: w_1/w_O plotted against the value for S = 0 for various values of k(S).

using the formulae of Kimura & Ohta (74, Appendix 4) for the equilibrium frequencies of the three genotypes for given values of S and the selection coefficients s and t of equation 4, with results that are shown in Figure 2. Here w_1 is calculated using genotype frequencies after selection, since these correspond to the frequencies among adults which would be used in experimental tests. It will be seen that, when selection is symmetrical so that $s = t$, increased selfing in the population in fact leads to an *increase* in the level of inbreeding depression, even at very high selfing rates. When s and t differ, this is true at low to moderate selfing rates, but a decline in δ occurs with high selfing. With too high S, asymmetrical selection cannot maintain polymorphism unless both selection coefficients exceed one half (74, pp. 195–96), and so δ is necessarily zero. By continuity, there must be a drop in δ at lower S, reflecting the approach of gene frequency to fixation. The increase in δ is more puzzling at first sight but presumably reflects the fact that individuals in equilibrium populations with partial selfing are inbred, so that their selfed progeny are more homozygous than those from a random-mating population. Hence, there is a larger difference in homozygosity between the progeny of

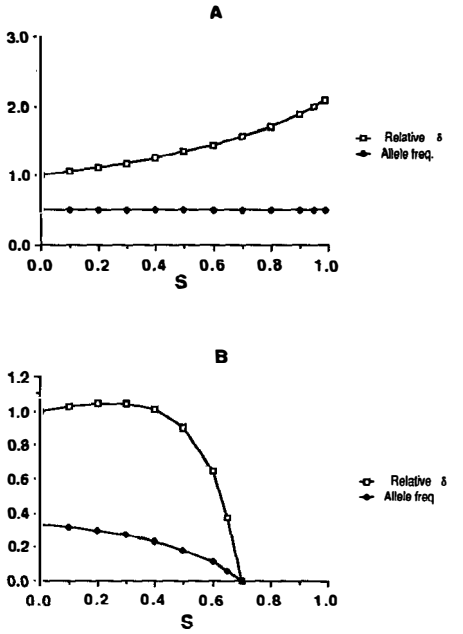

Figure 2 Allele frequencies and relative inbreeding depression (δ) values, compared with the values for S = 0, for various values of S for the case of a single locus with heterozygous advantage. A: $s = 0.1$, $t = 0.1$. B: $s = 0.2$, $t = 0.1$.

outcrosses and selfs, the larger S. Using the facts that the inbreeding coefficient of the selfed progeny of an individual with inbreeding coefficient f is $(1 + f)/2$, and the equilibrium value of f in a partially selfing population is $2/(2 - S)$ (30, p. 94), this difference is equal to $1/(2 - S)$, which is ½ when S is 0 and increases to 1 for $S = 1$. With the deleterious mutation model, this effect is obscured by the reduction in equilibrium gene frequency with increased S.

These results show that, provided the level of inbreeding decline in a random mating population due to mutations of small effect is sufficiently high, a large reduction in fitness to selfed compared with outcrossed progeny can be expected, even with high selfing rates. This agrees with the conclusion of Lande & Schemske (82), based on an analysis of weak stabilizing selection on quantitative characters. As we show below, there is abundant experimental evidence for such a sizeable contribution to inbreeding decline of mutant alleles with small effects. Similarly, loci with heterozygote advantage and approximately symmetrical selection coefficients will contribute significantly; only loci with such symmetry are likely to be maintained polymorphic in highly selfing populations (74).

There is one important caveat to this conclusion, however. Independence of genotype frequencies at different loci was assumed in the multi-locus version of the deleterious mutation model, but it is well known that deviations from random mating induce correlations between different loci of a kind that are absent with random mating (27, 60). Studies of electrophoretic and morphometric variation in plant populations have revealed the existence of such associations (3, 12). The probable effect of such correlations in the present case will be to cause the joint elimination of linked sets of deleterious alleles in progeny resulting from selfing, thus lowering their frequencies below those predicted with independence. On the other hand, a larger fitness reduction to selfed versus outcrossed progeny might be observed, so that it is unclear what the net effect would be. The extent of such nonrandom associations is likely to be even greater for loci having higher allele frequencies, as would usually be the case for loci maintained polymorphic by selection, so we have not carried out the multi-locus calculation for this case. No quantitative study of this difficult problem has been done as yet.

EXPERIMENTAL DATA

There are two main features of inbreeding depression that we wish to examine. First, how strong is it, and what stages of the life cycle are affected? Second, what is the effect of the mean level of inbreeding in natural populations on the extent of inbreeding depression? Clearly, these questions need to be reviewed together. The first question has been most thoroughly studied in *Drosophila*, and we will consider these data first. The second question is best studied in plants, which can have large values of inbreeding coefficients in natural populations.

