THE ROLE OF
GENETICS
IN DEER MANAGEMENT

DNA Adds A New Twist To Trophy Production

Part II

By Jim Heffelfinger

When it comes to deer management, our interest in genetics usually revolves around what effect humans might have on the gene pool. This effect could be positive or negative if our actions cause a shift in the overall proportion of "good" genes and "bad" genes.

Of course, genes are neither good nor bad, but if there is a characteristic we would like to retain or see more of, we consider that a desirable trait or a "good gene" that we would like to occur in a higher proportion among the animals in the population.

In domestic livestock production, that "good" trait may be high milk production or rapid weight gain. Usually our "good" deer genes simply boils down to larger than average antlers for a certain age.

We have the potential to alter the gene pool anytime we influence what deer are available to do the breeding for the next generation. This includes human activities such as selectively harvesting trophy bucks, culling bucks, establishing harvest restrictions based on antler size, trans-locating deer and establishing artificial breeding pens.

Each buck has a different genetic potential for antler size. How much envirnomental factors influence the expression of these genes in the wild is an important consideration for those wanting to improve the genetics of their deer herd.

GERRY PERRY PHOTO

In discussing the manipulation of the gene pool, we have to understand three main concepts: heritability, predictability and selection. Let's look at these concepts briefly and see how they play a role in the various ways humans potentially affect the gene pool.

HERITABILITY

In Part 1 of this series I highlighted some of the initial work that has been done in Mississippi and here in Texas regarding heritability, a term used to describe the inheritance of physical characteristics from the previous generation.

If you took a group of 5-year-old captive bucks fed the same diet and put all their Boone and Crockett scores on a graph, you would see a bell-shaped curve. There would be a few with unusually large antlers, some exceptionally small racks, but most fall in the middle around the average. In this case where age and nutrition are controlled, much of this difference in antler size is due to variations in genetic potential.

Early work with pedigreed captive herds illustrated that deer have a wide range of individual genetic potential for antler size and shape. It is clear that a buck's antler characteristics are related to those of his father or grandparents (in other words, they are "heritable"); but a characteristic can be "highly" heritable (offspring look a LOT like dad) or have low heritability (they only look a little like dad).

Different research projects conducted and analyzed somewhat differently have yielded some contradictions about how strongly various antler characteristics are heritable. Regardless, I think everyone would agree that antler characteristics are inherited to some degree and therefore we have the potential to influence that by altering whom is doing the breeding.

PREDICTABILITY

We know antler characteristics are inherited from previous generations, but how easy is it to predict a buck's future antler size from his antlers at 1-2 years old? The similarities in a buck's antler shape from year to year can be striking. If you have ever found more than one year of shed antlers from the same deer or seen the same buck in consecutive years you have seen this genetic predictability first hand.

Given this year-to-year similarity in antlers, it seems like we should have some ability to predict a young buck's potential for making it into the record books. This issue is at the heart of all the controversy surrounding whether or not shooting spikes can improve the gene pool.

In Part 1 of this series I highlighted the work done at the Donnie E. Harmel White-tailed Deer Research Facility at Kerr Wildlife Management Area (WMA) and at Mississippi State University. The research on pedigreed, captive herds at those facilities have yielded somewhat contradictory information about how well we can predict the future antler size

based on what a buck looks like as a yearling. Some of this confusion may be due to variation in individual deer performance and differing ways the research projects were designed and executed.

It is clear, however, from a Kerr WMA study where the next generation of sires were selected based on their yearling antler characteristics that a buck's first set of antlers can be used in predicting his genetic potential in their captive deer herd.

If there are contradictions about the predictability of antler size in controlled, captive situations, that does not bode well for our desire to design deer management schemes around it. In a free-ranging deer population, confounding factors such as fluctuating nutrition, sickness and fawn birth date can interfere with the expression of genes and muddy the issue considerably.

In recent years several studies have been, and continue to be, conducted to determine predictability in the wild. We will explore these studies on free-ranging populations in the next issue and see if any clarity comes from looking at this from the practitioner's perspective at the population level.

SELECTION

Selection refers to anything that removes future breeders from the population based on some characteristic rather than random removals. Examples of purposeful selection might include removing animals due to poor weight gain in beef cattle or poor antler development in deer.

Anything that removes deer from a population in a nonrandom way is exerting selection on the makeup of the gene pool. Anytime we shoot a trophy buck for the wall, shoot a spike or cull buck, or artificially inseminate does and release them, we are engaged in the selection of the next generation of breeders.

Selection can be intensive enough to rapidly change the genetic makeup of future generations or so light and sporadic that it is meaningless at the population level.

A 10-year experiment whereby you take 30 yearling bucks and each year only breed the five with the largest antlers to

20 does each in captivity is much more intensive selection than shooting three spikes per year on a 10,000-acre ranch. Both actions represent selection, but potential for changing the gene pool is dramatically different.

