Symposium Proceedings

The Role of Genetics in White-tailed Deer Management

2nd Edition

January 26-28, 1998
Texas A&M University
College Station, Texas

Acknowledgments

Conferences like this one cannot be conducted without a lot of help from a lot of people. The Steering Committee would like to thank the speakers who took the time to prepare a manuscript for these proceedings. Karen Spoo coordinated many of the daily tasks and communications to keep the ball rolling. Jacque Hand and her staff at the TAMU Conferencing Center coordinated pre-registration and many on-site functions. Belle Buscher and Karin Entrekin helped prepare manuscripts for printing, and Ron Day and his staff at Texas Agricultural Extension Printing Services put the finishing touches on this publication. Steve Byrns and Kathleen Davis with the Texas Agricultural Extension Service (TAEX) Department of Agricultural Communications assisted with publicity. Eugene and Steven Fuchs graciously allowed the use of their line drawings for the cover illustrations. Thanks to the Texas Wildlife Association for their assistance in publicizing the symposium. The contributions and participation of the commercial exhibitors was appreciated.

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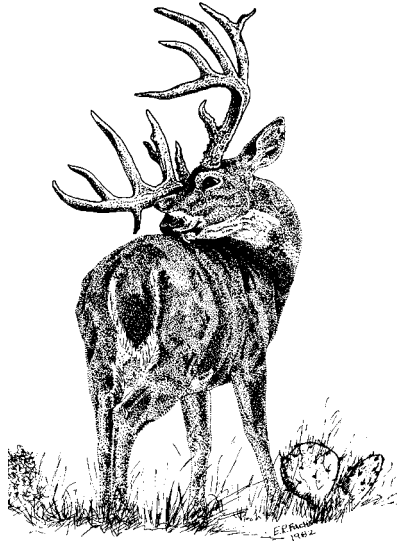**Rodney Honeycutt**

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The Role of Genetics in
White-tailed Deer Management

Proceedings of a Symposium
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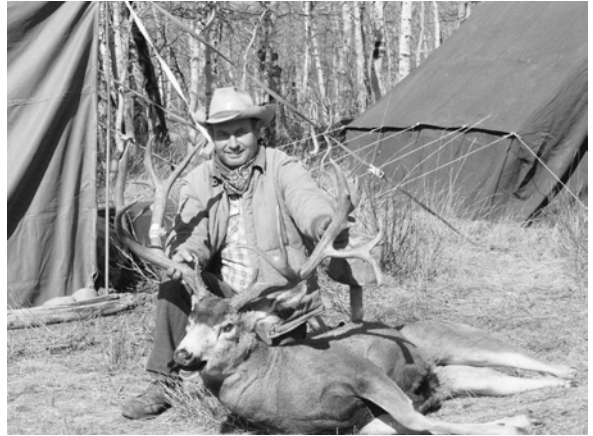**College Station**

Sponsored by:

Department of Wildlife and Fisheries Sciences
Texas A&M University System
Texas Chapter- The Wildlife Society

Edited by:

Kenneth A. Cearley, Extension Associate- Wildlife, and
Dale Rollins, Professor and Extension Wildlife Specialist
Dedication

*This symposium is dedicated
to the memory of*

Donnie E. Harmel.

Donnie Harmel died on October 19, 1997 after a hard fight with cancer. For 21 years Donnie was my boss. You learn a lot about a man in 21 years. Donnie had five loves. They were God, family, friends, hunting, and work. He found God in all he did. He worked at being a husband, dad and grandfather. He worked at being a friend. He worked at hunting. And he worked at working. He approached issues and tasks in a black and white manner. It was either right or wrong, and wrongs should be made right. Donnie did not live in a gray world.

If you knew Donnie, you know he was not hesitant about making a decision and you know he didn't spend a great deal of time second guessing himself on the decisions he made. That was probably one of his greatest strengths as a boss. He was definitely a "take charge" person. You knew what was expected from you and you knew that it better be done right. What you didn't always know was, "what will Donnie think is right?" He had a great deal of pride in a job well done, and you knew that if he didn't like it, you would have to do it over.

If you knew Donnie, you know he had a great love of the land and activities associated with it. Donnie always acknowledged that what God created was right and he was a dedicated steward of those natural creations. He taught that to his children. He shared that with his friends. He would have liked to share that with all who would listen, especially the kids. Donnie always saw that a lot of little things make up the Big Picture and he observed many things that most people overlooked. He was a firm believer that "you have to get out of the truck to see what's happening in the pasture."

One of his greatest pleasures was to sit around a campfire with friends and reminisce about hunting trips and things past and talk about deer. If the truth be known, some of best ideas about research and management of deer herds in Texas were the product of those campfire discussions.

The Kerr Wildlife Management Area was an extension of his personality and his love for the land. He put a lot of himself into it. Through his leadership and insight, the Kerr WMA became a recognized leader in the conservation world. His office wall was mantled with plaques to his achievements and successes. At his memorial, the pastor read a passage from a journal that Donnie kept. I don't remember the exact words, but part of the passage went something like this, "I wonder where I fit into God's plan." That kind of surprised me. Donnie was part of God's plan for almost 30 years. I'm sure the Kerr Area will go on. Donnie will be missed but his contributions, his caring, and his stories will be remembered around a lot of campfires.

- Bill Armstrong

(Editor's Note: The Texas Chapter of The Wildlife Society and the Texas A&M University Foundation are accepting donations to establish a Donnie E. Harmel Memorial Scholarship Fund. For more information, contact a member of the Steering Committee for this symposium.)

Foreword

Interest in white-tailed deer management has increased exponentially in the last 10 years. Much of this trend is aimed at growing bucks with larger antlers. Certainly, several factors are involved, including age, nutrition and genetics. In today's effort to "fast forward" antler growth, there is a special emphasis on genetic improvement. But there is also much confusion about the technology involved and its efficacy, i.e., what genetic manipulation can and cannot do. Finally, there are ethical questions about how such a "genetically engineered" approach to deer management will impact the future of deer hunting.

The goal of this symposium is to provide a forum for information exchange among leading scientific authorities and practitioners in the fields of deer management and genetics. As editor of these proceedings I guarantee you can find someone herein who will be espousing your arguments in the great spike buck debate. But as divergent as some of the theories on culling are, there is an equal convergence that deer genetics are just one tool in the deer manager's toolbox. Nearly every author herein exhorts readers to pay attention to the basics of habitat management as the foundation for any successful deer management endeavor.

The Texas Agricultural Extension Service initiated a series of annual symposia in 1993 to assemble the state of the science relative to wildlife issues in Texas. These symposia have addressed feral swine, coyotes, and supplemental feeding for deer. These symposia attempted to bring all sides of the issues to the table and provide an unbiased treatment of the issue. This genetics symposium was designed with the same intent.

– Dale Rollins

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OPENING COMMENTS

ROBERT D. BROWN, Head, Department of Wildlife and Fisheries Sciences, Texas A&M University, College Station, TX 77843

Welcome to the first symposium on the "*Role of Genetics in White-tailed Deer Management*." The planning for this symposium was based on the success of last year's symposium, "Supplemental Feeding of White-tailed Deer: Beyond Dogma." I expect that you will find this year's conference as enlightening and informative as last years', and I suspect you may find the issues as controversial, if not more so.

Certainly we have seen public interest in white-tailed deer management increasing exponentially in the past several years. Issues of interest have included habitat management, harvest management, leases and liability of landowners, private property rights, public versus private ownership of deer, what to supplementally feed, food plots versus feeders, the effect of nutrition versus genetics on body and antler growth, whether to cull spikes, and, more recently, questions about artificial insemination, embryo transfers, and possibly even "genetic engineering" of white-tailed deer.

What we have seen is a proliferation of scientific and not-so-scientific journal, magazine and newspaper articles about the possibilities of genetically manipulated antler and body growth in deer. Like nutrition and physiology, genetics is a highly technical field. The articles are often confusing, even if they are accurate, but often enticing, even if they are not accurate. With breeding bucks, buck semen, and even fawns selling for thousands of dollars, this new technology has the potential of financially making or breaking landowners and deer managers. But more importantly, both biologically and ethically, what might be the impact of this new technology, and the race for the "monster buck," on the future of our deer herd, our habitat, our landowners, and the future of hunting itself?

We have brought together a group of knowledgeable professionals to discuss these issues with you and with each other. Some are scientists with backgrounds in molecular biology, who can explain to you what genetic engineering can and cannot do, what DNA is, and whether a real "antler gene" might exist. Others have backgrounds in animal breeding and statistics, and will discuss the heritability of antlers and body weights, and the potential impact of introducing buck sires into herds, and the potential effect, or lack thereof, on the whole populations. Other speakers are mostly wildlife biologists, and they can discuss their real-life experiences at attempting to influence the antler size and body weights of their deer with a variety of techniques.

I will warn you, however, that you may not leave tomorrow with a lot of answers. Yes, we'll compare the "Mississippi" data with the "Kerr Area" data, and, we'll have the most knowledgeable scientists and managers in the country to do it. But, as I explained last year at the Feeding Symposium, the white-tailed deer may be the most studied wild animal in America, but we still know very little about it. Whereas there have been thousands of studies on millions of steers, hogs and chickens to give us what we know about their husbandry, nutrition and genetics, you can count the number of genetics studies done on white-tailed deer on one hand.

Because of that, you may hear conflicting results presented the next two days, and you may hear professionals disagreeing with each other, and even criticizing each other's work. We scientists and biologists are used to that; we regularly review each others manuscripts for publication or proposals for funding. We offer constructive criticism both in writing and in public at open hearings. So don't be surprised or offended if you've never seen two professionals disagreeing with each other. We are used to it, and in fact we welcome it; as professionals who are seeking to find the truth to our scientific questions about deer biology and management.

So I urge you all to pay attention and to ask questions. Remember that the only dumb question is the one that doesn't get asked. I can't promise you that by tomorrow you will know whether it was worth it to buy that expensive breeding buck, or to A.I. your does, or even whether you should shoot more spikes. What I can promise is that by tomorrow you will have had a very interesting two days, and that you will know everything we know.

DEER MANAGEMENT 101

STEVE NELLE, Natural Resources Conservation Service, 3812 Sherwood Way, San Angelo, TX 76901

*Abstract***:** The basics of deer management are important enough that a refresher course should be taken periodically, even by the "pros." We in deer management sometimes tend to drift off on tangents if not reminded of the foundational truths upon which our profession is based. While genetic manipulation is considered foundational by some deer managers, it is regarded as tangential by others. The degree to which antler quality in a wild population can be "tweaked" by genetic manipulation will be discussed and debated at this symposium and afterward. What is beyond debate is the fact that habitat management is the key to healthy, high quality, profitable deer herds.

In a college setting, a course designation of 101 means a freshman level course in some subject. A well taught 101 course lays the foundation and presents the framework for the subject. While it does not go into specifics, such a course will outline all of the essential elements of the topic and stimulate the student to seek deeper understanding of the subject. The course may also serve to remind the seasoned professor of the tenets of his profession. Such is the goal of this paper.

The title of this paper implies that there are certain basic doctrinal truths in deer management which are paramount. Even though many who read this would be considered advanced deer managers, the raw basics of our profession are important enough to bear repeating and re-emphasizing each time we gather.   In this way we may avoid the mistake of majoring in the minors.

What is Deer Management?

The dictionary defines management in these ways: "*to succeed in accomplishing a goal"; "to direct with a degree of skill*"; and "*to alter by manipulation*". We can combine these into a reasonably good definition of deer management:

"*success in directing and altering a deer population using the skills of manipulation in the accomplishment of a goal*".

This may be a good academic definition of deer management, but it tells nothing about how it is done. In 1933, Aldo Leopold described how game management might be thought of as the purposeful, creative and continuing alignment of these things:

(1) *axe* (brush or timber management)
(2) *plow* (farming or planting)
(3) *cow* (grazing management)
(4) *fire* (prescribed burning)
(5) *gun* (harvest management).

The basic tools used today in deer management have changed but little, although they have become a bit more sophisticated. The tools of the modern deer manager are illustrated in Fig. 1. Even though any or all of these tools can be effectively used by the deer manager, management does not consist simply of the use of tools, but rather of the planned and skillful use of them.   In fact, Leopold stated that the tools of progressive wildlife management are also the tools of wildlife destruction when used improperly.

The Circular Process of Deer Management

Leopold proposed that wildlife management is a continuing effort; it is never really an endpoint, but rather a process. The basic process of planned and skillful deer management is really no different than the management of a business, a forest or a football team. Management is a continuous and circular process of planning and re-planning using the 6 steps outlined in Fig. 2.

Step 1 - Goals. Deer management must begin with a goal or a set of goals. Goals may be a simple as a mental desire to have bigger bucks. They may be as elaborate as goals concerning sex ratio, deer density, body weight, fawn crops, and B&C scores contained in a written document. Goals may be both short term and/or long term. Goals should be specific, measurable and realistically attainable. Without goals, there can be little meaningful progress in deer management.

Step 2 - Resources. An inventory and assessment of resources is needed before one can proceed in deer management.   These resources would include: biological, physical, financial and human resources. The inventories needed might include: habitat assessments, deer census, an inventory of hunting facilities, labor, equipment and the availability of cash, credit or cost-sharing. An essential part of this step is to identify strengths and weaknesses. Knowing what

the weak links are will help one target management where it is needed most, as shown in Fig. 3. It is also during this step that the deer manager begins to distinguish between problems and symptoms. A prime example would be an abundance of yearling spikes and poor antler development in older bucks. These conditions usually are the symptoms of deeper and less obvious habitat and nutritional problems.

Step 3 - Alternatives. There is usually more than one good way to do something. Deer management is no different. This step involves the consideration of all the different options available to accomplish one's goals, and then analyzing the pros and cons of each. For example, there are a great variety of ways to increase deer nutrition including: decreasing deer numbers; decreasing competitive livestock; implementing a grazing rotation; prescribed burning; mechanical browse renovation; food plots; and supplemental feeding.

Step 4 - Decisions. This step forces one to choose among the alternatives presented. The wise deer manager is a patient and logical decision maker. With his goals clearly in mind, he must determine which of the many options open to him are best.

Step 5 - Implement. After firm decisions are made, it's time to get busy. This is the action step, the one that produces results. Many deer managers make the mistake of rushing into this step prematurely. However, implementation must only take place after going through the previous steps.

Step 6 - Evaluate. Not everything we do turns out as we plan. This step examines and critiques what was done and whether or not it helped accomplish the goal intended. What works well is kept and continued, What fails is discarded. What works in part is adjusted and improved. Common evaluations would include: habitat indicators; population changes; deer quality trends; financial returns; and hunter satisfaction. Written records are an important part of this step as well as casual observations.

When Step 6 is completed, the process is repeated with a re-examination of goals, an updated assessment of resources, a re-analysis of alternatives, a revision of decisions and actions and a re-evaluation of results. The working through of this process is deer management.

To reiterate, deer management does not merely consist of harvesting does, roller chopping brush, planting food plots, culling spikes or any of a number of activities. Deer managers are often tempted to take

shortcuts and try miraculous solutions to old problems. Nutritional quick fixes and genetic quick fixes are alluring, but rarely are they quick and seldom do they fix anything. It would do well for the modern deer manager to once again consider the words of Aldo Leopold: "*the success of wildlife management depends more on the exercise of skill than on heavy investments of labor or materials*"; and "*the recreational value of game is inverse to the artificiality of its origin*".

At this conference and in these proceedings, a group of intelligent, qualified and experienced professionals will discuss a popular and controversial subject. At the conclusion, some of our personal views and prejudices may have been challenged. Others may have been solidified. Regardless of what we come away with from this symposium, remember the simple, "old-timey" basics of Deer Management 101.

A Basic Manifesto of Deer Management

I. To value and conserve the habitat which supports thy deer herd. This is the first and greatest precept.

A. To keep thy herd within the carrying capacity of the habitat. The examination of thy deer weights, fawn crops, antler develop-ment and the abundance of spikes will tell thee if thy herd size is balanced to thy habitat. Surplus animals, thou must remove.

B. To learn to recognize and evaluate the herbs and bushes which thy deer use as food. Overgrazing of thy choice feeds is iniquity of the worst kind and will lead to the poverty of thy habitat.

C. To understandeth that deer need much shrubbery and woods for refuge. Excessive clearing art a transgression to be avoided.

D. To knoweth the relationships which govern the vigor of thy particular habitat and to practice those techniques which are known to maintain or increase that vigor.

II. To apply a selective harvest to thy deer herd to make it all thy heart desires.

A. To selecteth as to the gender of deer to be harvested to attain a desirable and balanced ratio of does and bucks.

B. To selecteth as to the age of bucks to be harvested relative to thy goals. If thou desires to have magnificent mature bucks in thy herd, thou must restraineth thyself against the taking of desirable young

bucks.

C. To selecteth as to the desirability of antlers possessed by bucks to improve future generations. To keepeth in thy herd bucks with antlers thou deemeth superior throughout his prime breeding years. To removeth from thy herd bucks with antlers thou deemeth undesirable for their age. This removal must be undertaken with utmost care, skill and restraint, lest it be counter to thy goals.

D. If these selections are considered of little worth due to the small size of thy land and the large wanderings of thy deer, thou should be diligent to enlist the support of thy neighbors in like-minded herd management. If thy neighbors refuseth, thou may have no choice but to erect a barrier suitable to manage thy herd prudently.

III. To have an appreciation and respect for the land, the wildlife, the tradition of hunting and other people.

A. To be a keen observer of all manner of wildlife as well as a predator of a few.

B. To savor the hunt regardless of the kill.

C. To seek not to needlessly offend the conscience of those who do not hunt.

D. To respect the property and wishes of the owner and caretaker of the land.

E. To submit to the statutes which regulate hunting.

IV. To do these things thyself and to teach others to do likewise.

When Deer Management Fails

The biggest failure in deer management is not small antler size, unbalanced sex ratios, poor age structure or low fawn crops. Deer managers have seemingly done a wonderful job of creating a huntable surplus of deer. Most suitable habitat has been filled to capacity. For a variety of reasons, there are now more deer than ever, more deer than needed, and more deer than many habitats can support. The biggest failure in deer management is failure to control excessive deer numbers.

The overabundance of deer is causing documented ecological damage across the northern, eastern and southern United States, including Texas. Deer managers have long been vocal opponents of overgrazing by livestock, and rightfully so, knowing the harm this can cause. Now, it is deer that are overgrazing and overbrowsing large areas of rangeland and forest land. In addition to harming the ecological health of the land, this overabundance of deer can also cause economic loss to ranchers, farmer, foresters, orchard owners, motorists and suburban home-owners.

A large and growing group of wildlife managers are much more concerned with the overpopulation of deer than whether they have spike or trophy antlers. In fact this overabundance has earned deer the nickname "rats with antlers". The traditional deer manager would do well to be aware of this growing problem and do his part to see that deer herds under his care do not contribute to the problem.

Questions for the Deer Manager

The following questions are asked to determine how serious you are about deer management. If you can answer them, you are probably an astute and serious deer manager who ought to be training others. If you cannot answer them, you might need a refresher course in the basic process and principles of deer management.

1. What are your specific deer management goals?

2. What is the average field dressed weight (using scales) of your mature does for the past 3 years? What does this tell you?

3. What percent of the bucks in your herd are in the mature age classes?

4. What percent of your yearling bucks are spikes in a "normal" year?

5. What percent of your buck harvest is made up of 5.5 year or older bucks?

6. What is the weakest link in your deer management program?

7. What is your net return per animal unit of deer?

8. What are the top 5 browse and top 5 forbs eaten by your deer?

9. Which choice deer foods are being overgrazed or overbrowsed?

10. Is you deer herd within carrying capacity? How do you know?

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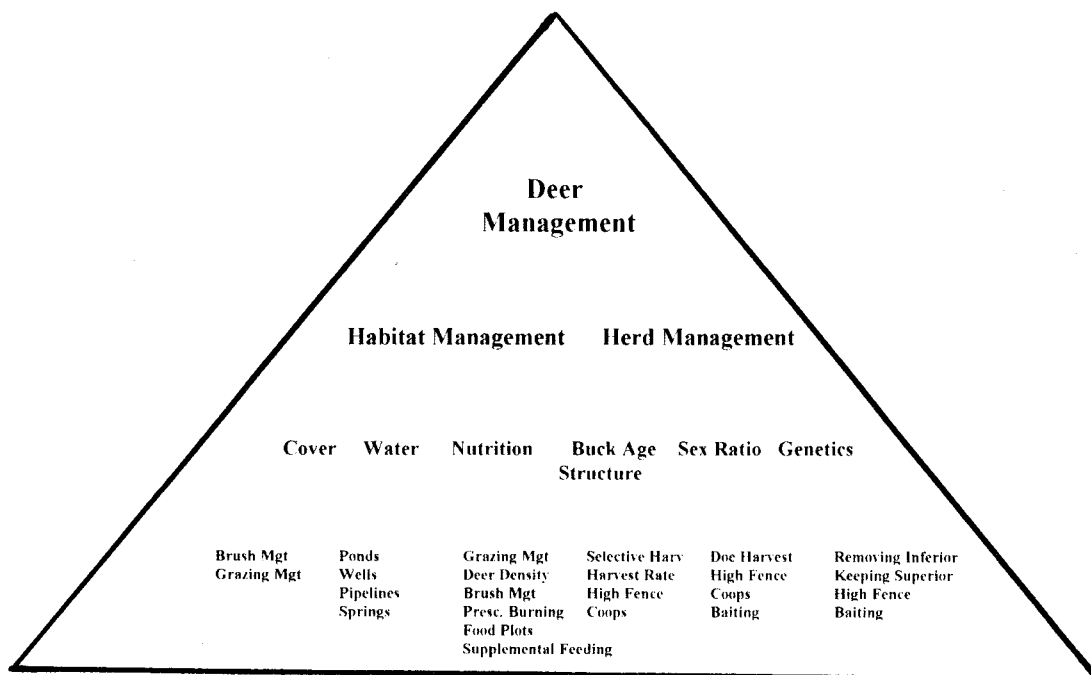
Figure 1. Deer management is initially divided into its 2 basic components (habitat and herd management). It is then subdivided into the 6 areas which are commonly manipulated by management. Finally, the tools used to implement management are listed.
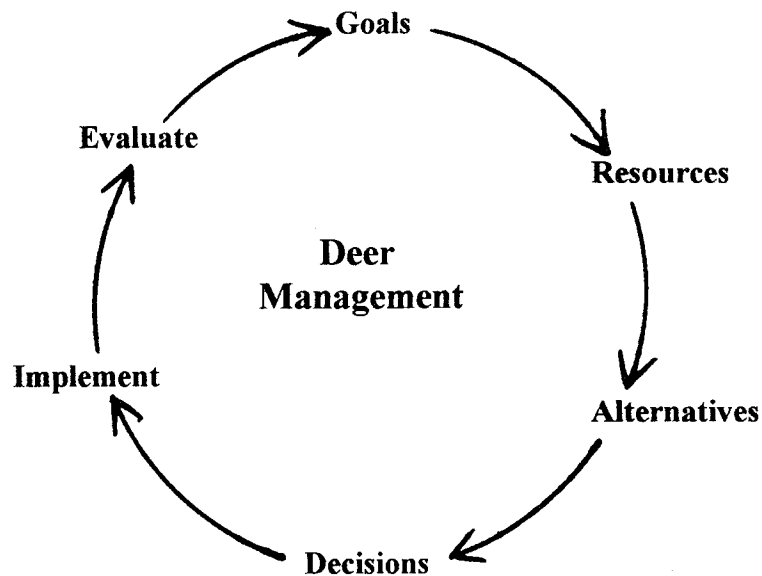
Figure 2. The circular process of deer management involves the continual application of these 6 steps.

Cover   Sex Ratio   Nutrition   Genetics   Buck Age   Water
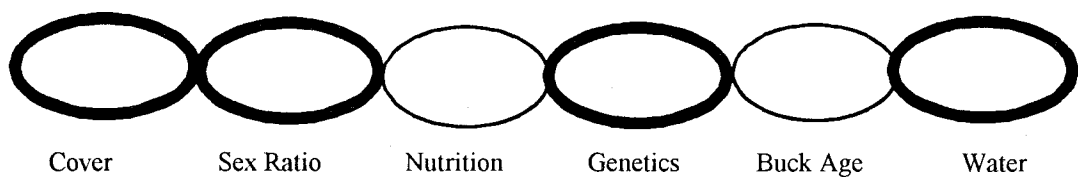
Figure 3. Deer management is usually a crude chain with some strong links and some weak links. In this example, buck age and nutrition are the weak links. It would not be wise to focus on genetic improvement or a better sex ratio. Management should concentrate on the improvement of nutrition and the development of an older age structure.

GENETICS 101: BASIC GENETIC CONCEPTS FOR DEER MANAGEMENT

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Abstract: Recent technological advances in molecular genetics and cloning now offer the prospect that humans may directly intervene and modify the genetic material of wildlife as well as domestic plants and animals. The implications of such interventions is the topic of this symposium. This presentation will review the organization and composition of DNA with special emphasis on the genome of the white-tailed deer and summarize the genetics principles controlling the inheritance of simple genetic traits and of polygenic (quantitative) traits. The concept of heritability of quantitative traits will be reviewed with application to the genetic and environmental determinants of antler growth and body weight in deer. Stabilizing selection as an opposing force to selective breeding in natural populations will be introduced as a topic for discussion.

It has been almost a century since the rediscovery of Mendel's experiments describing the laws of heredity. We now stand at the threshold of a brave new world in which we will have at our disposal the entire genetic blueprint for humans and several model organisms and the technical capability to modify those blueprints. The technological advances that have accompanied analysis of human genes also make it possible to intervene and manipulate the genetic material of other species including wildlife in ways that until recently were considered impossible. It is the potential of these technologies and their consequences as applied to the management of white-tailed deer that has motivated the organization of this symposium. The purpose of this presentation is to review some basic concepts of animal genetics as an introduction to subsequent presentations which will address specific aspects of genetic manipulation in the management of white-tailed deer.

In 1920, Winkler coined the term *genome* to define the basic (or haploid) chromosome set of plants and animals; hence the sum total of its genes. The cells of white-tailed deer and all other species of mammals normally contain two (diploid) chromosome sets, one from each parent. Genetic information is encoded in simple, thread-like molecules of DNA. The chemical composition of DNA is essentially identical among all forms of life and consists of a double helical structure of two antiparallel strands chemically bonded via pairing of the nitrogenous bases adenine (A) and thymine (T) or cytosine (C) and guanine (G). Genetic information is encrypted within the linear sequence of bases along a DNA strand, read as three bases (codon) at a time. The amount of DNA in the genomes of all species of mammals is surprisingly constant, at about 2.8×10^9 base pairs/genome and is packaged into a few, extremely long molecules, which together with associated proteins, can be recognized as chromosomes. Each chromosome contains only a single, linear double helix molecule of DNA. The genome of the white-tailed deer is packaged into 35 chromosomes (DNA molecules) that share many structural characteristics with chromosomes of cattle, sheep and goats (Gallegher et al., 1994). The similarities of the genomes of deer, cattle, sheep and goats at the chromosomal level mirrors the similarities of the genetic maps of these species and predicts that we may be able to apply genetic knowledge among these species based on their conserved genome organization.

We also know that each mammalian genome contains about 75,000 functional genes that encode the information necessary to produce a normal, fully functional individual. Surprisingly, these 75,000 genes account for only about 3-5% of the total genomic DNA, the balance of which is a collection of so-called "junk DNA" consisting of repetitive sequences, inactive (mutated) genes, constitutive DNA, etc.

The position of a gene on a chromosome is called a *locus* and because mammals possess two genomes, one from each parent, each cell in an individual contains two very similar/identical genes found at the same locus on each pair of homologous chromosomes. These alternative forms of a specific gene are called *alleles* and may be identical in DNA sequence or may contain a few differences. The estimated difference in the DNA sequences of allelic genes from unrelated individuals is about 0.1%. The allelic constitution at a genetic locus in an individual is often called a *genotype* although the term "genotype" may also be used to describe the allelic states at all loci in an individual. Alleles are transmitted from parents to offspring by

sexual reproduction in a predictable manner according to Mendel's Laws of Segregation and Independent Assortment in a process that we know as *inheritance*.

