

A Report on Population Genetics in Conservation

While conservation biologists have stressed the importance of genetic processes in the dynamics of extinction (e.g., Frankel and Soulé 1981, Schonewald-Cox et al. 1983), the staffs of many governmental agencies and Non-Government Organizations (NGOs) involved in conservation have little genetic expertise and are unsure of the utility of genetics to the practical problems of conservation. Few international conservation projects have incorporated genetic goals and methodologies. To discuss the uses of population genetics in biotic conservation programs, and to facilitate communication between conservation organizations and population geneticists, the World Wildlife Fund (WWF) held a workshop in Washington, D.C. on July 27–28, 1987. Participants included conservationists from WWF, biologists working in conservation and research at zoological parks, and academic population biologists and geneticists.

Workshop participants agreed that habitat destruction and the fragmentation of wildlife populations are the primary factors reducing biological diversity. Extinction is fundamentally a demographic process, the failure of one generation to survive and reproduce a subsequent generation. Wildlife populations are increasingly subjected to uncontrollable stochastic factors as a population declines in size. In addition, when populations become small, fragmented, and less stable, inbreeding becomes more likely, and genetic variation is lost due to increasing genetic drift. Thus, genetic processes in small, fragmented populations merit serious consideration

in management and recovery plans for endangered populations.

Among populations at risk of imminent extinction, there is diversity in population structures, selective pressures of the environment, modes of adaptation to the environment, and causes for population decline are examples of this diversity. Therefore, there will be no single critical population size, or even effective population size, below which genetic problems will be encountered and above which none would be expected, this is applicable to all populations. There is a pressing need for genetic investigations of threatened, as well as large, healthy populations. Conservation Biologists must better determine the genetic changes that result from and could contribute to declines in population. Workshop participants stressed the need for the study of demographic and genetic processes in each population of concern. The need for flexibility must be taken into account in the management of differences among endangered species. The participants agreed upon a number of inter-related recommendations on the application of population genetics to the conservation of wild populations. These recommendations are briefly summarized below.

Demographic considerations are of primary importance in managing populations for conservation. Genetic as well as behavioral and ecological processes are important because they directly affect demography. Genetic information can also provide insight into the demography of a population, revealing past geographic structure and distribu-

tion. Documentation of the demography of managed populations is essential to identify pending demographic and genetic problems, and to determine causes for the ultimate success or failure of the documented populations.

A thorough understanding is essential of the systematics of the populations that interest conservationists. Measurement of evolutionary divergence among populations, races, and named subspecies is necessary for the determination of the demographic unit(s) that need conservation action, and the appropriateness of managed migration between those units. If the existing taxonomy is based on a few specimens or characters, incomplete sampling across the species range, or outdated analysis of geographic variation, a thorough re-analysis of the taxonomic status should be undertaken. This should incorporate distributional morphological, molecular, ecological, and behavioral data.

Genetic data, as well as morphological data, should be used to assess relationships among all populations of concern that may have diverged genetically during periods of isolation. The genetic structure of local populations (within boundaries of formally named taxa) should be investigated to determine the likely amount of past interchange between populations and thus the possibility of local adaptations. Gel electrophoresis of blood and tissue proteins is currently the most cost-effective means of measuring genetic variation within and between most conspecific populations. If sufficient data cannot be obtained from starch or acrylamide gel electrophoresis,

further investigation may entail use of two-dimensional electrophoresis, or analysis of restriction fragment length polymorphisms (RFLPs) of mitochondrial DNA or of nuclear DNA for which hybridization probes are available. While electrophoresis of protein variation is effective for studying variation within species or between closely related species, there is often insufficient identity of allelic protein variants for analysis of genetic divergence among more distantly related taxa. More distant comparisons usually require analysis of RFLPs (though usually more useful within the specific and generic levels); DNA hybridization (useful at the familial and ordinal levels); measurement of immunological distance (for genetic, familial, and ordinal comparisons); or direct comparison of homologous DNA sequences (useful at all taxonomic levels). Nonmolecular measures of genetic variation may also be useful for studying variation within species. Quantitative variation within a species for morphological traits can be assessed from bones, skins, or other preserved material. Karyotypic variation between populations may be indicative (and possibly the cause) of reproductive barriers.

Recent studies of the systematics of taxa that are of particular concern for conservationists include molecular genetic data supporting separation of the black-footed ferret (*Mustela nigripes*) from the closely related steppe polecat (*Mustela eversmanni*) at the species level (O'Brien et al. 1988); confirmation of subspecies level genetic differentiation among the three lion tamarins (*Leontopithecus rosalia*) (Forman et al. 1986); the finding of minimal genetic differentiation among tiger (*Panthera tigris*) subspecies, more typical of within-subspecies estimates of populational divergence (O'Brien et al. 1987); and ongoing studies at Columbia University and the San Diego Zoo of the genetic separation among black rhino subspecies.

