Conservation Project Spotlight:

Big Questions/Little Genes

Maintaining accurate trophy records along the Blacktail/Mule Deer Boundary

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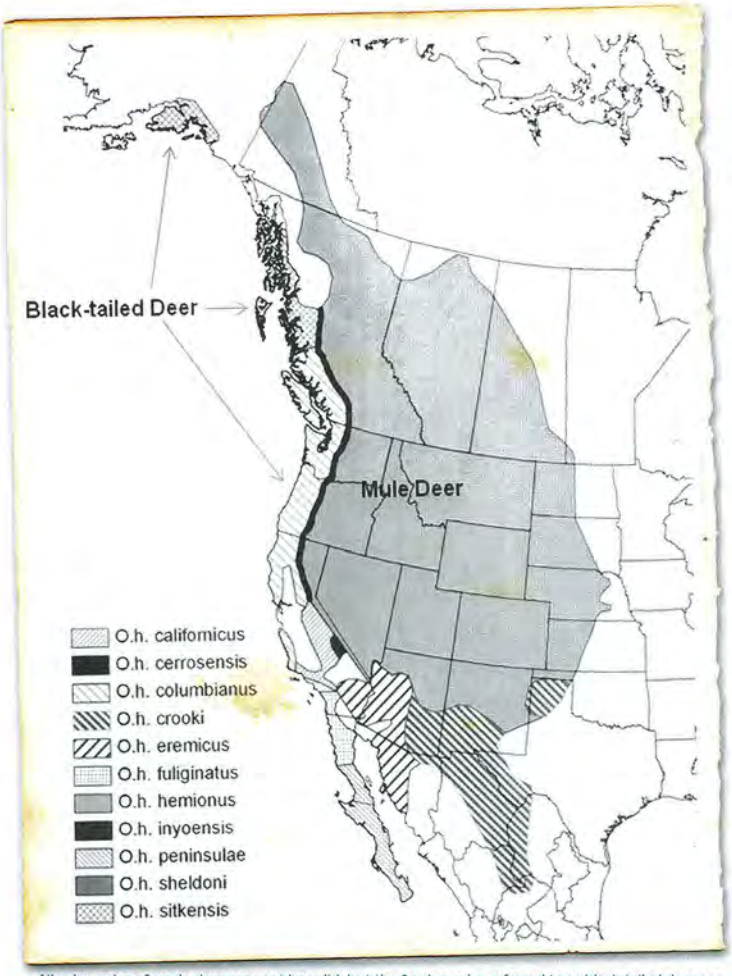


All subspecies of mule deer may not be valid, but the 2 subspecies referred to as black-tailed deer are genetically and physically different from the other mule deer subspecies.

Deer Diversity

Mule deer and their black-tailed deer subspecies are distributed throughout western North America from the coastal islands of Alaska, to southern Baja Mexico and from the Mexican state of Zacatecas to the Canadian provinces of Saskatchewan, Alberta, British Columbia, and southern Yukon Territory. Within this wide range of distribution, mule deer have adapted behaviorally and physically to local habitats and ecological conditions. These local adaptations have been described through the years as subspecies based on differences in fur coloration, antler shape, body size, appearance of their tails, and the size of the metatarsal gland. These subspecies designations have not been rigorously tested and many subspecies are probably not valid.

However two subspecies, the Sitka and the Columbian black-tailed deer in the Pacific Northwest, do appear to be different from all other "mule deer" subspecies in several ways. These differences and their implications to management and record keeping were the subject of a study recently completed by researchers working with the Pope and Young Club in collaboration with University of Wisconsin-Milwaukee, Boone and Crockett Club, Dallas Safari Club, Seattle Chapter of Safari Club International, California Deer Association, Camp Fire Club of America, Purdue University, and the Arizona Game and Fish Department. This research is part of a huge North American deer genetics project that started in 1996 and continues today.

