

COMMENTARY

Should We Select Genetic Alleles in Our Conservation Breeding Programs?

Robert C. Lacy*

Chicago Zoological Society, Brookfield, Illinois

The breeding strategy currently followed by almost all cooperative management programs for captive populations is designed to maintain the genetic composition of each captive population as close as possible to that of its wild source population, minimizing random genetic changes (genetic drift) and minimizing natural and artificial selection. The primary method for minimizing genetic change is to preferentially breed those animals with the lowest mean kinship to the overall managed population [Ballou and Lacy, 1995]. Thus, every attempt is made to breed animals whose alleles are at risk of being lost to the next generation, because of lack of prior opportunity to breed, poor behavioral, physiological, and/or genetic adaptation to the captive environment, or just bad luck. Recently, two articles examined effects of natural selection (or lack thereof) on captive populations and suggested that this breeding strategy may not always be desirable or effective. Although the papers contain important data and arguments, uncritical acceptance of their recommendations could be hazardous to the health of captive populations.

Lairre [1999] described a high prevalence of inherited disorders in captive populations and recommended that population managers should consider a program of selective removal of animals carrying deleterious alleles. The author was careful to discuss the possible risks of the accelerated losses of gene diversity, founder lines, and non-deleterious alleles that occur concomitantly with selective breeding and advocates cautious consideration of attempts to remove harmful alleles from captive populations. However, there are more problems with using artificial selection to get rid of "bad" alleles than just those discussed by Lairre. First, the effects of genes depend on the environment in which they are expressed. An allele can have an obvious deleterious consequence in one environment, but a very different expression and

effect in a different environment. For example, an allele that causes accumulation of iron in the liver may lead to iron toxicity when the animal is fed a diet high in iron, but may permit survival when iron is lacking. Unless we can be confident that the environment will not change over time (even if the animals are later released into natural environments), it is risky to presume that we can assess which alleles will be beneficial and which will be deleterious in the future. Even if we do think that we have identified an unconditionally harmful allele (as is probably the case with the albinism allele discussed by Lairre), we need to remember that it is likely that every animal carries at least one highly deleterious allele. Indeed, it is estimated that most mammals (including each of us) carry one or a few recessive lethal alleles [Morton et al., 1956; Ralls et al., 1988]. A rigorous program of selecting out animals carrying harmful alleles would require culling the entire population. The problem is not that deleterious alleles exist in our captive populations, but rather that the detrimental effects are expressed when the alleles become homozygous in inbred animals. In large, heterogeneous, well-managed populations, serious genetic defects are rare.

Because some captive populations are so small or mismanaged that inbreeding and rapid genetic drift have occurred, some deleterious hereditary traits have increased to high frequencies or by chance were unusually common in the few founding animals. It might seem wise to try to reduce the frequencies of such traits. However, such a strategy may be selective in ways other than that which is intended. For every deleterious trait that is apparent to our eyes, there are almost certainly a number of other deleterious alleles that have similarly drifted to high frequency. Relatively few genes have effects that can be easily observed from cursory examination of the external anatomy. I do not think we gain by selectively removing those animals that happen to carry the deleterious alleles with visible effects. Such a strategy will cause an increase (through more rapid drift and inbreeding) in the expression of many deleterious alleles that we cannot so easily see. The current zoo breeding programs encourage rapid population growth while preferentially breeding animals that have the lowest mean kinship to the rest of the population. These practices are designed both to minimize the rate at which deleterious alleles (seen and unseen) would randomly drift to high frequencies and to minimize the expression of any deleterious alleles in inbred animals. The strategy is based on the assumption that the original founders collected from the wild are equal in genetic value; each carrying an assortment of beneficial and harmful alleles.

Sometimes we may decide that it is necessary to selectively rid a population of a specific allele. On average, the fewest animals will need to die or be removed from breeding if we remove only homozygotes for problematic alleles (or we just let natural selection do the selecting for us), as each removed homozygote takes two copies of the offending allele with it. Faster reduction of the frequency can be achieved by removing known or presumed heterozygous carriers, but at the cost of more "genetic" deaths per incremental reduction in frequency of the allele. Lairre points out that in the absence of active selection against them, deleterious alleles can drift to even higher frequencies. However, they are just as likely (actually, slightly more likely) to return to lower frequencies even if we do nothing to remove them, particularly if they have strong effects on health or reproductive fitness. As stressed by Lairre, before any program of selection is imposed, it is important to determine how much variability across the genome and how many animals would have to be sacrificed to substantially change the frequency of the allele we do not want. (I should

*Correspondence to: Robert Lacy, Department of Conservation Biology, Chicago Zoological Society, Brookfield, IL 60513. E-mail: rlacy@czs.mtelcom.com

Received for publication August 11, 1999; Accepted July 20, 2000.

note that I fully agree with Lalkre that intentional selection *for* harmful mutations, as in the "white" tigers, is particularly damaging to conservation breeding and questionable ethically. The practice causes intentional loss of founder lines, increased genetic drift, rapid inbreeding, artificial amplification of abnormal phenotypes, and reduced health of animals.)