The coordinated expression of all genes (alleles) in an individual throughout development and the interaction of these gene products with environmental factors (nutrition, disease, etc.) produce an individual with certain recognizable characteristics - these characteristics are called *phenotypes* or *traits*. Some traits are controlled by alleles at a single locus and are largely uninfluenced by environmental factors. Such traits are called *monogenic* or Mendelian traits because they are inherited according to Mendel's Laws. Among domestic animals there are a large number of monogenic traits observable among individuals. These include polled vs. horned (cattle), various coat color phenotypes, spotting genes, and a number of genetic disorders. In contrast, most wildlife species are remarkably consistent in most phenotypes; there appears to be little tolerance in nature for genetic variation that is expressed morphologically as monogenic traits. There are occasional reports of melanistic deer, albino deer, or deer with white spotted phenotypes, but these animals are usually rare in natural populations; we have no difficulty in identifying and distinguishing the recognized phenotype of white-tailed deer, even from among the closely related mule-deer.

In general, monogenic traits observable as morphological differences are of interest primarily for cosmetic reasons, since they rarely are expressed as "production" traits. Production traits (weight gain, milk production, antler size, etc.) are usually determined by alleles at many different genetic loci and are called *polygenic* or *quantitative* traits.

Quantitative traits have the following properties:

(1) characters are measurable and the variation continuously distributed;

(2) contributions of any one gene to the phenotype are relatively small and interchangeable with other genes so that similar phenotypes might be observed among individuals with different genotypes;

(3) are subject to environmental influences.

To illustrate, let me use a modification of the data of Ott et al., 1997 for inches of antler, as scored by Boone and Crockett measurements, in a cohort of 140 pen-raised 4½ year old white-tailed bucks at the Kerr Wildlife Management Area (Fig. 1). The distribution of antler measurements in Fig. 1 is continuous and appears to be normally distributed (bell-shaped curve) with an

average score of 116, and a range of scores from 45 to 165.

The question of interest to deer managers then is how much if any of the variation observed among individuals for antler measurements or any other quantitative trait is controlled by genetic factors. To estimate the proportion of variation that is due to genetic factors, geneticists utilize a population statistic called *heritability*, (not to be confused with "*inheritance*"). Heritability is defined as the proportion of the total phenotypic variation (Vp) for which genetic differences (Vg) are responsible:

$$h^2 = \frac{Vg}{Vp} \text{ [where } Vg = (V_A + V_D + V_E)]$$

This is often called "broad sense" heritability because it does not distinguish among different types of genetic interactions measured as Vg (additive gene effects (V_A), dominance (V_D) and epistasis (V_E). In a practical sense, only the additive gene effects of Vg are useful in selective breeding programs to move the average of the population in a desired direction. Therefore, a second form of heritability, called "narrow sense", is the statistic usually employed as a measure of the "useful" genetic variation in a quantitative trait:

$$h^2 = \frac{Vg_{additive}}{Vp}$$

Although heritability estimates have been reported for numerous production traits in various breeds of domestic animals, there are only a few reports of heritability estimates for antler size and body weight in deer. Williams et al. (1994) reported moderate to high heritability estimates for body weight and several antler measurements in pen-raised 1½ year old white-tailed bucks in Texas. Lukefahr and Jacobson (1997) found somewhat lower heritability values across multiple age classes of white-tailed deer in Mississippi.

In the largest study to date, Van den Berg and Garrick (1997) analyzed heritability for antler weight and body weight in more than 2,000 red deer stags from 92 sire groups. They found h^2 values for antler weight from 0.43 (±0.09) in 2-year old stags to 0.85 (±0.29) in 8-year old stags and $h^2 = 0.48 \pm 0.36$ to 0.80 ± 0.12 for body weight (both sexes). Van den Berg and Garrick also found that antler weight/individual was highly correlated in successive years *(r* = 0.97). The studies by Lukefahr and Jacobson (1997) and Van den Berg

and Garrick (1997) both detected an increase in heritability for antler phenotype with age, except in the very oldest males.

The obvious question that follows from any selective breeding program based on "estimated" heritability for a trait is whether any genetic gain can be realized. The measure of genetic gain is known as *realized heritability* and is the measure of genetic change (G_1-G_2) divided by the selection differential (P_1-P_P) (Fig. 2).

$$h^2 = \frac{G_1 - G_2}{P_1 - P_p}$$

where P_1 = the mean of the entire population of parents (before selection)
P_p = the mean of the population of parents (selected as breeders)
G_1 = the mean of the entire population of offspring
G_2 = the mean of the offspring from selected parents.

The value of $P_1 - P_p$ (Fig. 2*a*) is called the selection differential.

Heritability is a population parameter, specific to the population and trait under consideration at a specified point in time. If either the genetic or environmental component of variation differs for the same trait in 2 populations, then h^2 will also differ in those populations. Moreover, h^2 will decrease as selection is repeatedly applied and the value of the trait is increased.

Stabilizing Selection - A caveat

Any discussion about the consequences of genetic manipulation of white-tailed deer in a natural population should address the concept of *stabilizing selection*. In natural populations a great deal of selection appears to be directed against individuals that deviate, in either direction, from the population average. In general, the fittest phenotype in natural populations is close to the population mean (see Crow 1986). There are no scientific studies that investigate stabilizing selection as a counter force in selective breeding of deer. The best management example suggesting stabilizing selection in herds selectively bred for increased antler size were the red deer herds of Nazi Germany in the 1920s - 1940s (V. Geist, pers. commun.). In this instance, antler size responded well to selective breeding practices, as one would expect for a trait with moderate to high heritability, but increased

antler size also resulted in accelerated natural mortality among stags. Mortality may have been directly associated with increased antler size or as a consequence of the correlated increase in body size (Huxley 1932).

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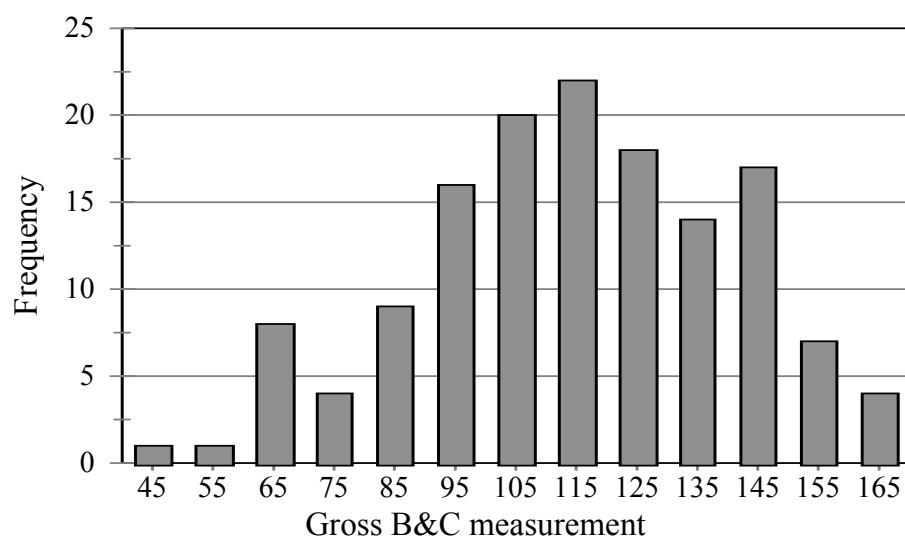
Figure 1. Distribution of antler measurements as gross Boone and Crockett scores for 140 pen-raised white-tailed bucks at 4 1/2 years of age at the Kerr Wildlife Management Area, Texas Parks and Wildlife Department, Hunt, Texas (original data from Ott et al. 1997).

a)

$\bar{P}_1$ $\bar{P}_p$

ΔP

b)

High

Medium

Low

$\bar{P}_1\bar{P}_{2l}$ $\bar{P}_{2m}$ $\bar{P}_{2h}$

$\bar{G}_1$ $\bar{G}_2 = \bar{G}_p$

ΔG

Figure 2. Illustration of the distribution of measurements for traits with high, medium or low heritability after one generation of selective breeding. Figure *2a* is the distribution of measurements in the original population, P_1. The hatched area identifies those individuals selected for breeding to produce the next generation, P_2.

GENETIC VARIATION IN WHITE-TAILED DEER: IMPLICATIONS FOR MANAGEMENT

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Introduction

The white-tailed deer, *Odocoileus virginianus*, occurs from Canada to Brazil (north of the Amazon River) and is represented by 38 subspecies (geographic races) in North and Central America and another 8 subspecies in South America. Over the past 60-70 years, numerous studies have been conducted on the general ecology and behavior of white-tailed deer. These studies have provided a wealth of information on nutritional and habitat requirements of deer, breeding biology, the dynamics of deer populations, and seasonal movements of deer.

More recently, there has been an increased interest in patterns of genetic variation in white-tailed deer, and a considerable amount of information derived from detailed genetic studies on deer offers great opportunity for those interested in the ecology and management of white-tailed deer, and large ungulate species in general. Because the white-tailed deer represents 1 of the most important game animals in Texas from a recreational and economic standpoint, this paper is an attempt to examine how genetic markers and genetic information can be used to understand more about basic deer biology and the management of deer populations.

Principles of Genetics and Importance of Genetic Variation

Basic Principles. Two of the most important principles of genetics are: (1) genetic information flows from the genotype to the phenotype; and (2) the identity of the basic units of heredity 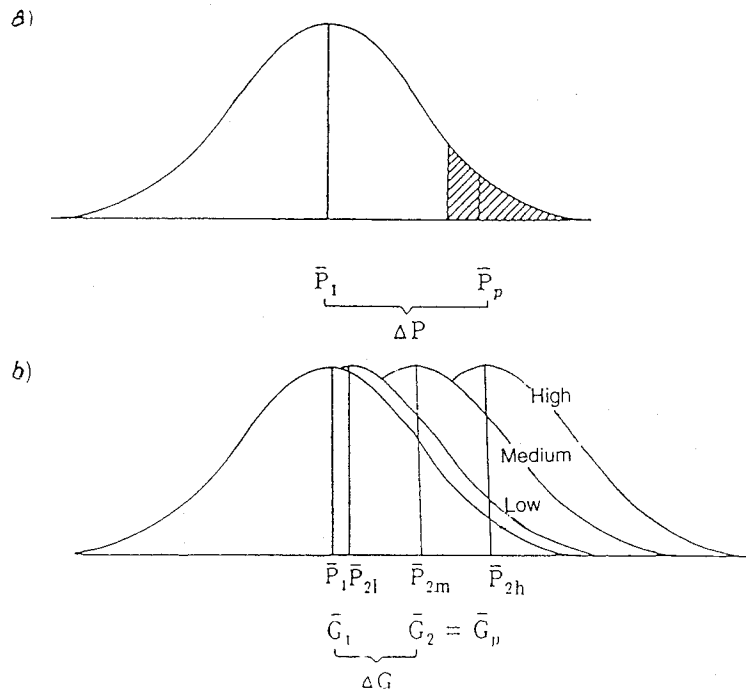is maintained from generation to generation. The ultimate source of genetic variation is mutation (changes in genes or chromosomes), with genetic recombination in sexual organisms allowing for the amplification and mixing of genetic variation into different combinations. Without such genetic recombination, populations and species would tend toward homozygosity (the lack of genetic variation). Genetic variation is seen as an essential component for the long-term survival and overall health of a species and/or population.

A major problem likely to be faced in attempts to preserve diversity will be how to define the unit to be managed and the appropriate scale upon which to base an effective management effort. The *minimum viable population* is a phrase used by managers to describe the minimum conditions necessary for maintaining viability and long-term survival of a local population. Genetically, the *effective population size* (actual number of breeding individuals) relates directly to a consideration of a minimum viable population, because the effective population size determines the rate at which processes that erode variation can occur. For instance, *genetic drift* is a phrase describing changes in the frequency of an *allele* (genetic variant at a particular gene or locus) within a population as a result of random sampling. Therefore, in populations with small effective population sizes, drift will have greater effects in terms of driving the population toward homozygosity. Some consequences of drift in small breeding populations are the loss of a population's ability to respond to a changing environment (e.g. introduction of a disease, parasite, etc.) and the potential fixation of deleterious alleles in the homozygous state. Many deleterious or harmful alleles are recessive.

From a management standpoint, genetic drift should be avoided because a small effective population size coupled with demographic and environmental variation can influence the overall survival and health of a population. Most factors that can influence the effective population size include events that result in a reduction in the number of breeding individuals and the restriction of gene flow (genetic exchange) between either individuals or populations. *Population bottlenecks* and *founder events* both relate to the overall reduction in the number of breeding individuals. Gene flow patterns can be disrupted by habitat fragmentation or any other means of retarding migration (e.g. high fence enclosures), and the breeding structure of a species in combination with reduced gene flow and smaller populations can enhance the rate at which genetic variation is lost in a population.

When dealing with small breeding populations, a major cause of the loss of genetic variation is

inbreeding. Inbreeding involves the mating between close relatives, resulting in an increase in the number of homozygotes (both beneficial and deleterious). Some of the consequences of close inbreeding are an increased accumulation of homozygous deleterious alleles, a decrease in the frequency of superior heterozygotes, and an overall decrease in genetic diversity among individuals. *Inbreeding depression*, a potential result of close inbreeding, has been observed in captive breeding programs, and can be associated with an overall loss in fitness. Some of the consequences of inbreeding depression are reduced fertility, birth defects, high infant mortality, slower growth rate, and increased susceptibility to disease.

Is the lack of genetic variation in a population bad? *Fitness* relates to the success of an individual's ability to contribute to the next generation, implying differential survival of individuals. If genetic variation contributes to the overall fitness of an individual, then it is important. *Heterozygosity* is a measurement used to determine the extent of variation within an individual and/or population. For instance, a gene with two identical alleles (DD) would be considered homozygous, whereas a gene with two alternate alleles (Dd) would be considered heterozygous. Overall heterozygosity for an individual can be estimated by totaling the number of genes (or loci) for which the individual is heterozygous. Previous studies have demonstrated correlations between heterozygosity and particular phenotypic and/or production traits such as developmental stability, growth and development rates, metabolic efficiency, fertility, survival, and resistance to disease.

In terms of deer, previous genetic studies have revealed a correlation between heterozygosity and antler size and symmetry, fetal growth weight, maternal weight, twining, body size, and fat levels. Although it is difficult to conclude from these studies that heterozygosity is a direct measure of fitness, one can conclude that the presence of genetic variation within a population is important to the long-term survival and overall health of a population.

Estimating Genetic Variation. How does one estimate genetic variation within and/or between populations? There are 3 major sources of genetic information, and each source has a different pattern of inheritance. The *nuclear genome* encodes most of the structural and regulatory sequences necessary for cellular function. In mammals the genome is diploid, containing representative haploid genomes from both the mother and father. In addition to this biparentally inherited component of the nuclear genome, *Y chromosome specific sequences* are inherited from males only, thus offering a means of examining genetic variation from the paternal lineage alone. The *mitochondrial genome* is located in the mitochondrion housed in cellular cytoplasm. Unlike the nuclear genome, mitochondrial DNA (mtDNA) is inherited from the mother. In addition, mtDNA is known to vary at a faster rate than standard nuclear genes, and as a result of its uniparental inheritance, it provides an excellent measure of geographic subdivision and restricted gene flow patterns.

The earliest technique employed for measuring genetic variation in white-tailed deer was protein electrophoresis. This technique measures genetic variation, including the identification of homozygotes and heterozygotes at a locus, by observed differences in net charge differences associated with the rate of protein migration through a starch or acrylamide gel connected to an electric power source. Variation at individual loci (variants known as allozymes) is identified by histochemical stains specific to a particular locus, and the result is a banding pattern that allows the identification of homozygous and heterozygous individuals. This method revealed an overall higher level of genetic variation in white-tailed deer than that seen for most large mammals, and this variation was used to both examine patterns of geographic variation in deer and evaluate the relationship between heterozygosity and fitness. There are two major disadvantages to this approach for measuring genetic variation. First, the technique underestimates genetic variation because it detects primarily changes in charged amino acid rather than all amino acid differences in a protein. For even white-tailed deer, which are highly variable, the estimated level of polymorphism is 20% and heterozygosity is 9%. This level of variation is too low to provide genetic markers that can be used to study the genetic structure of deer populations on a microgeographic scale, including the assessment of breeding patterns. Second, electrophoresis requires large amounts of freshly collected tissues that must be housed in ultracold freezers.

Within the nuclear genome there are classes of repetitive sequences known to demonstrate high levels of genetic variation that can be used to establish individual-specific genetic markers. DNA fingerprinting is a term associated with a class of hypervariable repetitive sequences distributed throughout the nuclear genome, and as implied by the name, DNA fingerprints provide patterns of variation that can distinguish between most individuals. The traditional DNA fingerprints, known as *hypervariable minisatellite loci* or *VNTRs*, are characterized by a tandem array of repeating units varying in length, and

variation can be detected by digesting DNA sequences outside this repetitive array so that differences in the number of repeats can be detected on the basis of band size. The major difficulty with VNTRs is related to the fact that alleles at a locus cannot be established, and this makes a direct estimate of heterozygosity difficult. Therefore, other than the assessment of parentage, the application of VNTRs to the examination of population level genetic variation is limited.

Recent advancements in molecular genetics offer a new set of tools and DNA sequences that can be used to not only establish parentage, as with traditional DNA fingerprints, but examine patterns of population structure and geographic variation in a similar fashion to that performed by protein electrophoresis. The *polymerase chain reaction* (PCR) is a method of enzymatic amplification of DNA sequences. The method utilizes thermal cycling to synthesize millions of copies of a target sequence. PCR is very sensitive allowing for the amplification of DNA sequences from small amounts of biological materials (e.g. single cells, single spermatocytes), and the procedure has allowed for automation of genetic typing, including individual genetic fingerprinting and the sequencing of specific genes and other fragments of DNA from individuals.

This automation and the low amounts of DNA required for PCR provide an inexpensive means of genetic typing for population studies, forensics, and the study of ancient DNA. For instance, DNA extracted from museum specimens has been used to gain historical information on genetic variation in populations through time, and recently, DNA extracted from feces has been used in both food habitat studies and the estimation of population size by indirectly determining the number of individuals on the basis of DNA fingerprints derived from PCR.

DNA microsatellite loci represent a recently discovered class of repetitive sequences found in the nuclear genome. Microsatellites represent short segments of simple repeat units of 2 to 4 bases distributed in tandem arrays throughout the genome. Variation at these loci occurs by the addition and/or deletion of single repeat units, and polymorphism and heterozygosity can be estimated directly. These genetic loci are highly polymorphic and can be used for the establishment of parentage, kinship, and examinations of gene flow patterns between individuals.

For instance, estimates from a pedigreed herd of white-tailed deer indicated that the probability of any 2 individuals having the same genotype (derived from microsatellites) was infinitesimal (2.6×10^{-8}). Therefore, these genetic markers have direct application for management. Deer-specific microsatellite primers

have been developed, and these primers allow for the direct amplification and genetic typing of variation with the use of PCR. In addition, genome projects being conducted for domestic ungulates, such as the cow and sheep, have provided hundreds of microsatellite primers that cover most of the cow and sheep genomes, and many have been mapped to specific chromosomes. In addition, some microsatellite loci map to gene of known function, and many of these functions relate to important production traits. A large percentage of these cow and sheep primers will work on white-tailed deer and other cervids, thus allowing for detailed genetic surveys to be conducted. Such detailed genetic typing has great potential in terms of allowing one to investigate the association of microsatellite variants with specific production traits such as antler size and antler configuration.

Finally, sex specific markers can allow a detailed examination of either female or male population structure. From a behavioral standpoint, deer demonstrate sexual differences in dispersal patterns where young males migrate but females remain in the natal group (place of birth). Females tend to form social groups containing an adult doe and her female offspring from previous seasons, whereas subordinate males (usually yearlings) are capable of long-range movements possibly as a result of social competition. Subsequent to leaving the natal group, females tend to establish home ranges adjacent to or overlapping with the mother's home range. Males establish home ranges outside their natal group, with their success in breeding related to maturity in terms of body size and antler development. There are regions of the mitochondrial genome that demonstrate high levels of genetic variation that can be assessed using PCR and nucleotide sequencing. This high level of poly-morphism and maternal inheritance of mtDNA provide a genetic marker that can be used to establish maternity and estimate dispersal patterns of females.

Although less polymorphic than mtDNA, Y-chromosome specific markers allow an assessment of paternity as well as patterns of male dispersal. Given the difference in movement between male and female deer and the difference in mating success among males, genetic markers that are gender specific are very useful for studying breeding structure and movement patterns of deer.

Applications to Management

Genetic Stock Identification. Patterns of genetic variation can be used to evaluate the degree to which populations or lineages within a species have been

separated over historical time, and they can provide clues as to past events responsible for the current level of variation. The identification of unique genetic stocks is important to deer management in Texas and other regions of the United States for several reasons. First, an objective demarcation of discrete stocks will allow wildlife managers to determine hunting quotas and management strategies of free-ranging herds based on the genetic identification of management units . Second, management practices involving restocking and translocation of deer can be organized in a manner whereby distinct stocks are not mixed. Third, the success or failure of stocking efforts can be determined based on genetic censuses subsequent to restocking or translocation. Fourth, the biological effects of mixing stocks can be evaluated.

For instance, deer are usually seasonal breeders (only once per year) throughout most of their northern distribution but some more southern populations demonstrate sporadic and/or extended breeding seasons. In South America females breed more than once per year, and in parts of Texas conception dates and length of the rutting season varies among regions. Such variation can influence fawn survival and overall productivity of the deer herd. Genetic factors, possibly as a result of past mixing of different deer stocks, may be contributing to this variation in breeding chronology.

Proper stock identification requires a knowledge of existing levels and patterns of genetic variation throughout a species' range, and information gained from such a geographic survey has direct management implications. One example can be seen from detailed geographic studies of white-tailed deer from the southeastern United States. Following the declines of deer populations in the southeastern U.S. during the 19th century, restocking efforts were employed to restore deer populations. A detailed study of mtDNA variation and allozyme diversity (using starch-gel electrophoresis) revealed patterns of geographic variation similar to other unrelated species. This suggested that population increases of deer in the southeastern U.S. was the result of increases in native herds, with restocking efforts having a minimal impact on the genetic composition of deer stocks in this region. It would be interesting to know the impact of past restocking efforts on Texas deer populations that were depleted earlier in this century but have subsequently recovered, presumably as a result of restocking efforts.

One obvious consequence of manipulating natural populations is an reduction of overall fitness as a result of poor management practices. Many species are represented by a series of populations differing genetically and adapted differentially to local environments. In deer this regional variation can be seen by the 38 subspecies recognized on the basis of morphological differences. If locally adapted populations are mixed, incompatibilities can occur that can reduce overall fitness. This loss of fitness from the mixing of divergent stocks is known as *outbreeding depression*.

There are 2 categories of outbreeding depression, 1 resulting from hybridization between locally adapted populations and another from intrinsic differences in chromosome number, morphology, and interacting gene complexes. When populations known to have regional differences in morphology and genetic variation are combined, the likelihood of outbreeding depression is increased. Small populations also especially vulnerable because outbreeding depression can alter the genetic and demographic structure of a population. This makes genetic stock identification critical for those interested in the management of deer populations, especially those maintained behind artificial enclosures. For instance, the introduction of deer from mixed genetic origins into a closed population can reduce the overall fitness of the deer herd.

Genetic Variation within Populations. An overall assessment of the degree of genetic exchange between populations, the overall level of genetic variation, and the breeding structure of deer populations are important information to wildlife managers. Genetic markers offer a means of evaluating the genetic structure of enclosed and free-ranging deer herds. In addition, they can be used to determine both the number of breeding individuals and relationships among individuals within a deer herd.

As the number of breeding individuals decreases, the level of heterozygosity (level of genetic variation) decreases. Deer populations with limited gene flow or migration between populations, such as seen for populations behind high fences, have the potential of losing genetic variation at a rapid rate. For instance, it is known that island populations, peripherally isolated populations, and populations established with a small number of founders demonstrate lower levels of variation than those seen in larger populations. This reduced variation is the consequence of the erosion of variants through population bottlenecks, genetic drift, and inbreeding. In terms of population viability this loss of variation may be accompanied by a loss in fitness and population sustainability.

One should consider basic deer biology when evaluating the influence of enclosures and barriers to gene flow on the amount and pattern of genetic variation observed. Social organization, sex ratios, and

other asymmetries in the demography of a population can influence genetic variability. In general, female *philopatry* (staying close to the natal group or birth site) in a *polygynous* species (a male defending a breeding territory and breeding with multiple females) can lead to increased levels of heterozygosity. Nevertheless, the proportion of variation depends on group size and the number of breeding males within the group. Recent genetic studies of white-tailed deer have demonstrated considerable population substructure over rather short geographic areas. In some enclosed and free-ranging populations this genetic substructure has persisted over multiple years. Detailed mtDNA studies on white-tailed deer in west Texas have revealed similar substructure of female lineages within the confines of a single ranch.

These studies suggest that the breeding structure of deer is geographically restricted with evidence of both female and male deer occupying well defined and restricted breeding ranges. If males were to breed within a social group for several generations, then a high level of relatedness or homozygosity within the group would be expected as a consequence of inbreeding. In a free-ranging deer herd this inbreeding probably is avoided to an extent by male dispersal and the establishment of territories outside their natal group. However, breeding of deer enclosed behind high fence can have different genetic consequences. In such a situation, males are not allowed to disperse as far, and they maintain territories over multiple years. This restriction of male dispersal coupled with the tendency of related females to remain close to their birth site increases the probability of inbreeding, which may eventually result in reduced fitness in the herd.

Testing Traditional Management Assumptions. Genetic markers also present some novel approaches for those interested in white-tailed deer management. First, ecological studies on white-tailed deer suggest asymmetries in male breeding structure that is associated with age. These asymmetries are related to sexual selection on the part of the female in conjunction with male/male competition for access to females. In many regions harvesting schemes are based on a presumed knowledge of breeding structure. Genetic markers, especially those that are highly polymorphic, offer a means of establishing accurate estimates of relationship and parentage in white-tailed deer. Therefore, the actual number of breeding males within a herd, especially an enclosed herd, can be determined when the genotypes of breeding individuals are known.

Even without known genotypes for all breeders, microsatellite markers can provide accurate identification of relationship classes. Second, as demonstrated by the numerous papers that have been written in the wildlife management literature, the assessment of total population size and sex ratio in a deer herd is a difficult task. Again, PCR and genetic typing offer another means of making such estimates. It is possible to extract DNA from antlers, bones, teeth, etc. and genetically type this material. Therefore, one has a means of determining the sex and genotype of this material, and this information can be compared to similar estimates of sex and number based on observation. Finally, food habit studies are abundant in the literature and are based on detailed observational data. PCR can be used to amplify DNA extracted from feces, thus allowing direct genetic verification of plant species being utilized by individual deer.

Introgressive Hybridization. White-tailed deer and mule deer are capable of hybridizing and producing fertile F_1 and F_2 hybrids. In regions of Texas and other parts of the United States where the ranges of white-tailed deer and mule deer overlap, evidence of hybridization has been reported. In the Trans-Pecos region of Texas the incidence may be as high as 6%. Most of the recent genetic information suggests that hybridization generally involves white-tailed bucks with mule deer doe. As a consequence of this asymmetry, in the west Texas area of overlap 67% of white-tailed deer share a common mtDNA haplotype with mule deer. In Oregon, 18% of the Columbian white-tailed deer were found to be heterozygous for nuclear genes found in black-tailed deer, suggesting a similar situation to that seen in Texas.

One consequence of this interspecific hybridization between white-tailed deer and mule deer is a high level of genetic similarity between these 2 species, at least in some regions of the United States. At the same time, other regions with less overlap show distinct genetic stocks for these 2 species. Evidence of interspecific hybridization has important management implications for both the regulation of deer harvesting and the translocation of deer populations.

Managed Deer Breeding Genetics of the Kerr Herd. In 1973 the Texas Parks and Wildlife Department established a captive breeding herd of white-tailed deer. The original purpose of this facility was to determine the heritability of traits associated with body size and antler conformation. The original herd was established from founders (6 buck and 42 doe) collected from different regions of Texas, and the herd remained closed subsequent to its establishment. Detailed records of pedigree and morphological features were maintained throughout most of this period, and from

these data the estimated degree of inbreeding was 12 to 14%, which is standard for most deer populations. The findings from this study strongly suggest that features associated with both body weight and antler characteristics have a high heritability. These results have led to some very important management implications with respect to spike versus forked yearling bucks, and they have been the source of considerable controversy.

