

INTRODUCTION

Endangered Genes of the Yellowstone Ecosystem



The Greater Yellowstone area is a premier ecosystem for conserving wild biodiversity in the 48 states. If we are to effectively practice conservation biology anywhere, it must be there. But important components of biodiversity are often neglected in wildlife management. Are important genetic elements of biodiversity being neglected in the Greater Yellowstone ecosystem?

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The most central concept of wildlife conservation is our obligation to leave adequate wildlife populations for future generations to use, enjoy and seek to understand. However, our attempts to fulfill this obligation are confounded by two related issues.

We can't leave animals to future generations of us. We can only leave population genomes – the many combinations of all the alleles in each population.

Given this fact of population genetics, we must define what is a genetically adequate population for purposes of wildlife conservation.

Here, I offer a definition for a genetically adequate wildlife population and assess the genetic adequacies of three important populations of wild mammals in the Greater Yellowstone Ecosystem. But, for perspective, we must begin with a little background information.

Genetics in the Practice of Wildlife Management in North America

In practice, wildlife management has been ignoring the above issues. Early wildlife plans emphasized only numbers of animals to be produced and managed. Eventually, there was

recognition that population age structures, often emphasizing trophy males, were elements of wildlife quality to be maintained. Recognition of genetic qualities of wild populations has occurred more recently, and is still in a rudimentary stage of acknowledgement, discussion and understanding.

Wildlife genetics began to infiltrate wildlife management curricula several decades ago (Soule and Wilcox, 1980). However, its application to most wildlife management is hampered:

- by a persisting cadre of older wildlife administrators with little or no background in genetics, perpetuating agency practices rooted in the past;

- by strong political oppositions from industries that oppose wildlife populations large and well-distributed enough to provide genetic adequacy, forcing management agencies to accept and focus on genetically inadequate populations; and

- by the complexities of population genetics and evolutionary biology that science is only beginning to reveal. There is a lack of understanding of wildlife genetics among wildlife managers and more so among the public, resulting in insufficient support for actions to preserve genetic qualities of populations.

Legal and Policy Mandates for Genetic Adequacy

Major legal mandates – the Endangered Species Act, The Park Service Organic Act, and state laws – for wildlife management and conservation predate today's understanding of wildlife population genetics. The ESA and most state laws provide only indirect allusions to conserving genetic qualities of wildlife populations. Only Park Service policy, interpreting its mandate, has provided clear guidance to justify concerns and actions that maintain genetic qualities of wild populations.

Under the Endangered Species Act, the Fish and Wildlife Service has provided a platform for arguing that components of genetic adequacy should be considered in decisions to list, or to delist, a segment of a population (Appendix 1). To my knowledge, vague standards for genetic diversity have been alluded to and weakly used in a few such decisions. However, environmental factors currently impacting and changing the allegedly adequate genetic diversities of imperiled species or populations have often been ignored.

The National Park Service has the clearest obligation and policy to define and maintain genetic adequacies of wildlife (Appendix 2). A 1916 mandate to leave resources “unimpaired” for future generations applies to all natural resources and natural processes, including evolution, and the genetic integrities of animal species. Pertinent here, “natural” is defined as an “absence of human dominance”. In cases of Park Service discretion, unimpairment of natural resources and natural processes must be the dominant basis for decisions.

In general, state laws provide the least mandate for conserving genetic qualities of wildlife. I use Montana laws as an example (Appendix 3). Montana law clearly and repeatedly emphasizes maintenance and control of wildlife numbers. The “wild” component of “wildlife” is not defined, whereas required wildlife management practices are often borrowed from livestock management. At best, Montana law provides only a few vague allusions to wildlife population quality. These appear to originate from a constitutional mandate that natural resources shall not be degraded.

A Genetically Adequate Wildlife Population for Wildlife Conservation

Goals for a genetically adequate wildlife population are to (1) avoid negative impacts of inbreeding, (2) retain valuable wild characteristics from past evolution, and (3) retain evolutionary potential for adapting to a changing future. Four micro-evolutionary processes influence these goals: inbreeding, genetic drift due to random events, and natural and human-caused selective forces of the environment. However, these processes also influence each other. The dynamic and complex micro-evolutionary system is described in Bailey (2016) and in *Population Genetics and Wildlife Management* at jamesabailey.com. For wildlife, the key determinants of genetic adequacy usually are the number of animals in a population and the number of those that are influenced primarily by natural selection.

The goal of retaining wild characteristics recognizes value in a wild population genome. But what is a wild genome? Most animal characteristics are **polygenic**, that is, determined by interactions of several genes at several gene-loci. For these characteristics, each gene, and whatever **allele** (type of gene) happens to occur at each gene-locus, has a small to moderate effect upon the animal's characteristics (Hendry 2013), and it is the combination of alleles that occur at a set of gene-loci that determine each animal characteristic. For each characteristic, there are many different combinations of alleles occurring across all the individual animals in a population. And this pattern is repeated for very many different characteristics of the animals.

A wild population, having suffered a preponderance of natural selection during its recent evolution, should contain a preponderance of animals having a preponderance of allele combinations that enhance **fitness** (survival and reproduction) in a wild environment.

Fitness to the wild environment ("**wildness**") may be diminished by (1) loss of valuable alleles from the population genome due to random drift, (2) accumulation of mildly deleterious alleles as drift replaces selection that normally would remove such alleles, and by (3) rearrangement of alleles throughout the genome due to drift and artificial selection, such that combinations of alleles that are best for wildness become rarer. In the short term (a few to several generations), rearrangement of allele patterns and accumulation of deleterious alleles are likely to be more involved in diminishing wildness than is allele loss (Hendry 2013). However, loss of alleles has a permanent effect on diminished wildness.

Genetic drift and artificial selection weaken or replace natural selection in determining the future composition of a population genome. For many populations of large mammals, the predominant artificial selection is a removal of animals by hunting or other management actions to limit population size and/or distribution. Effects of such artificial selection upon evolution of adult animal characteristics are numerous (Allendorf and Hard, 2009).

A genetically adequate wildlife population is (1) large enough to avoid inbreeding and to maintain genetic diversity for (a) retaining wild characteristics bequeathed from past evolution and (b) retaining evolutionary potential for responding to changing environments of the future; and (2) is influenced by a preponderance of natural selection rather than by small population effects and/or by weakening of natural selection with human interventions and impacts.

"Preponderance" of natural selection is an arbitrary standard that will be difficult to justify or measure with precision. It is intended that the effects of natural selection upon a wild population genome exceed the sum of effects of random factors (drift) and artificial

selection. A crude index is proposed: that the number of breeding-age animals dying due to natural causes exceeds the number dying due to human-caused mortality. Precision of the index may be enhanced by assessing mortalities separately for the sexes. This standard likely will be sufficient for genetic adequacy of a large population; but may not suffice for a small population in which the absolute number of animals subject to natural selection would still be small. For a small wildlife population, artificial selection should be minimized, preferably to zero.

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2017
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