Deer Divergence

The Pope and Young Club (and Boone and Crockett Club) recognizes 3 record-keeping categories for this species of big game: the Sitka black-tailed deer, Columbian black-tailed deer, and mule deer. These 3 types of deer look very different physically with black-tailed deer having a black upper tail surface, smaller body size and antlers, and a shorter metatarsal gland (this gland sometimes differs among deer subspecies and is used as a defining characteristic).

Genetically, blacktails also have very different mitochondrial DNA (mtDNA) than mule deer. MtDNA is not the nuclear DNA that is inherited from both mother and father and that codes for visible traits. Rather, it is DNA that resides in the cell outside the nucleus and so offspring get all their mtDNA only from their mother. This type of DNA is inherited down through the mother's side of the family just like a human last name is traditionally passed down through the male's lineage.

This genetic difference between blacktails and mule deer arose because a population of early blacktail/mule deer ancestors was isolated along the Washington and Oregon coast by the Ice Age glaciers sometime during the Pleistocene. The isolation was for a long enough period that after glaciers receded, these two forms of deer were somewhat different physically and genetically, but close enough to still reproduce. Today the distributions of the two subspecies remain in contact and the result is a zone of hybridization along the crest of the Cascade Mountains.

The Cascade Range runs through Washington and Oregon, dividing blacktails on the west and mule deer on the east.

This hybridization along the boundary between Columbian blacktails and mule deer in Northwestern North America created a pressing research need for the Pope and Young Club and the Boone and Crockett Club. It was widely known for quite some time that deer do hybridize along the crest of the Cascades in Oregon and Washington. In fact local hunters sometimes call them "benchleg bucks." There is nothing wrong with their legs, but this nickname clearly shows the local acknowledgment of this zone of hybridization. The important issue for the Club is that we can't have the smaller blacktail records category "polluted" with new record animals that are big only because they are part mule deer.

Using Little Genes to Answer Big Questions

The focus of the current research was to: 1) describe the extent of hybridization between blacktails and mule deer along the Cascades in Oregon and Washington; 2) evaluate the appropriateness of the currently recognized boundaries between the two types; and 3) develop a genetic test to diagnose animals that are not pure mule deer or black-tailed deer.

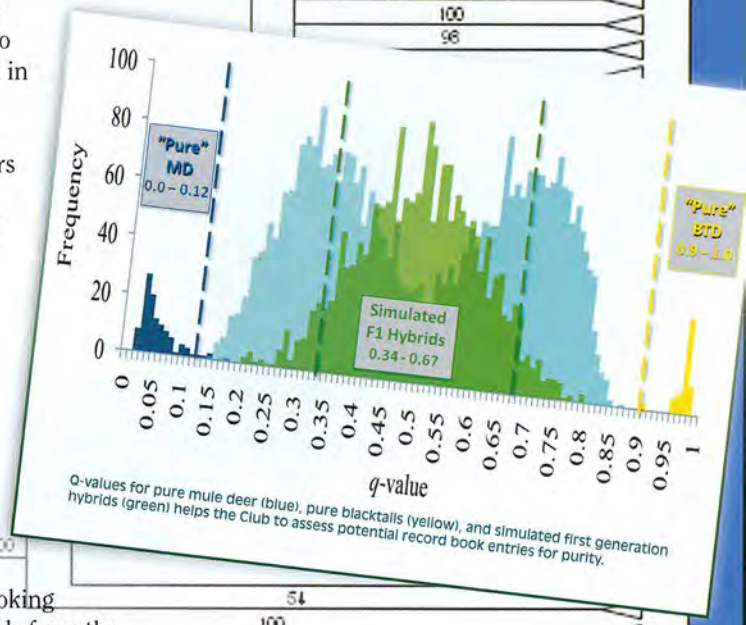
We had collected 2,800 deer tissue samples from all over North America, but re-sampled the zone of contact more intensively for this aspect of the study. The contact zone extends from Northern California northward into British Columbia, but we chose to focus our research in the heart of it all in Oregon and Washington. With the help of deer hunters and state biologists, we obtained 410 samples with accurate locations.

