



## Helping bighorn sheep keep their footing on the slippery slope of the genetic bottleneck

By Jerry Booth

*(This article was excerpted from a longer article, “Helping Endangered Species to Keep Their Footing on the Slippery Slope of the Genetic Bottleneck,” which appeared in the NRS Transect 24:1 (spring 2006). Reprinted with permission from the University of California Natural Reserve System.)*

With a growing number of species going extinct or teetering on the brink, conservation biologists are concerned that even species that manage to increase their numbers will later succumb to sudden, devastating infections. Susceptibility to disease can be one consequence of genetic impoverishment – which may happen when a large, apparently recovered population has only a few forebears. But such low genetic diversity is thought to cause generally low species-fitness, resulting in lower reproduction and poor survival. This is why conservation genetics is becoming ever more important to scientists struggling to ensure the long-term persistence of endangered species.

A genetic bottleneck occurs when a species’ population numbers decline to such a level that they are insufficient to maintain genetic diversity. The UC Natural Reserve System provides research access for several species that either have experienced or are currently experiencing such bottlenecks, including the desert bighorn sheep (*Ovis canadensis nelsoni*). The Natural Reserve System’s Sweeney Granite Mountains Desert Research Center in San Bernardino County provides an ideal location to study this most recognizable desert denizen.

### **The science beneath the surface**

A species’ genetic diversity is determined by the number of alleles – variants of specific genes within the overall genome – that are present across the population. Having multiple alleles available for each gene locus across a genome enhances a species’ ability to adapt to environmental changes. Even in individuals that are “heterozygous at a dominant locus” (that is, where two different alleles are present at a single locus, but only one is



expressed), the retention of the recessive allele is important because it provides flexibility. Populations that are genetically variable at a given locus are referred to as polymorphic; those that lack diversity are called monomorphic. Advances in microbiology have allowed scientists to better gauge the genetic fitness and diversity of species facing bottlenecks.

### **Taking the high ground**

Desert bighorn sheep inhabit a number of small, isolated mountain ranges throughout the Sonoran, Mojave, and Great Basin deserts of the U.S. Southwest. They live in small populations of usually less than 100 individuals. In California, biologists estimate the desert bighorn sheep population at about 4,300, spread across a territory that extends from the White Mountains east of the Sierras to the Mexican border. Their numbers are relatively stable, but during the last 60 years, 30 of 80 populations within the state have gone extinct. To maintain the species, scientists have moved sheep into seven ranges where extinctions have occurred. Three natural recolonizations have also been observed in recent years.

UC Berkeley postdoctoral researcher Clint Epps has spent much of the last six years tracking desert bighorn sheep throughout the California deserts. Epps often uses the Sweeney Granite Mountains Desert Research Center as his base of operations. “I started my genetics work right across the road (Interstate 40) from the Granites in the Marble Mountains,” he says. “I had originally anticipated that I would sample maybe six populations, but as I discovered I could follow them with genetic tests, chasing the next ridge became a bit of an addiction. I ended up doing about 30!”

Epps’s population genetics tests were conducted on the animals’ fecal samples, which contain DNA. “I was really interested in the question of metapopulation dynamics, extinction, and colonization,” he explains. “Colonization and dispersal have been difficult to study, because they’re relatively rare. It doesn’t take many individuals moving back and forth to maintain these processes, and the odds of detecting such movements are not very high. With genetics testing, we can match relatives and track individuals. In two cases, I detected the same sheep in two different nearby mountain ranges at different times, just from their droppings.”

In studying the flow of genes across the desert, Epps discovered that diversity varies greatly between populations. The Granite Mountains bighorns, for example, are quite

diverse and thus serve as a source population for recolonizing neighboring ranges. “The Granites are high elevation, which makes them ideal territory for desert bighorns,” Epps points out. “And they’re well connected with the Providence Range, which, in turn, is connected to another small chain of populations. Taken together, this area is one of the most genetically diverse areas in the desert.”

In the Newberry Mountains just outside of Barstow, however, the population’s genetic diversity was found to be just half of that in the Granite Mountains population. Epps attributes this circumstance both to recent bottlenecks and to that population’s geographical isolation. The Newberry Mountains animals live on an extremely remote range at the western edge of the territory, surrounded by long stretches of flat desert. Epps has found that desert bighorns will cross about 5 to 10 kilometers of flat ground, but seldom go much further. Such isolation can be devastating to small populations.

Epps has identified two major human-created obstacles that interrupt the movement of animals between populations: freeways and canals. Freeways are often fenced to prevent cattle from wandering into oncoming traffic, but they also prevent bighorn sheep from finding one another as well. A freeway has cut off the Newberry Mountains sheep population from its only known source of new animals. Even in the Granite Mountains, the heart of bighorn sheep territory, freeways have had an impact, as Epps discovered early in his study.

“I found populations just to the south of the Granites that should have been within easy dispersal range,” Epps recalls, “but an interstate built through the area in the 1960s cut off any interaction. And when I started working up my genetic samples in the lab, I noted that there was a surprising amount of genetic distance between these populations across the interstate and that the populations to the south were less genetically diverse. That’s when I really started getting interested in the impact of the interstates. One reason I sampled so widely was to increase my sample size so I could make these comparisons.”

