

THE ROLE OF GENETICS IN DEER MANAGEMENT

DNA Adds A New Twist To Trophy Production Part I

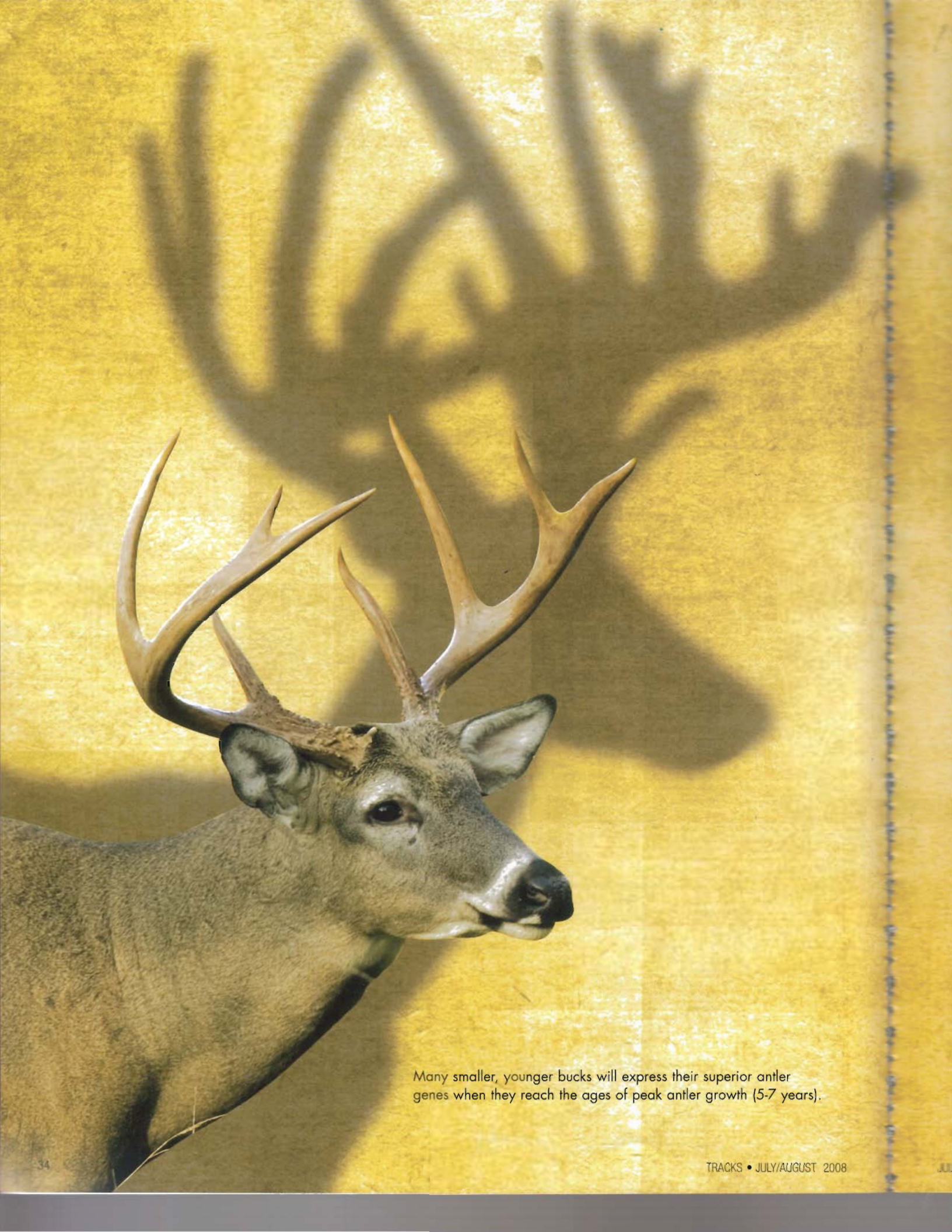
By Jim Heffelfinger

As deer hunters and managers, our hunger for producing bigger and bigger bucks is nothing new. We know there are three parts to the Boone & Crockett equation: age, nutrition and genetics. Age is the most obvious and easy to understand portion of the equation. We learned long ago that antler size increases with age through the years of peak antler growth (generally 5-7 years).

We then turned our focus to nutrition. Realizing that there was a relationship between antler size and diet quality, William Twiti in 1327 remarked "the head grows according to pasture, good or otherwise."

In the middle ages, enormous red deer racks decorated castles throughout Europe and were traded among royalty as objects of great value. During the 1930s and 1940s, a German chemist named Franz Vogt ran a series of experiments in an attempt to grow red deer antlers that would rival the monstrous medieval heads. Vogt knew that antler characteristics were

CONTINUED ON NEXT PAGE 36



Many smaller, younger bucks will express their superior antler genes when they reach the ages of peak antler growth (5-7 years).

somehow passed on to male offspring, but he chose to concentrate solely on age and nutrition.

