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A QUANTITATIVE-GENETIC PERSPECTIVE ON CONSERVATION ISSUES

Michael Lynch

INTRODUCTION

The multiplicity of populations, species, and higher taxonomic levels that we call *biodiversity* is a product of thousands to billions of years of evolution. Essentially everyone agrees that the short-term key to maintaining this diversity is the protection of critical habitat upon which species have depended historically. However, comprehensive strategies for preserving biodiversity require both prospective and retrospective views of the issues. Looking to the future, a primary consideration is the preservation of intrinsic genetic features that enable evolutionary lineages to cope with challenges from changing environments.

Whether intentional or a matter of chance, the current policy of the United States government in decisions to formally list species as endangered or threatened under the Endangered Species Act (U.S. Fish and Wildlife Service, 1992) has been to forego listing until a candidate population has dwindled to about 1,000 individuals in the case of animals, and 100 individuals in the case of plants (Wilcove et al., 1993). Based on our knowledge of the vulnerability of small populations to demographic and environmental stochasticity alone, such target sizes for listing are well within the range in

which the short-term risk of extinction is of significant concern (Ludwig, 1976; Leigh, 1981; Shaffer, 1981; Ginzburg et al., 1982; Goodman, 1987; Burgman et al., 1992; Lande, 1993; Foley, 1994). The results reviewed in this chapter provide a genetic perspective on the issues.

Most of the features of organisms that we value involve their outward appearances—morphology, behavior, and in some cases, physiology, the very characters upon which natural selection operates. Most characters of this nature appear to be products of tens to perhaps hundreds of genetic loci, and their expression can be modified by numerous environmental factors (Wright, 1966; Falconer, 1981; Lande, 1981), although there are exceptions (Gottlieb, 1984; Orr and Coyne, 1992). This conclusion is based on indirect statistical inference, rather than on direct observation of specific gene products. Nevertheless, over the past half century, a rich theory has developed to explain the emergent genetic and evolutionary properties of complex characters based on the assumption of multifactorial inheritance. This field of study, known as *quantitative genetics*, has been subject to considerable empirical scrutiny, and its long history of successful application in plant and animal breeding programs testifies to its practical utility (Falconer, 1981; Hallauer and Miranda, 1981; Pritchner, 1983; Wricke and Weber, 1986). There seems to be little question that the field of conservation genetics could profit from an influx of quantitative-genetic thinking.

When phenotypes are a function of multiple genetic and environmental effects, it is essentially impossible to ascertain an individual's genotype from its outward appearance. However, quantitative-genetic studies provide a basis for identifying sources of variation contributing to individual differences. Information on the relative contributions of genes and environment to the total variation in a population is acquired by comparing phenotypes of relatives. For example, a parent passes on a single gene per genetic locus to each of its offspring, but except in the case of cultural inheritance or strong maternal effects, most environmental effects are not transmitted. Consequently, the resemblance between parents and their offspring is largely, or entirely, a function of variable genes in the population. If all parents have identical genotypes, their phenotypic differences are due entirely to environmental effects, and their phenotypes are uncorrelated with those of their progeny.

One of the most familiar concepts in quantitative genetics is the heritability of a trait, h^2 , which is the fraction of the phenotypic variance for the trait that has an additive genetic basis. As a first-order approximation, the heritability of a trait is equivalent to the slope of a regression between midparent (mean value of the two parents) and offspring phenotypes. The heritability concept is important because it relates in a simple way to the ability of a population to evolve in response to directional selection.

A fundamental law of evolutionary biology is expressed by $\Delta\bar{z} = h^2S$, which states that the rate of evolution of the mean phenotype $\Delta\bar{z}$ is equal to the product of the selection differential S (the change in the mean phenotype in the population caused by selection prior to reproduction) and the heritability of the trait h^2 (Falconer, 1981). Often referred to as the breeders' equation, this formula provides the theoretical basis for most selection programs in plant and animal breeding. The breeders' equation nicely separates evolution into two components—selection and inheritance. Selection favors individuals on the basis of their phenotypes, regardless of whether the favorable features are due to genetic or environmental effects. However, the degree to which the selective change in the mean phenotype is transmitted across generations depends on the heritability of the trait. Since heritability has a zero-to-one range, it can be viewed as the efficiency with which a population responds to natural selection.

The goal of most conservation-genetic programs is to preserve significant pools of heritable variation, while simultaneously preventing the chance fixation of deleterious alleles (Foose et al., 1986; Falk and Holsinger, 1991; Hedrick, 1992; Hedrick and Miller, 1992; Lande, 1995). As testified by numerous chapters in this volume, progress toward these goals is generally monitored by use of molecular markers. Implicit in this approach is the assumption that molecular techniques do, in fact, serve as suitable surrogates for estimating adaptive genetic diversity and population-genetic structure. In the following section, I point out some of the limitations of molecular genetic approaches to conservation biology (see also Hedrick et al., 1986), and some reasons why molecular surveys might sometimes be misleading. That section motivates the remainder of the chapter, in which I advocate the use of quantitative-genetic principles as supplemental guides to developing management programs in conservation biology.

MOLECULAR VERSUS QUANTITATIVE-GENETIC APPROACHES TO CONSERVATION ISSUES

Several attributes of molecular markers, especially those that are DNA-based, have led to their widespread use in conservation studies. Molecular methods have the advantage of sampling broadly over the genome, and those that are based on the polymerase chain reaction can be applied to live organisms with little disturbance, and even to museum specimens, providing a historical perspective of gene turnover. DNA differences among individuals and/or populations have an unambiguous genetic basis, and the fact that most molecular polymorphisms behave in an essentially neutral fashion makes them very useful for ascertaining pedigrees, reconstructing

phylogenies, identifying phylogeographic patterns, and estimating patterns of gene flow (Avise, 1994; Milligan et al., 1994; Moritz, 1994).

Molecular studies in conservation biology often take the data a step further, using them to infer *adaptive* features of population-genetic structure. For example, a lack of molecular variation in the cheetah has been taken to imply an absence of genetic variation for adaptive quantitative characters and, by extrapolation, enhanced risk of extinction due to genetic homogeneity (O'Brien et al., 1985; see Chapter 3). The confidence that can be attached to such extrapolations is limited (Caughley, 1994). Although empirical data on the matter are in short supply, there are several good theoretical reasons to doubt that a strong connection will normally be found between levels of molecular and quantitative-genetic diversity within populations:

1. Variation at the molecular level (heterozygosity) is introduced to a population at the per-locus rate of mutation for the molecular marker, typically on the order of 10^{-8} to 10^{-5} per year (Kimura, 1983), whereas variation for quantitative traits (heritability) is introduced at a rate of approximately 10^{-3} to 10^{-2} per generation (Lynch, 1988a). Consequently, populations that go through significant-enough bottlenecks to lose most of their genetic variation will exhibit the molecular signature of such an event for tens to hundreds of thousands of years, while having ample time to recover normal levels of heritable variation (Lande and Barrowclough, 1987). A possible example of this situation is provided by a recent study of the highly endangered cotton-top tamarin. This species has a very low level of molecular heterozygosity, nearly identical to that in the cheetah, yet it exhibits a rather high level of heritability for body weight (Cheverud et al., 1994).