At Kerr Wildlife Management Area, researchers have run selection experiments where they used the largest-antlered yearlings in one trial and the smallest antlered yearlings in another as sire bucks for the next generation of captive deer.

Using the largest-antlered yearlings each year, they successfully increased antler size, by age class, over the course of the experiment. Using the smallest yearlings as sires each year for many years, they were able to nearly breed the antlers off the bucks in that bloodline! Simply turning the pages of this magazine illustrates just how effective controlled selection in captivity is.

INFLUENCING THE FREE-RANGING GENE POOL

Captive studies on heritability and predictability were important first steps to learning if we have the potential to influence the gene pool of wild populations. There has been some mixed research findings regarding just how

Rapidly developing genetic analysis techniques now allow researchers to correlate genetic relationships with some antler characteristics and population parameters.

heritable or how predictable antler characteristics are, but selection studies in captivity show that they are heritable and predictable enough to make physical changes to the herd through selection.

Years ago, Stewart Stedman published an article that addressed what he called the "Corral to County Continuum." What you can accomplish in a small scale, controlled corral (captivity), you might not be able to apply to an entire county (or even ranch) at the same intensity that produced the treatment effects in captivity.

It is the intensity of the selection that is the fulcrum upon which everything balances. I think everyone agrees that selection intensity is the cornerstone of any discussion about humans affecting the gene pool; however, it is uncommon to see it expressed as clearly as Stedman did (if it's mentioned at all).

We should not be taking the successful selection experiences in captivity and making definitive statements about how shooting spikes or older cull bucks will help the deer herd on your 40,000-acre ranch. Intensity has to be central to the discussion. Our ability to apply intensive selective pressures on a free-ranging population is hindered by many obstacles.

OBSTACLES TO SELECTION

We have no chance of selectively altering the gene pool unless we can get through or around most of the obstacles that inhibit our ability to remove undesirable breeders and encourage the genes we want to pass on to the next generation.

AGE

Many times the effects of age are confused with the effects of genetics. Although there are some physical characteristics we can use to age bucks on the hoof, it is an imperfect art to say the least.

Ideally, if we want to select poor-antlered deer out of the population we should know the age of the bucks in our scopes. It is important to know if we are looking at a "good" 2-year-old or a "poor" 5-year-old. In these cases, we don't have the benefit of a pedigree and the uncertainty of age represents an
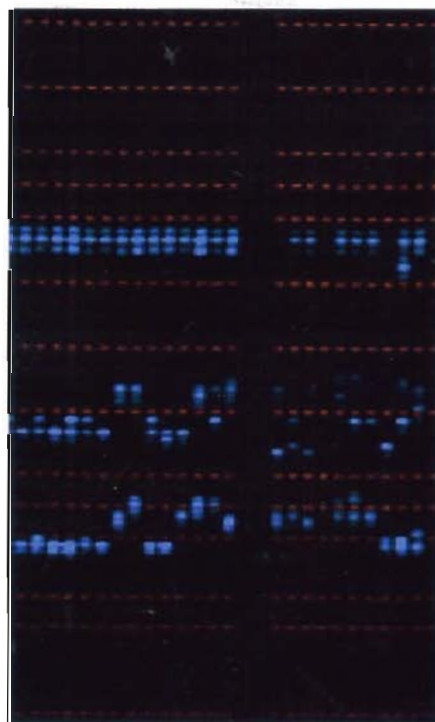
obstacle to efficiently selecting for antler traits after the buck's first year.

PATTERNS OF BREEDING SUCCESS

Research at the end of the 1990s by Dr. Randy DeYoung revealed some astounding insights into the patterns of male whitetail breeding success. DeYoung and several coworkers found that 30 percent of the fawns were sired by yearling and 2-1/2-year-old bucks. The remaining 70 percent of the fawns were sired by bucks 3-1/2 years old and older.

Rather than just a few dominant bucks doing most of the breeding, many bucks in the population were contributing genes to the next generation. This obviously complicates any attempt to cull or encourage certain breeding males in order to alter the gene pool.

DOE'S CONTRIBUTION

Most readers and students of deer management are aware that the doe contributes at least as much to the antler quality of her male offspring as the sire buck. Experiments have shown that fawns born from the same doe, but sired by very different bucks, often have antler conformations similar to each other and their mother's father.

If the buck:doe ratio is 1:2 or 1:3, this means that 66-75 percent of the total gene pool is made up of individuals (females) that cannot be subjected to selective pressures related to antler quality. It is hard to imagine how the quality of antlers could be manipulated by incomplete and sporadic selection on

only 25-34 percent of the gene pool.