The lack of protein variation de-

tectable by standard gel electrophoresis does not demonstrate that adaptive or potentially adaptive genetic variation does not exist in a population. No technique short of complete sequencing of the DNA of each organism (not now feasible) can reveal all genetic variation, and it should never be assumed that a population wholly lacks genetic variation of importance to the short- or long-term fitness of the population. It cannot be assumed that any population is so devoid of variation that it is of no conservation value or has no possibility of persistence (Lande & Barrowclough 1987). Yet, rapidly declining genetic variability, or the observation that a population has little genetic variation relative to conspecific populations (suggesting previous loss of genetic variation), should be cause for intensified concern for the persistence of a population. Inbreeding often results in reduced fertility, high mortality of offspring, slow or aberrant development, and accelerated adult mortality (Ralls & Ballou 1983, 1988). If inbreeding becomes common in a managed population fitness components should be monitored and evaluated relative to inbreeding coefficient.

Given a choice between otherwise equally appropriate populations, those containing more genetic variability are preferred as sources for re-introductions and translocations. Highly heterozygous individuals may have superior fitness relative to less heterozygous conspecifics (unless the population was created by a recent hybridization, lower fitness of heterozygotes is unlikely). The presence of more allelic variants may also allow the population to adapt to the new environment of the re-introduction or translocation site. If there isn't a source population that is genetically and ecologically similar to the former inhabitants of the release site, genetically diverse stock produced by crossing moderately divergent populations may provide the best source for re-introductions (e.g., peregrine falcon

re-introductions into the eastern USA; Cade 1980). A stock of this sort would have considerable variation on which selection could act to produce a locally adapted form. Except for some cases involving chromosomal incompatibilities between geographic forms, there is little evidence that hybrids, produced by crossing geographic populations which showed only incipient divergence suffer reduced fitness ("outbreeding depression"). Prior consideration should be given to avoiding crossing forms with so markedly different adaptations that their hybrids are unsuited for any habitat (Templeton et al. 1986).

Because electrophoretic techniques sample only a very small part of the genome, they are inefficient for assessing the relative heterozygosities of individuals within populations (Hedrick et al. 1986). Individuals should be chosen for re-introductions because of expectations of substantial genetic variability. This should be based on membership in populations that are measured or assumed, due to past history, to be highly variable, or based on pedigree analysis.

Demographic and genetic processes can be simulated by computer, or modelled analytically, allowing projection of the long-term fate of a population under management (e.g., Lacy 1987, Lande 1987). Although such models are simplified approximations of interacting natural processes, alternative management decisions should be examined for their expected effects on demographic and genetic stability of the population.

Genetic monitoring of managed populations can produce insights into aspects of population structure that affect conservation. Genetic markers, such as unique restriction fragment length variants at hypervariable or other loci (DNA fingerprinting), can be used to identify which individuals in a population contribute to future generations. The pattern of genetic variation throughout the range of the popula-

tion(s) can indicate past amounts of gene flow, and thus the amount of migration between areas (Slatkin 1987).

Pedigree determination is important in the management of very small populations. Pedigrees are requisite for the analysis of inbreeding, and allow for the most precise prediction of loss of genetic variability (MacCluer et al. 1986, Thompson 1986). Electrophoresis of proteins can be used to fill in the gaps in pedigrees (paternity or maternity exclusion) if sufficient allozymic variation is available for analysis. DNA fingerprinting is a much more powerful tool in pedigree determination, and can be used to determine genealogies even in the absence of extensive information about potential relationships (Jeffreys et al. 1985, Hill 1987, Burke & Bruford 1987).

Population geneticists, as well as demographers, ecologists, and behavioral biologists, should be consulted during the design of management and recovery plans. Guidelines for avoiding genetic problems and a monitoring program for detecting any deterioration of the genetic base of the population as soon as is feasible can promote more effective use of limited conservation resources and increase the chance of success. Even if no immediate benefit of the genetic analysis to a specific conservation program is foreseen, management and research programs could often incorporate genetic investigations that would broaden our understanding of genetic processes in wildlife populations. There is a need to build a data base on the genetics of wild populations, especially those in danger of extinction, from which to develop a more thorough understanding of the genetic processes in dwindling populations. It is unlikely that academic geneticists will soon explore a sufficient fraction of the diversity of wildlife species in need of conservation action unless they are drawn into wildlife conservation programs. For example, most programs that involve animal immobili-

zation (e.g., translocations, radio-tracking, monitoring of animal health) could provide blood and/or tissue samples for genetic analysis at little cost and with little interference to the overall program. Other opportunities for such sampling for systematics research, analysis of population structure, and genetic monitoring may be rare or nonexistent. Resources for wildlife management and conservation are limited; we need to obtain as much useful data as possible from each aspect of our conservation programs.

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