These samples were analyzed with a suite of 10 microsatellite markers (a way to identify genetic differences) and suspected hybrids were then subjected to mtDNA sequencing for additional information. We analyzed the microsatellites using a computer program called "Structure" that placed every individual deer into one of two genetic groups: mule deer or black-tailed deer. The analysis resulted in a "q-value" for each deer between 0 and 1, with 0 being a pure mule deer and 1 being a pure blacktail. Things are not always this clearcut, however. Because of genetic variability, most deer are not absolutely 0 or 1 so we first had to account for this.

The first step was to determine the range of values that represent pure blacktails and pure mule deer. We did this by going to our North American sample collection and selecting mule deer and blacktails from areas too far from the contact zone to be contaminated by hybridization (Idaho, Montana, and northern British Columbia). After looking at the range of variability in these pure animals, we then knew that animals from the contact zone with q-values outside these ranges probably were not pure.

First generation hybrids (F1) will have a q-value between the two parental types: near 0.5, but again, not exactly. To estimate the range of q-values for F1 hybrids, we used the computer to simulate matings between pure blacktails and pure mule deer to see what range of q-values we could expect to find in F1 hybrids. Q-values between 0 and 0.12 were indicative of pure mule deer and those between 0.9 and 1 were pure black-tailed deer. We defined any animal with a q-value between 0.34 and 0.67 as an F1 hybrid. Any animal that was not a pure individual or an F1 hybrid was probably the result of a hybrid breeding back (back-crossing) to one of the parent types or to another hybrid. Once we had the limits and range of values for these three categories defined (both pure parent types and their F1 hybrids), we now could test animals in

Analysis of mtDNA, which is inherited through the mother, shows a clear genetic division between blacktails and mule deer.



Q-values for pure mule deer (blue), pure blacktails (yellow), and simulated first generation hybrids (green) helps the Club to assess potential record book entries for purity.

Mule deer photo by George Andrejko/AZGFD.

the blacktail/mule deer contact zone for hybridization. Using a scoring system of q-values like this, we can be fairly confident in our designations of the pure parent types, and those that are not pure.

These defined ranges allow us to test individual animals on the scale of 0 (mule deer) to 1 (blacktail) and also to evaluate the extent of hybridization and back-crossing occurring in the contact zone. We know that the mule deer on the east side of the Cascade Range and the blacktails on the west side meet up on the crest of the mountains in summer. Since they don't migrate down to lower elevations until after most of the breeding is done, biologists have long recognized there is a zone of hybridization where they meet. When we looked at the distribution of pure and hybrid deer, we clearly saw that most deer sampled are one of the pure parent subspecies, but obviously a lot of hybridization is going on. Since we had locations where each deer was collected, we then colored-coded those locations according to that deer's q-value to describe the pattern of hybridization in this area.

We found that hybridization along the zone of contact was bidirectional and symmetrical, which means there were hybrids with both mule deer and blacktail fathers and this occurred in equal proportions. Of all the F1 hybrids, exactly half were fathered by mule deer bucks and half by blacktails. One might think that larger mule deer bucks would be able to out-compete smaller blacktail bucks and result in most hybrids being born to blacktail does, but this was not the case. We have some samples far from the contact zone with q-values indicating they are first generation hybrids, but these are most likely some second or third generation hybrids that have backcrossed with pure or hybrid individuals resulting in a q-value back in the range of F1 hybrids. These hybridizations have been occurring for a very long time and there is a wide variety of different combinations of mule deer and blacktails out there.

Using what we learned

The state agencies in Washington and Oregon have a long-established management boundary that they recognize as the division between mule deer and black-tailed deer. This boundary is very similar to the record-keeping boundary used by Pope and Young Club and Boone and Crockett Club. When we look at the location of all the pure individuals, we see that the Club boundary does a good job of defining the geographic division between these two deer types. Deer movement data from radio-collared deer in these two states are also consistent with the currently recognized boundary.

These results are already being put to use to keep trophy records accurate. The Club has developed a set of four guidelines to use in evaluating a deer that is questionable because of harvest location or physical appearance. The first guideline is simply the physical characteristics of the animal. There are well-known physical differences in coat color, metatarsal gland size, and antler shape. Secondly, the q-value is a powerful piece of information that allows us to base decisions on real data rather than simple appearance. Animals with a q-value between 0 and 0.12 are indicative of pure mule deer. On the other end of the scale, those deer with q-values of 0.9 to 1 are within the range of values for pure black-tailed deer.

