

KNOWLEDGE BASE

Making Sense of Mule Deer Distribution



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Since 1948 the Boone and Crockett Club has provided grants to support big game-related studies and to seed the careers of aspiring young wildlife professionals. The idea of these “seed grants”

is that relatively small investments can yield huge dividends further down the line. When it comes to the Club’s recent investments in deer genetics work, that strategy is working in spades!

A prime example is what has transpired since the B&C awarded modest conservation grants to biologist and deer enthusiast Jim Heffelfinger in 2005 and 2006. Jim teamed up with researchers Emily Latch, Jennifer Fike, and O.E. Rhodes to study genetic differentiation in mule deer. Recent advances in DNA analysis techniques enable researchers to address questions that were not thought possible just a couple decades ago, when many subspecies designations had very little scientific backing. Today, one of genetics’ most promising uses is in defining ecological management units throughout the range of a species. Let’s look at how the work of the mule deer research team is strengthening the scientific basis for management.

A New Look at Old Subspecies

The initial investment by the Club has grown into a coalition of conservation groups supporting one of the most ambitious projects of its kind: the genetic analysis of mule and black-tailed deer throughout North America. More than 2,700 tissue samples were collected from mule and black-tailed deer from over 70 sites throughout their entire range in North America. This evaluation of genetic differentiation will provide a basis for conservation efforts. Additionally, it will help solidify the range of different “types” of mule and black-tailed deer for accurate records-keeping purposes.

Science-based groups as units of conservation

The currently-recognized subspecies of mule deer have not been helpful in delineating

units of conservation and management. Managers require type designations that reflect actual genetic, ecological, and physical differences. Genetic differentiation of mule deer should help not only in answering subspecies questions, but also in highlighting unique problems that face animals in a localized geographic area. Additionally, the results may lead to positive changes by offering incentives for conservation. For example, a type of mule deer identified in Mexico might become a high-value trophy animal. Local residents, seeing this as a

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valuable asset, may be more likely to afford protection against poaching.

Building a solid, defensible basis for trophy records-keeping categories

Working out the geographic distribution of blacktail deer and mule deer is important for the integrity of trophy records systems. For example, deer harvested in the central portions of the northwestern states and provinces may be hybrid intergrades. As a result, larger hybrids harvested in an area officially recognized as “blacktail” range would have an unfair advantage over pure blacktail deer entered. This example illustrates that drawing lines based on “records-keeping purposes” rather than solid biological information may result in spurious records. Fortunately in the case of blacktail vs. mule deer, genetic research clearly shows that the two types differ substantially in their mitochondrial DNA.

This allows immediate application of genetic tools to map the current distribution of each deer type. Nuclear DNA can be used for something called an assignment test, whereby a sample from an unknown deer can be assigned to either “blacktail” or “mule deer” with a specified level of probability.

The team’s research helps resolve other issues

For example, does the “Inyo Mule Deer” really exist? With a very restricted range in eastern California, the deer’s unknown status makes it vulnerable to legal challenges by anti-hunting factions. Similarly, the “Burro Mule Deer” in southwest Arizona, southeastern California, and northwestern Sonora is said to be different than other desert mule deer to the east. Mule deer occupying the southern Baja California (Mexico) peninsula are mostly isolated from other mule deer and some physical characteristics, such as tail coloration, differ dramatically from mule deer in the northern part of the Baja peninsula. Some island populations of mule deer around the Mexican Baja Peninsula are isolated from the mainland—at least since the late Pleistocene—and physical descriptions suggest that they could be very

different from other mule deer. Two of these island populations of mule deer have been given unique subspecies names (Tiburon Island, Cedros Island); a third has never been described by science but the team has DNA samples from that island that should be revealing.

Unraveling Results from the DNA Molecule

The research team is beginning to interpret the results of its extensive analysis, starting with mitochondrial DNA because that analysis is most appropriate for evaluating the accuracy of existing subspecies designations and for defining large geographic units of similar deer. Next, they will turn to nuclear DNA to obtain a higher-resolution look at genetic diversity throughout North America and to address additional questions.

The first of at least three scientific papers has just been accepted by the prestigious journal *Molecular Ecology* for

publication in 2009. It reports findings that will be of interest to Boone and Crockett Club members and associates, such as: The previously described “Inyo Mule Deer” is not genetically different from other mule deer in California.

Confirming what other researchers have found, blacktails have very different mitochondrial DNA than all other subspecies of mule deer

Sitka and Columbian blacktail deer are not very different from each other compared to other subspecies. This may indicate, as some local authorities have suggested, that the Sitka deer is simply a maritime or island form of blacktail that has been shaped more by environment than long-term genetic isolation.

Sitka blacktails have much less genetic diversity than other subspecies, probably because of their history of existing mostly in island populations where gene flow and population size are limited. Consider, too, that a few deer colonizing a new island do not carry with them a lot of diversity to start with.

The team has identified the ice-free areas where deer survived during the last ice age; i.e., the source areas from which deer went on to populate the continent after the glaciers receded. We now see that today’s blacktails most likely expanded from coastal areas of Washington and Oregon, whereas earlier thinking had them expanding from areas further north. Mule deer survived the glacial maximum in several areas south of the ice sheets. Mule deer and blacktail deer were later reunited as the glaciers receded.

Other nuggets of knowledge will surface as the team gleans meaningful and practical information from its mitochondrial DNA data and, subsequently, from interpretation of nuclear DNA results. In the next phase of research the team will examine in greater detail the currently recognized subspecies, in order to better define the real boundary between blacktails and mule deer in the Pacific Northwest.

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Number and location of samples used for genetic analysis of mule deer and black-tailed deer.