Vogt analyzed the chemical composition of antler material and then fed the deer large quantities of protein and these minerals, and watched them grow through the peak antler growth years—and grow they did! When the fighting of World War II ended his experiments prematurely, 35 of his 36 stags scored in the top 100 heads ever measured.

That brings us to the third factor in our equation. Each buck has a different genetic potential for antler growth. Captive bucks of the same age, fed the same diet, show antler conformations that are very different from one another. Some bucks will be superior to others at the same age and some will never have large antlers, just as some humans never reach six feet tall regardless of diet or age. Every population has some individuals that have genetic potential for antler size that is far above or below average for that population.



A small piece of tissue or antler can be converted to genetic data that reveals a wealth of information about that deer and its relationships to other deer in the population. All photos by author.

DESCRIBING DEER DNA

I always thought talk of a deer's "DNA" referred to "Damn Nice Antlers." As fast as new genetic techniques are developed, they are being put to use by wildlife researchers, giving us a look at the genetic structure of deer populations in greater detail. These new techniques are beginning to unravel some of the mysteries of deer DNA and how it relates to real life, on-the-ground deer management.

As of yet, no one has located "the antler gene," and it is doubtful anyone will because the relationship between genes and physical characteristics is rarely that simple. There are probably many genes that act together to determine the shape, size and mass of a buck's antlers, and the expression of these genes is related to his ability to efficiently process his nutrient intake and survive to a ripe old age.

Searching for that magical gene is not what is keeping today's geneticists busy, but rather they are evaluating antler characteristics through many generations of captive and wild deer, and also comparing the variation between individuals and populations in the wild.

A short description of DNA itself is

important to get everyone on the same page. The DNA molecule resembles a twisted ladder with each gene represented as a ladder rung. The right side of the ladder is from the mother and left side from the father.

Each gene (ladder rung) has one side from each parent that come together when the egg is fertilized to form a complete DNA molecule in the offspring. An individual might get the same version of the gene from each parent (blue eyes from both) or a different version from each (blue eyes from one and brown eyes from the other).

Normally, one type of allele is dominant over another (which is fortunate or many of us would have eyes like a husky!). Those that receive the same version of the gene from each parent (blue/blue) are said to be homozygous for that gene, while those that received two different versions (blue/brown) are heterozygous.

YOU CAN BE HETEROZYGOUS AND STILL CELEBRATE DIVERSITY

Genetic tests can tell us whether an individual is homozygous or

heterozygous for a particular gene. Testing a large sample from a population allows us to estimate the percent of deer that are heterozygous. Comparing the percent of heterozygosity in different deer populations gives us a measure of how related they are and likewise how much genetic interchange there has been.

Looking at several genes in each animal also allows us to determine which individual deer are more heterozygous than others. It is an advantage for a deer to be heterozygous for many genes because good genetic diversity means they will be better able to adapt to changing conditions.

Whitetails, as a species, have very high levels of heterozygosity (good genetic diversity) among all large hoofed mammals. This may explain the great adaptability this species has shown throughout history.

Recent research showed that deer with a lot of heterozygous genes have higher Boone & Crockett scores, higher body weights and better reproductive rates. Genetic analysis of more than 16,000 whitetails harvested in South Carolina

CONTINUED ON PAGE 38



Before culling for antler quality can be implemented successfully in a practical situation, we must test what we learned in captive herds in wild free-ranging populations.

FROM PAGE 36

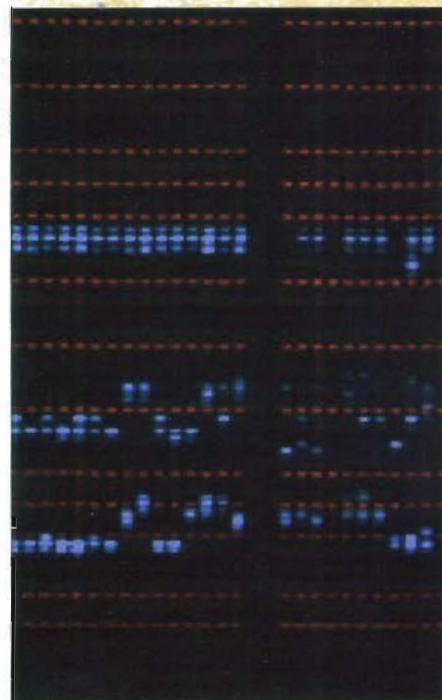
showed that heterozygous individuals had more antler points as yearlings. Now we're getting somewhere!