Global warming is another major factor affecting the movements of bighorn sheep and their ability to intermingle dispersed populations. Over the last century, the mean annual temperature in southwestern U.S. deserts has risen by 1.8 degrees Fahrenheit, while annual precipitation in California’s deserts has dropped 20 percent. Epps believes these conditions are already affecting the



region's bighorn sheep populations. "Losing 30 populations over the last 60+ years is an unsustainable rate of population extinction," he points out. "And those extinctions weren't random – they especially hit populations in lower, dryer ranges that lacked dependable springs. All of those are parameters related to climate." If global warming continues or even (as is often predicted) accelerates, the desert bighorn sheep population will become increasingly fragmented.

Epps is working on a number of possible solutions for the immediate problem of bighorn mobility. "One thing I'd like is to see what we can do about restoring the connectivity between the Granites and the Marbles to the south. The ideal thing for desert bighorn sheep would be a big overpass, but the odds of that happening are pretty low. There are some large culverts in the pass where the interstate cuts across the north end of the Marbles, but they're fenced. I'm hoping CalTrans can open those back up."

"The Granites and the Providence Mountains and that region are really key," he continues. "To ensure the long-term persistence of desert bighorn sheep, you have to maintain those core areas and the connectivity with the more outlying areas. You don't want to give up on those outlying areas. If disease or mountain lions hit the higher, wetter populations, those peripheral populations might be the saving grace."

Epps also hopes land managers will use his research and that of his colleagues to guide their handling of the different populations of desert bighorn sheep. By understanding the flow of animals and genes between populations, land managers will be able to react quickly when a local bighorn population goes extinct. If the area is still connected, they can wait for it to be recolonized naturally. If the area is not still connected, they can bring in bighorns to get the population going again.

"It's crucial for each of these small populations to have new individuals come in from other populations," Epps explains. "Otherwise, you will eventually lose that population. That's a standard feature of metapopulation models. The population may hang on for a long time, but if you don't make it possible for new animals to move in, you'll eventually lose these areas. You'll always have populations winking out here and there, but the system as a whole should remain pretty stable as areas are recolonized. Disrupt that, however, and you run the risk of breaking down the entire system. The harsh environment inhabited by desert bighorn sheep already has them walking on a knife's edge. It doesn't take much to push them off. The bottom line is that more than one-third of the population that was once known is now gone, and we could lose them all."

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### **For Further Reading**

- Clinton Epps webpage: [http://nature.berkeley.edu/BrasharesLab/Clinton\\_Epps.html](http://nature.berkeley.edu/BrasharesLab/Clinton_Epps.html)

*Photos by Larry Hogue*

## Key Terms Defined

**Allele** – Any of the possible forms in which a gene for a specific trait can occur. In almost all animal cells, two alleles for each gene are inherited, one from each parent. Paired alleles (one on each of two paired chromosomes) that are the same are called **homozygous**, and those that are different are called **heterozygous**. In heterozygous pairings, one allele is usually dominant, and the other recessive. Complex traits such as height and longevity are usually caused by the interactions of numerous pairs of alleles, while simple traits such as eye color may be caused by just one pair (from *American Heritage Science Dictionary [AHSD]*).

**Colonization/recolonization** – The spreading of a species into a new habitat. (*AHSD*) In **recolonization**, a species returns to an area of habitat where it had become locally extinct.

**Gene locus** – The position that a given gene occupies on a chromosome. (*AHSD*)

**Genome** – The total amount of genetic information in the chromosomes of an organism, including its genes and DNA sequences. (*AHSD*)

**Heterozygous** – see **Allele**.

**Metapopulation dynamics** – A **metapopulation** is generally considered to consist of several distinct populations together with areas of suitable habitat which are currently unoccupied. Each population cycles in relative independence of the other populations and eventually goes extinct as a consequence of “demographic stochasticity” (fluctuations in population size due to random demographic events); the smaller the population, the more prone it is to extinction. Although individual populations have finite life-spans, the population as a whole is often stable because immigrants from one population are likely to re-colonize habitat which has been left open by the extinction of another population. They may also immigrate into a small population and rescue that population from extinction (called the *rescue effect*). (*Wikipedia*).

**Monomorphic population** – a population that lacks diversity at a given gene locus.

**Polymorphic population** – a population that exhibits genetic variability (diversity) at a given gene locus.

**Population** – A group of individuals of the same species occupying a particular geographic area. Populations may be relatively small and closed, as on an island or in a valley, or they may be more diffuse and without a clear boundary between them and a neighboring population of the same species. For species that reproduce sexually, the members of a population interbreed either exclusively with members of their own population or, where populations intergrade, to a greater degree than with members of other populations. (*AHSD*)

**Recessive** – Relating to the form of a gene that is not expressed as a trait in an individual unless two such genes are inherited, one from each parent. In an organism having two different genes for a trait, the recessive form is overpowered by its counterpart, or dominant, form located on the other of a pair of chromosomes. In humans, lack of dimples is a recessive trait, while the presence of dimples is dominant. (*AHSD*)