2. Although the expected level of heterozygosity at neutral molecular markers declines linearly with the inbreeding coefficient, when significant sources of variation for quantitative traits are due to nonadditive gene action (dominance and epistasis), substantial departures from this behavior are seen. For example, due to the changes in the average effects of genes that occur as the frequencies of interacting genes are altered by genetic drift, it is possible for the expected additive genetic variance to increase with a population bottleneck (Robertson, 1952; Goodnight, 1988; Cockerham and Tachida, 1988; Whitlock et al., 1993; Willis and Orr, 1993). Such increases have been observed in bottlenecked populations of house flies (Bryant et al., 1986; Bryant and Meffert, 1993) and fruit flies (López-Fanjul and Vilaverde, 1989), although interpretation of the adaptive significance of these results is complicated by the fact that the inflation of the genetic variance is typically accompanied by a reduction in mean fitness.

3. For reasons purely related to statistical sampling, the relationship between molecular and quantitative-genetic variation is expected to be weak. Even for a quantitative trait with a purely additive genetic basis, the variation in quantitative-genetic parameters that arises among small populations can be enormous (Avery and Hill, 1977; Weir et al., 1980; Lynch, 1988b). Components of quantitative-genetic variance can drift substantially above or below their expected values, as López-Fanjul et al. (1989) have demonstrated in replicate populations of *Drosophila*. In addition, empirical estimates of quantitative-genetic parameters are subject to substantial sampling error.

4. Similar sampling problems exist in the estimation of heterozygosity with molecular markers—unless a substantial number of loci and individuals has been assayed, the sampling variance of measures of molecular variation can be very high (Nei and Roychoudhury, 1974; Mitton and Pierce, 1980; Chakraborty, 1981; Lynch and Crease, 1990; Lynch and Milligan, 1994). This point is well illustrated by an experiment that put replicate populations of mosquitofish through small bottlenecks (Leberg, 1992). Although the average response of the replicates was a reduction in allozyme heterozygosity, some replicates exhibited increases. Even when a large enough survey is done that one can be relatively confident that an accurate assessment of the molecular heterozygosity has been acquired, the molecular-marker loci will provide little insight into conditions at loci underlying adaptive variation unless a large fraction of the former are tightly linked to the relevant quantitative-trait loci. This seems unlikely except in species with very small chromosome numbers. In the absence of such linkage, marker data will provide little information as to whether past selective conditions might have led to abnormally low or high levels of genetic variation for adaptive quantitative traits.

All of the above caveats can also be used as arguments against the indiscriminate use of *interdemnic* measures of molecular divergence to derive inferences about *adaptive divergence*. Certainly, significant molecular divergence provides strong evidence that the *opportunity* for adaptive divergence has existed. However, a lack of molecular divergence is uninformative, an issue to which we will return later.

Not many empirical studies have been done on the relationship between molecular variation and quantitative-trait variation, and only two of these have actually considered the genetic component of phenotypic variance. In a comparison of several laboratory populations of *Drosophila melanogaster*, Briscoe et al. (1992) found a strong, positive correlation between allozyme heterozygosity and the heritability of bristle number. Since this character is

known to have an additive genetic basis and to be under only weak natural selection, it is much more likely to reflect the patterns of variation of neutral molecular markers than characters more closely related with fitness, which often exhibit a large nonadditive component (Falconer, 1981). In our studies of several *Daphnia* populations, we have yet to find an association between allozyme heterozygosity and the total genetic variance for fitness characters (Lynch and Spitze, in prep.)

Studies that have focused on phenotypic variation have yielded mixed results. Yezzerinae et al. (1992) found a very weak, but positive, correlation between allozyme heterozygosity and morphological variation within populations of rufous-collared sparrows (*Zonotrichia capensis*), and Strauss (1991) found a strong positive correlation between allozyme heterozygosity and phenotypic variation within populations of freshwater sculpins in the genus *Cottus*. On the other hand, in humans (Kobyliansky and Livshits, 1983), fox sparrows, and pocket gophers (Zink et al., 1985), there appears to be a weak, inverse relationship between the enzyme heterozygosity in a population and its morphological variation. Interpretation of these kinds of results is difficult. When the measure of morphological variation is purely phenotypic, it is unclear whether the fit would be better or worse if it were based purely on the genetic component of variation. Arguments have been made, with a fair amount of supporting evidence, that homozygous individuals are more developmentally unstable, and hence exhibit more phenotypic variation for purely environmental reasons than heterozygous individuals (Lerner, 1954; Soule, 1982; Palmer and Strobeck, 1986). If this is generally true, we should expect a negative correlation between molecular variation and the environmental component of phenotypic variation to obscure any positive relationship between molecular and quantitative-genetic variation.

In summary, some major challenges confront a science of conservation genetics that relies largely on molecular markers—most notably, to document a connection between molecular and adaptive quantitative-genetic variation, and to develop methods for rapidly assaying the latter in natural populations. Although the methods of quantitative genetics have almost never been applied to problems in conservation biology, in one sense, intensively studied populations of endangered species are ideally suited to such analysis. For captive populations with controlled breeding programs and for marked field populations, substantial information on genealogical relationships is often available, in which case the only additional labor required for a quantitative-genetic analysis is the measurement of the traits of interest. This, however, is where a difficult and perhaps unanswerable question arises. What characters should be measured? In almost all cases, it will be a judgment call as to which traits are currently most critical to survival and reproduction, and even more so as to which ones are most likely to be

confronted with future selective challenges. As will be argued later, quantitative genetics certainly has much to contribute to endangered species management, but as in the case of molecular analysis, there are limits to what can be accomplished.

Rather than focusing on the practical methodology of quantitative genetics, which is amply covered in many textbooks, the remainder of this chapter outlines several basic theoretical principles that have important and general implications for the management of species for long-term survival. Particular attention is given to the genetic consequences of small population size, one attribute that all endangered species have in common, with a goal of identifying the minimum effective population size necessary to secure the genetic integrity of a population. Much of the literature cited is quite technical mathematically, and an attempt has been made to reduce the basic results to simple qualitative relationships that may be useful to those involved in management decisions.