We have used recently developed DNA microsatellite loci for deer and related ungulates and the pedigree information to assess the overall genetic variation within the Kerr herd and compare that variation to free-ranging deer herds distributed throughout Texas. These genetic data are being used to address several questions:

1. Are Texas deer less variable than deer from other regions of the United States? Although deer are variable relative to other mammals, past studies using starch-gel electrophoresis suggest that Texas deer are less variable than those from South Carolina and other regions of the United States. The explanation for this presumed lack of variation is that deer populations in particular regions of Texas were depleted and restocked from restricted sources.

2. Is the Kerr herd representative of free-ranging white-tailed deer populations? If the answer is yes, the information derived from genetic typing with microsatellie markers and comparisons of genetic similarity to known relationships based on the pedigree can provide a yardstick for the determination of relationships between individuals where the actual pedigree is unknown. In studies conducted on inbred strains of mice and human families, estimates of genetic similarity and relationships based on microsatellite loci have been shown to be highly accurate.

3. Is there evidence for geographic variation of deer populations in Texas and how are these populations related? This is important for the identification of genetic stocks within the state and the evaluation of past restocking efforts and even future translocations.

Thus far, we have collected genetic data for 6 polymorphic microsatellite loci from several populations including: (1) Savannah River Ecology Site- South Carolina; (2) Kerr Wildlife Management Unit in Texas; and (3) several other Texas localities such as Canadian County in the Panhandle, San Angelo in central Texas, and Trinity, Sabine, and San Augustine counties in east Texas.

Several conclusions can be drawn from these preliminary data. First, in terms of overall heterozygosity and number of alleles, the Kerr herd is similar to free-ranging deer populations in the state. Second, Texas deer populations are highly polymorphic for the loci examined, and there is not indication of reduced variation to that seen in other states. Third, east Texas deer populations do not appear to form a cohesive group, possibly as a result of past restocking efforts. This finding needs to be further investigated. Fourth, the degree of population subdivision varies throughout the state but there is an indication that there is genetic subdivision among Texas deer populations. Finally, measures of relatedness based on estimates of similarity between pairs of individuals in the Kerr herd are correlated with relatedness estimates derived from deer of known pedigree. Therefore, these markers have potential for use in studies of free-ranging populations and populations behind high fence.

Studies of the Kerr herd and other Texas deer populations have demonstrated the potential utility of genetics to deer management. Continued genetic studies will follow several lines of investigation. First, the pedigree information of the Kerr herd and the information on phenotypic traits will be compared to an extended examination of microsatellite DNA variation. Second, deer of known relationship from the Kerr herd will be used to obtain information on relatedness using genetic similarity estimates from microsatellite loci. This information will be used to establish a baseline for estimates of genetic similarity and relationship classes. Such information will provide a genetic means for identifying individuals in natural populations that are both related and unrelated. Third, overall levels of genetic variation for both mtDNA and nuclear microsatellite loci will be estimated for both enclosed and free-ranging populations. This information will allow a direct evaluation of the impact of artificial enclosures on the genetic structure and overall fitness of deer populations. In addition, different management strategies of enclosed populations can be evaluated, and the overall breeding structure of enclosed and open populations can be determined. Finally, geographic variation in free-ranging deer populations throughout Texas will be examined in an effort to establish objective management units. This baseline information also will be used to both evaluate past restocking efforts and examine patterns of variation in breeding biology found in Texas deer.

HOW TO EVALUATE A DEER BREEDING PROGRAM

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When an evaluation of anything is proposed at least three questions should immediately come to mind. First, why is an evaluation necessary? Second, what is required to properly conduct an evaluation? Thirdly, how would be the evaluation be accomplished? There is another final question that might be asked after the evaluation. What should be done with the results of the evaluation? These questions and the answers to them will be discussed below.

There are many reasons why a program should be evaluated. Any effort such as a breeding program of white-tailed deer, at least any serious attempt, will necessitate the expenditure of considerable time and money. Such an effort will also require animals, personnel, equipment, real estate, and facilities. The investment of significant resources to a project almost demands the incorporation of some analysis or measurement of benefit achieved for the cost expended. A proper evaluation will be able to tell you if you did indeed accomplish what you set out to do. A cost benefit analysis and/or evaluation of any program will also be useful to others who are considering similar future operations.

Another reason why an evaluation of a breeding program should be done is that there are many variables and requirements involved in the production of deer with superior antlers. Genetics is definitely one of the major components which determine the size, shape, and mass of a deer's antlers, but as we know it is not the only factor. To conduct a breeding program implies that an attempt of some sort will be made to alter or change the genetic make-up of a population or a herd. If a program can grow animals with superior appearance and the program is to be pronounced a success, then it will be necessary to prove that this superior appearance is the direct result of a change of genetic alteration brought about by that program. The proof that the observed changes in antler characteristics seen in the deer are specifically attributable to that program will require a rigorous evaluation. For example, deer with superior appearing antler characteristics occur without breeding programs by chance alone, generally groups of deer on excellent rations or forage grow larger antlers than groups of deer on poorer forage, and also antler quality improves as the age of deer increase. If the deer in a breeding program show improvement in antler quality, then it must be shown that the improvement is due to a change in genetics rather than due to changes in nutrition or age. A properly designed, implemented, and analyzed method of evaluation will allow the cause of the observed changes to be known, and the success or the failure of the breeding program to be shown.

There are several requirements that must be in place and in proper sequence prior to any accurate assessment or evaluation of a breeding program or any program for that matter. The program must have a clear cut final objective or major goal, and it may or may not have some limited minor objectives or intermediate goals. For example a overall goal in a white-tailed deer breeding program might be the raise a single "book" deer on a particular ranch or in a set of pens, with an intermediate goal of increasing the percentage of "trophy" deer within certain age classes. A much more complex overall goal would be to produce a deer herd of superior and heritable antler characteristics for the sale of breeding animals and semen.

The importance or significance of the final goal can not be overemphasized. This overall goal must be the "north star" by which all other decisions regarding the program must be constantly measured, considered, adjusted, and aligned from the initial planning stages, through the implementation phases, management applications, achievement of preliminary milestones, and hopefully the successful achievement of the final goal itself. The final goal must be clearly stated by those in charge and understood by all involved at all levels in the process to allow progress toward the goal and to prevent confusion or counterproductive efforts.

The final goal of the breeding program must also be achievable, and measurable within the constraints of time, money, facilities, personnel, expertise, habitat, and most importantly the biology of the animal. The achievement of some future goal requires a coherent carefully thought out plan which considers the mentioned constraints, minimizes the risks, and maximizes the probabilities of success. The plan of the program is next only in importance to the establishment of the overall goal of the program. The worst of all possible situations in a breeding program is to have any

combination of the following: unclear, changing, unrealistic objectives; inadequate human, animal, or physical resources; lack of proper expertise, and guidance; insufficient time allowances; poor planning; and incomplete understanding (or perhaps worse, the misunderstanding) of the physiologic limits and requirements of the deer. Without clear, achievable, measurable goals, the probability of a successful breeding program is virtually zero, which means a total waste of time, money, and effort with possible deleterious effects to the deer and/or their environment.

Once the final goal (and any intermediate goals) has been clearly established, and the requisite realistic plan for achieving that goal has been accomplished, then a method to evaluate or measure progress toward that goal must be implemented. Without a method to evaluate the progress of the program, there is no "yardstick" or "compass" to measure the magnitude and the direction of the affects of the program or to determine the benefits of the efforts and resources expended on the program. No matter what the goal or what the plan, before any effect of the breeding program can be evaluated a baseline must be established. You simply can not determine how far you have traveled or in what direction you have traveled, if you do not know where you started The measurement and evaluation of the progress and achievements of entire program is based on the starting point. The baseline is the "gold standard" against which all other aspects of the program will be measured.

The type and amount of recorded data that is necessary to establish the baseline or starting point will vary with the individual program and the level of sophistication required. To return to our first example, if the final goal is to produce a single "book" deer and increase the percentage of "trophy" deer within age classes, then the actual production of one such a deer where none previously existed would achieve that somewhat simplistic goal. Progress toward the goal of a number of book deer within a deer herd, and the increase of "trophy" deer within age classes, would require at a minimum records indicating some type of annual morphomectric measurements of antlers and ages of a large number of bucks, these records would be utilized to first establish the baseline and then to determine subsequent progress or effect of the breeding program over time. If on the other hand, the goal was to produce male deer with clearly "superior" and heritable antler characteristics for sale as "breeding bucks" or for the sale of semen. Then methods to identify and select bucks with "superior" antler characteristics, breeding records, complete pedigrees, and clear evidence of similar "superior" antler characteristics in their offspring would be required. The unquestionable establishment of

parentage through blood typing or DNA fingerprinting would also be appropriate. If semen is to be collected and sold from bucks with established heritable "superior" antler characteristics, then records indicating the number and viability of sperm, as well as the number of successful artificial inseminations, and number of "superior" offspring produced would probably be required to properly evaluate the success of that breeding program. More subtle changes in the deer in a program may require very subtle measurements and even statistical analyses for the effects to be properly evaluated. Breeding programs at the phenotypic level may require data at one level while programs directed at the genetic level may require the collection of fairly sophisticated data and the use of statistical analyses. The power of these sophisticated tests and analyses is, however, much more powerful than those at the morphometric level, and therefore the confidence in both the evaluation and the program are increased.

To definitely determine the success (or failure) of a breeding program for improvement of antler characteristics, all other major variables that have influence in antler development must be either measured and known, or equalized. It is much easier and usually cheaper to equalize the other variables than to measure them. In scientific experiments that is why we utilize control groups. If the effect of a treatment (for instance a food additive) on weight gain is to be determined, the two groups are randomly chosen from a larger group of similar animals, and then one group is fed the additive with its food ration, and the other group gets exactly the same ration but without the additive. The animals are weighed before and after the experiment and therefore any observed differences in weights between the two groups can be attributed to the additive. Without control groups or other methods to equalize the influence and variation of other variables, it is difficult if not impossible to attribute the cause of observable differences to one particular treatment. For example in a deer breeding program, if two phenotypically similar bucks are being evaluated against each other on the heritability of their superior characteristics to their male offspring and twenty does are available in a pen situation. Then at a minimum, does should be selected at random by flipping a coin and assigned to two groups of ten. Each buck should be allowed to breed with one of the groups of ten does. The next year females in the same two groups of does should be mated with the other buck. The offspring from all matings should be permanently identified at birth and their antlers measured each year. If nutrition, pen characteristics, and all other variables are held equal. Then any differences of the average antler measurements observed between the offspring from the two sires within age classes should be attributable to the sire.

The proper evaluation of a breeding program can be an involved process, but without some sort of measurement of the final effect of the program, no one will ever be able to determine the success of the program, the biological or cost efficiency of the program, and no one who wishes to achieve similar goals in white-tailed deer will be able to know if a similar program can or will achieve similar results. As was stated at the beginning of this discussion, a serious breeding program in white-tailed deer requires a serious commitment of time, money, and other resources, why would anyone wish to initiate or emulate a similar program without some good probability of success. Perhaps the best reason for an evaluation of a breeding program would be to access the effects on the animals and possibly the wildlife resource. White-tailed deer are, without doubt, the premier game species in Texas. Anything that positively or negatively affects or even potentially affects populations of white-tailed deer in Texas will also have affects in attitudes and perceptions at the political, and economic levels. Nothing in Texas in relation to wildlife management ever seems to escape national attention, so some caution and attention to responsible action is well advised.

In summary, the only method to access the probability of success or the impact of breeding programs is through some type of proper evaluation. For an proper evaluation to be conducted the following at a minimum must be present:

1. a clearly stated achievable and measurable overall goal;

2. a realistic plan to achieve that goal;

3. the required resources available to implement the plan;

4. the necessary data collected and recorded at the proper times (most importantly including a baseline)at the proper level of sophistication, and with the required expertise; and

5. a method of adequate discrimination and appropriate power which allows measurement of the magnitude and direction of the effects program, and an analysis of the results.

Once an evaluation of a breeding program is completed at either the final or intermediate stages, then and only then, can one determine the success or the progress of the program, or can one make intelligent, informed decisions on the future direction of the program.

THE COMPARATIVE PERFORMANCE OF SPIKE- AND FORK-ANTLERED YEARLING WHITE-TAILED DEER: THE BASIS FOR SELECTION

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Abstract: The correlation between antler characteristics of yearling white-tailed deer and antler quality in later age classes is a poorly understood area of the biology of free-ranging white-tailed deer. This gap in our knowledge is particularly important since the success of management strategies that entail the selective harvest of yearling bucks based on antler characteristics is dependent on whether these characteristics reliably predict antler quality of mature deer. To address this question we compared the antler quality and body mass at 4.5 years of age (adult) of 140 white-tailed deer reared in a captive herd at the Kerr Wildlife Management Area (Hunt, Texas) from 1973 to 1990. Each yearling was classified as spike- or fork-antlered, measured for Gross Boone & Crockett (GBC) score, and weighed. Fork-antlered yearlings were further classified as having 3-5 points or ≥ 6 points ≥ 1 inch in length. All deer were reared in 4-acre enclosures and maintained on a 16% crude protein diet ad libitum. In ensuing years, antlers were removed and live body mass recorded. At 4.5 years, the GBC score of each buck was again measured. The average GBC score of adult deer that were fork-antlered yearlings (127.8) was significantly greater than that of spike-antlered yearlings (89.9). Adults that had forked antlers as yearlings had significantly greater tine lengths, beam lengths, beam circumferences, and spreads than did adults that were spike-antlered yearlings. The average body mass of fork-antlered yearlings was also significantly greater than that of spike-antlered yearlings at both 1.5 years (54.0 vs. 43.6 kg, respectively) and 4.5 years (78.7 vs. 66.7 kg). The GBC scores at maturity, and all components of GBC, differed significantly among spike-antlered yearlings, yearlings with 3-5 points, and yearlings with ≥ 6 points. Average GBC scores of adults that had ≥ 6 points as yearlings exceeded that of adults that were spike-antlered as yearlings by an average of 44 GBC points. The GBC score of yearlings reliably predicted their GBC score at age 4.5 years. Our results show that classifying yearlings as either spike- or fork-antlered was useful for predicting antler characteristics and body mass at maturity, and that spike-antlered bucks continued to produce smaller antlers at maturity in our controlled population.

In 1925 Texas law afforded protected status to spike-antlered white-tailed bucks throughout the state as part of an effort to stabilize declining deer herds (Thomas and Marburger 1965). In 1960, after 40 years of protecting spike-antlered bucks and selecting against fork-antlered bucks, this management decision was reversed statewide (Gore 1983). Currently Texas Parks and Wildlife Department (TPWD) advocates that spike bucks not receive differential protection in herds actively managed for improved buck quality (Armstrong et al. 1995). Despite the research conducted by TPWD that supports this management recommendation (Harmel et al. 1989, Williams et al. 1994), and efforts to popularize it (Baxter et al. 1981, Gore 1983, Harmel 1983, Williams 1994a, b, c,

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Williams et al. 1994, Armstrong et al. 1995), messages to the contrary continually crop up in the popular white-

tailed deer literature commonly read by sportsmen, landowners, and the lay public (Jacobson and White 1985, Haley 1993, Zaiglin 1994, 1996).

At the root of the scientific debate on the management of yearling bucks are the issues of (1) the relative importance of environmental and genetic factors in the expression of antler traits at age 1.5 years, (2) the comparative expression of antler traits of spike- and fork-antlered yearling bucks at later age classes, and (3) the reliability of yearling antler characteristics as predictors of antler quality of mature deer. Here we review issue 1 and investigate more fully the latter 2 issues.

Antler development in white-tailed deer is linked to body maintenance and growth (French et al. 1956, Moen 1978). Thus the expression of antler traits can be correlated with body condition within age-classes

(Smith et al. 1983) and correlated with body mass within and among age-classes (Severinghaus and Moen 1983, Williams et al. 1983, Williams and Harmel 1984). As a consequence, antler quality varies temporally within populations (Smith et al. 1983, Scribner et al. 1989) and spatially among populations with differences in habitat quality (Scribner et al. 1984, Shea et al. 1992*a*). Given these relationships variation in the nutritional quality of forage included in the diet plays a significant role in generating variation in antler trait expression (Teer et al. 1965, Ullrey 1983, Verme and Ullery 1984). Clearly, range management directed at improving forage quality is an effective way to improve mean antler trait expression in a herd.

Antler size and body mass of Texas white-tailed deer reared under controlled conditions vary also as a function of an individual's genotype as demonstrated by the finding of significant heritabilities for antler traits and body mass at 1.5 years of age (Harmel et al. 1989, Williams et al. 1994). The published heritability values of Williams et al. (1994) suggest that average antler quality in a herd can be increased or decreased by selectively choosing above or below average males to serve as breeders. A cautionary note however, is that because the heritability of a trait represents a ratio of genetic and environmental variances, estimates of heritability are specific to the environment and population in which the estimate was obtained (Falconer 1989). Thus, heritability estimates for white-tailed deer should be expected to vary between populations, among years, and between study herds of differing composition; (e.g., compare the heritability estimates for antler traits of Texas deer (Williams et al. 1994), and Mississippi deer (Lukefahr and Jacobson, *in press)*. Interestingly, antler quality has also been shown to vary as a function of heterozygosity within an age-class (Smith et al. 1983; Scribner et al. 1984, 1989; Scribner and Smith 1990).

Within the yearling age-class, the production of spike antlers in white-tailed deer appears to be influenced by both parental genotypes (Harmel 1983, Smith et al. 1983, Harmel et al. 1989, Williams et al. 1994, non-genetic factors, i.e., maternal effects (Lukefahr and Jacobson, *in press*), and parturition date (Knox et al. 1991, Shea et al. 1992*b*, but see Causey 1990). While there is general agreement that the incidence of spike-antlered yearlings varies temporally and spatially within and among populations within a region, and among regions, data directly addressing the relative importance of genetic and environmental factors in the production of spike-antlered yearlings in natural populations are nonexistent. As a result, there is continuing disagreement concerning the relative roles of environmental and genetic variation in the production of spike-antlered yearlings in the scientific and especially the popular literature, which is readily accessible to the land manager (Brothers and Ray 1982, Kroll 1991, Armstrong et al. 1995). Thus, the management decision to protect or remove spike-antlered bucks in natural or high-fenced populations remains controversial in Texas and throughout the southeastern United States (Jacobson and White 1985, Armstrong et al. 1995).

Herein we provide comparative data on antler characteristics and live body mass of spike- and fork-antlered yearlings reared under controlled environmental conditions to 4.5 years of age. We chose the Boone & Crockett scoring system (Boone and Crockett 1982) to compare antler characteristics of spike- and fork-antlered yearling white-tailed deer at 4.5 years of age for 3 reasons. First, this system provides a standardized metric for summarizing overall antler quality and the relative contribution of each component of antler quality. Second, the Boone & Crockett system is widely used in the popular literature. Third, white-tailed deer managers, guides, and hunters are adept at estimating gross Boone & Crockett scores under field conditions.

Methods

We examined antler characteristics and body mass of 140 male white-tailed deer reared from 1973 to 1990 in the pedigreed white-tailed deer herd at the Kerr Wildlife Management Area, a facility owned and operated by the TPWD near Hunt, Kerr County, Texas. The Kerr deer herd is representative of Texas white-tailed deer and has been shown to exhibit a level of heterozygosity comparable to natural deer herds throughout Texas (R. L. Honeycutt, Texas A&M Univ.,unpubl. data). All buck fawns included in this study were born into the captive herd and were reared on a 16% crude protein diet (Verme and Ullrey 1972, Harmel et al. 1989) ad libitum throughout the study. Each yearling was classified as spike- ($N = 43$) or fork-antlered ($N = 97$). Fork-antlered yearlings were split into 2 subclasses based on the number of antler points ≥ 1.0 inches in length: 3-5 points ($N = 33$) and ≥ 6 points ($N = 64$). All deer were reared in 4-acre enclosures. We captured, weighed, measured inside antler spread, and removed antlers 0.4 inches above the base of the pedicel of all bucks during the last 2 weeks of October and the first week of November. Gross Boone and Crockett score was computed for each buck at age 1.5 and 4.5 years using the formula:

$$GBC = \sum MB + \sum G_N + \sum H_N + SP + \sum NTPTS;$$

where $\sum MB$ = combined lengths of the main beams of the right and left antlers; $\sum G_N$ = total length of tines G_1 to G_N on both the left and right antlers; $\sum H_N$ = total beam circumferences H_1 to H_4 at the 4 measurement positions for both left and right beams; SP = maximum inside spread between the antlers; and $\sum NTPTS$ = total length of all nontypical points. Nontypical points were used in computing GBC scores at 4.5 years but were not further analyzed because so few deer of either class expressed such points. All measurements were recorded in mm by means of a flexible steel tape and were converted to inches to compute GBC scores (standardly expressed in inches). Both right and left antlers were measured for all deer.

Analysis of variance (ANOVA) was used to test for significant differences in GBC scores at 4.5 years and live body mass at 1.5 and 4.5 years between spike- and fork-antlered yearlings. ANOVA was also used to test whether each of the 4 GBC components differed at maturity between the 2 classes of yearling deer. ANOVA followed by means comparison was used to determine whether GBC scores at 4.5 years and live body mass differed among yearlings with spike antlers, 3-5 points, or $\geq$ 6 points. Linear regression analysis was used to predict the GBC score of each buck at maturity based on its GBC score at age 1.5 years.

Results

The average GBC score spike-antlered yearlings at 4.5 years old was less than that of fork-antlered yearlings ($\bar{x} = 89.9 \pm 2.8$ [SE], $N = 43$, and 127.8 ± 2.0, $N = 97$, respectively; $P < 0.001$). The distribution of GBC scores of the 2 classes of bucks overlapped minimally, and the production of "near trophy class" ($\geq$ 120 GBC) and "trophy class" ($\geq$ 130 GBC) bucks differed markedly between spike- and fork-antlered yearlings (Fig. 1). Most fork-antlered yearlings (62%) produced GBC scores $\geq$ 120 at 4.5 years, whereas only 2.3% of spike-antlered yearling had similar scores. All trophy-class bucks developed from fork-antlered yearlings. Spike-antlered yearlings also weighed less than fork-antlered yearlings at 1.5 years of age ($\bar{x} = 43.6 \pm 1.0$ kg, $N = 34$ and $\bar{x} = 54.0 \pm 0.7$ kg, $N = 87$ respectively; $P < 0.001$) and at 4.5 years of age ($\bar{x} = 66.7 \pm 1.6$ kg, $N = 43$ and $\bar{x} = 78.7 \pm 1.0$ kg, $N = 97$; $P < 0.001$; Fig. 2).

At maturity, fork-antlered yearlings produced higher scores than did spike-antlered yearlings for all GBC components (Table 1). These results indicate that the 42% increase in GBC scores at maturity for fork-antlered yearling bucks (38 inches) arose from differences in every component of GBC score. Most

notably, the total length of tines produced by fork-antlered bucks exceeded that of spike-antlered bucks by an average of 98%. This difference arose because of significant increases in the length of tines produced by fork-antlered bucks at each measurement position ($P < 0.001$ for all comparisons, Fig. 3). Similarly, the 26% increase in total circumference scores for adult fork-antlered bucks arose from significant increases in circumference at all measurement positions ($P < 0.001$ for all comparisons, Fig. 4).

Gross Boone & Crockett scores differed ($P < 0.001$) among adult bucks that as yearlings had spike antlers ($\bar{x} = 89.9 \pm 2.8$, $N = 43$), antlers with 3-5 points ($\bar{x} = 114.6 \pm 3.0$, $N = 33$), and antlers with $\geq$ 6 points ($\bar{x} = 134.0 \pm 2.3$, $N = 64$). This analysis indicates a general relationship between the overall quality of antlers produced at 1.5 years of age and those produced at 4.5 years. The 38-point difference in GBC score between adults that were either spike or fork-antlered as yearlings increased to 44 points when adults that were spike-antlered as yearlings were compared with adults that had $\geq$ 6 points as yearlings.

Each component of GBC score at 4.5 years of age also differed among the 3 classes of yearling deer ($P < 0.001$). Comparison of means for each GBC component at 4.5 years among the 3 yearling antler classes demonstrated clear differences between each of the yearling classes for each component and the intermediate performance of 3-5 point yearlings at maturity (Fig. 5).

Body mass of yearling bucks with spike antlers, antlers with 3-5 points, and antlers with $\geq$ 6 points also differed ($P < 0.05$) at both 1.5 and 4.5 years of age (Table 2). At maturity, spike-antlered yearlings attained only 83% of the live body mass achieved at maturity by yearlings with $\geq$ 6 points.

Linear regression of GBC scores at 4.5 years of age on GBC scores at 1.5 years of age showed that yearling GBC score is a reliable predictor of GBC score at maturity (Fig. 6). The best fit equation for this relationship: [(GBC 4.5 years = 70.5 + 0.92 (GBC score 1.5 years); $R^2 = 0.55$] shows that GBC scores at 4.5 years of age increase above the baseline of 70 GBC by about 1 GBC point for every GBC point scored as a yearling.

Discussion

Traditionally, participants in the controversy regarding alternative protocols to employ in managing spike bucks have considered yearling bucks to fall

neatly into 2 categories: spike or fork antlers (Brothers and Ray 1982 , Kroll 1991, Armstrong et al. 1995). Direct comparison of spike- and fork-antlered yearling bucks reared under controlled conditions demonstrated unequivocally that (at maturity) the average antler quality and average body mass of spike-antlered yearlings were less than those of fork-antlered yearlings. Fork-antlered yearlings reared during a 18-year study in the Kerr Wildlife Management Area captive deer herd consistently produced GBC scores and body masses that averaged nearly 140 and 120% greater than those of spike-antlered yearlings, respectively. Thus, classifying yearling white-tailed bucks as either spike- or fork-antlered is a reliable tool for predicting overall antler quality and live body mass at maturity. Our results were consistent with prior published studies of the relationship between antler traits and body mass of yearling deer and the expression of these traits in later age-classes (Williams et al. 1983, Scribner et al. 1984, Williams and Harmel 1984, Harmel et al. 1989, Schultz and Johnson 1992).

Our results show that differences in overall antler quality arose because of significant increases in each component of GBC score. Increased tine lengths and, to a lesser extent, beam circumferences, were the primary contributors to the increased GBC scores of fork-antlered yearlings at 4.5 years. Adult deer allocated resources similarly (i.e., no differences in the shape of the relationships between tine length or beam circumference and measurement position illustrated in Figs. 4 and 5), but fork-antlered yearlings committed more total resources to bone growth throughout antler development (i.e., at each successive measurement position).

Our analyses show clear differences between the size of antlers and body mass of adult white-tailed bucks that were spike- or fork-antlered as yearlings in our control herd. If the results of penned studies are applicable to free-ranging or managed populations, then the distinction between these classes of yearlings could be of value to those wishing to improve the average GBC scores of mature bucks. Improvement of GBC scores within a herd could be accomplished by selectively culling spike-antlered yearling bucks. This technique would increase mean antler quality at maturity within a cohort of bucks simply by reducing the number of small-antlered bucks contributing to the population mean (Armstrong et al. 1995). Improvement would be realized within the population, at the expense of cohort size, regardless of the genetic basis of antler traits.

Most management, however, is directed at habitat improvement and/or long-term (genetic) improvement

of herd performance. Both habitat improvement and genetic improvement seek to reduce the incidence of spike-antlered yearlings. For selective culling of spikes to produce long-term genetic improvement, not only must the expression of antler traits at the yearling stage reliably predict antler traits at maturity (as we have shown) but antler traits must exhibit heritable variation (Armstrong et al. 1995). Williams et al. (1994) demonstrated intermediate to high heritability in yearling Texas white-tailed bucks for number of points, main beam length, inside spread, basal circumference, and antler mass.