Another study showed that older bucks had a higher level of heterozygosity than young bucks, so they must have survived at a higher rate than homozygous deer. It appears then that there are measurable differences in the gene pool of deer herds that are related to real population characteristics.

With this in mind, we can begin to see the negative influence of inbreeding in a deer population. If a buck and doe are closely related there is a greater chance their offspring will receive the same allele from both parents and be homozygous for many genes. If it is a disadvantage to be homozygous for a lot of genes, then the deer herd experiences what is called "inbreeding depression"—smaller antlers, lower reproductive rate, etc. Their family tree does fork, just not as much as it should.

POPULATION GENETICS

We see significant genetic differences between portions of the deer herd, which should be able to freely interbreed. This is not caused by fences or other physical



Powerful genetic analysis software has brought the price for analysis low enough that large numbers of animals can be run, thereby maximizing sample size and strengthening the interpretation.

barriers, but rather the result of the breeding and dispersal patterns of white-tailed deer.

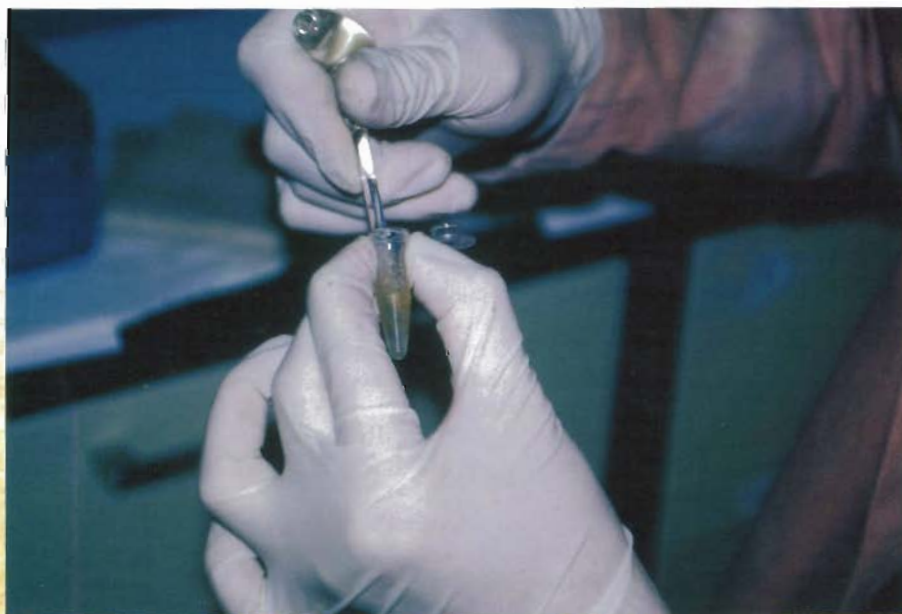
Males are the reason the gene pool gets "stirred up." Young males disperse to new areas at 1-1/2 years of age, while females usually hang around in or near their mother's home range. Because of this, genetic material from females generally stays in a localized area through the generations.

When we see forked brow tines or drop

tines consistently in a localized area we might attribute that to a sire buck with those characteristics. However, it may be a characteristic that is being perpetuated by a cluster of related, non-dispersing females. Researchers have found significant genetic differences between portions of deer populations only 2-3 miles apart.

How does this relate to deer-proof

CONTINUED ON PAGE 40



fences then? High fences definitely limit the dispersal of young bucks and ingress of hordes of your neighbor's does (that's why we pay so much for them!). Whether this will result in genetic problems (inbreeding depression) depends on the size of the fenced area, security of the perimeter and harvest strategies within the fence.

Larger fenced areas decrease the probability of inbreeding because males can disperse in a more normal fashion and the size of the gene pool is larger. A larger and more diverse beginning gene pool means there is a lower chance a deer will receive the same type of alleles from both its mother and father resulting in less genetic diversity.

As mentioned before, deer are generally pretty diverse and it only takes a relatively small amount of interchange to maintain that diversity. Fences are probably not a genetic issue for a population unless you have a small area with few bucks doing the breeding, either through the use of breeder pens or wide buck-to-doe ratios.

As we learn more in the future about the genetic variation of Texas deer herds under intensive trophy management, it may become beneficial to base management to a larger degree on preserving and enhancing the genetic component.

After decades under high fence, management of intensive trophy operations may include an exchange of deer with other ranches—not to obtain “good” genes, but merely to obtain “different” genes to increase the genetic variability (heterozygosity) of the herd.

SPIKE “GENE-OCIDE”

We have realized for a long time that antler characteristics are inherited, but there has been a lot of confusing and contradictory advice given about how genetics in a deer population might relate to practical management on the ground.

Starting in 1973, Donnie Harmel, John Williams, William Armstrong, Jim Ott and others began a series of progressively more complex experiments on the effects of genetics and nutrition on antler and body size in whitetails on the Kerr Wildlife Management Area (WMA).