MAINTENANCE OF ADAPTIVE VARIATION

Most populations, even those undisturbed by human activity, are exposed regularly to temporal and spatial variation in physical and biotic features of the environment. Although most organisms are endowed with an array of behavioral and/or physiological mechanisms for coping with short-term environmental changes, the range of environments within which such homeostatic mechanisms are operative is normally confined to the conditions experienced over recent evolutionary time. In principle, some species can cope with new selective challenges by simply migrating to suitable habitat (Pease et al., 1989). However, endangered species typically live in highly fragmented habitats with inhospitable barriers to movement. This leaves adaptive evolutionary change as the primary means of responding to selective challenges.

There is an additional reason why the maintenance of evolutionary flexibility may be especially crucial for the long-term survival of endangered species. The same human activities that threaten their demographic stability may also impose selective pressures that are substantially greater than those typically experienced in natural settings. For many species, habitat degradation, environmental pollution, global climatic change, species introductions, harvesting, and so on, impose an array of conditions that have never been experienced before. As noted previously, the ability to respond to novel selective challenges is proportional to the additive genetic variance for the selected trait. Thus, a common goal of genetic conservation programs, the maintenance of adaptive genetic variation, is well founded.

In small isolated populations, three factors interact to determine standing levels of genetic variation for characters associated with morphology, physiology, and behavior. First, most forms of natural selection cause a reduction in the genetic variance by eliminating extreme genotypes, the exact amount depending on the intensity of selection and the form of the fitness function (Shnol and Kondrashov, 1993). Second, small populations with an effective number of breeding adults N_e also lose an expected fraction $1/(2N_e)$ of their genetic variance each generation by random genetic drift. Finally, genetic variation is added to a population each generation by mutation, at the rate σ_m^2 . When populations are kept at a constant size and under constant selective pressures, a quasi-equilibrium level of genetic variance eventually evolves, at which point the loss due to selection and drift is approximately balanced by mutational input.

For populations with effective sizes smaller than a few hundred individuals, the expected amount of variation for a typical quantitative character is nearly independent of the strength of selection and is largely a result of mutation-drift balance (Keightley and Hill, 1988; Barton, 1989; Bürger et al., 1989; Howle, 1989; Foley, 1992). This situation arises with polygenic characters because the forces of selection are distributed over large numbers of loci, rendering the selective pressures on specific loci small enough to be overwhelmed by random genetic drift. Under these conditions, characters with an additive genetic basis have an expected genetic variance equal to $2N_e\sigma_m^2$. This result, which is also the neutral expectation (Lynch and Hill, 1986), is fairly general. It depends very little on whether gene action is nonadditive or on the linkage relationships of the constituent loci. Thus, for small populations, a doubling in population size effectively doubles the evolutionary potential of the population.

As the effective population size increases, random genetic drift becomes less significant as an evolutionary force, until with large populations, the equilibrium level of genetic variance is due entirely to selection-mutation balance. There is still some debate as to the magnitude of the genetic variance resulting from selection-mutation balance, as it depends on the gametic mutation rate and the distribution of mutational effects, neither of which are very well understood (Turelli, 1984; Barton and Turelli, 1989). However, there seems to be general agreement that the average genetic variance is essentially independent of population size once N_e exceeds 1,000 or so individuals. This does not mean that a population with $N_e > 1,000$ is genetically equivalent to an effectively infinite population.

Except in populations containing many thousands of individuals, random genetic drift causes the actual genetic variance in a population to wander around its expected value from generation to generation (Keightley and Hill, 1989; Zeng and Cockerham, 1991). The variance of the genetic variance is

inversely related to the number of mutations entering the population per generation, such that the coefficient of variation of the additive genetic variance is approximately $(2\mu N_e)^{-1/2}$, where μ is the genomic mutation rate for the character (the sum of the mutation rates for the constituent loci; Lynch and Hill, 1986; Barton, 1989; Bürger and Lande, 1994). Thus, if μ were 0.05, which appears to be reasonable for a typical quantitative trait (Lande, 1975; Turelli, 1984; Lynch, 1988a), the coefficient of variation of the genetic variance would be on the order of 0.3 and 0.1 for populations with $N_e = 100$ and 1,000. Due to inheritance, any random declines in the genetic variance are likely to persist for several generations. For N_e less than a thousand or so, the expected correlation of the genetic variance in the same population at times separated by t generations is approximately $e^{-t/(2N_e)}$ (Bürger and Lande, 1994), which declines only to 0.5 after $t = 1.4N_e$ generations.

The practical implication of these results is that by chance, even in the absence of a population bottleneck, in a population of moderate size the genetic variance for a quantitative trait can essentially disappear temporarily and remain at a low level for many generations until mutation has had an opportunity to replenish it. Such temporary excursions to low levels of genetic variance can jeopardize the survival of populations inhabiting changing environments (Bürger and Lynch, 1994).

One important caveat to the aforementioned results is that they apply largely to characters with a purely additive genetic basis, which may not include many fitness-related characters. Limited work has been done on the maintenance of genetic variance by drift-selection-mutation balance when genes exhibit dominance, and the results suggest that the predictions of the purely additive model are still reliable as a first approximation (Lynch and Hill, 1986; Caballero and Keightley, 1994). Whether this is true when epistatic interactions are important remains to be seen.

The Minimum Effective Size for an Adaptively Secure Population

Some past attempts to identify a critical minimum population size from a genetic perspective have focused on goals such as the maintenance of 90% of the genetic variability present in the ancestral (predisturbance) population for 200 years (Franklin, 1980; Soulé, 1980; Soulé et al., 1986; Lande, 1995). Short-term goals of this nature take into consideration the fact that populations that are dwindling in size cannot be in equilibrium. However, such goals are rather arbitrary with respect to choice of acceptable loss and time span.

For long-term planning, an alternative approach to defining a genetically

secure population is to consider the equilibrium conditions outlined previously. Beyond an effective population size of approximately 1,000 individuals, any further increase in N_e will not usually enhance the expected amount of genetic variance maintained in a population. For many species, the effective population size is often on the order of one-tenth to one-third of the actual number of breeding adults (Heywood, 1986; Lande and Barrowclough, 1987; Briscoe et al., 1992). Thus, from the standpoint of the maintenance of adaptive variation, the $N_e > 1,000$ criterion translates into the need for stable persistence of 5,000 to 10,000 breeding adults each generation. Programs to manage populations at a larger size solely to enhance their average evolutionary potential would be unlikely to achieve that objective, although a further reduction in the fluctuations of the genetic variance would be obtained. Additional considerations on the maintenance of adaptive variation in managed populations, including population subdivision and migration, are provided in Lande (1995).