Our results, in conjunction with those of Williams et al. (1994), imply that for Texas white-tailed deer, the average value of antler traits at maturity, or a measure that summarizes a suite of antler traits (e.g., GBC score), could be increased between generations in managed populations by selectively culling small-antlered bucks. This implication follows directly from a basic tenet of selection theory, namely that the response of a trait to selection is a product of the intensity of selection and the heritability of the trait (Falconer 1989). We concur with Scribner et al. (1984), Harmel et al. (1989), Schultz and Johnson (1992), and Armstrong et al. (1995) that selective culling of spikes could be considered as a component of management for improved average antler development of a herd.

Results of our 3-group analysis demonstrated large differences among spike, 3-5 point, and $\geq$ 6 point yearling bucks and suggest that for maximum antler expression, the decision of which yearling bucks to protect or remove from managed herds is not as simple as the convenient classification system "spike- or fork-antlered" would suggest. Indeed the regression of GBC scores at 4.5 years of age on GBC scores at 1.5 years of age indicates that expression of antler traits at maturity is highly correlated with expression at the yearling stage. The correlation in antler quality between years is high enough to allow the use of GBC scores of yearlings to reliably predict GBC scores at maturity. Thus, white-tailed deer managers and hunters must recognize that antler and body weight are continuously distributed traits whose expression at maturity may be correlated with their expression at the yearling stage. As indicated by basic selection theory (Lerner 1950) and discussed by Williams and Harmel (1984), management strategies that favor the removal of all but the largest-antlered yearling bucks (under the appropriate conditions) will lead to the greatest gain in mean herd performance.

The short-term cost of improvement in antler quality is fewer harvestable animals at maturity.

Obviously within different herds (and even the same herd in different years), the subset of the yearling population to be culled will differ, but in each population "top-end" yearling bucks should be identified and preserved, if the long-term management goal is to improve antler quality.

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Table 1. Comparison of Gross Boone & Crockett (GBC) component scores (in inches) between spike-antlered (N = 43) and fork-antlered (N = 97) yearling white-tailed deer at 4.5 years of age in the Kerr deer herd, Kerr County, Texas, 1973-1990.

GBC Component[1]	Spike-antlered		Fork-antlered			
	$\bar{x}$	SE	$\bar{x}$	SE%	increase[2]	$P > F$
$\sum$MB	31.8	0.7	39.0	0.5	+ 22.6	<0.001
$\sum$G$_N$	21.1	1.6	41.8	1.1	+ 97.6	<0.001
$\sum$H$_N$	22.2	0.5	28.1	0.4	+ 26.5	<0.001
SP	14.4	0.4	16.5	0.3	+ 14.3	<0.001

[1] Components are: $\sum$MB = combined length of right and left main beams; $\sum$G$_N$ = combined length of all tines on the right and left antler; $\sum$H$_N$ = combined circumference of the 4 measurement positions of both the right and left antler; and SP = maximum inside spread between right and left antlers.
[2] Percent increase relative to spike score = [(fork antlered - spike antlered)/spike antlered] *100.

Table 2. Live body mass (kg) at 1.5 and 4.5 years of age for yearling bucks with spike antlers, antlers with 3 -5 points, or antlers with $\geq$ 6 points in the Kerr deer herd, Kerr County, Texas, 1973-1990.

Yearling classification	Body mass (1.5 years)[1]			Body mass (4.5 years)		
	$\bar{x}$	SE	N	$\bar{x}$	SE	N
Spike antlers	43.6[A]	1.0	34	66.7[A]	1.6	43
3 - 5 points	48.6[B]	1.0	26	75.4[B]	2.0	33
$\geq$ 6 points	56.3[C]	0.8	61	80.5[C]	1.1	64

[1] Results based on ANOVA followed by means comparison using Tukey's studentized range test. For both 1.5 years,and 4.5 years $P < 0.0001$. Means followed by different letters within a year-class are significantly different at $P < 0.05$.
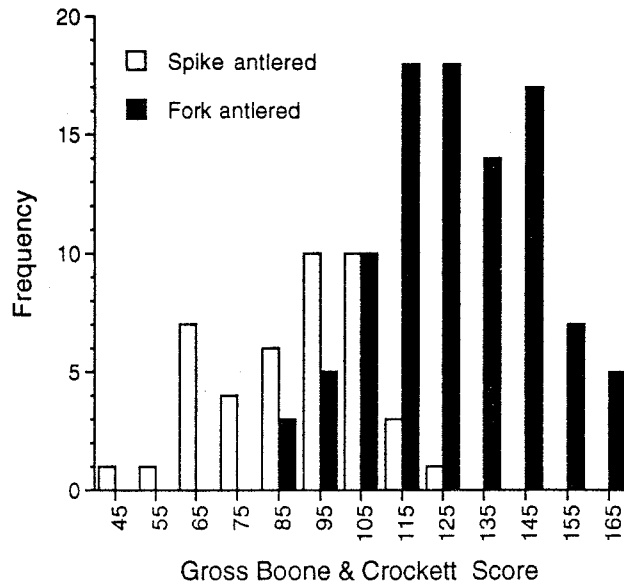
Figure 1. Distribution of gross Boone & Crockett (GBC) scores for white-tailed deer at 4.5 years of age that as yearlings were spike-antlered (N = 43) or fork-antlered (N = 97) in the Kerr deer herd, Kerr County, Texas, 1973-1990.
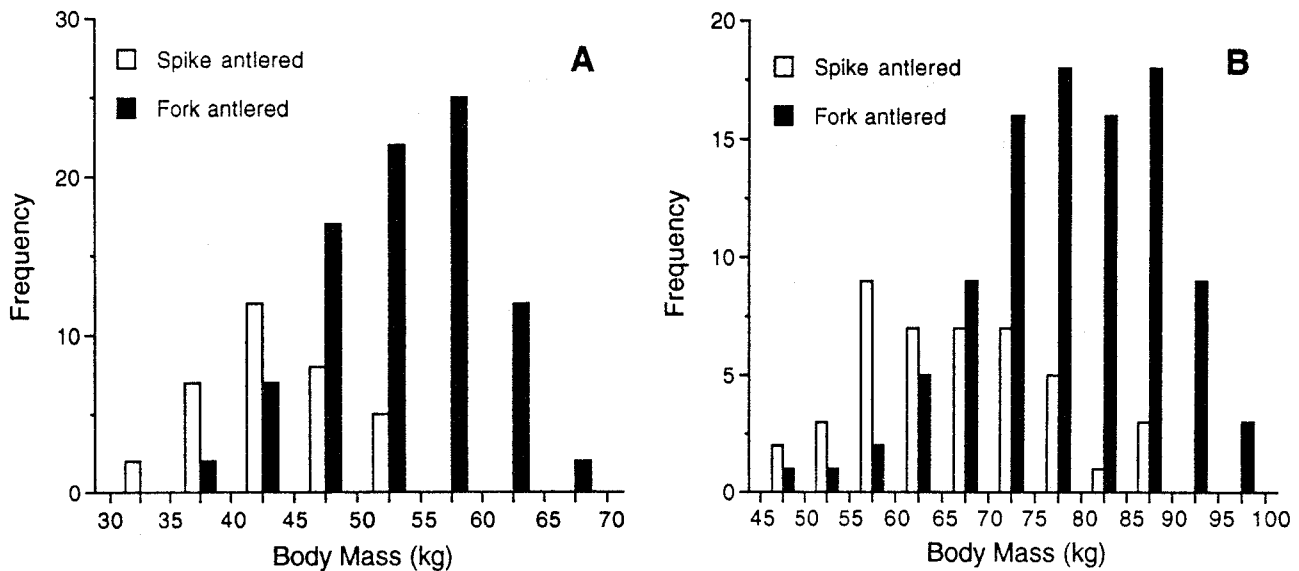
Figure 2. Distribution of body mass of (A) spike-antlered (N = 34) and fork-antlered (N = 87) yearling white-tailed deer at 1.5 years of age and (B) spike antlered (N = 43) and fork-antlered (N = 97) yearlings at 4.5 years of age in the Kerr deer herd, Kerr County, Texas, 1973-1990.
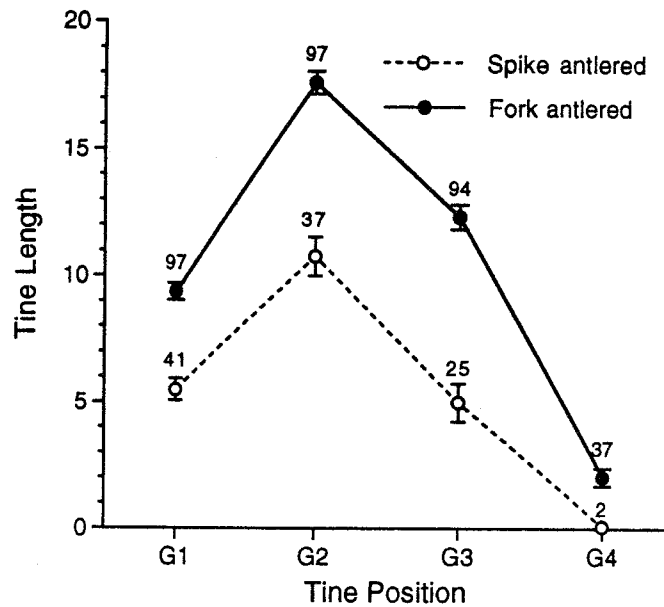
Figure 3. Mean (± SE) total length of tines at measurement positions G_1 to G_4 on the main beam ($\sum$ left + right antlers) at 4.5 years of age for spike- and fork-antlered yearlings in the Kerr deer herd, Kerr County, Texas, 1973-1990. Numbers above SE bars indicate the number of individuals in which total length of tines was greater than 0 at each measurement position. Total tine length is expressed in inches.
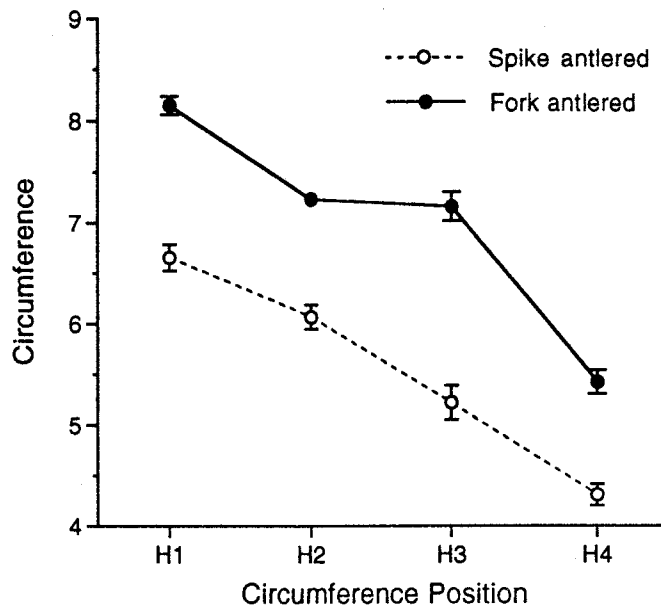
Figure 4. Mean (±) SE circumference as a function of measurement positions (H_1 to H_4) along the main beam at 4.5 years of age for spike- and fork-antlered yearling white-tailed deer in the Kerr deer herd, Kerr County, Texas, 1973-1990. Circumference is the sum of right and left antlers in inches; N = 43 and 97 at all measurement positions for spike and fork-antlered yearlings, respectively.
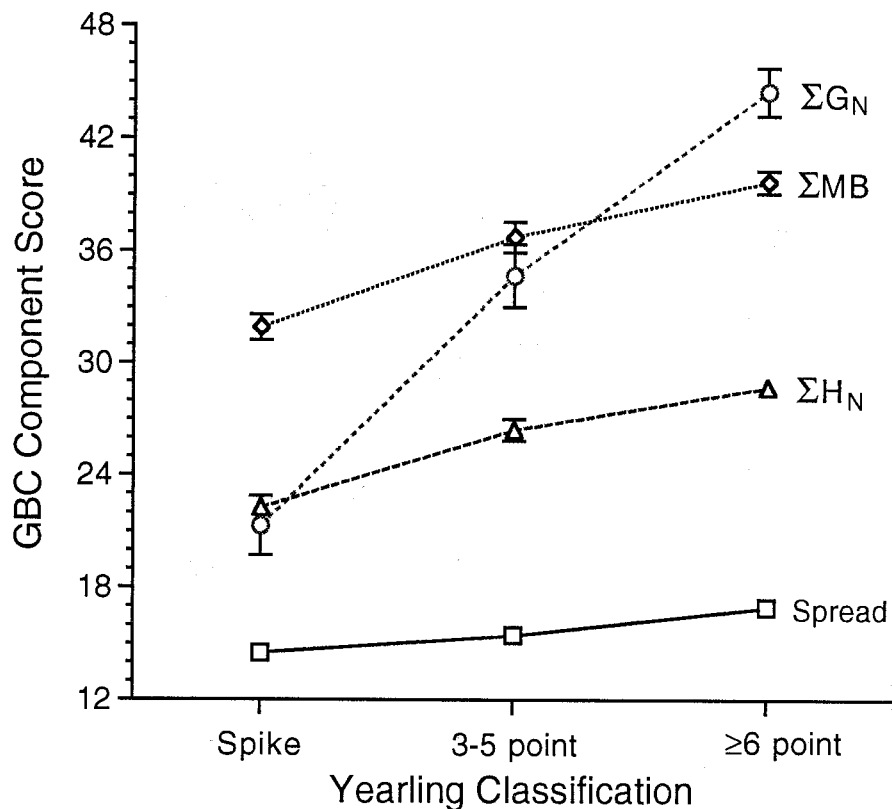
Figure 5. Means ± SE of GBC components ($\sum$MB = combined length of right and left main beams; $\sum G_N$ = combined length of all tines on the right and left antler; $\sum H_N$ = combined circumference of the 4 measurement positions of both the right and left antler; and spread = maximum inside spread between right and left antlers) at 4.5 years of age for spike-antlered yearlings, yearlings with 3-5 points, and yearlings with $\geq$ 6 points in the Kerr deer herd, Kerr County, Texas, 1973-1990. With the exception of mean values of spread for spike-antlered and 3-5 point yearlings, the mean scores of each GBC component differed ($P < 0.05$) among the 3 classes. Results based on individual ANOVAs ($P < 0.001$ for all components) followed by means comparison. Component scores are expressed in inches. Error bars are subsumed by symbols for some means.
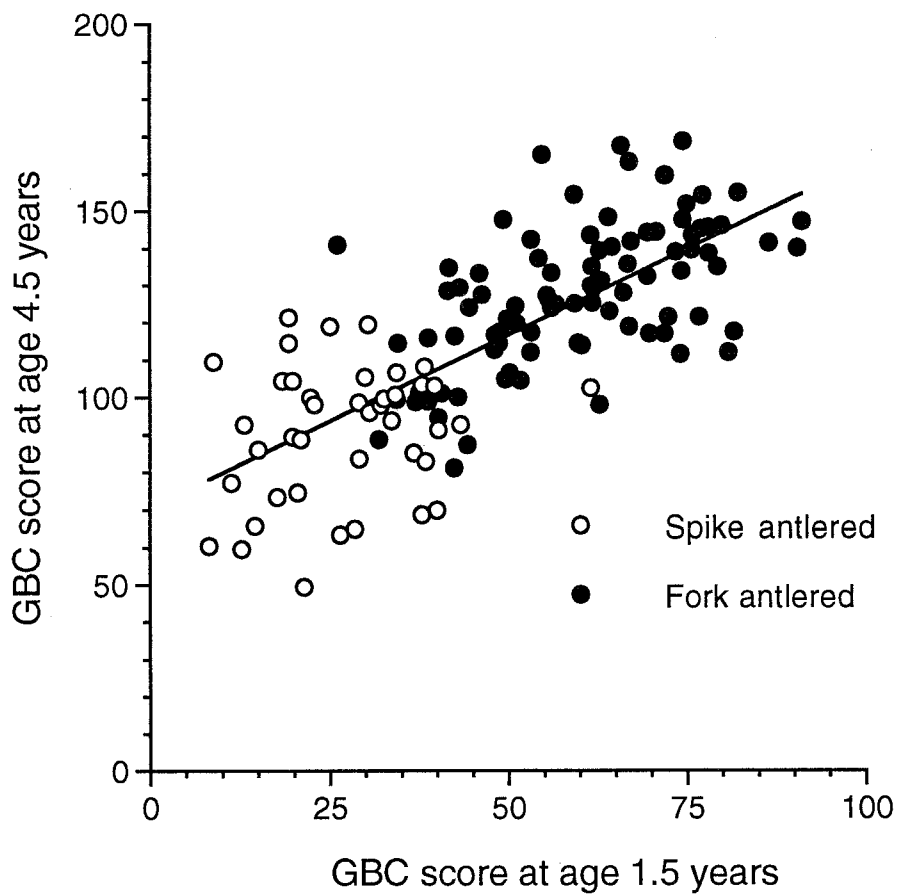
Figure 6. Gross Boone & Crockett scores at 4.5 years versus GBC scores at 1.5 years of age for both spike- and fork-antlered yearlings in the Kerr deer herd, Kerr County, Texas, 1973-1990; N = 41 and 93 for spike and fork-antlered yearlings, respectively. Gross Boone and Crockett score at 4.5 years = 70.5 + 0.92 x (GBC 1.5 years); R^2 = 0.55.

MANAGING FOR ANTLER PRODUCTION: UNDERSTANDING THE AGE - NUTRITION - GENETIC INTERACTION

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Abstract: Age, nutrition, and genetics clearly have significant impacts on antler development of white-tailed deer. Taken individually, each of these factors has clear and reproducible impacts on antler growth. Antler development increases with age up to a maximum at 5-7 years of age. Nutritional limitation can negatively impact pedicle initiation in fawns and growth of antlers in all ages classes. Genotype of a buck affects the ultimate expression of antler at some point in his life, although there is disagreement over when this takes place. Management programs should incorporate all three factors when possible. However, emphasis should be placed on addressing the most significant limiting factors. This approach will generally produce the most cost-effective results.

In our endless search for the "magic bullet" in management of our common passion, the white-tailed deer, we often look for simple solutions to complex management problems. This is not to say that the underlying biological principles are complex. Quite the opposite; most applied deer management involves application of several fairly simple, straightforward biological principles. However, it is the application of these "simple" principles to the complex reality of real-world management that often results in a fair share of material flying back onto our otherwise clean faces. It can be frustrating enough for an "educated" biologist when 2+2+2 just doesn't add up to 6, but add in an eager to understand landowner or hunter and there is more than enough frustration when the "laws of math" go awry.

Incorporation of genetics into white-tailed deer management has been mistakenly perceived by some as one of those "magic bullets." The resultant selective harvest of one type or another of inferior buck is expected to radically alter population-level gene frequencies tied to production of superior antler development. Reliance on manipulation of any one limiting factor, without understanding its relationship to other related, and perhaps more pressing, limiting factors domes many efforts to frustration, if not failure. My goal for this paper is to clarify the basic influences of nutrition, age, and genetics on antler development and then discuss how these fairly simple biological principles may interact to cause confusion and frustration within the deer management arena. The outcome should be an appreciation for the fact that there is only one simple, always-applicable, answer to the question "should we shoot spikes?" The

only simple, always-applicable answer that I have been able to come up with is "it depends."

Nutrition

Antler development is affected greatly by nutritional intake prior to and during antler growth. This basic relationship has been known as far back as King Edward II, whose huntsman declared "*The head grows according to the pasture, good or otherwise*" (Dryden 1908, cited in Chapman 1975). A number of nutritional components interact to generate the boney matrix of antlers, must importantly protein, energy, and minerals. The variety of experimental approaches to unraveling the nutrition-antler mystery rivals the variety of antler shapes found in white-tailed deer. However, experiments typically compare antler characteristics between an "optimally" fed group and one or more "sub-optimally" fed groups.

French and others (1956) began the modern search for nutrition-antler relationships. They showed that whitetail buck fawns fed 4.5 or 9.5 percent protein from weaning until 1.5 years of age grew smaller antlers than buck fawns fed 16 percent protein. This effect could have been due to retarded development of the pedicle (base from which the antler grows), which is related to nutrition (Lincoln 1971), or to negative effects on growth of the first antler. Red deer fawns raised on poor quality winter forage followed by poor summer forage were delayed in the initiation of pedicle development, the starting date of antler growth, and the date of velvet shedding and also grew lighter, shorter antlers compared to fawns raised on high quality winter forage followed by poor quality summer forage (Suttie and Hamilton 1983). Red deer fawns having unlimited access to high quality forage initiated pedicle development much earlier than those with access to only 70 percent as much forage (Suttie and Kay 1982). Whitetail fawns fed a diet simulating

an early green-up with access to acorns had about double the number of antler points at 1.5 years of age as fawns fed a diet simulating late green-up (Ullrey 1982). This apparent relationship between diet quality and a buck's first set of antlers is important to an understanding of the nutrition-birth date interaction to be discussed later in the paper.

Adult bucks also show antler responses to changes in diet quality. For example, antlers of 2.5 year old whitetails fed 16 percent protein had almost twice the antler mass of bucks fed 8 percent protein (Harmel et al. 1979).

Age

The first set of antlers typically are grown at 1.5 years of age. However, up to 20-30 percent of buck fawns may develop hardened antlers (usually only hardened buttons) at about 8 months of age (Jacobson 1995). In these cases, nutrition is adequate enough and birth dates are early enough to allow fawns to reach their critical body mass needed to initiate antler growth. Once initiated, antler size increases annually, in sometimes dramatic fashion, until maximum antler development is reached about 5-7 years of age. Based on averages of 23 bucks measured through 7.5 years of age (Jacobson 1995), 1.5 year old bucks grew the equivalent of about 26 percent of their ultimate maximum gross Boone and Crockett score. The percentage increased linearly each year, to about 63 percent at 2.5, 77 percent at 3.5, and 92 percent at 4.5 years of age. These particular animals peaked at 5.5 years of age and then dropped back to about 90 percent for years 6.5 and 7.5.

Genetics

Let's get a few facts clarified right up front. The fact that a buck's potential for antler development is contained within his DNA material must be accepted. Likewise, the fact that the sire and dam determine the genetic potential for antler development by their offspring also must be accepted. Given these facts, it really should matter which bucks breed which does.

In the abundant debate dealing with the application of genetics to deer management (i.e., selective harvest), never have I heard anyone dispute the importance of genetics in antler development of white-tailed deer. However, there has been significant controversy and/or confusion over the application of this genetic information to management of white-tailed deer. A big part of this issue involves the interaction of nutrition and age in the expression of genetic potential. In other words, how do nutrition and age affect our ability to evaluate the genetic potential of a young buck. Another large part of the issue deals with the wide range of extenuating management circumstances to which the biological principles are applied. In other words, under what circumstances would you want to attempt to genetically manipulate a population.

Evaluating Genetic Potential

To be effective in genetic manipulation of a population, you must be able to predict an animal's genetic potential for antler development (i.e., his genotype) and selectively remove him from the population. The ultimate expression of this potential can be affected by certain environmental factors (i.e., his phenotype). Any factor that negatively affects the expression of a young animal's genetic potential for antler development can inhibit success of a selective removal harvest strategy.

Factors which affect the initiation of pedicle growth during a buck's first winter and antler growth during subsequent springs and summers likely will affect the expression of a young buck's genetic potential for antler development. In areas where there is a long breeding season and subsequently a long fawning season with "late" fawns, date of birth can negatively affect antler development. The relationship between date of birth and subsequent antler development has been documented within the Mississippi State University deer pens (Jacobson 1995). For fawns born during late summer or early fall, the prevalence of spikes is much higher and the average number of antler tines much lower at 1.5 years of age compared to fawns born earlier in the summer. More importantly, this effect even carries over into the 2.5 year age class. Looking at gross Boone and Crockett scores further clarifies this relationship (H. Jacobson, Mississippi State Univ., pers. commun.). Scores of bucks born in September/October were only 32 %as high as bucks born in June at 1.5 year and only 79 % as high at 2.5 years of age. Bucks born in August had scores 54 % as high at 1.5 years of age and 83 % as high at 2.5 years of age compared to bucks born in June. The disparity among antler characteristics based on birth date disappears as the bucks mature, with no statistically significant differences discernible after 3.5 years of age, although the pattern is present for an additional year; this indicates that late born fawns are able to exhibit compensatory growth and "catch up" to early born fawns by adulthood. An alternative interpretation is that the bucks that exhibit early exceptional antler

development actually "slow down" and do not improve as much in subsequent years.

Poor nutrition during their first year of life can decrease antler size at 1.5 years of age, adding additional confusion to bucks' genetic potential. Remember the several examples discussed earlier in this paper. However, when comparing antler development of yearling bucks within the same habitat, it is reasonable to assume that all yearlings had equal access to the same forage quality and thus antler differences within a habitat likely would be due to factors other than nutrition.

Given that birth date and early nutrition can negatively affect expression of genetic potential, it should be asked at what age would selective harvest be effective? The results applicable to this question differ between the two main sources of research, Mississippi State University and Kerr Wildlife Management Area. Data from Mississippi indicate that a buck's true potential for antler development can not be judged accurately at 1.5 years of age and that selective harvest of this age class should not be promoted as part of a selective harvest program (Lukefahr and Jacobson 1998). Data from Kerr Wildlife Management Area indicate that antler development at 1.5 years of age is predictive of antler development at maturity and that classifying yearlings as either spiked or fork-antlered can be used as part of a selective harvest program (Ott et al. 1997).

When to Apply Genetic Manipulation

The role of genetics in the ultimate antler development produces a strong tendency for managers to attempt to incorporate it in selective harvest programs. However, selective harvest does not necessarily have to play a role in every management program. If the harvest of "average" mature deer without selective harvest is meeting the needs of the user group, then application of a tool based on potentially confounding factors may not be a good. Additionally, deer management programs typically involve a process of prioritization, where management efforts are targeted at minimizing the effects of the most seriously limiting factors. Often, improvement of the other antler factors, nutrition and age, will generate an overall satisfactory level of improvement.

Deer populations without adequate age structure within the buck segment are most limited by lack of an adequate number of older bucks, regardless of their genetic potential for antler development. Allowing younger bucks an opportunity to age and grow larger antlers often will produce acceptable results. For example, restrictions placed on harvest of yearling bucks using a minimum antler spread measurement in Dooley County, Georgia, reduced the prevalence of yearling bucks in the harvest from 41 percent in 1992 to 6 percent in 1993. The resultant age-related improvement in harvested bucks generated significant interest and support within the hunting public (Goldstein et al 1997). Protection of spikes from harvest at Tyndall Air Force Base in northern Florida increased older age classes in the harvest and significantly improved the quality of antlers harvested (Shea et al. 1997).

Control of overpopulation requires harvest of an adequate overall number of bucks. For populations with a balanced sex ratio and older age composition of bucks, there usually is a need to harvest excess bucks. Removal of bucks that have a likelihood of being "inferior" is highly advisable. The judgement of inferior status must be made relative to expectations on individual properties. Even though late born fawns may eventually catch up to early fawns, these animals could be considered candidates for selective removal, especially if most "mature" deer are harvested by 4.5 years of age. At this age the late fawns would likely still be lagging behind the early fawns in antler development. Even if you want to delay selective harvest to older age classes, you still must make a judgement as to which bucks have the least genetic potential for antler development. This conservative approach would involve selective removal of animals that have the smallest antlers within particular age classes.

Application of selective harvest to management of white-tailed deer populations is widely practiced and less-widely critically evaluated. If the potentially confounding factors influencing antler development on your property can be isolated and it appears that genetic potential is significantly limiting antler development, then selective harvest may be an option worth considering. Until those factors have been clearly evaluated, caution should be the watch word; cost-effective application of genetic manipulation to most deer populations really does "depend" on a number of other important factors.

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INFUSING NEW GENES: NATURAL OR ARTIFICIAL INSEMINATION?

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Abstract: Infusion of new genes into a population of white-tailed deer is best accomplished by selection and utilization of superior bucks. Superior bucks normally are found in temperate regions and usually are not adapted to southern states. Survival of northern bucks then is a problem for managers of white-tailed deer in southern states. Pen mating allows a buck to sire more fawns and a manager to know parentage of fawns. Artificial insemination allows for maximum impact of a single buck on the genetics of a white-tailed deer population. Estrous synchronization is an effective method to control reproduction in white-tailed does and facilitates artificial insemination.