In at least one of the Kerr WMA studies, researchers removed does from the breeding experiments if they produced two or more spike bucks. This was useful to prove that intensive selection can work in captivity, but we have no way of doing this outside of the "corral."

MATERNAL EFFECT

Does can have another, non-genetic influence on the health and quality of their offspring through a complex phenomenon called maternal effect. This effect is anything the doe does that increases or decreases the survival of the fawn. This might include providing antibodies to disease to the growing fetus or later in milk, or even just how well she selects a fawning site. Studies on many animals have identified maternal effects as a factor that may cloud attempts to exert selection on a herd for a particular trait.

NUTRITION

It is no secret that in dry years or on overpopulated deer habitat, a higher percentage of yearlings will have spikes because of poor nutritional conditions. It has been written by many (including myself) that removing spikes during these years would be bad because you could remove a lot of deer that are just nutritionally stressed and not genetically inferior. This may be true, but you really have to know your herd and what it produces under good and bad conditions to evaluate the relationship between nutrition and genetic potential.

If you are trying to maximize your

selective intensity on the herd, dry years may be exactly what you need to gain some ground. Mitch Lockwood, Don Frels Jr. and coworkers introduced the well-reasoned theory of "swing deer" that made me start thinking differently.

They suggested that there were three types of deer. Some deer that produced good antlers no matter what nutrition they received (#1), others produced poor antlers regardless of nutrition (#2) and a third group (swing deer) that grew big antlers in good years and poor antlers in dry years (#3).

To effectively alter the gene pool, you would ideally want to remove most of the bucks out of groups #2 and #3 each year and leave those that produce big antlers no matter what. The only time you can identify these bucks is during poor nutritional situations. This all makes theoretical sense and would be the way to go if you were trying to implement these principles intensively enough on the "county" end of the continuum.

DATE OF BIRTH

Much has been written about the effects of the fawn's birth date (early or late) on antler development the next year. Late-born fawns probably have a higher proportion of spike antlers when 1-1/2 years old because they are a little behind in body development and have less "extra" energy to put into antlers growth.

The years of raw data from Kerr WMA (or additional research) could be analyzed to investigate this further. If being born late in the year artificially masks a yearling buck's true genetic potential it could be culled for the wrong reason, thus adding yet another complication to our quest to select for big antlers.

LINKED GENES

Genes reside together on chromosomes and if we had enough time and money we could map all the genes on all the chromosomes as they have done with the Human Genome Project. We don't know where most genes are located, but we do know that genes located close to one another on the chromosome are usually inherited together.

If, for example, a gene related to antler size resides close to one that causes poor quality milk production,

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

JIM HEFFELFINGER PHOTO

these two genes may show up together most of the time. This means that as we are diligently selecting to increase the proportion of these types of deer, Mother Nature is selecting poor quality milk producers out.

In captivity, artificial feed may mask problems associated with us selecting for traits that would reduce survival in the wild. Not only can linked genes present an obstacle to efficient selection, but also if we are successful in altering the frequency of "antler-related" genes in a population, one has to wonder what affect we have had on other important genes that are linked.

OTHER ENVIRONMENTAL PRESSURES

Even if managers were able to exert an intensive selective removal of genetically inferior individuals from the population, it would not be the only selection taking place. Many other factors remove deer from the population irrespective of genetic potential for big antlers. These other removals are not always at random, so selection may be taking place.

In most populations, factors such as malnutrition, coyotes and disease take more than half of each year's fawn crop. If all these removals by other mortality factors were at random, this would not affect our efforts to alter the gene pool. But we don't have a good grasp of how genetic makeup is related to susceptibility to various sources of mortality.

For example, some individuals are genetically predisposed or immune to certain diseases. Some humans have a genetic sequence that appears to offer complete immunity to AIDS. If there are deer out there that are genetically immune to CWD or tuberculosis, we should hope that gene is not linked to the one for spike antlers!

USING WHAT WE KNOW IN MANAGEMENT

The obstacles listed here are just that— obstacles, not barriers. I have outlined the difficulty of effectively altering the frequency of certain genes in a free-ranging deer population, but this does not mean it is impossible.

These days the deer management world is a-buzz with cussin' and discussion about the effectiveness of culling spikes, culling inferior mature

bucks, establishing breeding pens, removing only the best-antlered deer on the ranch, trans-locating big deer from greener grass elsewhere and antler-based harvest restrictions.

All of these have a solid theoretical basis that indicates they should work on free-ranging wild populations. Under some circumstances they might work, but we should be careful about applying information from the "corrals" to our "counties."

In the next issue (Nov/Dec) I will pull together all these concepts, along with some new research now being conducted, and we will explore what can realistically be done to the gene pool when we apply the results of a lot of good research on the role of genetics in deer management programs. 🦌🦌

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