Drosophila

Evidence from numerous experiments on *Drosophila* has been admirably reviewed by Simmons & Crow (31, 133). We here do little more than summarize their main conclusions and draw attention to a few more recent studies. The chief character that has been studied is egg-to-adult viability, using the technique of balancer chromosomes carrying inversions and dominant genes with recessive lethal effects, to make single chromosomes derived from wild males homozygous at all loci on the chromosome in question (i.e $f = 1$). Greenberg & Crow (54) developed a methodology for partitioning the load revealed by this method into "lethal" and "detrimental" components. Chromosomes are generally classified as homozygous lethal if they have a viability of less than 10% (133); since individuals with such low fitness will be unlikely to survive in nature, it is reasonable to estimate the contribution of lethals to the mean viability of chromosomal homozygotes by weighting the

observed frequency of lethal chromosomes by zero. Nonlethal chromosomes are lumped together as detrimentals, and the net reduction in fitness associated with detrimentals is given by the mean viability of homozygous detrimentals relative to chromosome heterozygotes. Greenberg & Crow (54) expressed the data in terms of genetic loads derived from the absolute values of the natural logarithms of the frequency of lethals, and of the ratio of detrimental homozygote to heterozygote viability, respectively, on the assumption of a basic multiplicativity of gene action (see theoretical section above). This procedure has been widely followed in the *Drosophila* literature; in Table 1 we summarize data on viability both in this way and in terms of the raw ratios of inbred to outbred viabilities. The values presented are obtained from the mean values of the viabilities from many studies (31, 38, 133, 142). The detrimental load can be further partitioned into a component due to semi-lethal chromosomes (homozygotes with a viability less than 50–60% of the mean for heterozygotes) and the remainder, attributable to mildly detrimental genes. The bulk of the detrimental load comes from the mildly detrimental chromosomes (an average of 63% for the autosomal viability loads for the species listed in Table 1).

Two features stand out from this table. First, the contributions to inbreeding decline from lethal chromosomes and detrimental chromosomes are approximately the same: The mean detrimental load is 1.11 times the lethal load (the mean load due to mildly detrimentals is 70% of the lethal load). This has some bearing on the question of the causes of inbreeding depression, as we discuss below. Second, the magnitudes of these effects are fairly similar across species and chromosomes (it should be noted that the data on species other than *melanogaster* are scanty), except for the much smaller effect on viability for the *melanogaster* X chromosome (chromosome 1) which is expected on theoretical grounds, due to the higher rate of elimination of deleterious alleles in hemizygous males (38, 59). This is unexpected in view of the differences in the sizes of the autosomes, among these species (112). The viability of nonlethal chromosomal homozygotes is about 70–80% of that of heterozygotes, and the net effect on viability of homozygosity for a single autosome is a reduction of 50–60%. The reduction in viability due to detrimentals of a *melanogaster* individual homozygous for both autosomes would thus be approximately 0.60.

The effects of homozygosity for nonlethal chromosomes on net fitness have been determined in several systems by means of an ingenious technique devised by J. A. Sved (147, 148). This involves allowing a set of laboratory populations, each containing a balancer chromosome and an extracted nonlethal single wild chromosome, to equilibrate. Since the balancer chromosome is recessive lethal, the homozygous fitness of the extracted chromosome can be estimated from its equilibrium frequency, using the familiar formula

for equilibrium frequency with heterozygote advantage. If, as occasionally happens, the balancer chromosome is eliminated from a population, the fitness of the homozygotes for the extracted chromosome can be estimated from the rate of elimination. Control populations with the balancer and a mixture of extracted chromosomes can be used to standardize fitnesses relative to those for wild-type chromosome heterozygotes. The results of several experiments are summarized in Table 1. It will be seen that the effects of inbreeding on net fitness are very much greater than for viability, especially for *melanogaster*. If net fitness effects of different loci combine multiplicatively, these data suggest that a fly which is homozygous for its autosomal complement would have a fitness of only 3% of normal. The effect of homozygosity for the X chromosome on net fitness is much greater than on viability; this probably reflects sex-limitation of deleterious mutations affecting female fertility (38, 163).

Finally, the *Drosophila* data are the best source of evidence concerning the adequacy of the assumption of multiplicative effects of different factors of fitness, which is the basis for much of the theory discussed earlier. This evidence has been reviewed by Simmons & Crow (133), who conclude that the joint effects of deleterious alleles at different loci are somewhat larger than would be predicted by the multiplicative model, i.e. there is synergistic epistasis. The effect of epistasis is not, however, very large. Temin et al (150) found that the sum of the mild detrimental loads for the second and third chromosomes of *D. melanogaster* was 0.217, whereas the (nonsignificant) additional contribution from interactions between the two chromosomes was 0.021.

Mammals and Birds

There is much evidence that inbreeding depression often has major effects in mammals and birds (115, 165). Evidence from natural populations is, however, scanty (56, 154).

Ferns

In homosporous ferns, there is an opportunity to measure the genetic load as it affects one component of fitness (80). Gametophytes produce gametes by mitosis, and a single gametophyte generally produces several female gametes (78). If male gametes are produced simultaneously with archegonia, as happens during part of the reproductive period in some species, the failure of isolated gametophytes to produce diploid sporophytes is an indication that the gametophyte carries recessive sporophyte lethals, and the frequency of such failure can be used to give an estimate of the genetic load. Ideally, the control experiment of growing unrelated gametophytes together in the same culture

conditions should be done to show that reproduction can take place in those conditions (77). However, this is rarely done.

The results of such experiments have been reviewed by Klekowski (79). The frequency with which isolated gametophytes give rise to sporophytes ranges from virtually 100% in some species to less than 40% in *Osmunda regalis* (76). The causes of these differences in genetic load are not at present understood. It seems likely that they are related to the breeding systems of the species, with the more highly inbreeding species having lower genetic loads. This has been suggested by Lloyd, who studied genetic loads in several Hawaiian fern species and found lower frequencies of "sterile" gametophytes in "pioneer" species that colonize lava flows than in rainforest species (91). Similar results have been reported in other sets of species (78, 134). Unfortunately, there are so far no quantitative estimates of the inbreeding coefficients for these species. Recently, a number of fern species have been surveyed electrophoretically, and it is clear that there is a wide range of breeding systems, from essentially outcrossers to highly inbreeding species (101, 136, 137). However, genetic load data are at present available for very few of these species (137).