Because of the ability of the male to sire progeny from multiple females during each breeding season, infusion of new genes is usually accomplished through introduction of males carrying the desired new genetic material. As antler characteristics are the most important trait for white-tailed deer selection, the male having desirable traits is detected more easily than the female. Offspring from the introduced male have the advantage of being born to an adapted female which will transfer immunity to many diseases through immunoglobulins in the colostrum. If an unadapted female is bred to an adapted male, the offspring will not receive the same immunity through the colostrum and will be at a disadvantage. Both matings would transfer the desired new genes at similar rates but survival of offspring would differ dramatically.

Many questions remain unanswered with respect to both natural service and artificial insemination of white-tailed deer. The white-tailed deer is a seasonal breeder with breeding season varying in time of onset depending on origin of the deer. The manager of a white-tailed deer breeding facility would benefit from being able to induce onset of the breeding season in does for either natural service or artificial insemination. Furthermore, the manager would benefit from being able to control the estrous cycle for artificial insemination. Artificial insemination using frozen semen is the most efficient method to introduce new genes into a population without moving unadapted animals into a new environment. As animals acquire improved genetics, managers must provide an adequate environment for these new genes to be expressed.

Considerations for Natural Service

Most scientific breeders will pen mate does to bucks with desirable traits in individual breeding groups. Seldom can the manager justify turning a valuable buck into a multiple sire breeding group. When a buck is spending a large proportion of his time seeking does and in protecting does he cannot breed as many does and will sire fewer offspring. With individual sire groups it also is an advantage to be sure of the sire of the fawns. Each mature buck should be capable of breeding at least 20 does during each breeding season in an individual breeding group. The manager should remove the hard antlers from pen mated bucks to avoid bucks killing non-receptive does (Warren et al. 1978).

Estrous Synchronization

Methods for estrous synchronization of deer include prostaglandin F2α (Haigh, 1984; Hoekstra et al., 1976; Asher et al. 1990), progesterone delivered via intravaginal controlled internal drug release device (CIDR; Haigh and Waldham, 1991), half of a norgestomet (synthetic progestin) ear implant (Synchro-Mate ; Willard et al., 1996) or intra-vaginal sponges containing medroxyprogesterone acetate (MAP; Magyar et al., 1991). For the system with prostaglandin F2α to be effective the doe must be experiencing estrous cycles. Magyar et al. (1991) reported 60% of does treated with prostaglandin F2α had synchronized estrus while 75% of the does treated with a progestin had synchronized estrus. Does nearing their breeding season can be induced to begin

experiencing estrous cycles by progestin treatments (Asher et al. 1990).

Most managers will want to use estrous synchronization at the beginning of the breeding season. For the best results, a system based on a progestin should be used for estrous synchronization of white-tailed deer because it will induce estrous cycles to begin (Asher et al. 1990). The most often utilized system for estrous synchronization in deer employs the CIDR. This device is manufactured outside of the U.S. and is not approved for use by the Food and Drug Administration. Availability of the CIDR is therefore limited. The Synchro-Mate B system for estrous synchronization includes a norgestomet (synthetic progestin) ear implant manufactured in the U.S. and approved for use in cattle by the Food and Drug Administration. The norgestomet ear implant therefore is available.

In a study (Willard et al. 1996) making a direct comparison between the CIDR and half norgestomet ear implants, sika hinds showed estrus at similar times (CIDR = 35 hours vs norgestomet 37 hours) with similar pregnancy rates (CIDR = 60% vs norgestomet = 67%). Time of onset of estrus was hastened in these sika hinds by treatment with 50 IU of PMSG (pregnant mare serum gonadotropin). As the treatments are both working through the same mechanisms they appear to be having the same results for estrous synchronization of deer.

The recommended treatment for white-tailed deer is to use either half of a norgestomet ear implant (Synchro-Mate B , without the estrogen plus progestin injection) or the CIDR device which are left in the doe for 13 to 14 days. In a study in South Texas (unpublished data), white-tailed deer were in estrus 58 + 4 hours after removal of the norgestomet ear implant with 87% (26/30) showing synchronized estrus detected by fertile white-tailed bucks. From 75 to 87% of white-tailed does should show estrus following either CIDR or norgestomet treatment in an average of 58 hours from treatment removal.

Estrous Synchronization with Natural Service

Estrous synchronization can be used for natural service in pen-raised white-tailed deer. Comparison of estrous synchronization and natural service with non-synchronized natural service in white-tailed deer shows fawns were born an average of 10 days earlier when does were estrous synchronized and bred by natural service. During the first 10 days of the fawning season, 68.6% of the fawns were born to the estrous

synchronized does compared with 18.8% of the fawns born to the non-synchronized does. These does were bred in individual groups of 10 does/buck and bucks achieved a 70% first service conception rate in the estrous synchronized groups compared with 55% in the non-synchronized groups. Pregnancy rates for the entire breeding season were 83.3% in estrous synchronized does and 70.0% in non-synchronized does.

Artificial Insemination

There are two systems for artificial insemination of white-tailed deer. Laparoscopic artificial insemination is accomplished by placing semen in each uterine horn of an anesthetized doe. Transcervical artificial insemination is accomplished by passing an artificial insemination pipette through the cervix of a restrained doe. Willard et al. (1997) reported fertility was similar in sika does which were bred using laparoscopic or transcervical artificial insemination. Requirements for laparoscopic insemination include anesthesia of the doe and the equipment for laparoscopic insemination. Usually a veterinarian is required for anesthesia and a highly skilled technician for insemination using the laparoscope. Requirements for transcervical artificial insemination are facilities to restrain the doe, a light source, speculum and artificial insemination pipette. A technician familiar with semen handling and placement is required for transcervical artificial insemination. Both techniques are effective but require either estrus detection or synchronization of estrous with proper timing of artificial insemination. Using estrous synchronization via half norgestomet ear implants, in the ear for 13 days, white-tailed does had a first service conception rate of 66.7% when inseminated transcervically about 65 hours after implant removal compared with estrous synchronized does bred natural service which had first service conception rates of 70.0%.

Artificial insemination has the advantage of breeding several does with one ejaculate from a buck and can allow a buck to sire many fold more fawns in a breeding season compared with natural service. Semen which is collected, extended and frozen can be stored indefinitely. This allows a manager to easily transport new genetic material and to provide insurance that genetic material will be available from a valuable male even after his death.

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CASE STUDY: THE KERR AREA PENNED DEER RESEARCH FACILITY

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Abstract: The Kerr Area deer pen is a 16-acre research facility in which 7 distinct and separate research studies have been conducted to understand the role of genetics, nutrition, and selected environmental factors play in antler formation in white-tailed deer. Each study has had its own objective and research design. Information learned from each study has been used to design future studies. Studies have included the effects of 8% and 16% crude protein controlled diets on antler formation, influences of fork antlered sires versus spike antlered sires on antler formation, comparison of antler production of spike-antlered yearlings to fork-antlered yearlings in later years, heritability estimates related to body size and antler formation, and the combined effects of nutritional stress and selection on improving antler quality. Research results have been published in Federal Aid reports as well as Texas Parks and Wildlife publications and the Journal of Heredity. Combined information from all studies suggest (1) that antler quality in later years can be predicted based on status of yearling antlers, i.e. spikes as a group do not produce as good as antlers at 4.5 years of age as yearlings that produced 6 or more points; (2) that antler formation is genetically controlled and environmentally influenced; and (3) that selection for antler quality based on yearling antlers can improve overall antler quality of future cohorts. In addition, insight from data gained in the primary studies has been useful in understanding the role in the age of the dam, effects of birth date, and time of weaning on antler production.

In 1974, a 16 acre research facility to study antler growth in white-tailed deer was built on the Kerr Wildlife Management Area. This facility has been used in a series of research programs to determine the role of nutrition and/or genetics in the antler development process. Each program had its own research design and objective. The first of these studies was to determine the effects of nutrition of antler development. The second study was to determine if genetics was involved and still a third compared antler development at 1.5 years of age to antler development later in life. Because it was determined that antler development was genetically controlled and nutritionally influenced, a heritability study was initiated to determine how heritable were antler traits. Currently, the pens are being used in a study that combinations the effects of nutrition and genetic influences on antler production. In addition to the above studies, the pens have also been used to study the effects of early weaning on fawn survival. A so called " spike line" of deer bred to produce small antlers on a high protein diet has not been used in any "official" study but has been maintained in the pens.

Effects of Nutrition on Antler Development Study

In this study, a group of male fawns were placed on controlled diets and their antler production monitored for four years. It was determined from this study that an animals diet was an important component in antler development. The results of this study are published in the 1989 Texas Parks and Wildlife bulletin, "*Effects of Genetics and Nutrition on Antler Development and Body Size of White-tailed Deer*".

Genetics' Role in Antler Development Study

In this study, a male deer that was a spike as yearlings (1.5 years of age) was placed in an individual pen and was bred to a group of does. There were seven spike sires used throughout the study. The male deer were then bred to their daughters to concentrate the gene pool of the sires. The original does (those that were originally bred to the deer that were spikes as yearlings) were then bred to a large antlered male that had six points as a yearling. There was a significant difference in progeny antler production between the three types of matings. The results of these matings strongly indicated a genetic role in antler development. All deer throughout this study were fed a free choice 16 percent protein diet. Nutrition was not a factor in this study. This study is also reported in the 1989 Texas Parks and Wildlife bulletin, "*Effects of Genetics*

[1] *Deceased*

and Nutrition on Antler Development and Body Size of White-tailed Deer".

Spike vs. Fork Antlered Yearlings

In this study, antler production of deer that were fork antlered as yearlings and deer that were spike antlered as yearlings were compared yearly until 4 years of age. Fork antlered deer produced almost twice the antler mass each year as their spike antlered counterpart. Results of this study are also published in the 1989 Texas Parks and Wildlife bulletin "*Effects of Genetics and Nutrition on Antler Development and Body Size of White-tailed Deer*". This study has been complimented and updated since 1985 by investigations by James Ott and R W. Scott and data presented at both the Texas Chapter of the Wildlife Society and the 1997 Southeast Deer Study Group. The papers' title is *"Comparative Antler Characteristics of Spike- and Fork Antlered Yearling Whit-tailed Deer in Texas at 4.5 Years"*. Results of the updated study are being presented at this seminar by Jim Ott.

Another related study compared antler production under *field conditions* of deer that were spike or fork antlered as yearlings. This study was conducted in a 96 acre deer proof pasture over a four year period. Deer were "range grown" without supplemental feed. Although small sample size prevented the two groups of deer from being *statistically* different, trend data indicated that antler production of fork antlered deer surpassed that of spike antlered deer. Results of this study are reported in Federal Aid Performance Report *W-109-R Job 38 : "The Effects of Genetics on Antler Development and Body Size Under Field Conditions"*.

Heritability Study

In 1986, a study was begun to determine the heritability of selected antler traits in white-tailed deer. Only *yearling deer* were used as brood bucks. All fawns were weaned in October. Heritability estimates were analyzed by three different statistical methods. It was determined from this study that antler traits are highly heritable. Results of this study are published in the scientific journal *"Heredity"*. In 1997, a fourth statistical method was used to analyze the original heritability data set using an animal model and MTDFREML software. Standard errors were very large and no statistical conclusions could be drawn. Results of this fourth analysis are published in a TPWD paper entitled *"Genetic and Environmental Parameters for Antler Development Traits in White-*

tailed Deer Using an Animal Model " by S. D. Lukefahr. (Final Report On Interagency Contract No. 386-0692). Based on phenotypic observations, heritability is considered to be moderately to highly heritable.

Genetics vs. Environment Study

This study began in 1991 and currently has 5 years of antler data. In this study, fawns are weaned in October and are placed on an 8% protein ration in which daily intake is also restricted. The deer are raised on this ration until they have completed their antler growth the following October. They are then placed an a 16% ad lib ration and their antler production monitored until they are four years old. The five yearlings that exhibited the best antler growth each year on this limited diet are used as brood bucks and bred to unrelated does. Their offspring are then placed on the limited ration. This process is repeated yearly. This study is scheduled to be completed in 2003. Yearly reports of this study are published in Federal Aid Performance report *W-127-R Job 96: "Genetic/Environmental Interactions in White-tailed Deer"*. See Figure 1 for preliminary antler production trends.

Spike Line Herd

Since 1974, a breeding herd of deer has been maintained separate from other studies. This herd has been selectively bred to produce small antlers. No formal report on these deer has been published. They have been used primarily as demonstration animals to illustrate how selection for poor antlers can influence antler production.

Effects of Early Weaning on Fawn Survival

The E*ffects of Early Weaning on Fawn Survival* study was a two year project with two different fawn crops in which fawns were weaned at 60, 90, and 120 day intervals. Growth rates and other physical measurements were made to measure the effects and were compared to fawns which remained with their mothers. There was no difference in growth patterns between fawns weaned at 60 days and those that were left with their mothers. This data is published in Federal Aid Performance Report *W-109-R Job 42: "White-tailed Deer Growth and Development"*.

Other Related Facts

Age of Doe: Early in the studies, the effect of age of the does and their influence on antler production became a concern. No studies were specifically designed to determine the effect of dam age on antler production. However, in the deer pens, 73% of the spikes born were born from 3 year old or older deer (Figure 2). When age of doe is analyzed by study, only the study where spikes were bred back to their daughters did a large number of young does produce spike offspring. This was to be expected since bucks that were spikes as yearlings were bred to does from spikes (Figure 2A).

Time of Birth: Also early in the studies, the time of birth became a concern. It was felt by some that fawns born in later August or September would be spikes just by virtue of their late birth date (Figure 3). Again, this concern was not specifically addressed in a separate research program. In the deer pens, over 80% of the spikes were born before July 15th. A 3 year, state wide study in Texas indicated that 95% of Texas deer are born before July 15th. Again the only study to produce a significant number of spikes after July 15 was the study in which spike bucks were bred back to their daughters. This was to be expected.

Removal of a Cohort of Deer: A concern of some biologists dealt with the removal of spike antlered deer being removed from a cohort of deer. The concern was that no young deer would remain if all spikes were removed. A study of harvest data in the Edwards Plateau Region of Texas indicates that approximately 60% of the harvest of yearling deer are fork antlered. Removal of spikes and protection of the forked antlered cohort would insure more yearling deer would remain after harvest.

Role of the Doe: The doe carries 50% of the genetic material for antler development. In the deer pens, some does consistently produce small antlered offspring and some consistently produced large antlered offspring. When spike antlered males were bred to "spike antlered" females the off spring were often spikes at 1 and 2 years of age with a few being spikes at 3. When females from forked antlered sires were bred to fork antlered males, the offspring were often large antlered.

Nutritional Spike vs Genetic Spike: There is no such thing. All animals have a genetic potential that is influenced by its environment. Antler development is neither nutritional or genetic. It is a combination of both. A long spike is not a genetic spike. A small spike is not a nutritional spike. Within a given year and on the same range, a small spike has less potential than the long spike. To improve overall antler quality both should be removed, the smaller one first.

Implications of Combined Studies

Management Implications: Implications of combined studies are that a comprehensive management program that addresses *nutritional and genetic* influences in antler development of white-tailed deer is necessary to produce quality antlered deer. When compared to other members of their cohort, deer that have poor antler quality at 1.5 years of age will more than likely have poor quality antlers in later years. As a group six point yearling deer produce larger antlers later in life than spike antlered deer. Management programs should be aimed at removing deer with poor antler potential (spikes and/or 4 points) at an early age (yearling) to insure that better quality deer enter the breeding pool. Herd reduction programs should be aimed at removal of "bottom end males" and older does to insure that those does remaining on the range were produced from better quality bucks. Ranges should be managed to insure that quality habitat is maintained to insure proper nutrition so that all animals can reach their genetic potential. The nutritional-environment study suggests that the best time to select for quality yearlings is during a drought period. Those deer that perform well under stress are the ones desired as brood bucks.

Heritability Estimates: A trait is either heritable or not. If it is heritable, then the question becomes "Is it highly heritable, moderately heritable, or poorly heritable". Data can be analyzed to determine how heritable a particular trait is. Also, if a trait is heritable (greater than 0), then selection can be used to enhance that trait. How quickly you get measurable results depends on how heritable a particular trait is. Different statistical methods are used to analyze the data to make estimates of heritability . Depending upon sample size, statistical method used, and research design, varying heritability estimates can result. Geneticists often argue about statistical methods, research design and sample size. Figure 5 demonstrates the heritability estimates at the 95% confidence limit for the various statistical methods used to analyze the data. These data indicate wide ranges of estimates. There are reasons for that. Each statistical test has its own assumptions and biases. The variance, means and progeny tests were conducted on a designed heritability study and published in the scientific journal *"Heredity"*.

Possible reasons for differences between the

animal model analysis for the Kerr and Mississippi data sets, are (1) the animal model method (AM) used on both the Kerr and Mississippi deer pen data requires a large sample size and (2) it was applied to all deer in all studies used in deer pen research on both the Kerr and Mississippi populations. Data sets for the animal model analysis were a conglomerate of studies unlike the designed Hereitability Study *(ibid.)* conducted at the Kerr Area Deer Pens. Depending on how these various studies were conducted (ie. nutritional status, time of breeding, time of weaning, etc.) would greatly influence the analysis. Neither data set was designed to be used with the animal model (the population was not randomly bred). To overcome this biases, sample sizes must be very large. The sample sizes of the animal model analysis are too small for statistically conclusive data. As stated in the conclusions of analysis of Kerr data using the animal model, Lukefahr *(ibid.)* states, "*the 95% confidence range for antler mass is 0 to .81. Obviously, it is unclear whether these traits are lowly, moderately, or highly heritability in this population.*"

Because data cannot be proven statistically valid by one statistical method does not mean it not a biological fact. When all study results and analysis are viewed as a whole, antler traits appear to be at the minimum heritable and more realistically moderately to highly heritable. In all studies in the Kerr WMA deer pens where antler development characteristics were selected for, the desired results were obtained within a relatively short period of time. Regardless of the variances of statistical methods used to analyze data, we know antler characteristics can be selected for and achieved and that selection is a practical management tool. We've done it.

ANTLER POINT CLASSIFICATION FOR 138 YEARLING BUCKS REARED ON A LIMITED 8 PERCENT PROTEIN RATION
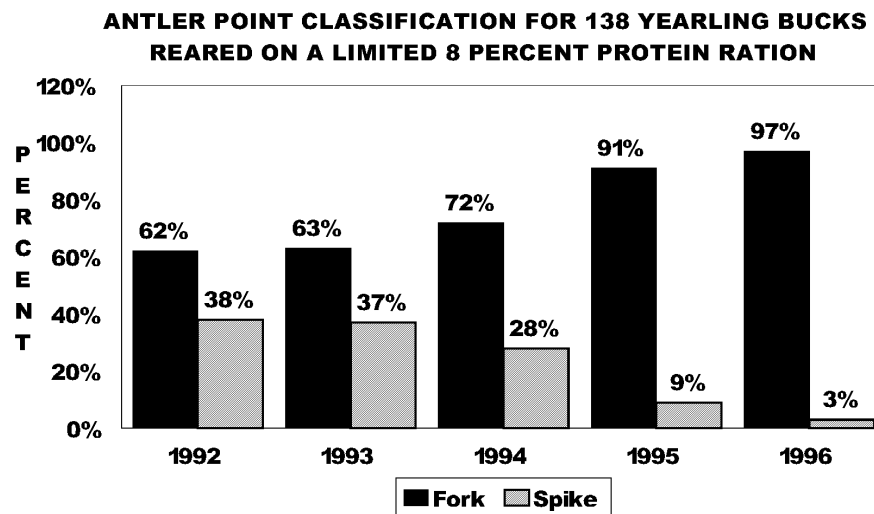
Figure 1. Percent forked antlered deer vs. spike antlered deer in the *Genetics /Environmental Interaction in White-tailed Deer* study over a 5 year period. Note: In 1992, there were only 38% 6 point yearlings with none being 8 points or better. In 1996, 65% had 6 or more points with 50% of those being 8 points or better.

PERCENT SPIKE / FORKED ANTLERS
BASED ON AGE OF DOE
KWMA DEER PENS

73 % of Spikes Born Were From 3+ Does

Study not intended to measure this parameter
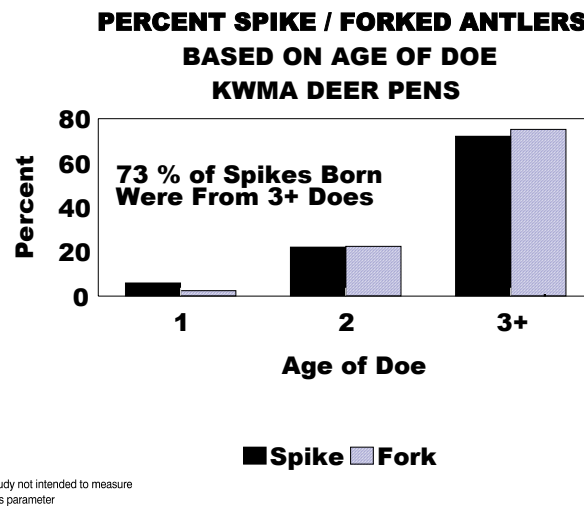
Figure 2. Percent spikes vs. forked antlered yearlings born in Kerr WMA deer pens based on age of doe. Data for this chart is a combining of all data from all studies. There was no formal study to determine effects of age of doe on antler characteristics.

Figure 2A. Percent of spikes produced by doe age class at birth and by study. All sires used in the Heritability, Stress, and New Spike studies were yearling bucks. The Heritability and Stress Study sires were the better fork antlered yearlings based on points and mass. The New Spike Study sires were the lesser mass spike antlered yearlings. The Old Spike Study sires were spikes as yearlings. The Fork Study used a sire that was a forked antlered yearling. All males for all studies were weaned in October. With the exception of the Stress Study, all deer were fed an unlimited 16% protein diet. Stress Study deer were fed a limited 8% protein diet.

PERCENT SPIKE/FORKED ANTLERS
By BIRTH DATE
KWMA Deer Pens

81 % OF ALL SPIKES WERE
BORN BEFORE JULY 15
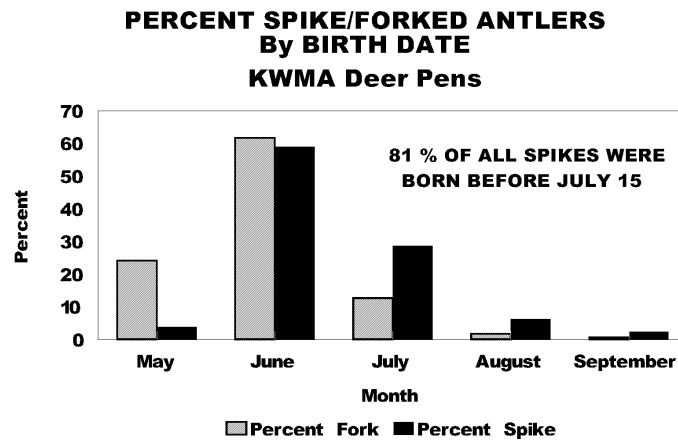
This study not intended
to measure this parameter

Figure 3. Percent of spike vs. fork antlered yearlings born in the Kerr WMA deer pens based on birth date. Data is a combining of all data from all studies. There was no formal study to determine effects of age of doe on antler characteristics.

Percent Spikes in Harvest
Edwards Plateau - Yearlings

Average Forked 58%   Spike 42%

Max Spikes = 70%
Min Spikes = 27%
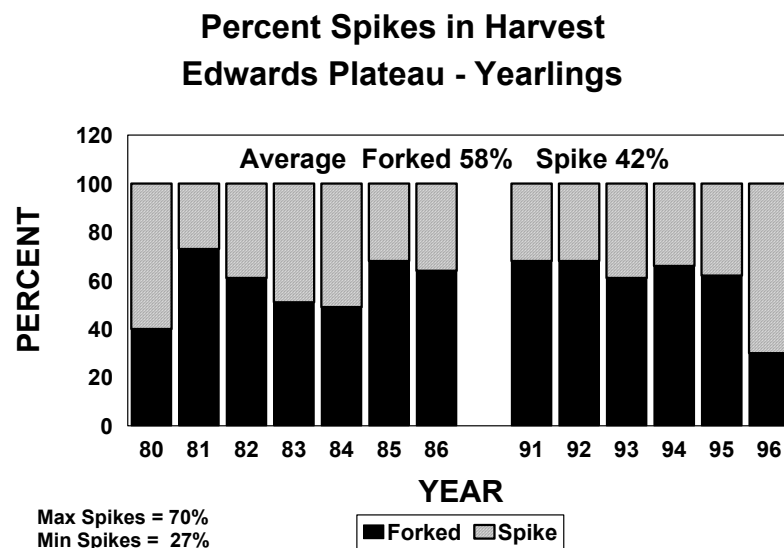
Figure 4. Percent forked vs. spike antlered yearling deer in Edwards Plateau harvest.

Heritability Estimates for
Antler Mass
95% Confidence Limits
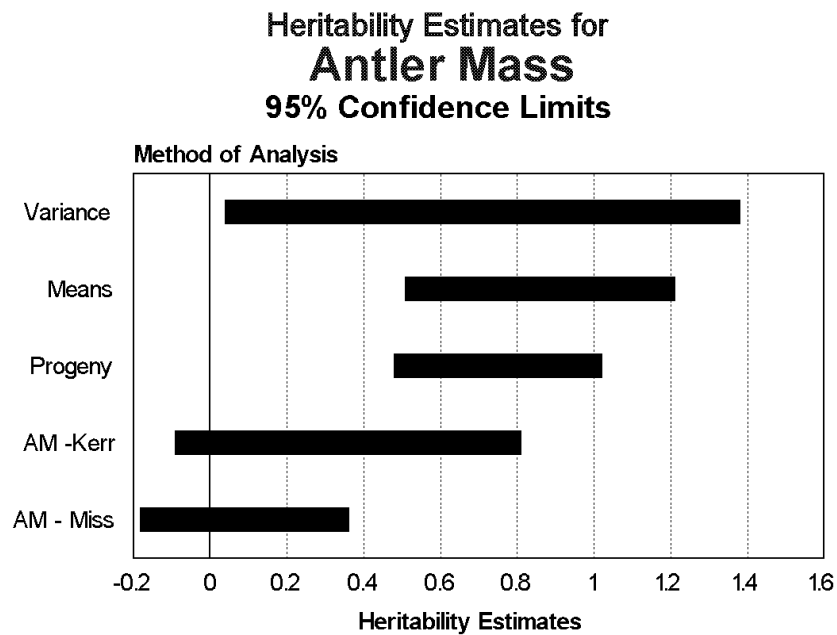
Figure 5. Heritability estimates for antler mass at the 95% confidence limit using various statistical methods. The variance component analysis, family means, all progeny and AM- Kerr (AM = Animal Model) confidence limit bars for each statistical method are for Kerr WMA data set (n=146). The AM - Miss. confidence limit bar is based on Mississippi State data (n=199). The Animal Model method requires much larger sample sizes than were available for either the Kerr or Mississippi State data. Biologically, heritability cannot be lower than 0 or greater than 1. Confidence intervals shown here are statistical values.

CASE STUDY: GENETICS RESEARCH ON CAPTIVE WHITE-TAILED DEER AT MISSISSIPPI STATE UNIVERSITY

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Abstract: Studies on captive deer at Mississippi State University demonstrate heritability of antler traits for yearling bucks are low and that more important than heritability was the significant influence of the dam. Results of these studies argue against the practice of culling spikes for the purpose of genetically improving antler traits. Mature buck antlers do demonstrate moderate heritability for some traits such as antler points and antler mass. Genetic selection based on pedigree information, in particular, can be expected to result in genetic progress. In a translocation study of deer from Mississippi to Michigan and visa versa, we found a genetic basis for timing of the rut, disease resistance and body weights. Photoperiod differences between study areas resulted in a two to three week shift in timing of fawning for deer which were translocated, but genetic differences of five to seven weeks were seen between deer of different geographic origin. Northern deer experienced significantly higher mortality from hemorrhagic disease than did deer of Southern origin. Offspring were intermediate in rut timing and disease resistance to their parents. Body weights of Michigan bucks averaged 23-45 lbs heavier than Mississippi bucks. Crossbred offspring were intermediate in size to their parents. Crossbreds in Michigan had slower growth rates than those in Mississippi, most likely as the result of late birth dates causing more stunting in Michigan due to a more extreme environment than Mississippi. These results demonstrate the importance, yet need for caution, in making genetic management decisions and also the need for caution in genetic introduction. It is clearly evident that more research is needed.