The Maximum Rate of Sustainable Evolution

In the development of policies for species protection, the major focus is usually on short-term local issues such as dam and road building, logging and mining, grazing, housing development, and so on. However, the evidence is mounting that human activity is causing, and will continue to cause, global changes in the temperature and chemical composition of the atmosphere (Abrahamson, 1989; Wyrman, 1991; Kareiva et al., 1993). These types of changes, particularly when combined with habitat fragmentation, pose threats to all species, even those that are currently abundant, and raise a fundamental question: What is the maximum rate of environmental change that can be tolerated by a species?

Laboratory studies with several species of plants and animals have shown that continuous programs of intense directional selection on quantitative traits often lead to approximately linear changes in mean phenotypes for several dozens of generations (Jones et al., 1968; Kress, 1975; Dudley, 1977; Eisen, 1980; Weber and Diggins, 1990). Although the effective sizes of the populations involved in these studies are generally on the order of only a few dozen individuals, it is not unusual for the evolutionary change of the mean phenotype to exceed five to ten phenotypic standard deviations before the response to selection begins to diminish. Such results clearly indicate that even small isolates of natural populations typically harbor enough quantitative-genetic variation that, when confronted with a novel environment, mean phenotypes well outside of the observed range of variation in the initial population can evolve rapidly.

After a few dozen generations of fairly strong selection, laboratory experi-

ments usually exhibit a selection plateau due to the evolutionary advancement of genes with major effects on the selected trait and negative pleiotropic effects on fitness (i.e., to a conflict between artificial and natural selection). Such antagonisms are less likely to arise in more natural settings, where genes are selected for their total effects on fitness. Nevertheless, in small populations, the rate of phenotypic evolution can become limited by the availability of additive genetic variance.

Once the favorable genes in a founder population have been advanced to fixation by natural selection or lost by random genetic drift, all future evolutionary change will be dependent upon the input of new variation by mutation. This transition certainly takes on quantitative significance by the time N_e generations have elapsed (Clayton and Robertson, 1955; Lynch and Hill, 1986). For example, even in the absence of selection, the fraction of initial additive genetic variation surviving after t generations of isolation is approximately $e^{-t/(2N_e)}$, whereas the variation resulting from mutations subsequent to the founder event has expected value $2N_e\sigma_m^2(1 - e^{-t/(2N_e)})$. Thus, after approximately $1.4N_e$ generations have elapsed, 50% of the genetic variance in the founder population is expected to have been lost, while the new variation due to mutation will have increased to 50% of its equilibrium value. After approximately $4.6N_e$ generations, 90% of the variation in the founder individuals is expected to have been lost, while the new variation from mutations will have increased to within 10% of its equilibrium value.

Consider a population confronted with a gradual long-term change in a critical environmental parameter (e.g., temperature, humidity, prey size, etc.). If the rate of environmental change is sufficiently slow and the amount of genetic variance for the characters needed to cope with it is sufficiently high, then the population will be able to slowly track the environmental change evolutionarily, without a major reduction in population size. If, however, the rate of environmental change is too high, the selective load (reduced viability and fecundity) on the population will exceed the population's capacity to assimilate new genetic variation and maintain a positive rate of growth. In this case, although the population may respond evolutionarily, it will go extinct in the process. Thus, for any population, there must be a critical rate of environmental change that allows the population to evolve just fast enough to maintain a stable size.

Theoretical studies on the response to long-term directional selection show that as populations settle into a new equilibrium level of genetic variance, they also settle into an evolutionary trajectory that is parallel to the moving optimum for the selected trait, provided the optimum is not out of the range of possible adaptive variation (Lynch et al., 1991; Lynch and Lande, 1993; Bürger and Lynch, 1994). Thus, the critical rate of environmental change is equivalent to the maximum rate of sustainable evolution. The amount by

which the mean phenotype lags behind the moving optimum is determined by the strength of selection and the magnitude of genetic variance for the trait. The magnitude of the lag in turn determines the degree of maladaptation of the population and hence its demographic potential.

To gain some appreciation of the magnitude of environmental change that can be tolerated for a sustained period of time, consider the situation in which a population is exposed to a Gaussian (bell-shaped) fitness function with a constant width but moving optimum for the selected trait. In units of phenotypic standard deviations, the critical rate of environmental change (rate of movement of the optimum) beyond which such a population is incapable of replacing itself is less than $\phi \bar{h}^2 [2r_{\max} - (1/(2N_e))]^{1/2}$, where $\phi = \sigma_z/\sigma_w$ is the ratio of the phenotypic standard deviation of the trait, and r_{\max} is the fitness function, \bar{h}^2 is the equilibrium heritability of the trait, and r_{\max} is the rate of population growth in a constant environment (assuming in that case that the population is fully adapted, such that the mean phenotype coincides with the optimum; Lynch and Lande, 1993; Bürger and Lynch, 1994). What does this expression imply about the maximum sustainable rate of evolution?

First, we note that if the effective population size (N_e) is less than $1/(4r_{\max})$, a population has no long-term viability even in a constant environment. With such small population sizes, the mean phenotype drifts to a large enough extent from the optimum phenotype that the average selective load exceeds the demographic potential.

For populations with larger size (i.e., $N_e \gg 1/(4r_{\max})$), the critical rate of environmental change depends on the product $\phi \bar{h}^2$. Only limited work has been done on the equilibrium heritability of quantitative traits experiencing directional selection. However, it appears that for large populations, \bar{h}^2 is elevated somewhat above $2\mu/\phi^2$, where μ is the zygotic mutation rate for the trait (Bürger and Lynch, 1994). Thus, even for populations with effectively infinite size, the critical rate of environmental change is less than $2\mu[2r_{\max}]^{1/2}/\phi$. As noted previously, estimates of μ for typical quantitative traits appear to be on the order of 0.05 or smaller. ϕ appears often to be on the order of 0.1 to 0.4 (Turelli, 1984; Endler, 1986), and on time scales of generations, r_{\max} is usually less than 1.0. Since the preceding expression overestimates the critical rate of environmental change if the directional trend in the environment contains a stochastic component (Lynch and Lande, 1993), which is essentially always the case (Boag and Grant, 1981; Kalisz, 1986; Hairston and Dillon, 1990; Weis et al., 1992), our results imply that even large populations are unlikely to sustain rates of environmental change that exceed a few percent of a phenotypic standard deviation per generation. The situation is even more stringent in small populations (Lynch and Lande, 1993; Bürger and Lynch, 1994).