Gymnosperms

The gymnosperms present a favorable situation for studying inbreeding depression in the early stages of embryo development, because it is often possible to distinguish between the various fates of an ovule, i.e. whether it remains unfertilized, is fertilized but then dies or is aborted, or whether a surviving embryo is produced (121, 138). The results are especially valuable as data on genetic load, because there is no endosperm in gymnosperms, so that inviability of a zygote can be attributed to its own genotype rather than to a nonfunctioning endosperm. It is, however, important to remember that in many species each ovule contains several archegonia, so that failure of an ovule, resulting in an unfilled seed, probably represents the death or abortion of more than one product of fertilization (139). The effects of inbreeding at the later stages of life can also be measured. These data are very interesting, as there are very few data on inbreeding depression in long-lived plants, such as trees, among the angiosperms.

Strong inbreeding depression effects have frequently been measured in gymnosperm species (e.g. 44, 141). Table 2 summarizes the data for species where there is some quantitative estimate of the selfing rate. For some of the gymnosperm species, there may be a significant differential loss of selfed progeny before the time at which the genotypes can be scored (i.e. as viable embryos), because the products of selfing and crossing often differ greatly in their survival to the stage at which viable embryos that can be used for

electrophoresis are formed. In some species, seeds are held in the cones for more than a year, so the opportunity for differential mortality is especially great (26). In any case, it is clear that for gymnosperms the selfing rate at fertilization cannot be measured. We have therefore indicated in Table 2 whether the selfing rate estimates are derived from electrophoresis of surviving seedlings. An alternative method of estimating the selfing rate uses this difference in the results of selfing and crossing. Suppose the fraction of filled seeds from selfed cones is p_s and that from outcrossing is p_x, and suppose also that one observes the fraction of filled seeds under natural pollination to be p_w. Then an estimate of the selfing rate is given by

$$S = (p_x - p_w)/(p_x - p_s). \qquad 6.$$

We have used such estimates in Table 2 when the data were available to calculate them. A problem with these data is that bagging the cones often appears to lower their production of filled seed, so that one can only obtain

Table 2 Inbreeding depression estimates in gymnosperms calculated as ratio of value for selfed seed or progeny to value for outcrossed seed or progeny.

	Character affected				
Species	% filled seed	Germ. rate	Size[a], fertility[b], or survival[c]	Selfing rate	References
Pinus attenuata	—	—	0.63[b]	0.50	145
Pinus sylvestris	0.12	—	0.63[a]	0.11–0.24	44, 58, 107, 149, 166
Pinus taeda	0.12	0.86	0.96[c]	0–0.04†	46, 45, 118
Pinus radiata	<1	0.78	0.88–0.98[a]	0.04	45, 57, 162
Pinus elliottii	0.16–0.22	0.47	0.78[a]	0.06	44, 124, 141
Pinus banksiana	0.42	0.98	0.95[a]	0–0.17†	26, 44
Pinus jeffreyi	—	0.91	0.54[a]	0.06	47, 44
Pinus ponderosa	0.37	—	0.64[a]	0.04–0.19†	41, 140, 141
Picea glauca	0.20	ns	0.37[a]	0.60	43, 75, 111
Picea mariana	0.46	ns	0.80[a]	0.08	10, 110
Picea abies	0.50	0.25	0.89[a]	0.11†–0.49	37, 44, 94
Abies procera	0.69	ns	0.76[a]	0.41	140
Pseudotsuga menziesii	0.11	0.89	0.82[c]	0.07–0.1†	44, 117, 131, 138, 139
Larix decidua	—	—	0.84[a]	0.71†	37
Sequoia sempervirens	1.02	—	0.27[a]	0.59	85

—: No information
ns: No significant effect of selfing
†: Selfing rate estimate is for surviving progeny, not time of fertilization (see text).

such estimates when the open- or wind-pollinated cones were also bagged for as much time as possible, except during the period of pollination itself.

The table shows clearly that there is usually a large disadvantage to the products of selfing, compared with outcrossed progeny. The data for proportion of filled seed and size measures of inbreeding effects are shown in Figure 3, which shows that there is no evident relationship with the degree of inbreeding of the population, for these two characters. The few populations which appear to be quite highly selfing show significant inbreeding depression, while the populations whose selfing rates are near zero have varying levels.

Angiosperms

Although it has been known for a long time that inbreeding depression effects can occur in flowering plants, few studies of nondomesticated species exist, and few studies attempt to quantify the effects of inbreeding on more than a single component of fitness (2, 32, 165). Darwin (35) studied a total of 57 species, of which perhaps 39 were based on material derived immediately from populations with a reasonably natural population structure; he obtained data on size from all of the noncultivars and on female fertility for 15 of these species. Most species showed inbreeding depression for one or both of the characters, and all the estimates are probably underestimates because Darwin did not take survival into account but measured the characters on survivors only, and survival of selfed progeny was often low. On the whole, Darwin's data suggest that inbreeders sometimes show little inbreeding depression, though in such cases he often found that there was great benefit from crossing to a "fresh stock." However, it is also clear that many such species did show considerable inbreeding depression.

