

NEWS AND COMMENTARY

Selection and the rate of loss of genetic variation

Natural selection and genetic diversity

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Evolutionary geneticists and conservation biologists are very much interested in how various evolutionary forces interact to determine the amount and type of genetic variation found in natural populations and how, in turn, that genetic variation affects the fitness and evolutionary potential of populations. In populations smaller than a few thousand individuals, it is generally believed that genetic variation is lost via random genetic drift faster than mutation can replace it. This is of particular concern with regard to the conservation of endangered species of plants and animals, as the loss of genetic diversity through random genetic drift can compromise the future ability of populations to evolve in the face of changing environmental conditions. Thus, a recent paper published in the *Proceedings of the Royal Society B* (Kaeuffer *et al.*, 2006) demonstrating that an isolated population of mouflon (*Ovis aries*) introduced to a remote island as a single founding male–female pair, has apparently increased in heterozygosity (a measure of genetic variation) over the course of approximately 23 generations is of great interest. Kaeuffer *et al.* (2006) suggest that this increase in heterozygosity is due to natural selection acting against inbred individuals.

The idea that natural selection can act as a force to help maintain genetic diversity is not new. Associative overdominance is the term used to describe the fitness difference between heterozygotes and homozygotes at a neutral locus. Since the locus itself is typically a noncoding portion of DNA being used as a molecular marker in the study (for example, microsatellite loci), differences in genotype do not directly contribute to fitness. The correlation between heterozygosity at neutral loci and the fitness of an individual can come about because the marker loci are directly linked to loci that do directly affect fitness ('local effects') or heterozygosity at these markers can correlate with fitness because they accurately reflect genomic heterozygosity ('general' or 'genome-wide

effects'). The latter occurs because individuals within the population vary in their inbreeding levels. Kaeuffer *et al.* (2006) suggest that their results are more likely to be due to local than general effects, but admit that there is no concrete way to test this. The inability to discriminate between these two hypotheses is not, in my opinion, of great concern as ultimately all genome-wide effects must have a local cause. The real question is whether inbreeding depression is due to increased homozygosity at a few loci with large effect or a large number of loci with small effect.

Several studies of inbred populations performed in the laboratory had already suggested that the decrease in heterozygosity at neutral loci is slower than that expected by theory (for example, Rumball *et al.*, 1994; Latter *et al.*, 1995; Gilligan *et al.*, 2005). However, there are two reasons why the paper by Kaeuffer *et al.* (2006) is so intriguing. First, they did not just see a slower decline in heterozygosity than what is expected under common models of neutral expectations. They actually saw an increase in heterozygosity, as estimated from 25 microsatellite loci, in a population with a harmonic mean population size of less than 20 individuals. This suggests that the strength of selection against inbred (more homozygous) individuals may be much stronger than was previously suspected and therefore the ability of selection to maintain genetic diversity greater. Second, this is not a highly fecund species in a laboratory environment. The fact that these changes in heterozygosity occurred in a wild population of a vertebrate makes it more compelling.

Kaeuffer *et al.* (2006) performed a number of computer simulations to test how various founder scenarios and selection regimes are predicted to impact genetic variation in the introduced population of mouflon. They found that truncation selection against individuals with heterozygosity levels less than 0.40 resulted in an increase in heterozygosity similar to the one they observed over time in this population. This is very

strong selection! Perhaps such strong selection should not be surprising, given the harsh climate and the limited grass cover of the island. It is becoming very clear that inbred individuals are more sensitive to environmental stress (for example, Armbruster and Reed, 2005; Reed *et al.*, 2006) and that this is an important consideration in conservation biology. A combination of high fecundity, a large variance in inbreeding coefficients among the offspring born in a given year and strong selection against inbred individuals creates ideal circumstances for selection to maintain heterozygosity levels within a population, even in the face of the potential for significant genetic drift.

Like most good studies, this one raises more questions than it answers. It has generally been felt that selection strong enough to maintain or increase genetic variation, would also be strong enough to imperil small populations with rapid extinction. However, Kaeuffer *et al.* (2006) state that selection had a negligible effect on the demography of the population in their models. This might reflect reality if there is considerable reproductive excess and mortality is determined primarily by intraspecific competition. If mortality is strictly density-dependent and due primarily to competition for limited food resources, then truncation selection such as that modeled is possible and would not push the population to extinction. The fact that the goats are not native to the island and there are no predators, makes this type of scenario not so far-fetched. However, the population remained very small for at least five generations after introduction, as though struggling with inbreeding depression. Then after a short climb to carrying capacity, the population began to cycle in a way that suggests strong food limitation. This suggests that there must have been strong selection against inbred individuals for survival to maturity in the absence of limited food supplies early on, or there would have been little genetic variation to preserve in the later density-dependent phase.

The biggest question was raised by Kaeuffer *et al.* (2006) themselves: Can the results from this population be generalized to other populations? Was there a special set of circumstances that allowed genetic variation to increase in this small population following the bottleneck or are the conditions for this type of phenomena fairly liberal? Or is this type of scenario rare but will show up often in surviving populations

because only the subset of bottlenecked populations that maintain genetic variation survive long enough to be tested? This paper should spur further research on natural and experimental populations to test the boundary conditions where genetic diversity can be maintained in small populations and what it means to their future evolution and persistence.

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