The practical implication of these results is that sustained periods of environmental change of fairly small magnitudes can eventually cause the selective mortality of a population to exceed its demographic potential. This conclusion applies to both common and rare species, and there is reason to believe that the demographic consequences of environmental change may be threshold in nature. The extent to which current long-term trends of global warming and atmospheric change will translate into a major extinction episode will depend on the degree to which such changes exacerbate the intensity of natural selection. In principle, climatic changes may induce shifts in the optima for multiple physiological characters required for coping directly with such changes, as well as generate secondary changes in species' ecological settings (abundances and phenotypes of predators, competitors, and prey items). Thus, for isolated populations in particular, it is conceivable that global climate change may impose as substantial a threat to long-term survival as habitat destruction currently poses for short-term survival.

POPULATION BOTTLENECKS: PURGING VERSUS FIXATION OF DELETERIOUS GENES

For many quantitative traits, the fitness effects of mutations may be context dependent (i.e., a mutation for smaller body size may be beneficial or detrimental depending on the current direction of selection for body size). However, it has long been thought that a large fraction of mutations is unconditionally deleterious. Such mutations influence the mean fitness of an isolated population in three ways. First, segregating mutations inherited from the ancestral population may either be purged by natural selection or they may rise to fixation by random genetic drift. Second, mutations arising in the isolated population lead to the establishment of a new segregational load defined by the balance between the present forces of drift, mutation, and selection. Third, a fraction of the mutations entering the population each generation becomes fixed by random genetic drift at some future time. Unlike the first two sources of mutation load, the fixation of recurrent deleterious mutations leads to a progressive loss in fitness. In the following sections, I consider how the accumulation of deleterious mutations can influence the mean fitness and risk of extinction of small populations.

Deleterious Genes in the Ancestral Population

Most attempts to model the genetic risk of extinction for small populations have focused entirely on rare deleterious genes carried in the founder

individuals (Senner, 1980; Barrett and Charlesworth, 1991; Lacy, 1992, 1993; Halley and Manasse, 1993; Hedrick, 1994; Mills and Smouse, 1994). The primary concern of these studies has been to ascertain the expected buildup of inbreeding depression due to the random increase in frequency of deleterious recessive genes. However, with the exception of Hedrick (1994), who confined his analysis to full-sib mated lines, all of these studies have used rather *ad hoc* genetic models. For example, Senner (1980) simply assumed that the load due to inbreeding depression increases linearly with the average coefficient of inbreeding at neutral loci. Whereas Mills and Smouse (1994) allowed for a nonlinear response, their approach, as well as that of Senner, is phenomenological, ignoring the underlying genetic basis of inbreeding depression and failing to take selection against deleterious alleles into account. Lacy (1992, 1993) modeled inbreeding depression with a genetically explicit model, but he assumed that all of the recessive load is due to lethals at a single locus, with each founder individual carrying a unique allele. Such a scenario is inconsistent with extensive observations that the load in populations due to recessive deleterious genes is spread over many loci, a large fraction of which have small individual effects (Charlesworth and Charlesworth, 1987).

A popular idea in the design of captive breeding programs is that intentional inbreeding, combined with rapid population expansion, can lead to a purging of the deleterious genes from a population (Templeton and Read, 1983, 1984). Such a purging of inbreeding depression has, in fact, been recorded in short-term studies with flies (Bryant et al., 1990), plants (van Treuren et al., 1993), and mice (Bowman and Falconer, 1960; C.B. Lynch, 1977; Connor and Bellucci, 1979), although in the latter case it has only been accomplished at the expense of extreme selection (extinction) among replicate lines. Were this procedure to be generally successful, it would provide a powerful way for managing captive populations for viability. However, a close look at the issues raises questions about the utility of such a treatment.

The effects of small population size on the evolution of inbreeding depression need to be considered from two frames of reference. By eliminating the genetic variation within an isolated population, long-term inbreeding can lead to a situation in which any further inbreeding has essentially no effect on the number of homozygous recessive genes expressed per individual. Once this situation has been reached, from the standpoint of the current population, there is no inbreeding depression. However, this is certainly not the case from the standpoint of the ancestral population if, during the inbreeding process, deleterious genes have become fixed. This point is nicely illustrated by a study of self-fertilized lines of the normally outcrossing aquatic plant *Eichhornia paniculata* (Barrett and Charlesworth, 1991). Inbreeding

caused an immediate depression in fitness, but after only two generations of selfing there was no further decline, suggesting that the vast majority of loci affecting fitness had become homozygous within lines. Nevertheless, despite the absence of inbreeding depression within the derived lines, crosses between lines exhibited a substantial increase in mean fitness, as expected if the different lines had become fixed for different deleterious recessives. Similar results have been obtained for other species of habitually self-fertilizing plants (Charlesworth et al., 1990; Holtsford and Ellstrand, 1990; Ågren and Schemske, 1993). The salient point here is that the absence of local inbreeding depression does not eliminate the possibility that a population harbors a substantial mutation load.

A general understanding of the consequences of deleterious genes contained in founder individuals can be achieved as follows. Consider an ancestral population containing N individuals, each of which incurs an expected μ new deleterious mutations per generation. Let the relative fitnesses at a genetic locus for mutation-free homozygotes and mutant heterozygotes and homozygotes be, respectively, 1, $(1 - 2hs)$, and $(1 - 2s)$, where h is a measure of the degree of dominance ($h = 0.5$ denoting additivity). For large populations with reasonably stable sizes, there is a mutation-selection balance between the number of deleterious mutations arising each generation ($N\mu$) and the number eliminated by natural selection. Assuming that the mutant alleles do not have epistatic effects on fitness, this equilibrium load of mutations causes the mean fitness of individuals to be reduced to approximately $e^{-\mu}$ of that expected for an individual free of deleterious mutations (Haldane, 1937). Haldane's result has some remarkable features. First, it applies to all populations with effective sizes greater than $5/s$ (Kimura et al., 1963; Bürger and Hofbauer, 1994). Even with s as small as 0.001, this requires only that the population contain at least a few thousand individuals. Second, it depends only on the genomic deleterious mutation rate, not on the effects (s or h) of the individual mutations. This is because there is an inverse relationship between the effect of a mutation and its equilibrium frequency.

Haldane's result allows a prediction about the number of deleterious alleles that are likely to be inherited by a founder population. Let \bar{n} be the mean number of deleterious genes per individual in the ancestral population. Making the reasonable assumption that most deleterious alleles have low enough frequencies in the ancestral population that they are almost always in the heterozygous state, and assuming that mutations at different loci influence individual fitness independently, the mean fitness of an ancestral individual is approximately $(1 - 2hs)^{\bar{n}} \approx e^{-2hs\bar{n}}$. Setting this expression equal to Haldane's $e^{-\mu}$, the expected number of deleterious genes carried by a founder individual is found to be approximately $\bar{n} = \mu/(2hs)$.

regating mutations is approximately $(1 - 2hs)^{2N_e\mu} \simeq e^{-4N_e\mu hs}$. This value is greater than the expectation for an effectively infinite population, $e^{-\mu}$, if $N_e < 1/(4hs)$.