Wright (165) reviews data from several domesticated species, which suggest that inbreeding depression may occur in habitual inbreeders but that it is

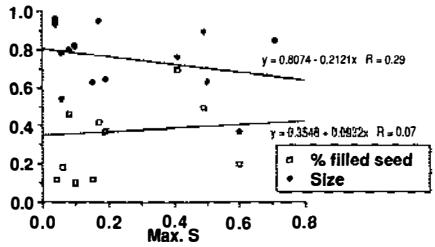

Figure 3 Relative values of two types of character (percentage of filled seed and size, measured at various ages) for inbred progeny, compared with outcrossed progeny in several species of gymnosperms.

usually less severe than in species that are normally outbred. This is mainly because of the lack of strong inbreeding effects in highly selfing species; partially outcrossing species showed effects of various magnitudes (2). However, the fact that the above data are only for certain components of fitness and that they were collected for agricultural purposes, in which the yield of some product is usually the focus of interest, means that these studies are not very relevant to evolutionary considerations, though they do of course indicate something of the potential for inbreeding depression.

What we really need are studies of the effects of inbreeding on as many components of fitness as possible, using plants recently taken from natural populations whose inbreeding coefficients have been measured. If possible, the fitness components should be estimated using plants grown in the field; this entails planting seeds from hand self- or cross-pollinations into natural populations. Very few studies of this kind have been done. Even though it is likely that inbreeding depression will be most severe in outcrossers, it remains possible that substantial inbreeding depression will exist even in partially selfing populations, and it would be very valuable to have some idea of its magnitude in such species. For naturally selfing species, one certainly might not expect to find much evidence for inbreeding depression if one compared the results of selfing with those of intercrossing individuals from the same local population, because there may be little genetic variation within local populations of such species (but see 123). However, crosses between populations might show luxuriance which would indicate higher fitness of such crossed progeny in the natural situation. Few such data exist.

Table 3 shows the available angiosperm data. We have included all studies based on natural material of which we are aware, as there are so few of them, and have attempted to get estimates of selfing rates when any relevant data were available. As with gymnosperms, it might be possible to estimate selfing rates by comparing the values of progeny of naturally pollinated flowers with those for selfed and crossed flowers if it were known that the bagging necessary to do the controlled pollinations had no effect on the progeny quality. Unfortunately, when this type of data is available, it usually shows that the seeds from the natural pollinations are superior to those of crossing (e.g. 122), so one cannot use such data. It would be valuable to collect data from seeds of naturally pollinated, but subsequently bagged, flowers. All the species listed in Table 3 are herbs. All show clear evidence of inbreeding depression at some stage of their life history, and there is no indication that inbreeding species have no inbreeding depression. All the estimates except that of Schoen (126) are likely to be underestimates, as they either ignore one or more stages in the life history or are based on comparisons between sets of progeny that are not as different as self and outcrossed progeny (70, 155). We have not included here species which have very low fertility on selfing compared with crossing, as it is difficult to tell whether self-incompatibility or

Table 3 Inbreeding depression estimates in angiosperms calculated as ratio of value for selfed seed or progeny to value for outcrossed seed or progeny.

	Character affected				
Species	Number of nonaborted seed per poll	Germination rate	Size[(a)], fertility[(b)], or survival[(c)]	Selfing rate	References
Gilia achilleifolia	ns	ns	0.56[c]	0.04	126
Papaver dubium	–	–	0.80[b]*	0.75	4, 67
Costus allenii	0.67	0.88	0.75[a†]	~0	122, 125
Costus laevis	0.63	1.07	0.80[a†]	0	122, Schemske, pers. commun.
Costus guanaiensis	0.66	0.94	0.81[a†]	0	122
Impatiens capensis	–	ns	0.59[a]–0.93[c†1]	High	81, 155
Impatiens pallida	–	–	1.5–0.6[b3]	High	Schemske, pers. commun.
Thlaspi alpestre	–	0.82	–	0.95	116
Limnanthes alba	–	–	0.40–1.00[b2]	0.03–0.57	70
Delphinium nelsoni	0.57	–	0.156[c]	–	114
Limnanthes douglassii	–	–	0.78[b†]	0.23	73
	–	–	0.93[b†]	0.06	
Silene vulgaris	0.66–0.82	0.57–0.73	0.81[b†]–0.40[b†]	~0.1–0.3	72, own data
Phlox drummondii	0.83	–	0.83[c†]	SI	83
Thymus vulgaris	0.69	0.66	0.70	0.1–0.70	5, 53, 153
Erythronium americanum	0.25	–	–	0.38[2]	61

†: Data from greenhouse-grown plants. *: More than one generation of inbreeding in the selfed lines.
SI: Self-incompatible.
[1] Based on differences between progeny of cleistogamous and chasmogamous flowers.
[2] Based on differences between seed set of selfed and open pollinated flowers.
[3] Higher value for shaded environment (similar to environment of parents) and lower value for open environment.

late-acting inbreeding depression is involved (22, 130). We have also excluded species for which the only data are fruit and/or seed set on selfing or crossing, for the same reason, though it seems likely that some of these are in fact self-compatible species and the low values on selfing are due to early acting inbreeding depression.

