NEWS AND COMMENTARY

Conservation genetics

Genetics at the brink of extinction

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A comprehensive new meta-analysis provides strong evidence that goes some way to dispelling the influential nagging doubt in the minds of conservation geneticists, first raised in the 1980s, that genetic considerations might be irrelevant to the conservation of species on the brink.

What happens when a species goes extinct? In the recent past, we have watched many species go down this route, and the characterization of the factors involved has been a major goal of conservation biologists. There are many logical arguments for the importance of genetic factors involved in extinction, but some extremely challenging arguments that genetics does not matter have also been raised (Lande, 1988). Basically, these counter-arguments suggest that demographic factors are more important, to the extent that genetic variability and other genetic factors are irrelevant as a species approaches extinction. Now, Spielman et al (2004) have used a meta-analysis approach to address if indeed genetic factors impact species as they are driven to extinction. Their analyses of genetic variability and heterozygosity strongly indicate that genetic factors impact most species on the road to extinction.

Conservation genetics has now survived three major challenges to its utility for helping to make conservation management decisions (DeSalle and Amato, 2004). The first challenge was raised with respect to species definitions and boundaries and the role of genetics in delimiting conservation units (Ryder, 1986). The second concerned Caughley's (1994) critique that there was too much focus on technical approaches to conservation (including conservation genetics) resulting in the neglect of more important issues, such as habitat threat and disease. The third challenge, the focus of this report, and perhaps one of the most contentious subjects in conservation biology, is the role (if any) that genetic factors play in the extinction and endangerment of wildlife.

Simply put, the argument for the importance of genetics in conservation is based on the assumption that genetic variability is good and genetic homogeneity is bad. More specifically, genetically diverse populations or species are more likely to avoid inbreeding and loss of variability due to stochastic factors. Such avoidance allows genetically diverse populations to adapt to stochastic events or events that might be selective forces in microevolutionary contexts. The classic example of this concept involving the genetic impact of low variability is the case of the cheetah. Cheetahs were shown to have extremely low levels of genetic variability at the major histocompatibility complex (MHC) loci (O'Brien et al, 1985). This lack of variability at loci responsible for immune response was thought to be an important factor in the negative response of cheetah populations to environmental challenge.

Lande (1988) challenged this notion of the importance of genetic factors in endangered species in a landmark paper when he suggested that demographic factors (such as those that influence population growth and life history) were much more important than genetic factors in the endangerment and extinction of species. Consequently, the challenge of providing strong evidence for the importance of genetic factors in endangerment of species has fallen upon practicing conservation geneticists who use genetic variability as a tool in plying their trade. Most previous approaches to examining this problem have focused on single or a few specific species.

Enter Spielman et al (2004) with their recent meta-analysis of a large sample from the literature of genetic variability studies of critically endangered, endangered, and vulnerable (the categorization system of the IUCN-The World Conservation Union Red List) species. They collated results from 170 threatened taxa with either allozyme, microsatellite, or minisatellite data available. By comparing the heterozygosity of the 'threatened' (Ht) species with the heterozygosity of the nearest related nonthreatened (Hnt) species (Figure 1), they show a clear trend of threatened species having lower heterozygosity than nonthreatened. In 77% of the paired comparisons, overall Ht was less than Hnt, a result that was highly statistically significant. Why, then, does the 'no genetic impact hypothesis' not apply to most threatened taxa? Spielman et al (2004) give four reasons why the original challenge to the importance of genetic factors underestimated the impact of inbreeding and loss of genetic variability on threatened species (Table 1).

Any meta-analysis has the shortcoming of combining inconsistent data from broadly divergent sources. While the Spielman et al (2004) study is carefully conducted, to avoid this problem in future similar analyses, we need to develop standardized approaches for estimating the relative decrease of genetic
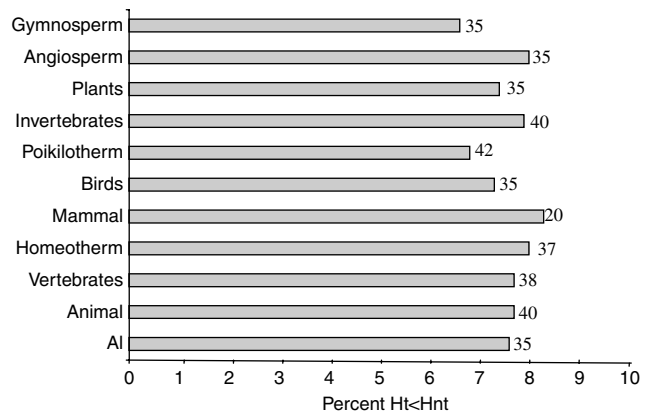

Figure 1 Percent of total paired comparisons where Ht (heterozygosity of threatened) is less than Hnt (heterozygosity of nonthreatened). In any paired comparison, the larger measure of heterozygosity was used as the denominator ($100 \times$ (nonthreatened−threatened)/nonthreatened or $100 \times$ (nonthreatened−threatened/threatened). The statistical approach to analyzing the information on these 170 species and their subgroupings as listed on the Y-axis was a nonparametric Wilcoxon's signed-rank test. The numbers at the end of the histogram bars indicate the mean difference in percent between Ht and Hnt.

Table 1 Conclusions from the new meta-analysis and their implications for the importance of genetic factors in conservation

Conclusion from meta-analysis	Implication with respect to the previous challenge to the importance of genetic factors
Inbreeding and loss of genetic diversity occur at a substantially higher rate than was originally thought	Ratio of effective population size to census size was inflated
Effective population sizes were underestimated, which led an underestimate of the effects of inbreeding and loss of genetic variability	Impact of stochastic factors and genetic factors was underestimated
Inbreeding depression now appears to be four times greater than originally thought	Impact of inbreeding depression was underestimated
Purging by selection has a very small effect on the fate of deleterious alleles compared to previous expectations	Natural selection was overestimated as a factor in purging deleterious alleles

variability in threatened species. The potential for DNA barcoding (Stoeckle, 2003) and DNA registries (DeSalle and Amato, 2004) to accomplish the standardization of such measurements is great, and the application of these novel approaches to characterizing biodiversity should be encouraged.

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