In the other recent article, Bryant and Reed [1999] report that the lack of selection acting on captive populations can lead to rapid deterioration of aspects of fitness that could be important for population persistence under more natural conditions if the animals are ever to be used in re-introduction programs. They found that late-life fecundity diminished in populations of houseflies that were maintained under a regime that bred flies only when they were young. They suggest that captive breeding programs should not try to minimize selection (through schemes such as minimizing mean kinship), but rather should allow the alleles of less adapted individuals to be lost from the population. I think that Bryant and Reed overstate the seriousness of the problem of fitness deterioration when natural selection is relaxed and overlook a number of problems associated with the strategy they propose:

The problems with allowing natural selection to act with full force on captive populations include the more rapid loss of genetic diversity (including adaptive diversity) and more rapid accumulation of inbreeding because of smaller numbers of breeders and less equal genetic contributions. Adaptation to captive (as opposed to wild) conditions [Frankham and Loebel, 1992] would also be more rapid if we do not counter "natural" selection within our zoos. The rate of loss of late-life fecundity in the houseflies was 0.5% per generation. The decline in overall fitness would be much less than this, as other fitness components, such as early-life fecundity, did not decline. Yet, conservation breeding programs usually accept an increase in inbreeding of approximately 1% per generation and cumulative inbreeding of approximately 10%, as the inevitable cost of trying to maintain populations at manageably small numbers. For the typical captive population of mammals, this rate of "acceptable" inbreeding causes a reduction in survival of approximately 1.5% per generation, and 15% cumulatively, as the population declines to 90% of original heterozygosity [Ralls et al., 1988]. Other fitness components, such as fecundity (both early and late) are similarly affected by losses of diversity. A breeding scheme that promotes natural selection may halve the effective population size and therefore double the rate of inbreeding. As a consequence, Bryant and Reed's suggestion may do much more harm than good. Bryant and Reed avoided the problems of inbreeding in their fly populations by keeping population sizes above 2,500. We do not have that luxury with most captive populations of wildlife. At the small population sizes that can be maintained in zoos, random genetic drift and inbreeding are much more dominant forces than is selection [Lacy, 1987]. Fortunately, empirical work on *Drosophila* indicated that the rate of fitness decline due to accumulation of deleterious mutations is likely to be too slow to be of consequence for most conservation breeding programs [Gilligan et al., 1997]. This more optimistic conclusion is not inconsistent with the modest decline in fitness observed over 100 generations in Bryant and Reed's houseflies.

What are the important messages for conservation breeding programs? First, as reported in the articles discussed here, loss of natural adaptations, random increases of deleterious traits, and expression of recessive alleles in inbred animals may be occurring more rapidly and with greater frequency in our populations than we might

282 Lacy

like. These problems can be minimized by using a reasonable number of founders, keeping adequate population sizes, and maximally retaining genetic diversity through the generations. Once genetic problems have arisen, however, they are not easily reversed. A strategy of artificial selection, or even allowing natural selection to work unchecked, will often exacerbate the problems it is intended to fix. Selection inevitably reduces the number of founders, reduces gene diversity, and ultimately, therefore, increases inbreeding. The lesson is that we should not expect small or poorly managed populations to remain genetically healthy for more than a few generations in captivity. We need more rather than less diligence in following strategies, such as minimizing mean kinship, that are effective and robust at maintaining genetic diversity, minimizing inbreeding [Ballou and Lacy, 1995], and preserving adaptations to wild environments [Montgomery et al., 1997]. Early and consistent application of genetic management that preserves as much of the natural variety as possible can keep us out of the genetic troubles described in these recent articles.

ACKNOWLEDGMENTS

I thank the Small Population Management Advisory Group of the American Zoo and Aquarium Association for valuable discussions on these topics. Two reviewers and the editor made a number of helpful suggestions on the manuscript.

REFERENCES

Ballou JD, Lacy RC. 1995. Identifying genetically important individuals for management of genetic diversity in pedigreed populations. In: Ballou JD, Gilpin M, Foose TJ, editors. Population management for survival & recovery. Analytical methods and strategies in small population conservation. New York: Columbia University Press. p 76-111.

Bryant EH, Reed DH. 1999. Fitness decline under relaxed selection in captive populations. *Conserv Biol* 13:665-9.

Frankham R, Loebel DA. 1992. Modeling problems in conservation genetics using captive *Drosophila* populations: rapid genetic adaptation to captivity. *Zoo Biol* 11:333-42.

Gilligan D, Woodworth L, Montgomery ME, Briscoe DA, Frankham R. 1997. Is mutation accumulation a threat to the survival of endangered populations? *Conserv Biol* 11:1235-41.

Lacy RC. 1987. Loss of genetic diversity from managed populations: interacting effects of drift, mutation, immigration, selection, and population subdivision. *Conserv Biol* 1:143-58.

Lalkre L. 1999. Hereditary defects and conservation genetic management of captive populations. *Zoo Biol* 18:81-99.

Montgomery ME, Ballou JD, Nurnhen RK, Englund PR, Briscoe DA, Frankham R. 1997. Minimizing kinship in captive breeding programs. *Zoo Biol* 16:377-89.

Morton NE, Crow JF, Muller HJ. 1956. An estimate of the mutational damage in man from data on consanguineous marriages. *Proc Natl Acad Sci U S A* 42:855-63.

Ralls K, Ballou JD, Templeton A. 1988. Estimates of lethal equivalents and the cost of inbreeding in mammals. *Conserv Biol* 2:185-93.