THE CAUSES OF INBREEDING DEPRESSION

In this section, we discuss experimental evidence relevant to discriminating between the two rival theories of inbreeding depression. This evidence falls into two broad categories: that obtained from data on properties of random mating populations and inbred lines derived from them, and that obtained from biometrical genetic studies of the properties of lines descended from a cross between a single pair of inbred lines.

Evidence from Population Properties

It is first worth pointing out that the *Drosophila* data are unfavorable to the notion that lethal genes are often maintained in populations by heterozygote advantage. Most lethals seem to represent point mutations rather than epistatic complexes of genes with drastic net effects on fitness (84, p. 46). While lethal-bearing chromosomes are often present in a frequency of 30% or more and contribute a correspondingly large fraction of the total inbreeding load (Table 1), the frequency of allelism between random pairs of lethal chromosomes is usually low, of the order of 1% or less (68, 93). The same is true of sterility genes (93). There is little room for any selective advantage to heterozygotes for recessive lethal genes in these studies, since any appreciable average such effect would raise lethal gene frequencies far above the level expected from mutation-selection balance and so lead to much higher rates of allelism than those observed. Furthermore, measurements of the heterozygous effects on viability of lethal-bearing chromosomes derived from equilibrium populations suggest that they normally reduce fitness by about 2% (31, 133). At least as far as *Drosophila* is concerned, we can safely conclude that recessive lethals are overwhelmingly maintained by mutation-selection balance. The problem thus reduces to explaining the source of the sizeable fraction of the inbreeding load that is due to nonlethal chromosomes (Table 1).

Morton et al (104) suggested that the B/A ratio defined earlier would provide a method for distinguishing between the mutational and heterozygote advantage hypotheses, since (as is evident from Equations 3 and 4) this ratio is unity for the case of heterozygote advantage with two alleles but is very large for nearly recessive deleterious mutations such as recessive lethals [of the order of 25 for the $\bar{h}$ values estimated for lethal chromosomes from *Drosophila* populations (133)]. But, as is evident from Table 1, a large fraction of inbreeding decline is due to detrimental rather than lethal alleles, and it seems clear that the $\bar{h}$ value for such alleles is far from zero. With the h of approximately 0.20 for mildly detrimental viability mutations from natural populations of *Drosophila* (31, 133) the value of B/A is 1.5. The contributions of different classes of mutation to the overall values of B and A are weighted by the corresponding mutation rates (Equation 3; this is more than 0.10 for detrimental mutations on the second chromosome of *D. melanogaster* but only 0.005 for lethal mutations; 133). The weighted B/A ratio for viability mutations of *D. melanogaster* is approximately 2.7. This is close to the value for heterozygote advantage with two or three alleles per locus, and so a low ratio cannot be taken as evidence for heterozygote advantage. For this reason alone, this method cannot provide useful evidence concerning the source of the detrimental load, unless high values of B/A are consistently obtained, which does not seem to be the case with the human data on survival prob-

abilities for which the method was originally developed (69, pp. 261–68; 129). Some other difficulties have been discussed by Lewontin (84, pp. 74–80). The method unfortunately does not seem to be capable of providing a rigorous test.

Data on the mutation rate to detrimental alleles in *D. melanogaster* provide a means of testing the ability of the deleterious allele model to account for inbreeding decline in viability. The results of Mukai and his collaborators (31, 133) suggest that this rate [equivalent to U in equation (3)] is approximately 0.1 per second chromosome per generation. Using the above value of $h = 0.2$ and substituting into Equation 3b, the inbreeding load due to mildly detrimental genes on the second chromosome is expected to be 0.3. This is in fact somewhat higher than the observed value for the total detrimental load given in the top line of Table 1. The observed effect of X chromosome homozygosity on viability in *D. melanogaster* is similarly consistent with the predictions of the mutation-selection model (38). There is thus little doubt that the mutation-selection balance model is quantitatively capable of explaining the data on inbreeding depression in viability in *D. melanogaster*. There is, however, at present no evidence concerning the total mutation rate for mutations affecting net fitness, so that no such comparison can be carried out for the case of the net effects of chromosomes shown in the lower part of Table 1.

Evidence from Crosses between Single Pairs of Lines

This evidence comes mostly from studies of the genetic basis of heterosis in plants. If a cross is made between two lines fixed at all loci, the gene frequencies at each locus for which the lines differ must be one-half. Neglecting effects of linkage and epistasis, the genetic variance in populations derived from such an F_1 can be completely described by additive and dominance components $\Sigma_i a_i^2$ and $\Sigma_i d_i^2$ respectively, using the notation introduced at the start of the section on the theory of inbreeding (96, 119). The mean level of dominance can be measured by the ratio

$$a = \sqrt{\left(\frac{\sum_i d_i^2}{\sum_i a_i^2}\right)}. \qquad 7.$$

This ratio will be greater than one if there is overdominance at all loci and will be less than one if there is partial dominance at all loci. The genetic parameters can be estimated from analyses of variance of F_2s and other populations derived from the F_1 (96, 97, 119).

In maize, biometrical studies of F_2 populations have sometimes suggested overdominance for such characters as yield that display heterosis, although

many heterotic characters show only partial dominance (28, 49, 119, 143). As pointed out by Robinson & Comstock (28, 119), these estimates of average dominance are biased upwards by linkage between loci controlling the trait in question, if the parental lines are fixed for groups of recessive or partially recessive deleterious alleles. The effect of this bias is expected to decay in later generations derived from the F_2 by random mating, and the study of Moll et al (103) of seven traits showed that the average degree of dominance did indeed decline significantly over the generations. Yield was the only trait that showed apparent overdominance in F_2, but it failed to show it in later generations. A recent review by Sprague (143) has concluded that it is unnecessary to appeal to overdominance in order to explain heterosis in maize. A large body of additional theory on line crosses has been developed by the Birmingham school of biometrical genetics (97), and its application to the analysis of heterosis has been reviewed by Jinks (71).