The third guideline is to consider what kind of mtDNA the animal in question has. If a first generation hybrid with a mule deer mother breeds back to a blacktail buck, her offspring will be 3/4 blacktail and yet have mule deer mtDNA (from its mother and grandmother). If that female second generation hybrid breeds with a blacktail buck, we now have a deer that is 7/8 blacktail, but has all mule deer mtDNA because it is passed down through the female line as a complete package. Some deer tested might actually look very blacktail-like, but the presence of mule deer mtDNA helps us identify hybridization in its past.

Lastly, we can consider what are called "subspecies-specific alleles." These are genetic markers from the microsatellite analysis that are always, or almost always, found in either mule deer or blacktails. If a certain genetic marker is found in mule deer 99.8 percent of the time and we find it in a deer thought to be pure blacktail, it causes us to scrutinize that specimen a little more closely. Some of these guidelines may not work out 100

This Washington blacktail buck is beautiful, but is not nearly as big as Rocky Mountain mule deer to the east. Photo by Scott McCorquodale.

percent of the time when used alone, but together the suite of four guidelines offer a powerful and data-driven way to inform a trophy record-keeping decision.

Records Program Integrity

We documented extensive hybridization between mule deer and blacktails along the Cascade crest of Washington and Oregon and that has serious implications for record-keeping. This hybridization is occurring in both directions and with equal frequency on both sides of the zone of contact. There is nothing we can do about the existing level of hybridization; however, these are two well-supported trophy categories. Therefore we have to acknowledge the presence of this zone of hybridization and make sure the dividing line is in the most logical place given the best available data.

It is very important to the Pope and Young Club that trophy records be kept free of errors. Genetic contamination results in records contamination. With the smaller blacktails as separate records categories, it is very important that none of those high-ranking bucks contain a large dose of mule deer. It is well known that mixing two species or subspecies often results in "hybrid vigor," where the hybrid offspring are larger than either parent for at least the first generation. It is very easy to see the problems associated with hybridization between these categories.