At first sight, this result might suggest that populations could be managed for a minimal mutation load by simply maintaining them in small isolates. However, the fact that very small populations have a reduced load due to segregating mutations is again misleading. In large populations, the mutation load results almost entirely from a balance between the input of new deleterious genes by mutation and their removal by selection. In small populations, selection is less effective, and the input of new mutations is balanced by some selective removal and fixation by random genetic drift. The progressive and permanent decline in fitness due to fixation of recurrent mutations in small populations is not inconsequential. With μN new deleterious mutations entering a population each generation, each with initial frequency $1/(2N)$, for populations with effective sizes small enough that selection is overwhelmed by random genetic drift, $\mu/2$ fixations are expected to occur per generation. This implies a decline in fitness per generation of $[1 - (1 - 2s)^{\mu/2}] \simeq (1 - e^{-\mu s})$, or approximately 2.2% with the *Drosophila* parameters.

The preceding discussion provides a qualitative framework for understanding the consequences of deleterious mutation accumulation for the viability of populations. Suppose that the maximum number of progeny produced per adult in the ancestral population is R . If the fitness load due to deleterious mutations increases to the point at which the probability of survival to maturity is less than $1/R$, the per capita reproductive rate will be less than one. At this point, the population is no longer capable of maintaining a stable population size, and as it begins to decline, a synergistic interaction between random genetic drift and mutation accumulation is set in motion (Lynch and Gabriel, 1990; Lande, 1994; Lynch et al., 1994, 1995). As the population size declines, random genetic drift becomes a more significant evolutionary force and the rate of accumulation of deleterious mutations increases, causing a further decline in population size. We refer to this extinction phenomenon, which can be quite rapid, as a *mutational meltdown*.

We have modeled the mutational meltdown using the *Drosophila* mutational parameters. For populations with effective sizes smaller than several dozen individuals, the mean time to extinction due to the buildup of mutation load is typically on the order of a few tens to a few hundreds of generations in the absence of any demographic or environmental stochasticity (Lynch et al., 1995). Of course, virtually all populations continuously experience both kinds of stochasticity (in the form of fluctuations in sex ratios, carrying capacities, and survival and reproductive rates). Such conditions

cause a reduction in the long-term effective population size, which under realistic conditions can reduce the time to entry to a mutational meltdown by an order of magnitude or more (Lynch et al., 1994, 1995).

There are additional reasons why the preceding results probably underestimate the threat of deleterious mutations to population survival. First, we have relied upon the mathematically tractable, but biologically implausible, assumption that mutations have constant effects s and h . However, it is primarily the effectively neutral fraction of mutations, that is, those with selection coefficients smaller than $1/(2N_e)$, that contributes most to the mutation load. If significant numbers of deleterious mutations have effects that are smaller than $1/(2N_e)$, as suggested previously, the rate of mutation accumulation will be substantially greater, and the mean time to extinction substantially smaller, than anticipated on the basis of the average mutational effect (Lande, 1994).

Second, the problem of deleterious mutation accumulation may be exacerbated in endangered species that are confined to breeding facilities. Since captive environments are usually quite benign (including services from dietitians, veterinarians, artificial inseminators, etc.), a real possibility exists that mutations that are significantly deleterious in nature are rendered nearly neutral. If that were the case, regardless of the population size, deleterious mutations would accumulate at nearly the neutral rate, $\mu/2$ per generation, although their effects would go undetected until the population was reintroduced into the wild. At that point, the population might no longer be capable of sustaining itself without continued human intervention.

Third, empirical evidence supports the idea that the expression of deleterious mutations is magnified in harsh environments. Relative to controls, *Drosophila* lines that have accumulated mildly deleterious mutations have substantially reduced fitness when raised under stressful conditions ($< 10\%$ of that in a benign environment; Kondrashov and Houle, in preparation). Moreover, numerous studies have shown that the expression of inbreeding depression, a consequence of deleterious recessive genes, is exacerbated in extreme environments (Parsons, 1971; Barlow, 1981; Dudash, 1990; Jiménez et al., 1994; Pray et al., 1994).

In summary, what little we know about deleterious mutations raises the real concern that their recurrent introduction can threaten the persistence of even moderately large populations over timescales of several dozens of generations. The issues are complex, and there is a serious need for more data in other species so that firmer quantitative statements can be made. However, for captive breeding programs in particular, there seems to be little question that management programs whose genetic focus is entirely on the deleterious genes contained in founder individuals are misguided.

The magnitude of \bar{n} depends on the mutational properties μ , s , and h . Unfortunately, estimates of these parameters are only available for a single higher organism, the fruitfly, although in this case the data are extensive (Mukai, 1964, 1969, 1979; Mukai et al., 1965; Mukai and Yamazaki, 1968; Ohmishi, 1977; Houle et al., 1992). A survey of the available data suggests that $\mu \approx 1.5$, $\bar{s} \approx 0.01$, and $\bar{h} \approx 0.36$ (Lynch et al., 1995). These estimates exclude lethal mutations which, in *Drosophila*, appear to arise at the rate of approximately 0.02 per genome per generation. These data imply that the average number of mildly deleterious segregating genes per individual is on the order of $\bar{n} \approx \mu/(2h\bar{s}) \approx 140$. The effects of individual mutations are, of course, variable. Some indirect evidence supports the idea that the distribution of deleterious mutational effects is approximately exponential (Gregory, 1965; Edwards et al., 1987; Mackay et al., 1992; Santiago et al., 1992; Keightley, 1995), with the frequency of a mutation decreasing with increasing effect.

Research on the fitness effects of spontaneous mutations in other organisms is necessary before we can be certain about the generality of the *Drosophila* results, but there is no reason to expect that they will be highly unusual. Thus, it seems reasonable to conclude that, since most individuals are expected to carry unique sets of rare deleterious genes, even small founder populations are likely to harbor segregating deleterious genes at several hundred loci. All such genes are subject to eventual chance fixation in a small founder population.

The worst-case scenario is realized when the size of the founder population is so small that random genetic drift completely overwhelms the power of natural selection. Roughly speaking, this requires that the effective size of the isolated population, N_0 , be $< 1/(2s)$, or using the *Drosophila* data, that $N_0 < 33$. Under these circumstances, the probability that a deleterious mutation goes to fixation is close to its initial frequency in the founder population. Thus, for deleterious mutations with additive effects, the average impact of a population bottleneck on mean fitness is essentially zero, although in any particular population, random genetic drift will cause the realized mean fitness to be above or below this expectation. For populations with sizes $> 1/(2s)$, some or all of the ancestral additive deleterious mutation load will be purged, and when $N_0 > 10/(2s)$, essentially all of it will be eliminated (Lynch et al., 1995).