While some contribution of overdominance cannot at present be completely ruled out, these very careful biometrical studies of heterosis in plants have failed to provide positive evidence for a role for overdominance but instead have strongly supported an important role for partial dominance, together with contributions from epistatic interactions (71, 143).

EVOLUTION OF INBREEDING AND INBREEDING AVOIDANCE

Evolution of Inbreeding and Outbreeding: General Models

Theoretical studies of the evolution of inbreeding versus outbreeding have mostly assumed single-locus determination of the degree of outbreeding. Fisher (42) studied the change in frequency of an allele that causes self-fertilization in the absence of any inbreeding depression. Selfing is automatically favored, due to the higher representation in the progeny generation of an allele that causes selfing, in comparison with an allele for outcrossing, except if the selfing genotypes make no contribution to the pollen pool (108). This has been termed the "cost of outcrossing."

Recently, these models have been extended in various ways, including the addition of inbreeding depression as an explicit parameter. Using three models of how selfing rates could be controlled, Lloyd (86) showed that inbreeding depression is a critical parameter in determining the outcome of selection on an allele that affects the selfing rate. Outbreeding is favored when inbreeding depression exceeds ½, whereas selfing is favored when it is less than ½, and a selfing allele will spread to fixation. However, several other models predict intermediate selfing rates. When selfing and outcrossing are related automatically (for example if changes that promote selfing also decrease the

chance that an ovule is fertilized by foreign pollen), "competing" self fertilization produces this result, for certain intermediate values of the inbreeding depression parameter (86). This also occurs if successive generations of inbreeding have a progressive and increasingly deleterious effect on fitness (99, 100, p. 126; see also 14), if selfing is favored when rare, but increases seed production and thus competition between seedlings as it becomes more prevalent. If inbreeding depression affects competitive ability, this leads to a negative frequency-dependent element in the fitness of a selfing genotype, so that a polymorphism could result (88, pp. 79–81). It can also occur when progeny of selfing suffer not only reduced survival or fertility when growing in the same population as their maternal parents (inbreeding depression), but also reduced ability to disperse to, or establish in, another population ("migration depression"; 65, 128). If inbreeding depression reduces the fitness of selfed progeny by less than half and migration depression reduces it by more than half, an intermediate level of selfing can be evolutionarily stable for some migration rates. This result remains true even when some proportion of the pollen is used up by selfing, so that an increase in the selfing rate would decrease the contribution to the outcrossed pollen pool, as would probably be true in a facultatively cleistogamous species. It has been observed in such species that there are always some chasmogamous flowers, at least in some growth conditions (92). This is an example of Darwin's observation that nature "abhors perpetual self fertilization" (33).

In summary, some but not all models suggest that selfing rates will evolve either to near zero or to near 100%. At present, it is not clear whether plants fall into two categories, outbreeders and inbreeders (1, 156), despite the claim (124) that such a bimodality exists. Most of these models also include an effect of reduced fertility of nonselfed ovules, which increases the advantage of selfing or, equivalently, reduces the effective level of inbreeding depression. A very crude model of inbreeding depression is usually used, with no model of the genetic basis of the inbreeding depression (except for 82, see above). Most also ignore the possibility of differences in inbreeding depression in different genotypes, and the possibility that some nonself matings may be between relatives (but see 152). In models assuming an initially inbreeding hermaphrodite population, the "cost of outcrossing" is lowered when the population into which a selfing allele is introduced is itself somewhat inbred, so that the more inbred a population is, the lower the selective advantage of a given increase in selfing rate (16, 66, 87).

Inbreeding Avoidance: Specific Mechanisms

A number of different phenomena have been thought to have evolved as means of avoiding inbreeding. In this section, we discuss these from the viewpoint of assessing whether inbreeding avoidance is indeed a likely factor,

or at least a major one, promoting the evolution and maintenance of these characters. The characteristics we discuss are self-incompatibility and dioecy in plants, and dispersal and incest avoidance in animals. Before discussing these "outbreeding mechanisms" we wish to point out that one must not assume, just because some feature is associated with a decrease in inbreeding, that this is the sole reason for its evolution. Lloyd & Webb (90) review the evolution of protandry and protogyny in plants and show that, although these features of a plant breeding system have the effect of reducing the selfing rate, they may also have one or more of several other important evolutionary advantages, such as a longer period or a better spatial arrangement for pollen presentation or avoidance of interference between the very different functions associated with male and female reproduction. Another example is the case of monoecy in plants, with separate male and female flowers on the same individual. Even if it were known that this separation of the sex functions has the effect of reducing selfing, this might not be the major factor in the evolution of monoecy (23).

There are a number of other systems that prevent inbreeding, such as mating types in lower plants, and these might be thought to have evolved in response to inbreeding depression. However, we have little evidence at present that this is so. In a study of a theoretical model for the evolution of mating types in an isogamous organism, Hoekstra (64) found that avoidance of inbreeding depression is unlikely to be a major factor.