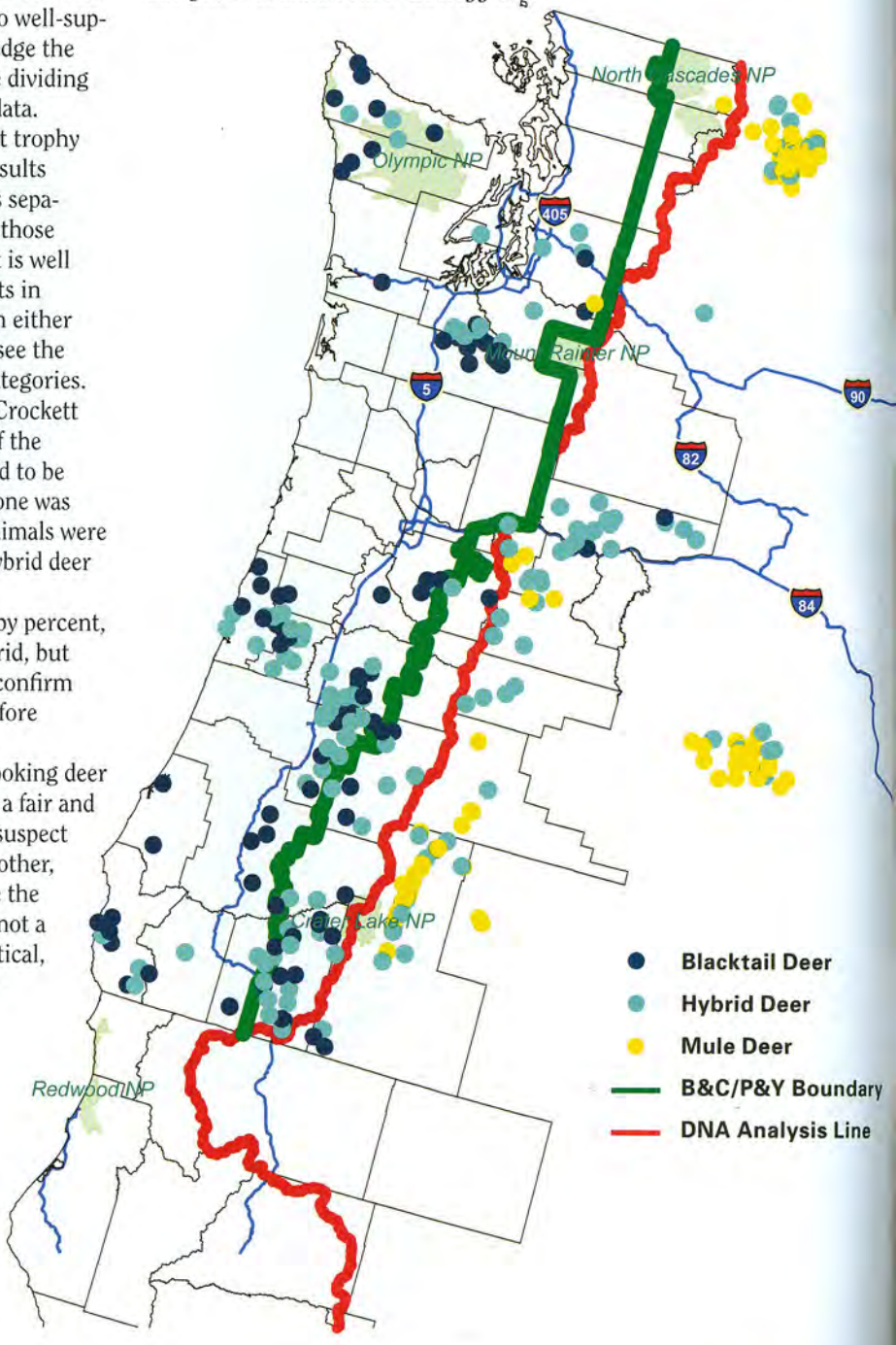
So far this protocol has been used by the Boone and Crockett Club to test eight individual deer to assure the integrity of the records categories. Of those eight deer, one was confirmed to be pure mule deer, six were found to be pure blacktails, and one was identified as a hybrid from northern Oregon. The pure animals were celebrated and entered, but the entry application of the hybrid deer was rejected from the records program.

We may not be able to tell a hybrid's exact pedigree by percent, or even if it is a first or second (or more) generation hybrid, but that is not important. What is important is that we can confirm the purity of an individual deer as defined by the Club before allowing it to be entered in the records book.

The Club now has a protocol for how questionable-looking deer and suspected hybrids will be processed and dealt with in a fair and transparent way. In the future, if the Club has reason to suspect a deer is not a pure representative of one category or the other, the person submitting the trophy will be required to have the deer tested with this approved protocol to show that it is not a hybrid as defined by the Club. It is not possible, nor practical, to require animals already in the book to be tested so the best we can do is to scrutinize entries from this point forward.

Finally, after years of trying to keep records clean and accurate by relying on physical characteristics, we now have a much more informed process upon which to base record-keeping decisions.

Jim Heffelfinger is a member of the Pope and Young Club and this study was part of a larger research effort supported by the Club and its partners to use genetic analysis to inform practical decisions on wildlife management and record-keeping integrity. Visit www.deernut.com or follow Jim on Twitter: @Gametrax. Dr. Emily Latch and Elizabeth Kierepka represent the Latch Laboratory of Applied Evolutionary Ecology at the University of Wisconsin-Milwaukee, and Dr. O. E. Rhodes, Jr., is the Director of University of Georgia's Savannah River Ecology Lab



The boundary line used by the Boone & Crockett Club and the Pope and Young Club to separate pure mule deer (blue) and black-tailed deer (yellow) may be the best that can be done given the surprising amount of hybridization (aqua color) along this contact zone.

Map courtesy of Boone & Crockett Club