Research with captive deer at Mississippi State University was initiated in 1977 when a group of 12 fawns were captured as newborns from the wild and bottle reared. Offspring from these animals, additional wild caught fawns, and donation of animals from other captive facilities made it possible to increase numbers to a maintenance level of about 100 deer. Between 1977 and 1996 several hundred deer were raised in these facilities and records maintained on the pedigrees of all animals along with measurements on antler traits and records of reproductive events.

Deer genetics research at Mississippi State University has centered on two separate issues. The first study was initiated to examine the practice of selective harvest of male white-tailed deer by managers for the purpose of genetically improving antler qualities of selected deer populations. In this study, the data base for captive deer maintained by Mississippi State University was analyzed to _____

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determine genetic and environmental determinants of antler quality and to derive heritability estimates for antler traits. Results of that study have been published

(Lukefahr and Jacobson 1998). The second study was initiated to examine potential benefits and detriments from translocating deer from one geographic location to another. In this study, we examined genetic versus environmental effects by translocating deer from captive deer facilities of the Michigan Department of Natural Resources at Houghton Lake Michigan to Mississippi State University and vice versa. Our objectives in this later study were to determine relative contribution of genetics and environment for breeding dates, molting, antler events, disease resistance, and body growth.

Methods

From 1977 to 1996, a variety of studies were conducted with deer in the Mississippi State University captive animal facilities. Although most animals used in the genetic data base were not exclusively used for genetics research, the nutritional conditions and general animal husbandry practices were the same, or very similar, for all animals in the study. All animals were fed a pelleted commercial dairy-cattle ration containing >16% crude protein, 2.5% crude fat, 17% crude fiber, 45% nitrogen-free extract, and 65% total digestible

nutrients. Deer were maintained in pens of 0.4-1.4 ha, planted annually in fall to rye grass (*Lolium* spp.) and clover (*Trifolium incarnatum, T. Repens).* Deer densities were not allowed to exceed 20/ha.

To examine variance components of antler traits, we used an animal model procedure (Boldman et al. 1993) to estimate genetic and environmental variances. Antler traits included spikes versus forked (yearling bucks only), number of points, beam length, beam circumference, inside spread, and antler mass. Antler trait records were analyzed from 220 yearling males, 166 2.5 year-old males, and 146 3.5-7.5 year-old males, along with pedigree information from their sires and dams. Although number of antler points were available for all deer, some antler measurements were incomplete with subsequent sample reduction. The minimum number of animals recorded for any trait was 199 for yearling antler mass, 168 for 2.5 year-old antler mass and 138 for 3.5-7.5 year old antler mass. Description of these analysis are provided by Lukefahr and Jacobson (1998). Although a summary of the results of these analyses are provided in the present paper, the reader is referred to the original paper for an in depth treatment of the subject.

In the translocation study, we translocated 6 female and 2 male fawns from Michigan to Mississippi in 1988 and 1 male yearling, 4 female and 2 male fawns in 1989. An additional adult male was translocated from Michigan to Mississippi in 1992. Although original plans were to translocate Mississippi deer to Michigan at the same time as the Michigan translocation, prevalence of hemorrhagic disease titers in Mississippi deer prevented translocation until 1989. Michigan required all deer entering the state to be negative to hemorrhagic disease. In 1989, 1 male yearling and 2 female fawns were translocated from Mississippi to Michigan and in 1990, one yearling and 5 fawn females were translocated. Husbandry practices were similar between the two study sites, with the exception that agricultural plantings of rye grass and clover for supplemental forage were not an option in Michigan.

From 1989 through 1992, translocated males and females of breeding age were crossbred to resident deer in the respective locations. In 1993, translocated males were bred to translocated females at both locations. All resulting offspring were allowed to reach breeding age and their reproductive cycle documented. Fawning dates, velvet shed dates, antler cast dates, and body weights were recorded for all deer.

Results

Heritability of Antler Traits. Heritability of antler traits for yearling bucks tended to be low (range 0.00 to 0.13), except for mean beam circumference (h^2= 0.25) and no trait was significantly different from zero (Fig. 1). Generally more important than heritability was the significant influence of the dam, referred to as maternal effects (Fig. 1). To explain low heritabilities in yearling bucks, potential sources of variation attributable to the dam include: time of birth (early or late in the fawning season), type of birth (single versus twins), milk production, general mothering ability, age and health status of the doe, etc. The maternal effect was even more pronounced when records from bottle reared bucks were deleted and the analysis repeated. This analysis suggested a very important influence of milk production by the dam. In addition, environmental effects of a non-maternal origin accounted for most of the variation (54-79% of the total variation) in antler characteristics. This type of environmental effect could include, for example, the deer's own grazing ability, diet quality following weaning, health status, and social status or other behavioral aspects.

Heritability of antler traits for 2.5 year old bucks were low to moderate (0.08 to 0.39) and also were not significantly different from zero. Increasing values are best explained by the diminishing general maternal influence as young bucks further approached maturity. Environmental effects of a non-maternal origin still accounted for most of the variation range (43-81% of the total variation) in the same antler characteristics.

Heritability estimates for mature bucks (>3 years-old) were low to moderate (range 0.03-0.43). Only the estimate for antler weight (h^2= 0.43) is considered highly heritable. Maternal effects were not important for any "mature" antler traits studied. There tended to be an inverse relationship between genetic versus permanent environmental effects, whereas temporary environmental effects had a narrower (0.25-0.52) range than the latter (0.09-0.57). Permanent environmental effects could reflect positive (e.g., abundant nutrition or acquired immunity) and (or) negative (e.g., a physical injury or disease affliction) circumstances occurring early in the animal's life that have a lasting influence on the trait of interest.

Translocation Study

Mortality Associated with Genetic Background. Of 6 male and 10 female Michigan deer originally transported to Mississippi State University research facility, only 3 females survived to the end of the study. Six of the Michigan deer died as fawns from

suspected cases of hemorrhagic disease, four adult deer died at 2-3 years of age from pneumonia and 3 died from documented hemorrhagic disease.

The Mississippi deer fared better in their adaptation to life in the North than did Northern deer to life in the South. Although 3 Mississippi female fawns died from incidental injuries soon after their transfer to Michigan, all remaining females survived for the duration of the study. The 1 buck sent to Michigan survived until the last year of the study, but did die while being treated for a bacterial infection in 1995.

During the final year of the study, in the summer of 1995, a hemorrhagic disease outbreak occurred in the Mississippi State captive deer facilities. At that time, there were a number of Texas and Mississippi crossbreds, as well as some Wisconsin bloodline crosses in the pens, in addition to the purebred Michigan and Mississippi deer and their crossbred offspring,. When deer were partitioned out on the basis of mortality to hemorrhagic disease and their genetic background as to percentage of northern or southern bloodlines (Fig. 2), a highly significant effect due to genetic background and susceptibility to hemorrhagic disease was documented (Jacobson 1996).

Body Size. The most obvious difference that can be seen in the 2 breeds of deer is in their body size. On average, the Mississippi deer are considerably smaller in stature than their Northern counterparts. Within the same age classes, Michigan bucks outweighed Mississippi bucks by an average of 23 to 45 lbs. (Table 1). Similar differences were noted for does, although does were not weighed in all years of the study and subsequently sample sizes too small for meaningful comparisons to be presented. There was an obvious difference between the crossbred offspring in the two geographic locations. Crossbreds in Michigan were 30-50 lbs. lighter than the same crosses in Mississippi (Table 1). The obvious explanation is that later births, of Mississippi crosses than purebred Michigan deer, resulted in severe stunting in Michigan due to a more extreme environment than their counterparts in Mississippi.

Reproductive Events. Although body size differences are dramatic, other less obvious differences, may ultimately prove to be more significant to the biology of the white-tailed deer. One surprise finding of our study was that the Mississippi buck in Michigan was not able to breed Michigan does at their normal breeding time. As evidenced by the fact that the Mississippi buck, in Michigan, was still in velvet antler when Michigan does were in their normal first estrous cycle (see information presented below on antler velvet

shedding). We postulate the buck was physiologically incapable of a fertile mating until does reached their second cycle. The result was Michigan does he bred had fawns one month later than normal (Table 2).

With the exception of those Michigan does bred the Mississippi buck in Michigan, fawning dates of Michigan does have averaged almost 5-8 weeks earlier, in both study locations, than Mississippi does (Table 2). However, both Mississippi and Michigan does had fawns an average of 2 weeks earlier when in Michigan than in Mississippi.

The relationships between gonadal trophic hormones and antler events in male deer are well known. Antler velvet shedding signals the ability of a buck to produce viable sperm and the casting of antlers marks the end of his annual breeding cycle (Jacobson 1994). That the rut can be genetically controlled in male white-tailed deer was seen when we examined the timing of antler events. Hardening of the antlers and shedding of antler velvet has averaged 3 to 4 weeks latter for Mississippi deer than Michigan deer, whether in Mississippi or in Michigan (Fig. 3). Crossbred offspring were intermediate to the two parent breeds. Similarly, the casting of antlers averaged more than 6 weeks later for Mississippi deer than Michigan deer and crossbred offspring were again intermediate to the parent breeds (Fig. 4).

Discussion

It has been reported that yearling antler traits are highly heritable (Williams et al. 1994). This has led to suggestion that culling of yearling bucks can upgrade genetic quality of a deer herd. However, our results also demonstrated no differences between offspring of spike antlered yearlings and multi-pointed yearling bucks (Fig. 2). Additionally, when the data presented by Williams et al. (1994) were reanalyzed by Lukefahr (1997), the results demonstrated even lower values for heritability estimates than did the Mississippi State study (Table 3). The higher heritabilities reported by Williams et al. (1994) reflect highly significant variation due to birth year and Julian birth date (age), factors which were not accounted for in their analyses.

An example of the lack of relationship between yearling antler traits of sires and mature antler traits of their sons can be seen in Figure 5. It should be noted that distribution of antler points for mature bucks has no predictability based on the sire's yearling antler traits. In addition, there appears to be a poor relationship between yearling antler traits and

estimated breeding value (genetic transmitting ability) at maturity (Fig. 6).

On the basis of our results, we can not recommend the practice of culling yearling bucks to improve genetics. Our results do, however, indicate genetic selection of bucks based on mature antler traits can be used to change antler traits of white-tailed deer. Pedigree information and an animal model procedure was used to estimate breeding values for all bucks and does in this population. An example demonstrating predicted breeding values for total antler points of three different bucks from the Mississippi State captive facilities is shown in Table 4. On the basis of pedigree, the buck 8839 would be expected to produce offspring with more antler points. Additionally, when breeding values for all traits expressed at maturity were examined, this buck (8839 Whitehouse) had superior breeding values for all traits except spread. However, his breeding value for body weight was close to the population average, whereas buck 8347 (Kenny) had below average breeding values for all antler traits, but above average breeding value for body weight (Table 5).

For many years it has been known that daylight regulates the timing of reproductive events of deer. Findings from the translocation study suggest that the photoperiod differences between the 2 locations caused these normal seasonal events of reproduction and molting to occur 3 weeks earlier or latter, depending on the geographic location. However, what is surprising about our results is that reproduction appears not only to be governed by photoperiod signals, but also by a genetic clock which caused the 2 races of deer to respond at different times to the same photoperiod signals. Thus, regardless of geographic location, Mississippi deer fawned 5 to 8 weeks later than Michigan deer in the same location and the crossbred offspring had fawning dates intermediate to the parents, confirming a genetic basis for breeding timing of does. Similarly, antler events and rut timing for males was 3 to 6 weeks different for bucks between

breeds with crossbred offspring again intermediate to parent breeds.

In addition to physiologic differences related to breeding season timing, our results also demonstrated a genetic basis for disease resistance of Northern breeds and Southern deer. In particular, susceptibility to hemorrhagic disease was linked to genetic background, and like reproductive events, crossbred offspring were intermediate in resistance to this disease.

Management Implications

The results of our studies demonstrate the need to understand genetic influences on wildlife populations. Our efforts at managing deer affect not only the population structure and habitat of these animals, but also we can influence traits of these animals through our management actions that ultimately affects the survival of this animal and its ecological interactions with other animals and plants. Hardly a state has not had introduced deer from other geographic locations (Marchinton et al. 1995). More recently, the quest for big antlers and the economic values of trophy deer has created a stimulus for translocation of animals with superior antler qualities.

Our results suggest that genetic progress can be made through selection for specific antler traits. However, we also know that white-tailed deer populations have evolved with dramatically different selection pressures across their geographic range. We have now demonstrated reproduction, disease resistance, body growth and other traits are also genetically controlled. Thus, before we advocate or engage in management for or against specific genetic traits, we should at least evaluate what other traits we may be selecting for or against in our management process. It is clearly evident that more research is needed.

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Table 1. Body weights of male deer, by genetic origin, in Michigan Department of Natural Resources captive deer facilities, Houghton Lake, Michigan, and in Mississippi State University captive deer facilities, Mississippi State, Mississippi, 1990-1995.

Location/genetic origin (Sire/dam)	Number	Mean (lbs.)	Range	SE
Yearling males				
In Michigan				
MI/MI	14	147.6	120-177	4.83
MS/MS	1	113.0	-	-
MI/MS	8	97.3	77-114	4.59
MS/MI	10	117.6	70-149	9.73
In Mississippi				
MI/MI	3	139.5	112-172	21.31
MS/MS	8	114.9	97-133	5.78
MI/MS	13	137.8	112-171	4.97
MS/MI	2	133.0	129-137	5.66
2.5 Year-old males				
In Michigan				
MI/MI	13	186.3	152-219	5.62
MS/MS	1	149.0	-	-
MI/MS	5	125.2	91-152	12.07
MS/MI	10	147.5	89-182	9.07
In Mississippi				
MI/MI	3	197.7	167-212	19.42
MS/MS	7	159.0	134-201	10.08
MI/MS	12	189.2	122-218	7.84
MS/MI	2	190.0	188-192	2.83
3.5 Year-old males				
In Michigan				
MI/MI	11	193.3	152-220	9.05
MS/MS	1	170.0	-	-
MI/MS	2	175.0	170-180	7.07
MS/MI	3	156.3	146-167	7.42
In Mississippi				
MI/MI	2	234.0	230-238	5.66
MS/MS	7	189.3	150-244	12.44
MI/MS	7	226.3	195-260	10.27
MS/MI	2	210.0	202-218	11.31

Table 2. Fawning dates of deer in Michigan and Mississippi based on genetic origin, 1990-1995.

Location/genetic origin (Sire/dam)	Number	Mean	Range	SE
Michigan				
Michigan/Michigan	39	142.2 (May 22)	115-173	2.16
Mississippi/Mississippi	7	205.9 (Jul 26)	160-224	8.90
Michigan/Mississippi	14	199.5 (Jul 19)	166-238	6.27
Mississippi/Michigan	13	183.3 (Jul 2)	158-244	8.57
Crosses	19	181.3 (Jun 30)	145-211	4.27
Mississippi				
Michigan/Michigan	5	154.4 (Jun 3)	144-165	4.48
Mississippi/Mississippi	154	217.8 (Aug 6)	175-275	1.71
Michigan/Mississippi	16	209.6 (Jul 29)	180-259	5.96
Mississippi/Michigan	21	160.5 (Jun 10)	140-234	4.48
Crosses	28	183.8 (Jul 3)	164-220	2.71

Table 3. Literature comparison of heritability estimates for yearling antler traits of captive, male white-tailed deer.

Trait	Report[1]		
	Lukefahr and Jacobson (1998)	Williams et al. (1994)	Lukefahr (1997)
Antler points	0.05	0.22	0.00
Antler spread (mm)	0.00	0.03	0.00
Antler mass (g)	0.09	0.71	0.00
Beam circumference (mm)	0.25	0.80	0.00
Beam length (mm)	0.00	0.49	0.05

[1]The study by Lukefahr and Jacobson (1998) involved Mississippi State University data, whereas studies by Williams et al. (1994) and Lukefahr (1997) involved Kerr Wildlife Management Area data.

Table 4. Potential application of genetic evaluation of white-tailed deer based on pedigree data and animal model procedures.[a]

| | Buck | Maternal | | |
		Sire	Dam	Grandsire
Buck Number 8839				
Average Antler Points[b]	19.0	13.6		12.5
(number of records)	(4)	(5)		(2)
Estimated Breeding Value[c]	+6.2	+3.7	+3.8	+2.7
(Accuracy of breeding value[d])	(0.78)	(0.82)	(0.60)	(0.72)
Buck Number 8947				
Average Antler Points	16.5	14.7		14.5
(number of records)	(2)	(3)		(4)
Estimated Breeding Value	+4.6	+3.4	+2.6	+4.0
(Accuracy of breeding value)	(0.71)	(0.80)	(0.58)	(0.81)
Buck Number 8437				
Average Antler Points	6.3	7.5		8.0
(number of records)	(4)	(4)		(5)
Estimated Breeding Value	-2.5	-2.3	-1.3	-1.1
(Accuracy of breeding value)	(0.81)	(0.82)	(0.61)	(0.55)

[a] The pedigree analysis provided inbreeding coefficients of 0.063, 0.000, and 0.125 for bucks #8839, #8447, and #8437.
[b] Phenotype as average of mature (3.5 - 7.5 years of age) records for antler points.
[c] Estimated breeding value for antler points.
[d] Range of values from 0 to 1, which implies low to high accuracy, respectively.

Table 5. White-tail deer genetic evaluation for antler traits and body weight based on mature records from 3.5 to 7.5 years.

WHITEHOUSE (#8839)

- Excellent in AP, AM, BC, and BL   Sire: Orin
  (Ranks in top 1% for AP and AM)   MGS: Montana
- Average for mature body weight
- Poor in SPR
- Average mature gross B&C score of 195

Trait[a]	AP	SPR	AM	BC	BL	BW
BV[b]	+6.2	-.23	+1.83	+.78	+.53	+2
ACC[b]	.78	.24	.72	.67	.49	.82

JETHRO (#8947)

- Excellent in AP and BC   Sire: Tough Stuff
- Heavy mature body weight   MGS: BC
  (Ranks in top 5%)
- Poor in SPR and BL
- Average mature gross B&C score of 160

Trait	AP	SPR	AM	BC	BL	BW
BV	+4.6	-.11	+.57	+.64	-.32	+31
ACC	.71	.22	.68	.61	.45	.76

KENNY (#8437)

- Poor in all antler traits   Sire: Arthur
- Above average for mature body weight   MGS: Donnie
  (Ranks in top 15%)
- Average mature gross B&C score of 88

Trait	AP	SPR	AM	BC	BL	BW
BV	-2.5	-.08	-.68	-.05	-.86	+20
ACC	.81	.29	.76	.70	.54	.84

_____

[a] Traits: AP = total antler points; SPR = inside antler spread (inches); AM = total antler mass (pounds); BC = beam circumference (inches); BL = beam length (inches); BW = body weight (pounds).

[b] Codes: BV = estimated breeding value; ACC = accuracy of BV (range of values from 0 to 1, which implies low to high accuracy, respectively).
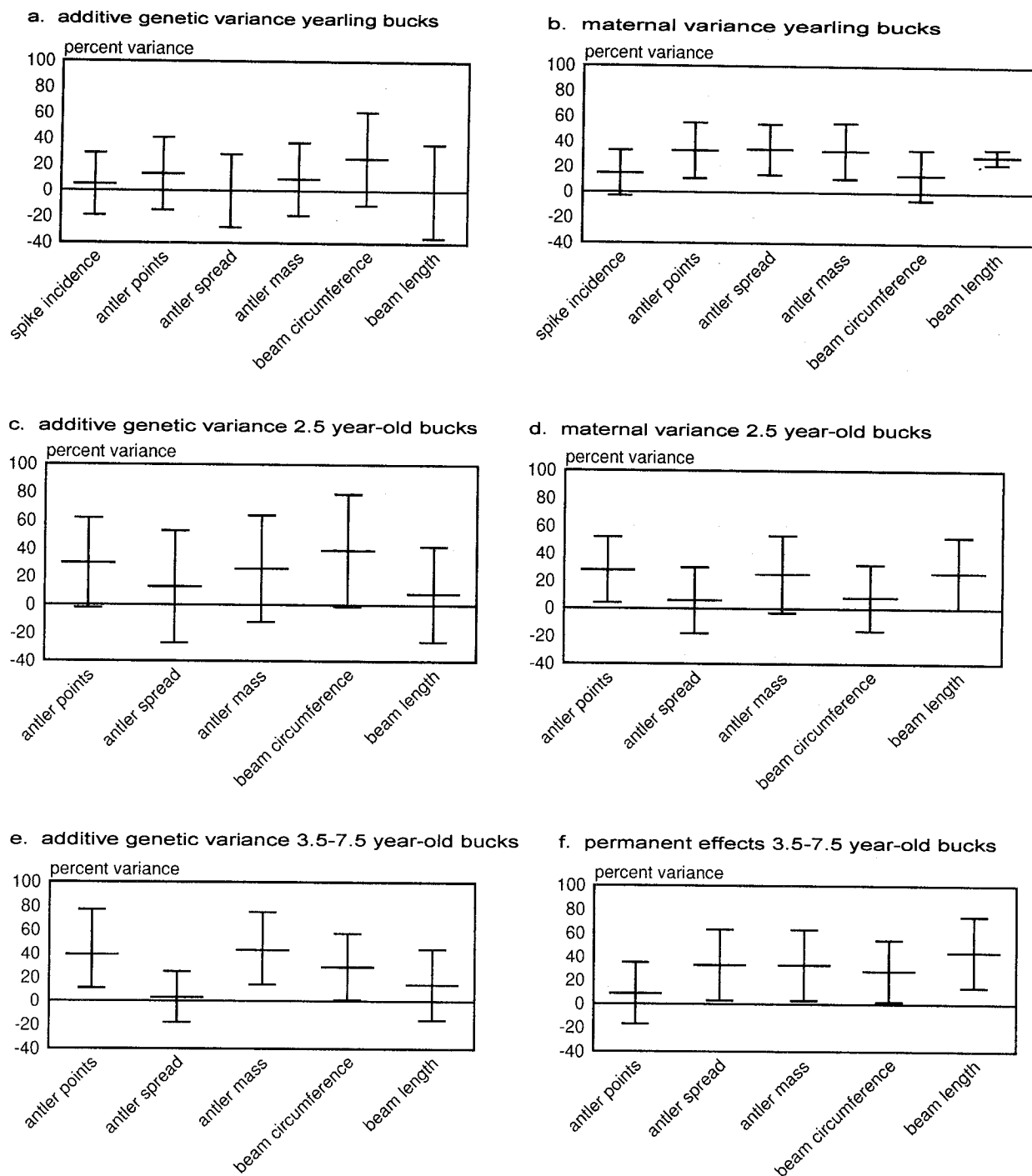
Figure 1. Variance components for antler traits (+- 2 S.E.) of captive white-tailed deer in Mississippi. (a.) Variance of yearling buck antler traits attributed to additive genetic effects of male. (b.) Variance of yearling antler traits attributed to maternal (genetic and permanent environmental) effects. (c.) Variance of 2. 5 year-old antler traits attributed to additive genetic effects of male. (d.) Variance of 2.5 year-old antler traits attributed to maternal effects. (e.) Variance of 3.5-7.5 year-old antler traits attributed to additive genetic effects of male. (f.) Variance of 3.5-7.5 year-old antler traits attributed to permanent (nonadditive genetic and permanent environmental effects) of the male.

ALIVE☐	6	25	24	21
DEAD☐	11	19	5	3
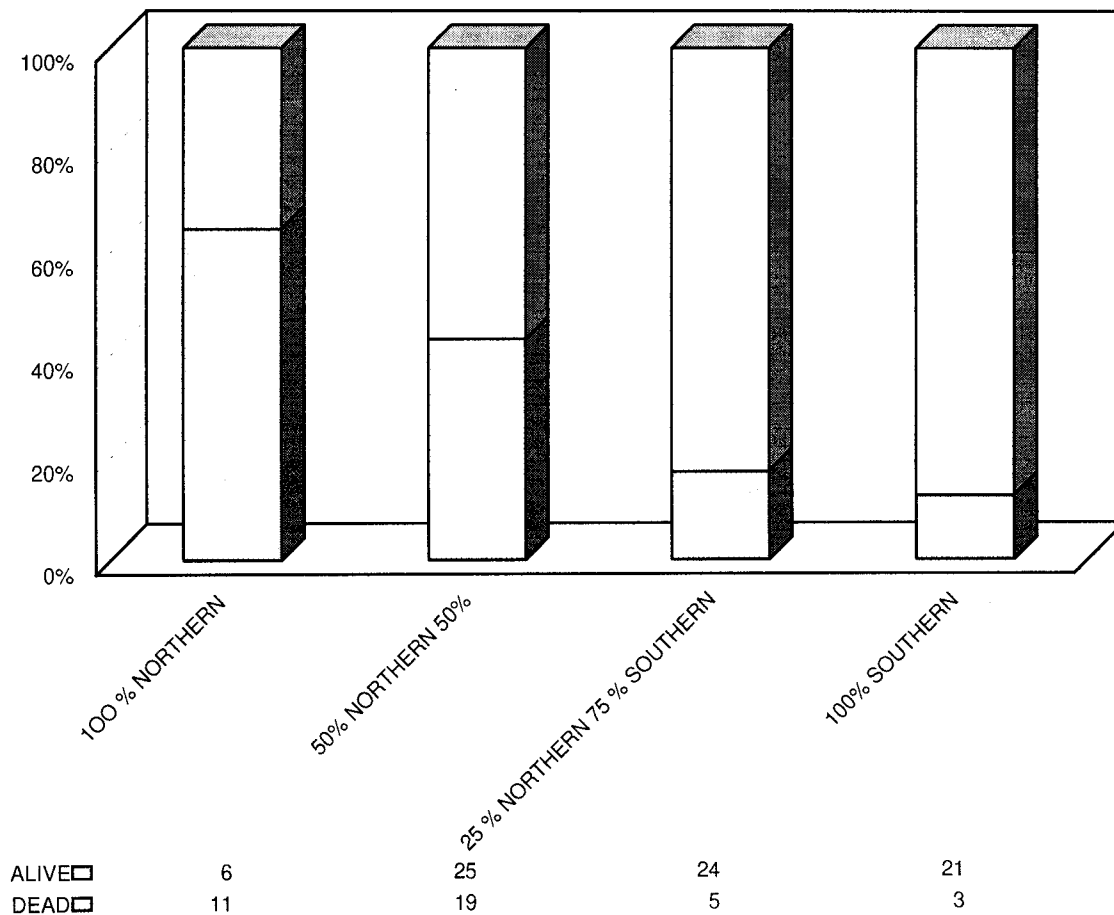
All but 6 deer were born in Mississippi and had the same history of prior exposure. Five of the 6 exceptions were born in Michigan but transported to Mississippi as fawns and were at least 5 years-old at the time of the outbreak. The remaining exception was a 9 year-old male that had been in Mississippi one year.