HOMOMORPHIC INCOMPATIBILITY Many flowering plant species have genetically determined self-incompatibility systems which ensure that they do not produce seeds when fertilized with their own pollen. In homomorphic systems, there are no overt morphological differences associated with the incompatibility type, which is controlled by alleles at one or more incompatibility (*S*) loci. There are two classes of self-incompatibility systems which differ in the genetic control of the incompatibility reactions in pollen. In gametophytic systems, the pollen type is controlled by its own genotype, while in sporophytic systems the genotype of the plant that produces the pollen determines the pollen's incompatibility type. Gametophytic systems are known in at least 16 angiosperm families (three of them with systems controlled by more than one locus), and sporophytic systems in at least 7 families. At present, we have no satisfactory account of how self-incompatibility in plants evolved, nor do we know whether it arose only once or more than once (8, 161). Since there are no evident phenotypic differences between the different genotypes at the incompatibility loci, it would seem at first sight most likely that self-incompatibility systems must have evolved in response to selective pressures to avoid inbreeding (either selfing or mating between close relatives). If the first step is a mutation in an initially faculta-

tively selfing species, to an allele conferring self-incompatibility of either type, a necessary condition for it to spread is that the inbreeding depression δ be greater than one-half (24; and D. Charlesworth, unpublished). Nevertheless, the original "self fertility" allele is not usually eliminated. In other words, a consistently rather high degree of inbreeding depression is necessary for the population to maintain these types of self-incompatibility systems. This is not necessarily a serious problem for the evolution of self-incompatibility since it is not thought that such systems evolved many times.

HETEROSTYLY This type of self-incompatibility, in which the flowers of the incompatibility types are morphologically distinguishable, is known in 22 angiosperm families (48). It is likely that these mostly represent separate, independent evolutionary origins, since there are no evident relationships between the different families that have heterostylous self-incompatibility (22). Any model for the evolution of heterostyly must be consistent with the known inheritance of the incompatibility types and the associated floral differences. There are at present two classes of theory about the origin of the distylous form of heterostyly (with two floral morphs). One view is that heterostyly originated from initially self-incompatible species (presumably with a sporophytic system, as this is the kind of system in distyly) by loss of alleles (105, but see 20); on this view, the evolution of heterostyly has nothing to do with inbreeding avoidance, as this is already assured. However, there is no known case of sporophytic incompatibility in any of the families which have heterostyly (22). Another view is that the type of self-incompatibility system found in heterostyled plants might have evolved from a self-compatible state, and then the morphological heterostyly evolved in response to selection pressures imposed by the pollination mechanism. On this view, at least the first step in the evolution of distyly is a means to avoid inbreeding. This idea is the basis of a theoretical model of the evolution of distyly (25). The model is problematical in that the first step (the spread of a sporophytically acting allele that makes the pollen self-incompatible) requires the unlikely circumstance that the product of the selfing rate and the inbreeding depression must exceed one half. As in the case of homomophic self-incompatibility, heterostyly may have evolved so few times that one can accept that unlikely circumstances have been involved. It would be more satisfactory if we had definite evidence that avoidance of inbreeding was indeed a factor in promoting, or is today important in, the maintenance of such systems.

The tristylous kind of self-incompatibility system (with three floral morphs) is even less well understood although some attempts have been made at modelling its evolution and breakdown (19). At present, it is not known for certain how often the breakdown of heterostyly is due to an increased selec-

tive advantage for selfing, for example due to insufficient pollination (18, 113), so that any disadvantages of inbreeding are outweighed. There appear to be correlations between loss of the heteromorphism and of the self-incompatibility with colonization of marginal areas (160) as is also seen in distyly (7).

DIOECY The rôle of inbreeding depression in the evolution of dioecy in plants has been very controversial, probably because for this type of breeding system it is relatively easy to imagine alternative selection pressures that would favor separation of the sexes on different individuals over the hermaphrodite or other cosexual state. It is also clear from theoretical considerations that dioecy cannot evolve solely as a system for avoidance of inbreeding (see below). Darwin (36) pointed out that: "As we must assume that cross-fertilization was assured before an hermaphrodite could be changed into a dioecious plant, we may conclude that the conversion has not been effected for the sake of gaining the great benefits which follow from cross-fertilization." It therefore seemed likely to Darwin that the reason for the evolution of dioecy was that it makes the most effective use of limited resources for reproduction.

It is clear that inbreeding avoidance alone cannot account for the evolution of dioecy (17). Although females can invade a cosexual population, provided that the product of the selfing rate and the δ parameter exceeds one half, their spread becomes much more likely if they also receive some direct fitness benefit from ceasing to have male function, e.g by reallocating resources so as to increase female fertility or survival. Also, once females have become established in a population, which is now polymorphic for females and cosexuals, alleles that make the cosexual type more male can be favored, but this requires that any decrease in their female fertility is compensated for by a greater increase in male fertility (17). The evolution of dioecy therefore need not involve avoidance of inbreeding, though it is likely to have played a part. Empirical evidence in support of this view is that the pathway via polymorphism for cosexual and male morphs appears to be rare or absent, although it could occur as easily as that via females if inbreeding avoidance were irrelevant because the ancestral state is one of complete outbreeding (21). Furthermore, whenever the closest relatives of dioecious species have been tested, they appear to be self-compatible, which is unlikely if dioecy commonly evolves in self-incompatible forms (22, but see 52). Finally, dioecy appears to show a negative association at the taxonomic level with self-incompatibility (22, 151), as would be expected if avoidance of inbreeding has been a factor favoring females. Since a positive association might be expected if self-incompatibility also evolved as an outbreeding system (6), the finding of a negative association would give fairly strong support to the view

that avoidance of inbreeding is generally a factor in the evolution of dioecy. It is likely that other factors have also been involved in the evolution of dioecy; several such factors are reviewed by Lloyd (89), who makes it clear that the explanations for associations between dioecy and demographic and ecological (e.g pollination or fruit dispersal systems) factors are unlikely to be found in the strength of inbreeding depression.