In the first experiment, eight bucks that were spikes as yearlings and one

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buck that was a large 10-point at 3-1/2 years old were bred to does and the antler development of 10 generations of offspring were recorded. Researchers showed that antler size and body weight were genetically based and influenced by environmental factors like nutrition.

Data collected from this captive population indicated a buck's future antler size could be predicted by looking at his first set of antlers. On the average, bucks carrying spike antlers when they were yearlings did not grow antlers as big as those that were forked-antlered yearlings. Yearling spikes also went on to produce more spike-antlered offspring in their lifetime than bucks with forked antlers as yearlings.

A more intensive analysis of the inheritance of antler characteristics was later conducted on these captive deer and most antler characters were considered to have high levels of heritability.

The early studies from Kerr WMA set off the “spike wars.” If spikes were prone to producing and passing on inferior antler genes then removing spikes might be a way to cleanse the gene pool. The widespread slaughter of spikes commenced in the name of genetic purity.

One of the reasons this “Gene-ocide” became so popular, so fast, was that it was fun. Finally, there was something we could actively do to improve the gene pool—and it involved shooting deer! However, as more information became available, the idea of genetic improvement became more complex and managers were understandably confused.

During this time I was completing my Master's Degree at Texas A&M-Kingsville

under Drs. Sam Beasom and Charlie DeYoung and then managing the Rio Paisano Ranch in Brooks County. This spike culling made all the sense in the world and we killed spikes on the ranch at every opportunity.

I then started working for Dr. Harry Jacobson at Mississippi State University and Jacobson was giving talks and showing pictures from his captive deer herd that showed some spikes that became tremendous bucks at maturity.

SPIKES RALLY BACK

Some people started to point out that poor nutrition and late birth dates will also produce spike antlers in a yearling irrespective of what kind of genetics the buck has. Removing those deer would not improve genetics and may even be counterproductive.

In some areas of the country with chronically poor nutrition, most yearling bucks are spikes and if culled intensively, deer managers could nearly wipe out the yearling age class. When it comes to gene pools, you don't want to drain it in order to clean it.

There were criticisms that Jacobson's anecdotal slides showing a spike-to-monster progression was not data, but simply pictures of the exceptions. So Jacobson teamed up with geneticist Steven Lukefahr to conduct an analysis of antler measurements and pedigrees of over 200 captive white-tailed deer housed at Mississippi State.

Analysis of this herd from 1977 to 1993 indicated that the occurrence of spike antlers in yearling bucks was related

CONTINUED ON PAGE 42

more to environmental factors than genetics. Antler characteristics of yearlings are probably more dependent on nutrition and birth date (early or late born) because their bodies are still growing and nutrients available for antler growth may be limited.

The genetic influence of antler conformation was more detectable in older bucks (2-plus years); as their bodies matured, antler size was related more to their genetic potential than their nutritional intake.

The Mississippi data and the Texas data yielded what looks like contradictory results, which has led to decades of controversy.

According to an independent review by Texas A&M animal geneticist Daniel Waldron, the different conclusions derived from these research efforts may simply be the result of the researchers asking slightly different questions and analyzing their data with different statistical methods.

Dr. Waldron also pointed out that some Kerr WMA studies did not account for factors such as the birth date of yearling bucks, year, maternal influences

or the fact that many of the sires in the Kerr herd were related to one exceptional sire buck.

The Mississippi captive herd consisted of deer from the Midwest and Southeast, and this may be a problem when applying the conclusions to Texas deer. Waldron felt that neither the Texas nor the Mississippi analyses resolved this issue definitively.

It seems logical that during a buck's first year of growth, nutritional variation would have a lot to do with the size of his first set of antlers. And yet, the Kerr data showed clearly that the antler size at the yearling stage does hold some predictive value in what that animal's antlers will look like at maturity.

There is also no doubt that antler characteristics of male offspring are related to those of their sire, but definitive statements about how this relates to management actions on a free-ranging deer herd must be reserved until we are able to see the results of pending and future research.

Investigations have illuminated surprising differences in genetic variation between ages, years and neighboring subpopulations. We don't have all the answers, but we now know a lot more

about the heritability and the predictability of antler traits. This foundation of genetic knowledge is already being used to design still more complex studies to determine what affect our actions can exert on the genetic makeup of a deer population. Can we, through our actions, actually change the gene pool of a free-ranging deer herd?

Editors Note: This is the first of a ³two-part series on the role of genetics in deer management. After highlighting some of the most important research on this topic (Part 1), the author will discuss the effects culling, breeder pens, trophy hunting and antler restrictions can have on the genetics of a free-ranging deer herd (Part 2). *!!!*

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