Suppose now that the ancestral mutations are partially recessive, rather than additive, again averaging $\mu/(2hs)$ in number per individual. Assuming that these mutations are distributed over a large number of loci, then there are approximately $N_0\mu/(2hs)$ deleterious genes in the founder population, each with approximate frequency $1/(2N_0)$. Thus, if selection is completely ineffective (so that the fixation probability equals the initial frequency), the

number of deleterious mutations expected to become fixed in a permanently bottlenecked population is approximately $\mu/(4hs)$. In this extreme situation, the mean fitness would be $(1 - 2s)^{\mu/(4hs)}$, compared to $(1 - 2hs)^{\mu/(2hs)}$ in the ancestral population. The ratio of these two quantities is approximately $e^{\mu(1 - 1/(2hs))}$, which with the *Drosophila* parameters equals 0.56.

These simple qualitative arguments validate the idea that population bottlenecks can lead to a reduction in the average fitness of individuals. However, they also suggest that the depression in mean fitness due to the fixation of unconditionally deleterious mutations inherited from the ancestral population is unlikely to be more than 50% or so. This conclusion still needs some major qualification. First, the results cited indicate only what is expected to happen on average; in any particular case, random genetic drift will result in a situation that is somewhat better or somewhat worse than the expectation. Second, we have yet to consider the fate of the substantial number of deleterious mutations that arise subsequent to the founder event.

New Deleterious Mutations in the Isolated Population

As noted previously, for populations of moderate size, one may reasonably expect natural selection to lead to a substantial purging of the deleterious genes carried in the founder individuals. However, this gives a rather distorted picture of the true mutation load. At the same time the deleterious mutations inherited from the ancestral population are being eliminated, new ones are appearing. Indeed, so long as $N_0 > (5/s)$, a population will behave as though it is effectively infinite—the loss of old mutations by selection will be balanced by the input by mutation each generation, and the fitness due to segregating mutations will remain stable at $e^{-\mu}$, as predicted by Haldane (1937).

For populations with effective sizes smaller than $5/s$ breeding adults per generation, the fitness associated with segregating deleterious mutations can decline to a value less than $e^{-\mu}$, the minimum occurring when the effective population size is approximately $1/(2s)$ when mutations have additive effects (Lynch et al., 1995). With the *Drosophila* parameters, this result implies that populations with effective sizes of about 33 individuals will exhibit the highest load of segregating mutations. It may seem counterintuitive that the segregational load declines in populations below this point. However, as noted, in very small populations, the mutations behave as though they are effectively neutral. Under drift–mutation equilibrium, the expected heterozygosity per locus is $4N_0\mu$, where μ is the genic mutation rate, and the expected number of heterozygous loci per individual is $2N_0\mu$. Thus, for very small populations, the expected fitness associated with seg-

The Threat from Elevated Mutation Rates

An important issue relevant to long-term species survival is the presence of environmental mutagens. Over the past century, the release of environmental pollutants through human activities has almost certainly increased the mutagenic potential of the environments of many species beyond our own. For example, concern over the depletion of the ozone layer is largely motivated by the resultant increase in the intensity of ultraviolet radiation, a significant source of somatic mutations, and presumably of germline mutations in organisms with exposed gametes and embryos. Although a massive amount of bioassay research has been done on the short-term effects of various pollutants on survival and reproduction, almost no quantitative information exists on the consequences of environmental mutagens for the genomic mutation rate and spectrum of mutational effects in natural populations.

A simple extrapolation of Haldane's result provides some insight into the long-term consequences of an increase in the genomic mutation rate. For a large population, an increase in the genomic mutation rate by a factor of x will reduce the fitness from segregating mutations from $e^{-\mu}$ to $e^{-x\mu}$. Even disregarding the fixation of new mutations, it is clear that populations for which $x > \ln(R)/\mu$ are doomed to rapid extinction. If the genomic mutation rate estimate from *Drosophila* is reasonably representative of that in other organisms, the critical value of x is not very large. For example, with $R = 20$, a generous situation for many birds and mammals, and $\mu = 1.5$, it is only 2.0, and even with $R = 1,000$, it is 4.6. Thus, if the *Drosophila* estimate for μ is correct, the long-term consequence of a doubling of the genomic mutation rate would be extinction for many species. It is worth emphasizing that this argument applies to all species, regardless of their current population size, including our own. Although most governmental policies on the disposal of toxic pollutants are guided by human concerns about carcinogenesis, it is clear that the long-term effects of environmental mutagens on ecosystem stability warrant close attention.

POPULATION AGGMENTATION

An increasingly common strategy for maintaining wild populations of endangered species is augmentation with stock from breeding facilities. An implicit assumption of such procedures is that recipient populations, when they still exist, actually derive some benefit from an artificial boost in population size. There are, however, several reasons why the long-term deleterious consequences of supplementation may outweigh the short-term advantage of increased population size.

First, over evolutionary time, successful populations are expected to become morphologically, physiologically, and behaviorally adapted to their local environments. This principle has been most convincingly documented through reciprocal transplant experiments with plants, which have often shown adaptive divergence on spatial scales as small as a few meters (Schemske, 1984; Waser and Price, 1985; McGraw, 1987; Schmitt and Gamble, 1990; Galen et al., 1991). Thus, there is little question that the introduction of non-native stock has the potential to disrupt local adaptations.

This type of problem takes on added significance when the population employed in stocking has been maintained in captivity. As noted, captive environments are often radically different from those in the wild. Given the amounts of genetic variation that exist for most quantitative characters, over a period of several generations captive populations will naturally evolve behavioral and/or morphological phenotypes that perform best in the novel environment. Such "domestication" selection has been clearly documented with invertebrates and fish (Doyle and Hunte, 1981; Doyle, 1983; Frankham et al., 1986; Ruzzante and Doyle, 1991; Frankham and Loebel, 1992; Reisenbichler, in preparation). To the extent that the genes advanced by selection in captivity are actually deleterious in nature, as seems likely, given that they had previously been kept at low frequencies, domestication selection can only further detract from the potential success of a reintroduction program. Fairly convincing circumstantial evidence now exists that phenotypic changes that evolve in hatchery-reared salmonids are deleterious in nature (Reisenbichler, in preparation; see also Chapter 8). On the other hand, as noted previously, an overprotective captive breeding program may simply result in a relaxation of natural selection and the gradual accumulation of deleterious genes. For example, for hatchery-raised salmonids, egg to smolt survivorship is typically 50% or greater, as compared to 10% or less in natural populations (Waples, 1991).