Figure 2. Loss of captive deer on the basis of genetic background during the summer of 1995 due to hemorrhagic disease in facilities at Mississippi State University.
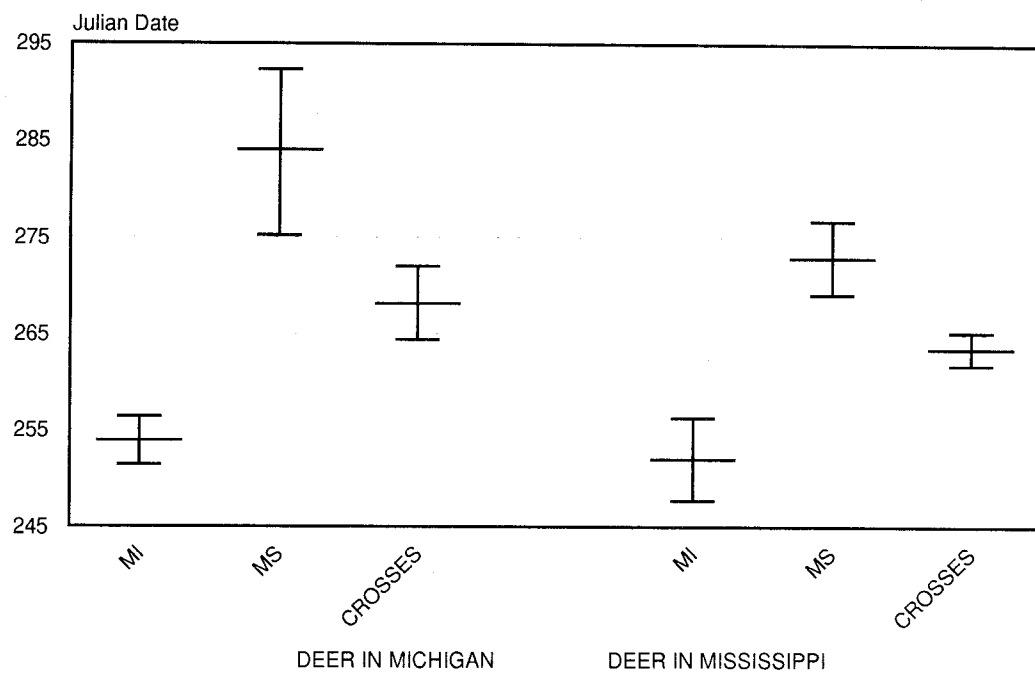
Figure 3. Mean velvet shedding dates (+- 2 S.E.) of bucks in Michigan and in Mississippi by genetic origin, 1990-1995.
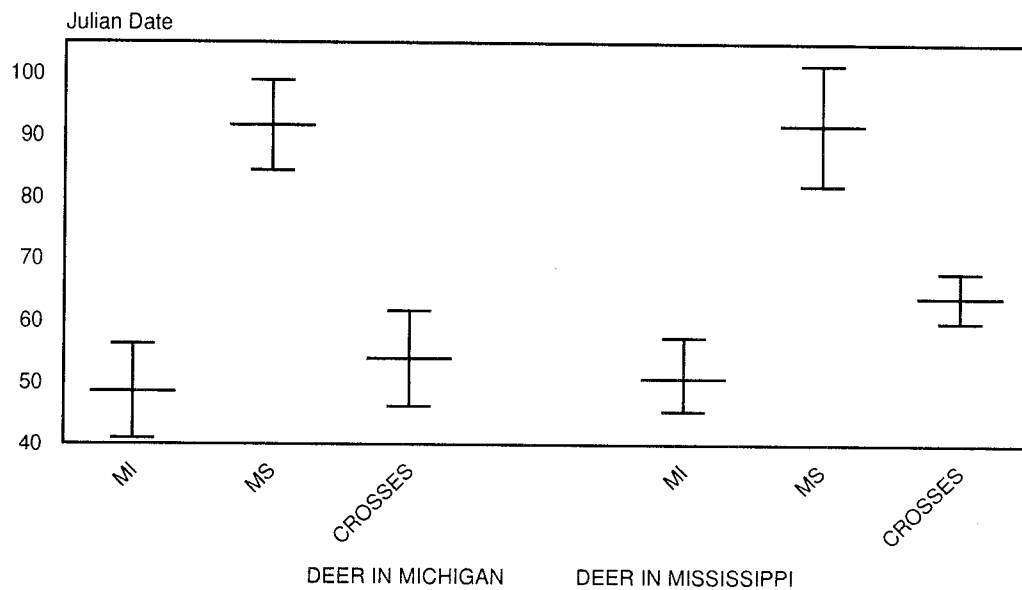
Figure 4. Mean antler casting dates (+- 2 S.E.) of white-tailed deer in Mississippi and Michigan by genetic origin.
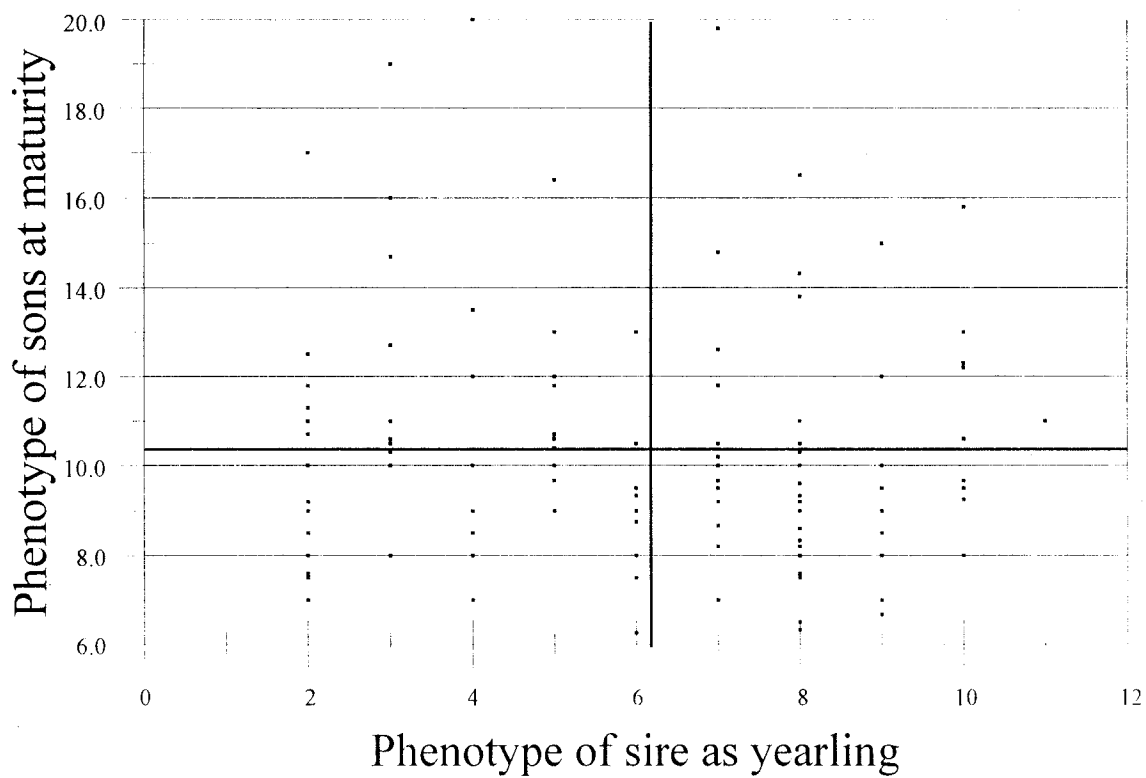
Figure 5. Distribution of phenotypes for total antler points.
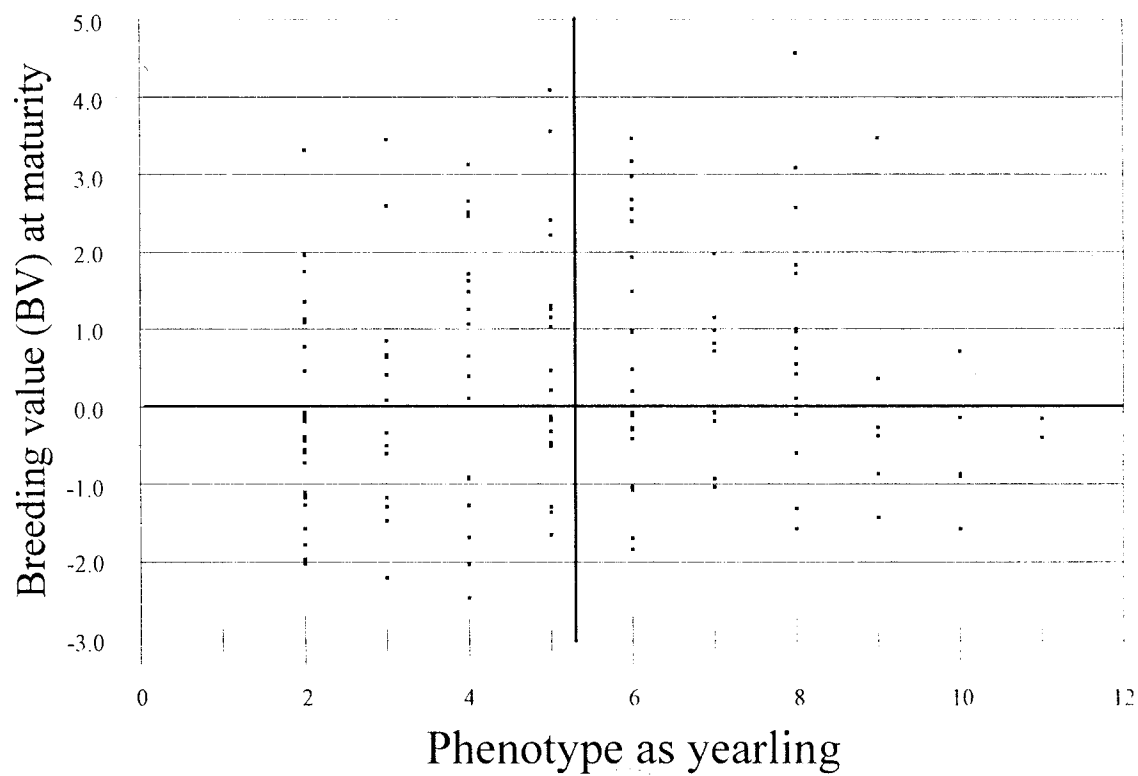
Figure 6. Distribution of BV by phenotypic class for total antler points.

CASE STUDY: THE FAITH RANCH HERD

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Abstract: The advisability of culling segments of male white-tailed deer populations has been debated in recent years. Two major studies of penned deer, one in Texas and the other in Mississippi, have provided a considerable amount of information. However, studies of issues related to culling of free-ranging deer have been lacking. From 1985-1997, 631 bucks were captured on the Faith Ranch, Dimmit County, Texas, and antler measurements recorded. Many (23%) of these bucks were recaptured or harvested, providing repeated antler measurements. Repeatability analysis and correlation analysis were used to determine if antler characteristics at 1.5 years of age predicted antler size or characteristics at 4.5 years or older. Antler points were the least repeatable measure, suggesting points were a relatively poor culling criterion. There was a poor correlation between antler size at 1.5 years and later. However, sample size was small. Managers are encouraged to study available data and make their own culling decisions, recognizing there is a risk that the option selected may prove to be undesirable.

Genetic management of white-tailed deer populations has been an interest of biologists and land managers for over 20 years. Two long-term studies of penned deer, one in Texas (Williams et al. 1994) and the other in Mississippi (Lukefahr and Jacobson 1998) have contributed to considerable interest, debate, and confusion. In particular, there have been differing interpretations of the findings of these studies relative to the advisability of culling spike yearling (1.5 year old) deer. Given that we accept the validity of these two studies, and we should, why is there so much confusion? One answer, in my judgement, is that the topic is much more complex than first thought. It seemed so straight-forward in the beginning that we could cull spike yearlings and expect phenotypic and genetic improvement in deer populations. However, I argue that this is not a straight-forward, but rather a complex, topic. This means that no one study is going to provide "the answer." This has been part of our problem, i.e.,different factions claiming that they have the answer. In reality, we have had 2 useful studies that provide insight into culling yearlings and other genetic management practices. However, it will be some time in the future, and several more studies, before the mystery is completely solved.

One major drawback is that neither the conclusions of the Texas studies, nor the Mississippi work, have been field-tested under natural conditions. Both penned studies provided considerable control over the environment of the study deer, for example, constant nutrition. It appears that the Texas studies provided more constant conditions versus the Mississippi work. It would seem reasonable that free-ranging deer would be subject to much more environmental variation than occurred in either study, and that resulting phenotypic antler expression could largely mask genetic factors. Young deer could be particularly vulnerable to environment because they have not gained physical maturity.

On the Faith Ranch, Dimmit County, Texas, we have been capturing about 50 or more bucks at random per year for 13 years (1985-1997). All bucks have been individually marked with ear-tags and ear-tatoos, and immediately released. Many bucks have been recaptured one or more times, providing insight in a free-ranging population to some of the issues raised in the penned studies. The objective of this paper is to report results of this ongoing study relative to antler development at maturity of yearling bucks with 2-7 points, as well as other issues bearing on genetic management of white-tailed deer.

Study Area

The 44,000-acre Faith Ranch is located mostly in Dimmit County, Texas, with a small portion in Webb County. It is located about 25 miles southwest of Carrizo Springs, Texas and borders the Rio Grande River. The habitat consists of mixed brush communities dominated by mesquite, blackbrush, guajillo, guayacan, kidneywood, lotebush, and prickly

pear. Dominant grasses include tanglehead, Arizonia cottontop, plains bristlegrass, green sprangletop, and lovegrass tridens. Common forbs include orange zexmenia, bushsunflower, menodora, dayflower, and dalea.

Unadjusted, complete coverage helicopter surveys of deer on the ranch have generally varied in the range of one deer per 30-70 acres. Such surveys usually count about one-third of the deer (DeYoung 1985). Deer on the Faith Ranch have generally been very lightly harvested during the study period. However, about one-fifth of the ranch was subjected to a harvest of 40% of the raw helicopter counts during 1986, 1987, and 1988. Generally, a small number of mature bucks have been harvested each year, and no does. Young bucks have not been culled during the study period. In recent years, a small number of mature bucks with poor antlers have been taken.

In 1995, several food plots were installed on a portion of the ranch and planted to warm-season and cool season forages. The ranch is not enclosed by high fence. However, in 1995, high fence was erected along part of the south boundary. In 1996, about 3,000 acres were high-fenced and pelleted supplemental feed offered to deer. We have not captured in the supplemental feed area since it was fenced off and feeding begun. In recent years, cattle grazing has been light to moderate. The ranch has consistently produced large, trophy bucks, including several in the Boone and Crockett records.

Methods

Bucks were captured annually during 1985-1997 by drive net or net gun (DeYoung 1988) in September, October, or November. Helicopter pilots were carefully instructed to catch the first buck encountered, regardless of size. Leon et al. (1987) reported that these capture techniques can result in a sample containing a reasonable cross-section of the animals present. At capture, each buck was aged by the replacement and wear technique (DeYoung 1989), and antler and other measurements recorded. For several years a small incisor tooth was extracted and an age also obtained by the cementum annuli method (DeYoung 1989). All bucks were individually marked with colored and numbered cattle ear tags and an ear tatoo. Several hundred were also fitted with a radio transmitter collar for use in various studies. Standard Boone and Crockett antler measurements were taken in inches as per Nesbitt and Wright (1981), except that only the basal circumference measurement was taken. The remaining 3 circumference measurements on each

antler were not made in order to release the deer faster and thus reduce stress. Also, in 1985, point length measurements were not taken. After measurements were completed, bucks were released at the capture site. Sullivan et al. (1991) reported that the capture-related mortality rate using these procedures was 1.1%.

Many marked bucks were recaptured over the years. Also included in the data set were 51 marked bucks killed by hunters. These were treated in the same way as recaptures. Using antler and age data from all deer (recaptured and not recaptured), repeatability (Falconer 1981:126) was calculated. Repeatability is additive genetic plus permanent (or fixed) environmental effects. An example of a permanent environmental effect would be a severe infection of the pedicile of a buck causing permanent damage that affected all subsequent antler growth from that pedicile. This is as opposed to a temporary environmental effect, such as a drought year, which affects antler growth that year, but not in future years. In the absence of pedigree information, repeatability is useful in that it sets the upper limit for heritability (additive genetic influence of a trait). As stated in Hohenboken (1985), repeatability provides an answer to 2 important questions:

(1) "*What portion of the total differences among individuals are attributable to '...(permanent)...' effects*?"; and,

(2) "*What proportion of an individual's superiority or inferiority (based upon a single measurement of a trait) is expected to be expressed in future measurements as well*?".

Repeatability is used as the basis for culling management decisions in livestock, and may also be useful in deer management. Repeatability was computed using the software of Blouin and Saxton (1990). I compared repeatability estimates for antler traits from the Faith Ranch to repeatability estimates from the Mississippi study [calculated by summing values for additive genetic (heritability) and permanent environmental effects in Table 3 of Lukefahr and Jacobson (1998)]. Comparisons were made for antler points over 1 inch, inside spread, basal circumference, and beam length. Groups compared were bucks 3.5 - 7.5 years old for the Mississippi data and 3.5 - 12.5 years old for the Faith Ranch. It was not possible to make similar comparisons with data from the Texas study (Williams et al. 1994) because only yearling bucks were involved.

Correlation analysis was used to assess relationships in recaptured bucks between antler size in

years 1.5 versus 4.5 or older, 2.5 versus 4.5 and older, and 3.5 versus 4.5 and older. An antler index was used for these comparisons, as follows:

Index = inside spread + left and right beam length + left and right basal circumference + total point length.

This index was highly correlated with gross typical Boone and Crockett score ($r = 0.99$). If an individual was captured more than once after reaching 4.5 years, the "mature" age indices were averaged.

For recaptured deer, there were sometimes discrepancies between the known interval between captures and the interval resulting from estimated ages using the replacement and wear technique (DeYoung 1989). In such cases, ages were adjusted to the known interval by one of the following rules:

1. one age was 1.5 years and this was considered a known age;

2. cementum annuli age was available and resolved discrepancy;

3. age for third or fourth capture was adjusted to conform with two or three previous captures;

4. adjustment made recognizing bias in technique toward over-aging young deer (DeYoung 1989);

5. adjustment made recognizing bias in technique toward under-aging older deer (DeYoung 1989);

6. and, in a few cases where none of the above helped, the discrepancy was resolved by coin flip.

Results

There were 760 buck captures and 51 harvested marked deer over the study, which involved 631 different bucks (Table 1). Yearling (1.5 year old) deer appeared to be under-represented in the sample, because over a period of years, this should have been the largest age class if deer were caught at random, as reported by Leon et al (1987). I speculate that yearlings were encountered by the helicopter at random, but were under-represented because helicopter pilots at times did not see their small antlers and therefore thought they were females. DeYoung (1989) reported that the replacement and wear aging technique tended to result in over-aging of young deer and under-aging of old deer. This bias tends to "pile up" deer in the middle age classes, and this is apparent in Table 1,

with the 5.5 age class being among the largest. The abrupt drop in deer after age 8.5 is partly due to many old bucks being aged at "8.5+". The ages after 8.5 were generally assigned when the buck was captured at a young age, and then caught or shot years later, providing more confidence in the old age. For example, buck #115 was caught in 1987 and aged as 2.5 years. He was caught again in 1997, 10 years later, making him 12.5 years, if the first age was correct.

Antler measurement means for the data set are shown in Table 2. DeYoung (1990) reported that antler size of Faith Ranch deer did not differ appreciably from antler measurements on the Zachry Randado Ranch in Jim Hogg County, Texas. Antler measurements of Faith Ranch deer also did not differ much from deer on Crab Orchard National Wildlife Refuge in Illinois or the George Reserve in Michigan. Antler measurements of Faith Ranch deer generally tended to increase with age until 5.5 years, and then level off. It was not unusual for some bucks to attain impressive antler growth up to 10 years or more of age.

For simplicity, recaptured deer and harvested marked deer will cumulatively be termed "recaptures". For recaptures, 146 bucks (23%) were caught more than once (Table 3). Of these 146 bucks, 118 had 2 records, 22 had 3 records, and 6 had 4 records, resulting in 326 total records from bucks with repeated measurements.

Repeatability for various antler measurements and combinations of the data (models) are shown in Table 4. For all combinations of data, number of antler points had the lowest repeatability. This suggests that number of points on a buck is the least reliable criterion on which to base a culling program. Alternatively, antler spread was consistently the most repeatable antler measurement. This is interesting given that both Williams et al. (1994) and Lukefahr and Jacobson (1998) reported spread to have low heritability relative to other antler traits. Apparently, spread is largely determined by environmental factors that are fixed early in life.

Among yearling bucks in the entire data set, 35% had 2 points (spikes), 9% had 3, 24% had 4, 9% had 5, 8% had 6, 6% had 7, and 3% had 8 points. Removing the spike yearling antler measurements only tended to increase repeatability (model 1 versus model 2, Table 4). However, when all antler measurements (yearling and subsequent years) of spike yearlings were removed, repeatability changed little (model 2 versus model 3, Table 4). This suggests that the antler records in subsequent years from spike yearlings differed little from antler measurements in subsequent years from

forked yearlings. The main effect on repeatability was from the yearling spike records. Repeatability generally kept increasing as the data set was restricted to older and older animals (models 4-7, Table 4). This suggested that the reliability of culling decisions would become greater in older age classes.

Repeatability was similar between bucks 3.5 - 7.5 years from the Mississippi study (Lukefahr and Jacobson 1998) and bucks 3.5 - 12.5 years from the Faith Ranch (model 5 versus model (MS), Table 4). However, because of the dual nature of repeatability (i.e., genetic and environmental parts), it cannot be concluded that heritability was similar.

Twelve bucks provided antler measurements at 1.5 years and then again at 4.5 years or older (Table 5). Five of these bucks were recaptured twice. There was a good distribution of antler points as a yearling, ranging from 2-7 points. Figure 1 shows a scatter plot of antler size at 1.5 years versus the older age. The correlation was poor for this relationship ($r = 0.46$, $P < 0.13$). The yearling antler index accounted for only 22% of the variation in antler index at older age. The relationship for a sample of 22 bucks was better between the antler index at 2.5 years versus 4.5 years and older ($r = 0.62$, $P < 0.002$). The relationship for a sample of 36 bucks with an antler index at 3.5 years versus 4.5 years or older was not stronger ($r = 0.47$, $P < 0.003$). Aging inaccuracy undoubtedly adds increasingly to variation in the data (DeYoung 1989) as the independent variable becomes an older age. That is, when comparing 3.5 year olds, it is likely that some were actually 2.5 or 4.5 years of age. I assumed that all yearling ages were accurate, thus the relationship in Fig. 1 should not be influenced by aging inaccuracy.

Discussion

Repeatability has been used for antler traits in the deer family. Zhou and Wu (1979) reported repeatability of 0.76 for velvet antler weight in sika deer. Likewise, van den Berg and Garrick (1997) reported repeatability of 0.64 for velvet antler weight in red deer. In livestock, repeatability has been used for repeated traits such as milk production in dairy cows, wool production in sheep, twinning in sheep, weaning weight in beef cattle, and racing ability in horses (Bourdon 1997). Again in livestock, traits with repeatabilities below 0.2 are considered lowly repeatable, traits with repeatabilities between 0.2 and 0.4 are considered moderately repeatable, and traits with repeatabilities above 0.4 are considered highly repeatable (Bourdon 1997). It is difficult to assess if these ranges are relevant to reliability of culling criteria in white-tailed deer. In a relative sense, antler points had the lowest repeatability (0.28) in Faith Ranch deer

(Table 4).

Only 12 bucks in this study provided antler data at 1.5 years and again at 4.5 years or older. Caution must be used in drawing conclusions from this small sample. On the other hand, data from free-ranging deer are lacking and very difficult to obtain. The annual mortality rate of yearling bucks is approximately 37% in south Texas (DeYoung, unpublished data). Thus many marked yearlings are lost before they even reach 2 years of age, much less 4.5 years or older. Additionally, dispersal of several miles is common in yearling males (Holzenbein and Marchinton 1992). Thus, marked yearlings may leave the study area and not be available for recapture or harvest. Correlation analysis is strongly influenced by sample size, and had there been a larger sample of yearling versus mature records, the relationship may have been stronger. Nevertheless, based on these limited data, antler size of yearling deer appears to be a poor predictor of antler size at maturity.

In summary, this study provides data on antler development from a free-ranging population to compare to the previous penned studies. In some instances, sample sizes were small and the Faith Ranch study site was not replicated. However, the data suggest that neither antler points, nor an index of overall antler size in yearling bucks is a reliable predictor of future antler development. Neither this study, nor the previous penned work, provides conclusive answers to the practicality under free-ranging conditions, of antler improvement by culling certain segments of the buck population. It is 1 piece of data that needs to be fitted with results of past and future studies until reliable answers to the culling dilemma in white-tailed deer are available.

So, what is a manager to do? Managers need to assess the available data and make their best judgement of what, if anything, to cull. In making a judgement, it should be understood that complete information is not yet available, and that there is risk that the management practice you select may prove undesirable. Managers may also wish to conduct their own management research to provide new or supporting information, but should seek the advice of a professional in the design of such research. Also, managers should monitor the results of new studies as they come available and adjust management accordingly.

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Table 1. Number of white-tailed deer bucks of each age caught or harvested by year on the Faith Ranch, Dimmit County, Texas, 1985-1997. Number of harvested deer included in each datum is indicated in ( ).

Age	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	Total
1.5	2	13	13	4	2	0	6	10	3	8	2	13	12	88
2.5	8	3	8	18	16	4	3	7	8	5	13	8	25	126
3.5	13	4	3	10	13	13	8	7	8(2)	10(1)	15	12	8	124(3)
4.5	13	9	5	4	8(1)	9	8	3	3	6(1)	18	7	11	104(2)
5.5	8	11	6	4	3	11	11(1)	14(2)	11	9(1)	13	13(3)	14	128(7)
6.5	4	7	10(1)	6(1)	4	4	7	12(7)	7(1)	9(2)	8(1)	18(2)	11	107(15)
7.5	1	4(1)	5	3	3(1)	2	1	4(1)	4	7(3)	5(1)	5(1)	11	57(7)
8.5	1	0	1	5(2)	3	3(1)	4(2)	1	12(3)	4	9(3)	10(1)	9	61(12)
9.5	0	0	0	0	0	0	1	0	0	1(1)	2(2)	6(2)	0	10(5)
10.5	0	0	0	0	0	0	0	0	0	0	1	0	1	2
11.5	0	0	0	0	0	0	0	1	0	0	0	0	2	3
12.5	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Total	50	51(1)	51(1)	54(3)	52(2)	46(1)	49(3)	59(10)	56(6)	59(9)	85(7)	98(9)	101	811(51)

Table 2. Means for antler measurements on 631 male white-tailed deer captured on the Faith Ranch, Dimmit County, Texas, 1985-1987. Also included in the data set are antler measurements from 180 records of recapture or harvest of these bucks.

		Antler Measurement[1]						
Age	AP	PL	LBC	RBC	LBL	RBL	SPR	
1.5	3.8	6.7	2.3	2.3	8.6	8.5	7.3	
2.5	7.5	20.7	3.3	3.3	15.2	15.2	12.8	
3.5	8.2	28.3	3.6	3.6	17.9	17.8	14.9	
4.5	8.9	38.8	4.1	4.1	19.7	19.8	16.4	
5.5	9.3	41.1	4.4	4.4	21.2	21.3	17.7	
6.5	9.5	43.8	4.5	4.5	21.6	21.6	17.3	
7.5	9.4	42.0	4.3	4.3	21.2	21.4	17.9	
8.5	9.5	42.1	4.3	4.3	21.4	21.5	18.4	
9.5	8.5	33.2	3.9	3.8	19.4	20.1	17.8	
10.5	9.0	42.8	4.6	4.5	20.6	20.9	15.8	
11.5	9.0	38.2	4.4	4.3	20.8	20.3	16.0	
12.5	9.0	32.8	4.5	4.1	20.0	18.0	16.0	

[1]Antler Measurement: AP = antler points over 1 inch; PL = total length of all points (inches); LBC = left basal circumference; RBC = right basal circumference; LBL = left beam length; RBL = right beam length; SPR = inside spread.

Table 3. Frequency of age at capture versus age at recapture for male white-tailed deer on the Faith Ranch, Dimmit County, Texas.

Age at Capture	Age at Recapture											Totals
	2.5	3.5	4.5	5.5	6.5	7.5	8.5	9.5	10.5	11.5	12.5	
1.5	9	6	5	3	2	2	3	1	1	0	0	32
2.5		10	6	7	7	3	3	1	0	0	1	38
3.5			10	11	10	8	4	4	0	1	0	48
4.5				14	12	6	4	0	0	0	0	36
5.5					12	11	1	1	1	0	0	26
6.5						10	7	1	0	3	0	21
7.5							12	3	0	0	0	15
8.5								3	0	1	0	4
9.5									0	0	0	0
10.5										0	0	0
11.5											0	0
12.5												0
Totals	9	16	21	35	43	40	34	14	2	5	1	220

Table 4. Repeatability for various antler measurements and combinations of data (models) for male white-tailed deer captured or harvested on the Faith Ranch, Dimmit County, Texas, 1985-1997.