INCEST AVOIDANCE AND DISPERSAL IN ANIMALS In many animal species, individuals tend to disperse before mating, which has the effect of reducing the chance of mating with relatives. However, it is not clear whether this provides the main evolutionary pressure that maintains or initiates dispersal behavior in any species. The fact that the two sexes often show different tendencies for dispersal strongly suggests that inbreeding avoidance is not the only advantage for dispersal, but that other, sex-specific costs and benefits must exist. Several possibilities and theoretical models have recently been reviewed (55, 159); the importance of inbreeding avoidance remains uncertain.

There is some evidence that animals of several species avoid mating with relatives when they happen to be in situations when this is a possibility (see references in 62), but in other cases there is no evidence for any nonrandomness to the mating, so that matings with relatives occur at frequencies expected from the chance of coexistence of relatives on the same area, taking the dispersal patterns into account (56, 154). Behavioral studies in laboratory situations suggest that close inbreeding as well as distant crossing is sometimes but not always avoided (reviewed by Bateson, 9). In total, therefore, there is a certain amount of evidence for avoidance of close inbreeding in animals, but it is by no means universal or absolute.

CONCLUSIONS

As will be seen from the data presented above, the magnitude of inbreeding depression can be very great, in some species of animals and plants, and it seems fair to say that it has if anything been generally under- rather than overestimated. This is mainly due to the fact that it is difficult to measure inbreeding depression at all possible stages of the life cycle, so that the data usually underestimate the impact of inbreeding on net fitness. This is clearly brought out in the studies on *Drosophila* (Table 1). Even when only a single component of fitness is measured, however, substantial inbreeding depression is sometimes found, as in the gymnosperm data reviewed above. Shields (132, p. 59) suggests that inbreeding depression is often less important than appears from the size of effects found, because these effects are mainly manifested at the earliest stages of life. Thus, if there is competition between

siblings, the loss of some progeny due to inbreeding depression might be unimportant for the parents' fertility. Although not nearly enough data are currently available from natural populations, it is clear that inbreeding depression often affects growth and survival of progeny after the time when this early competition is occurring, and there are substantial effects on fertility in many species studied. Inbreeding depression therefore is a strong force acting to reduce the genetic value of inbred progeny.

It is important, in estimating the magnitude of inbreeding depression, to be clear that its evolutionary consequences depend on the difference between the progeny of inbreeding, such as selfing, and progeny produced by outcrossing; this is the comparison that one should therefore make when collecting this type of data. It is not relevant to compare inbred progeny with naturally produced progeny, such as open pollinated progeny in plants, because the matings that produced these may be a mixture of inbreeding and outcrossing, and the relative proportions of the two are usually unknown. Several studies of inbreeding depression are rendered less useful because that was the only comparison made—for example those noted in Table 3, including comparisons of the progeny of cleistogamous (selfed) flowers and chasmogamous (partly outcrossed) flowers in *Impatiens* species, and also several studies on gymnosperm species which we have therefore omitted from our review.

We have also examined the evidence for the view that inbreeding depression is as a rule low in partially inbreeding populations, while it has high values in outbreeders. This view has been very widely accepted. For example, Stebbins (144, p. 165) states: "In nearly every major subdivision of the plant kingdom some species require cross-fertilization, and if self fertilized produce either no offspring or else weak and degenerate ones, while other species, often closely related, are regularly self fertilized and seem to suffer no ill effects of this continued close inbreeding." Shields (132, pp. 55–56) also emphasizes that normally inbreeding populations will suffer little inbreeding depression. But such statements ignore the effects of crossing with unrelated individuals in normally self-fertilizing species or populations, which may result in a significant fitness gain. From the theoretical results and the data reviewed above, it seems clear that, even in quite highly inbred populations, inbreeding depression in the sense defined above can be of substantial magnitude. The data available at present are not very extensive, however, and it would be very valuable to get more inbreeding depression data from natural populations with known breeding systems. There is also a need for more theoretical work, particularly to investigate the effect of associations in transmission of alleles at different loci under selection, which are likely to be an important feature of partially inbred populations. The theoretical results obtained so far do not incorporate this propcrty and their general validity must therefore remain uncertain.

The effort to make better models of inbreeding depression is likely also to yield further understanding of its causes. At present, it seems clear that mutational load is of sufficient magnitude to account for a substantial part of observed inbreeding depression in those few organisms for which there are adequate data, and it is unnecessary to assume a large contribution from loci with overdominance, though this does not of course rule out the existence of some such loci.

Whatever the causes of inbreeding depression, it seems clear that it is often a strong effect and, as such, seems very likely to have played a part in the evolution of plant breeding systems such as self-incompatibility (including heterostyly) and dioecy, of course in conjunction with other factors that must affect plant reproductive success. The situation is not so clear when one considers the evolution of animal behavior patterns that reduce inbreeding, because these could also be selectively favored for other reasons.

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