Second, local gene pools can be coadapted intrinsically (Dobzhansky, 1948; Templeton, 1986; Lynch, 1991). Just as the external environment molds the evolution of local adaptations by natural selection, the internal genetic environment of populations is expected to lead to the evolution of local complexes of genes that interact in a mutually favorable manner. The particular gene combinations that evolve in any local population may be largely fortuitous, depending in the long run on the chance variants that mutation provides for natural selection. By breaking up coadapted gene complexes, hybridization can lead to the production of individuals that have lower fitness than either parental type, and can even occur between populations that appear to be adapted to identical extrinsic environments. Burton (1987, 1990a, 1990b) has provided extensive evidence for the breakdown

of physiological competence in crosses between populations of the intertidal marine copepod *Tigriopus californicus* separated by only tens of kilometers. Other dramatic evidence of outbreeding depression comes from observations of reduced fitness in crosses of inbred lines of flies (Templeton et al., 1976) and plants (Parker, 1992) adapted to identical environments. Crosses between outbreeding plants separated by several tens of meters can exhibit reduced fitness (Waser and Price, 1989), as can crosses between fish derived from different sites in the same drainage basin (Leberg, 1993) and crosses between clones of *Daphnia* from the same pond (Lynch and Deng, 1994). Populations that exhibit outbreeding depression upon crossing are clearly on different evolutionary trajectories.

Third, augmentation of wild populations with stock from captive breeding programs can have ecological consequences that have both immediate demographic effects and long-term evolutionary implications. For example, high-density hatchery populations of fish are prone to epidemics involving diseases that are uncommon in the natural environment. Such events provide strong selection for disease-resistant varieties of hatchery-reared fish, which subsequently can act as vectors to the wild population. The Norwegian Atlantic salmon is now threatened with extinction because of a parasite brought to Atlantic drainages by resistant stock from the Baltic (Johnsen and Jensen, 1986).

These three arguments strongly suggest that augmentation programs be used only as a last resort in the recovery and/or management of endangered species, even when both phenotypic and molecular data indicate strong similarities among demes. The studies cited here provide ample evidence that the absence of any obvious molecular divergence gives little, if any, insight into the potential for negative impacts of outcrossing. Even when the population subdivision of an endangered species is obviously due to human-induced fragmentation, a decision to manage the isolates as a single genetic entity by encouraging gene flow among demes can be shortsighted. Reproductively isolated groups created (or exaggerated) by human disturbance might reflect more natural units of genetic diversity that had arisen from long-term ecological and evolutionary forces, including isolation by distance. Alternatively, isolation induced by habitat loss may directly promote adaptive differentiation of demes to local conditions created by human activity. In either case, a management scheme that encourages interdemal migration might actually have the negative consequence of eroding local adaptation.

A particularly difficult issue underlying practical assessments of the potential for outbreeding depression concerns the timescale over which outbreeding depression is revealed. It is extremely common for the F_1 progeny of interpopulation crosses to exhibit enhanced fitness relative to their parents (Lerner, 1954; Thornhill, 1993), only to have a dramatic reduction in

fitness occur in the F_2 generation (Wu and Palopoli, 1994). In some situations, the development of negative consequences of mixing coadapted gene complexes can be more subtle, taking several generations to emerge fully (Lynch, 1991). Thus, what might initially appear to be a successful management decision, encouraging further augmentation, may later become a liability to the wild population (Reisenbichler, in preparation).

Arguments have been made that populations suffering from outbreeding depression will eventually recover by evolving new coadapted gene complexes out of the hybrid gene pool, and perhaps even benefit from the influx of genetic variation (Templeton, 1986; Templeton et al., 1990). However, given that we know essentially nothing about the timescale over which such recovery might occur, subjecting a small population to even a few generations of increased genetic risks of extinction seems hazardous. Once an augmentation program has proceeded to the point at which F_2 individuals have begun to appear, it will often be next to impossible to erase the process of introgression.

SUMMARY

1. The vast majority of research in the field of conservation genetics has been focused on the use of molecular markers to elucidate patterns of variation. Such information provides a valuable perspective on numerous issues such as phylogenetic and pedigree relationships, patterns of gene flow, and phylogeographic domains. However, molecular genetics has yet to provide much insight into the fundamental genetic problems confronting most small populations of endangered species: the accumulation of deleterious mutations, the loss of adaptive potential, and the negative effects of population augmentation. Quantitative genetics, the branch of genetics that deals directly with the evolutionary properties of morphological and behavioral traits, provides a foundation for understanding the relevance of these issues to conservation biology.

2. An overview of theoretical and empirical results in quantitative genetics provides some insight into the critical population sizes below which species begin to experience genetic problems that exacerbate the risk of extinction. Populations that regularly contain fewer than 100 individuals are extremely vulnerable to both deleterious mutation accumulation and loss of adaptive potential. Security from long-term deleterious-mutation degradation requires a harmonic mean population size of at least 1,000 reproductive adults. Moreover, populations with fewer than 10,000 reproductive adults are likely to be limited with respect to adaptive genetic variation. It is

perhaps not until 10^5 or so adults are regularly present that a population begins to behave genetically as if it were effectively infinite.

3. Current national and international policies are such that endangered species are usually only endowed with formal protection after their total census number has dwindled to several hundred or fewer individuals. Based on the aforementioned, such population sizes are two to three orders of magnitude below the point at which the genetic integrity of species begins to be at risk. Thus, on genetic grounds alone, there is a need for much higher standards in the protection of species.

4. Although most of the focus of genetic conservation is on the immediate deleterious consequences of small population size, human activities also potentially threaten the long-term persistence of very large populations. Due to the fact that natural selection imposes a load on a population through reduced individual survivorship and/or fecundity, there is a maximum rate of sustainable evolution beyond which the demographic cost of selection exceeds the ability of a population to replace itself. Rates of environmental change (such as global warming) that exceed a critical value can cause the extinction of any population. This problem is particularly acute for natural populations confined to fragmented habitat, because this eliminates migration as an alternative strategy for coping with environmental change. The critical rate of environmental change beyond which extinction is inevitable is quite low, even for populations that are effectively infinite in size from a genetic perspective. In some cases, increased deleterious mutation rates induced by human activities may impose an additional load on species, especially those with low demographic potential. Thus, the genetic consequences of human activities extend well beyond those species that currently appear to have dwindled to small population sizes.

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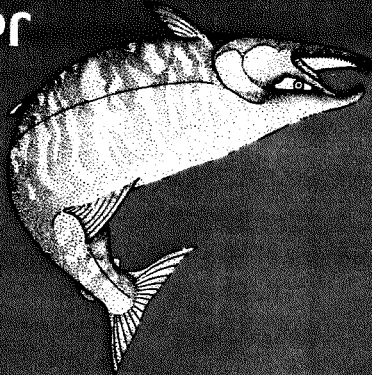
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