Antler Measurement[2]	Model[1]							
	1	2	3	4	5	(MS)	6	7
AP	0.28	0.39	0.38	0.43	0.48	(0.48)	0.63	0.65
PL		0.46	0.46	0.46	0.55	0.60	—	0.61	0.83
LBC		0.41	0.43	0.42	0.53	0.53	(0.57)	0.61	0.69
RBC		0.38	0.42	0.43	0.59	0.63	(0.57)	0.64	0.73
LBL		0.35	0.44	0.44	0.56	0.61	(0.58)	0.72	0.67
RBL		0.32	0.41	0.42	0.46	0.59	(0.58)	0.65	0.61
SPR		0.46	0.57	0.57	0.68	0.71	(0.60)	0.85	0.87

[1]Model: 1 = 1.5 - 12.5 years (all data); 2 = 1.5 - 12.5 years (spike yearling data excluded); 3 = 1.5 - 12.5 years (spike yearling at all ages excluded); 4 = 2.5 - 12.5 years (all yearling data excluded); 5 = 3.5 - 12.5 years; MS = repeatabilities for males 3.5 - 7.5 years calculated from Lukefahr and Jacobson (1998); 6 = 4.5 - 12.5 years; 7 = 5.5 - 12.5 years.

[2]Antler measurement: AP = number of antler points over 1 inch; PL = total length of all points in inches; LBC = left beam circumference; RBC = right beam circumference; LBL = left beam circumference; LBL = left beam length; RBL = right beam length; SPR = inside spread.

Table 5. Antler points (Pts) and an antler index (Idx) for bucks caught at 1.5 years of age and recaptured or harvested at 4.5 years or older, Faith Ranch, Dimmit County, Texas.

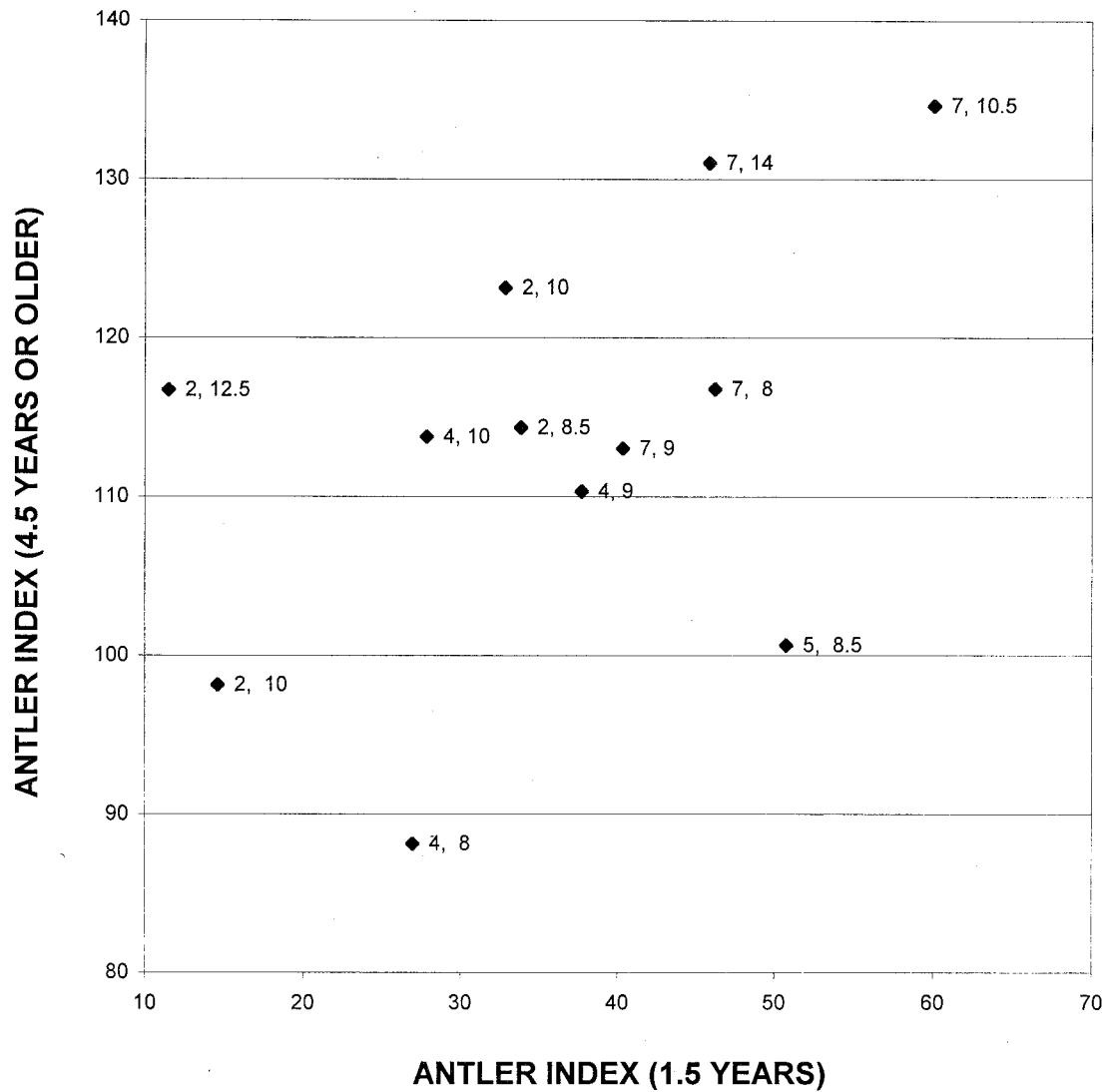| Buck ID#	1.5 Years		4.5 Years or Older												
			4.5		5.5		6.5		7.5		8.5		9.5		10.5
	Pts	Idx	Pts	Idx	Pts	Idx	Pts	Idx	Pts	Idx	Pts	Idx	Pts	Idx	Pts	Idx
63	4	28									10	114				
79	7	46									14	131				
126	4	38							8	108			10	113		
161	5	51			9	97									8	105
163	2	12					12	114			13	119				
512	2	34			8	109			9	120						
530	7	46					8	117								
614	7	60	11	140	10	130										
624	2	15	10	98												
735	4	27	8	88												
826	7	40	9	113												
9057	2	33	10	123												

Figure 1. The relation between an antler index at 1.5 years of age and the same index at 4.5 years of age or older in male white-tailed deer from the Faith Ranch, Dimmit County, Texas. Numbers by data points are antler points at 1.5 years and antler points at 4.5 years or older.

A CRITICAL EVALUATION OF STUDIES ON THE GENETICS OF ANTLER TRAITS OF WHITE-TAILED DEER

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Abstract: A critique of studies addressing questions about consequences to selection for antler traits is presented from a scientific journal editor's perspective. The studies that addressed: "Is the fact that a yearling has spike or fork antlers a good predictor of his antler traits at maturity?" seem to differ in their stated conclusions. However, some of the differences can be attributed to differences in models used for statistical analyses. The evidence suggests yearling antler class does have limited value for prediction of antler traits at maturity. The use of a more comprehensive statistical model that includes year and other effects was suggested as a means to provide more meaningful conclusions. Studies that addressed: "Is the fact that a yearling has spike- or fork- antlers a good predictor of his progeny's antler traits at maturity?" also differ in their stated conclusions. Although the data sets used are the largest of their kind, they are not large enough to justify definitive conclusions about heritability. Differences in models used for statistical analyses were shown to account for some of the difference in results and suggested that assumptions made in earlier analyses were not adequately justified. Including more sources of variation and accounting for relationships among animals in models used for analyses will provide more precise estimates of the parameters of interest. The size of the data sets suggests the most powerful statistical tools available should be used in order to obtain the most useful information possible.

I have learned much about the history and controversy of deer antler genetics in the last ten days. I have learned several new terms this week: Boone and Crockett score, spike, forked, spread, and main beam circumference. The vocabulary and traits of deer antler genetics are new to me and there are several who are more knowledgeable than I am about these traits. But, the issues involved in the controversy, the experimental design, statistical analysis, and interpretation of results from animal measurements and pedigrees, are those which I can confidently address. My training is in animal breeding and genetics and in my own research I primarily use sheep and goats. I describe my job as trying to determine better ways to select the parents of the next generation, so that we will have more productive animals. With sheep and goats, the goals are varied and include: increasing quantity, quality, efficiency or profitability of meat and/or fiber, adaptation to environments, and resistance to disease. With respect to deer antlers, the traits of interest may be different, but the concept of choosing the parents, in order to influence traits in future generations is the same.

I have been asked to give an evaluation of previous studies. I am, therefore, approaching this from a reviewer's perspective. Reviewers, in the context of scientific publications, play a significant role. Scientists conduct research to address unanswered questions. Most good experiments start with a well-defined question for which the answer is not known. An experiment is then conducted with the objective of providing an answer to the question. The measurements are then analyzed using statistical methods that have been shown to produce results with known properties. The results of the statistical analysis are interpreted and then the scientist writes a paper explaining how the experiment was conducted, how the analysis was conducted, what results were obtained and the implications or meanings of the findings. The scientist then submits the written paper to a journal for publication. The editor of the journal sends the paper to reviewers (usually 2 to 4 other scientists familiar with the methods used) for evaluation. Reviewers are chosen because they have demonstrated competence in specific areas of research. The reviewer's task is to evaluate how the experiment and analysis were conducted and provide the author with suggestions that will improve the paper. Reviewers typically remain anonymous and are asked to recommend either a) accept the paper for publication, b) accept the paper after it is revised by incorporating changes the reviewer suggests, or c) reject the paper. The editor then evaluates the reviews and makes a decision about the fate of the paper. This process is necessary, even though it is time consuming, to ensure readers of the journal that the paper is not merely an opinion, but that the experiment was conducted in such a way that the results are meaningful and that the interpretation of those results is valid.

My situation here, as a reviewer, is unusual in that I can not remain anonymous, and the authors of the

papers that I am reviewing are present. When I receive, from an editor, comments from the reviewers, my usual reaction is that I want to have that reviewer present because I want to explain some things that he or she didn't understand. I might be frustrated that the reviewer didn't understand what I meant, when I thought I wrote my paper so carefully. After I have read the reviewer's comments, I put it down and come back to it when my emotional frustration has subsided. I often find that the reviewer didn't understand because my wording wasn't clear enough. I make the reviewer's suggested changes, or redo the analysis with a more appropriate method, or justify my interpretation with additional supporting evidence, or admit the limitations of the experiment. I ultimately have a paper that is a better product.

For the authors of the papers under review, please remember that my purpose is to evaluate the methods and presentation. I will question certain aspects of the papers. My questions may be from a different perspective than your own. But the ultimate purpose of my evaluation is to provide more information to the audience or reader. I did have an advantage, that a reviewer doesn't usually have, in that I was able to talk with some of the authors, asking them to clarify things for me about their papers.

I will focus on the statistical analyses in these papers. One purpose of statistical analysis is to summarize many measurements and distill them down to a few, very meaningful numbers. If a scientist showed many pages of antler measurements, deer ages and pedigrees, the reader would be left to wonder what it all means. By using all the data to calculate a few meaningful statistics, a scientist can better communicate the results and explain the implications of those results.

I was told that there was controversy about the "question". On my first read through the abstracts of the papers I have been asked to review, I realized that part of the controversy might be due to the fact that there is more than one question. I think the realization that there is more than one question is essential to greater understanding of the meaning of the papers.

Before I consider the results of these research projects, I will first consider the different questions that are being asked. I want to break it down into two questions. The first main question is: Is the fact that a yearling has spike or fork antlers a good predictor of his antler traits at maturity? However, even this question could be specified more precisely. There are several individual measurements that I have called 'antler traits'. I will not attempt to address specific measurements, but have chosen to address antler traits in a general sense.

I realize that generalizations, including this one, have limited value. Maturity should also be defined. For my review, I will define maturity as the four- to five-year-old range. The second main question is: Is the fact that a yearling has spike or fork antlers a good predictor of antler traits in the next generation at maturity? There are two main questions. They are distinct, but related questions.

Question #1: *Is the fact that a yearling has spike or fork antlers a good predictor of his antler traits at maturity?*

The paper by Ott and others, titled "The comparative performance of spike- and fork-antlered yearling white-tailed deer: The Basis for selection", the paper by Jacobson, titled "Culling as a management practice for white-tailed deer: The Dark side, and the paper by DeYoung, titled "Case studies: The Faith ranch herd" all addressed Question #1. This question is the easier question to answer because pedigree records are not required. Question #1, as posed, does not require an explanation of why, but is merely asking if yearling antlers can be used to predict the future for a buck.

I will now give my reviewer's comments on the papers with respect to question #1. I noted that the paper by Ott and others had a good-sized data set, there were measurements on enough animals to safely make a conclusion from the data. I acknowledge that the statistical methods used and the question that he was trying to answer were clearly explained. The results from the statistical analyses justify the conclusion. I suggested to the authors that the analysis could be improved. This could be a stronger paper if the author did try to address the question of *why* yearling antler class (spike- or fork-antlered) is or is not a good predictor of antler traits at maturity. There appears to be sufficient data to warrant an attempt to attribute variation in antler traits at maturity to different causes such as: sire of the buck, body weight of the buck, or year of measurement. I was left questioning if there were other effects that can explain some of the variation in antler traits in maturity. It was not the author's purpose to answer this question, but I suggest that they could have tried to answer more questions with this data in order to produce a more informative paper.

I realize the deer were raised in a pen and all fed the same ration, and therefore one can argue that the environment was controlled and not a factor. I have been told that a sample from every truckload of feed was analyzed for nutrient content. This does provide some measure of control of the nutritional environment.

But, there is variation in content among batches of feed mixed with the same recipe by the same feed company. The protein and energy content of the feed are probably the most important to control on such a trial. However, having total control of the diet involves additional factors. Levels of macro and/or micro minerals can significantly affect performance in sheep and goats and I expect the same is true for deer. Other factors that may affect antler traits include: health status of the animals. There may be a sub-clinical infection affecting performance in a given year. In animal breeding research we typically include a year or season effect in a statistical model because we recognize that we do not have complete control over the environment and accounting for this in the model used for analysis allows for better estimates of the effects of the factors of interest. If there were significant differences in other factors that affected antler traits, those factors could be accounted for by including a year affect in the statistical model.

If one is attributing variation in antler traits to different causes, the inclusion of a year effect is especially important when the spike- and fork-antlered yearlings are not evenly distributed across years. In this data set the ratio of spike- and fork-antlered yearlings is not the same in each year. The records of the 140 bucks were collected over an 18 year period. If there were particularly unfavorable conditions in a year in which the bucks that were measured at 4.5 years of age were mostly, or all, fork-antlered as yearlings, the estimates would be biased. This type of effect, which could be considered as an environmental effect for a specific year, can bias results in either direction. The unfavorable conditions could be a result of disease, or unusually high or low environmental temperatures, or high humidity or other factors which may affect antler traits. The statistical consequence of including a year effect is that, if the effect is a significant source of variation, the estimated error variance will be smaller and hypothesis tests will have more power. Other factors that may be significant sources of variation are age of dam and date of birth within a year. If other factors that explain significant amounts of variation are included in the model, more meaningful evaluations of the traits of interest are expected.

The second paper addressing Question #1, by Jacobson, also has a good-sized data set of 95 bucks over several years. The question that Jacobson tried to answer was a slightly different question than Ott tried to answer. Ott addressed the question, "Is the fact that a yearling has spike or fork antlers a good predictor of his antler traits at maturity?" Ott also added a second question which was, "Are there significant differences in antler traits at maturity among groups of bucks that

were either, a) spike-antlered, b) 3-5 points or c) 6 points or more?" Jacobson asked a slightly different question, which I would word: "Are there significant differences in antler traits at maturity among groups of bucks with different numbers of antler points?" There were 8 groups: 2, 3, 4, 5, 6, 7, 8, and 9+. The fact that these two papers address slightly different questions, explains part of the difference in their conclusions. I notice that in Jacobson's Table 1, the spike yearlings had the lowest, and the 9+ point yearlings had the highest, average Gross Boone & Crockett (GBC) scores, antler weight, and beam length. But, there is not a consistent increase from 2 points to 9+ points in these or other traits. Spike yearlings had lower GBC and antler weight and these differences were statistically significant. However, the variation within each yearling antler point category was not small enough for the authors to conclude that there were significant differences among different categories for any of the other traits presented. Because the bucks were divided into several categories, based on number of yearling points, the number of bucks in each category is quite small and this limits the power of statistical tests used to detect significant differences. Because Jacobson and Ott answered slightly different questions, the reader is left to decide which question is more relevant. If the goal is to evaluate the effect of culling based on spike versus fork yearling antlers in order to improve average antler traits at maturity in this group of bucks, then I think Ott asked the more relevant question. If the goal is to compare antler traits at maturity for each of the 8 yearling categories (2, 3, 4, 5, 6, 7, 8, or 9+ points) then I think Jacobson asked the more relevant question.

I have some of the same criticisms of the Jacobson paper that I have of the Ott paper. There were some environmental effects that could be taken into account that were not accounted for in the statistical analysis. The 95 deer records were collected over approximately 15 years. At the least, year effects could have been included, other possible effects that may have been included, if the data were available, include day of birth within year and /or age of dam. Estimation of environmental effects such as these, in one comprehensive model, effectively accounts for these effects so that the entire analysis provides more meaningful information.

The Jacobson paper did not explain the statistics in as much detail as the Ott paper did. I consider that a negative, but most of the audience for this conference probably considers it a positive, not to have complicated statistical details. I understand that this is a symposium paper and not a paper to be submitted to a refereed journal and this is why the author chose not to include more of the statistical details. I did ask the

author some detailed questions about the statistical methods used. He explained what was done and I saw no errors in his analysis.

If the authors want to make steps toward resolving the different conclusions of these papers, I suggest that they use each other's methods on their own data set and see how the conclusions may differ. A joint paper resulting from cooperation between the authors of the present papers would probably be in demand by several publications.

The paper by DeYoung, which is not something that would be submitted to a scientific journal (I think the author recognizes this), serves the purpose of trying to answer Question #1 out in the field rather than in a pen study. The most significant revelation for me from DeYoung's paper is that it is very difficult to get relevant data out in the field. The data presented does give an indication that there is some level of predictability of antler traits at maturity from spike-versus fork-antlered yearlings. The data are not sufficient to answer Question #1 conclusively. But, for what they have to go through to capture the bucks again at 4.5 years of age after they catch them as yearlings, I realize why they have a relatively small data set. The data that was presented does contribute additional information to the answer of Question #1. The author admitted the limitations of the data set and did not encourage readers to make final conclusions based on the results. The relationship that was shown was not statistically significant, but it was a positive relationship.

After reviewing the three papers that addressed Question #1, it appears to me that although yearling antler class (spike- and fork-antlered) does not explain all of the variation in antler traits at maturity, yearling antler class does have limited value for prediction of antler traits at maturity. Figure 1 of Ott's paper shows that the distributions did have some overlap. There are examples in Jacobson's Table 1 where spike-antlered yearlings were superior to some of the other categories. I expect that if Ott's data were presented in the same way, similar examples could be found. However, individual examples do not support general conclusions. The use of a more comprehensive statistical model may provide more meaningful answers to Question #1 from both Ott's and Jacobson's data.

Question #2: *Is the fact that a yearling has spike- or fork- antlers a good predictor of his progeny's antler traits at maturity?*

Question #2 is the harder question to answer and, from my perspective, also a more interesting question.

The conference papers that address Question #2 are "The Kerr area penned deer research facility" by Harmel and others and "Genetics research on captive White-tailed deer at Mississippi State University" by Jacobson and Lukefahr. Different methods have been used in attempts to answer question #2. Some of the details of those differences are beyond the scope of this paper, so I will cover only the most significant points and refer the reader to publications that address the differences in more detail.

Antler trait records and pedigree records are used together to answer Question #2, whereas pedigree records were not required to answer question #1. The Harmel paper does not give full details but refers the reader to a paper by Williams, Krueger and Harmel (1994) which reported heritability estimates of .71 for antler weight using a sire model, and .86 and .75 using variations of sire-offspring regression. Heritability estimates for other traits were also reported, with several of them being above .40. The Jacobson paper similarly does not give full details but refers the reader to a paper by Lukefahr and Jacobson (1998) which reported a heritability estimate of .09 for antler weight using an animal model. Heritability estimates for other traits were also reported, with several of them being below .30. Both conference papers refer the reader to a third TPWD publication (Lukefahr, 1997) which used a variety of estimation methods. A comparison of the results from the different methods provides useful information about why estimates differ.

Sire model vs. Animal model

The sire-offspring regression and sire model methods both use the relationship between sire and son as the pedigree information. An animal model uses all relationships between all animals in the data set as the pedigree information. This includes relationships between sire and son, dam and son, uncle and nephew, grandsire and grandson, maternal grandsire to grandson, ... When more genetic relationships are taken into account, more accurate estimates of heritability are obtained. Prior to the 1980's, sire models were used in most genetic evaluations and estimation of genetic parameters because the computing requirements for animal models with large data sets could not be met. Advances in computer hardware and software allowed for the use of animal models which included all available relationships. For more information on animal models see Henderson (1988) and other papers in the "Proceedings of the Animal Model Workshop". The sire model was, and still is, a very useful statistical tool. The relationship between sire and son is the most important relationship in most animal breeding

analyses. But, when dams, grandsires and other relatives are known, the inclusion of these additional relationships results in less bias of the estimates. Using all available information is especially critical in data sets such as those being discussed at this conference because antler traits are only observed in the males. If antler traits are heritable, the dam's contribution should be taken into account and will affect the heritability estimates. An animal model has the ability to extract more information from the same data set. Larger data sets with records on more animals would be desirable regardless of estimation methods used. However, small data sets are more of a concern with sire models than with animal models.

For any heritability estimation method, sample size and method of sampling are important issues. However, results from sire models, are subject to more bias than animal models from method of sampling, non-random selection of mates, and fixed environmental effects which are not accounted for, such as year, contemporary group or age of dam. Use of a sire model requires more assumptions (random selection of sires, sires unrelated to mates, mates unrelated to each other) than an animal model. Relationships among sires can either be accounted for or assumed not to exist in a sire model.

Accounting for other effects

When estimating heritability of a trait, the goal is to analyze the data in order to attribute portions of the observed variation to different causes. The portion attributed to additive genetic variation is used in calculating an estimate of heritability (See paper by Skow in this proceedings). In order to have a reliable heritability estimate, other sources of variation should be taken into account by the statistical model used. If sources of variation are not accounted for, a biased heritability estimate can result. An intentional way to bias a heritability estimate would be to provide preferential treatment based on sire groups. If the sons of Sire A were fed better, or maintained in a more favorable environment than the sons of Sire B, the heritability estimate obtained would be biased. Unintentional bias can arise from factors which may affect different sire families to different extents. For example, if Sire A's sons were all measured in 1992, and 1992 was an unusual year for antler traits (possibly the result of unusual temperature, precipitation, disease or other factors mentioned earlier) this would result in a biased estimate of heritability. A comprehensive model, which includes factors that are known to affect antler traits should be used in order to explain the cause for as much of the observed variation as is feasible.

These non-genetic factors can be taken into account in the same model from which heritability estimates are calculated, or the data can be adjusted for these factors prior to estimating heritability. The factors that I would suggest be considered and tested for significance are age of dam, birth date within year, and the year that the antler trait was measured. When the data are available, these factors should be tested to determine if they are significant sources of variation. Those that know more about factors affecting antler traits may suggest including other factors as well. All of the variation in antler traits will not be explained by any one factor. Ignoring some factors when estimating the effects of others is likely to produce incorrect results. The variety of reports cited in the Harmel paper clearly show that there are non-genetic factors that may affect antler traits.

Review of other reports

In reviewing papers, one of the questions considered is: do the results obtained support the conclusions of the author? Another way to word this question is: did the author interpret the results logically? If an author states that A caused B, the reviewer's job is to question if there might have been another explanation of what caused B. If the scientist has a well-designed trial that was analyzed correctly and interpreted logically, the conclusions will withstand the review. I will now discuss Williams et al. (1994), Lukefahr (1997) and Lukefahr and Jacobson (1998) and the associated papers in this proceedings from a reviewer's perspective.

The analysis reported by Williams et al. (1994) used relationships between sires and sons and assumed that 1) sires were unrelated to each other, 2) sires were unrelated to their mates, 3) mates were unrelated to each other. If pedigrees are known, as I understand is the case in most, if not all, of the data of Williams et al. (1994), all relationships should be taken into account to avoid potential bias from non-random mating and obtain more accurate estimates. Williams et al. (1994) explicitly assumed that the year and pen effects did not need to be taken into account. This assumption was not tested (Williams, pers. com.). I understand that they had as much control over the environment as anybody has in a deer situation, but I also understand that they did not have control over everything (see previous discussion on Question #1). Therefore, in my review, I would say that unless the assumption, that year and pen effects would not affect the results, was tested and proven to be valid, the analysis is not acceptable. At the least, I would request that the authors indicate to the reader the limitations of drawing conclusions from this

analysis because the results are subject to bias because of this assumption. Lukefahr (1997) did include year and day of birth within year in a sire model analysis using the same methods and TPWD records as were used by Williams (1994). When year and day of birth within year were taken into account, the sire model yielded substantially lower heritability estimates than reported by Williams (1994). This demonstrated that the assumptions used in the data analysis of Williams (1994) were not valid.

Figure 2 in Harmel's paper has the caption "73% of Spikes Born were from 3+ (yrs of age) Does." Looking at the bars of the graph, one can see that 1-yr-old does produced more spike- than fork-bucks while 3-yr-old and older does produced more fork-than spike-bucks. Therefore, the data suggest that age of doe is a factor that affects antler traits and that bucks from younger does are more likely to be spike-antlered yearlings. Similarly, Figure 3 in Harmel's paper has the caption "81% of all spikes were born before July 15." The bars on this graph show that, of the bucks born in May and June, there were more fork than spike while of the bucks born in July, August and September, there were more spike than fork. The data suggest that month of birth does affect yearling antler points and bucks born earlier are more likely to be fork-antlered yearlings. The disclaimer of "This study not intended to measure this parameter" is on Figures 2 and 3. As a reviewer, I would suggest that the authors clarify why Figures 2 and 3 are included. It is acceptable to estimate effects from studies designed for other purposes, if the statistical analysis used takes known sources of variation into account. If attempts are made to estimate effects, such as age of doe or day of birth, a statistical model must be used which accounts for other sources of variation that may bias the results. The captions on Figures 2 and 3 and the discussion seem to suggest one conclusion while close observation of the figures suggests a different conclusion. Without a comprehensive statistical model to account for all significant effects, neither conclusion can be logically defended.

Lukefahr and Jacobson (1998) used an animal model, which took into account all the relationships between animals in the data from Mississippi State University. The model also included an effect for birth year and nursing background (natural dam or artificially reared). The animal effect in the model was used to calculate the heritability estimate and the model also included a maternal effect. A maternal effect can be used to explain some of the variation due to the fact that all dams are not equal as mothers. One example of a maternal effect is where a doe produces a greater than average amount of milk. This could be an advantage to the offspring. The reason that a dam may be superior to another dam can be either genetic or environmental. With an adequate number of offspring from each dam and proper accounting for relationships among dams, one can separate the maternal genetic effects from the maternal environmental effects. On the average, each doe that had offspring in this data set, had approximately two sons with antler measurements. An average of two sons provides a very limited amount of information for estimating maternal genetic and maternal environmental effects. With the fact that there were, on average, only two offspring/dam, a compromise had to be made. The authors' choices were to 1) ignore all maternal effects and accept the risk of results being subject to associated bias or 2) include a single maternal effect that would include both maternal genetic and maternal environmental effects and realize that to ascribe a meaning to the 'general' maternal effect would be speculative. Neither alternative for analysis is desirable. The authors had to choose the 'lesser of two evils'. The authors chose to combine the maternal genetic effect and the maternal environmental effect into one maternal 'general' effect.

Lukefahr (1997) also used an animal model on the TPWD data set. The TPWD data set used in Lukefahr (1997) also had approximately 2 sons/dam. Although there was not good agreement between the results presented by Lukefahr (1997) using TPWD records and Lukefahr and Jacobson (1998) using MSU data, there were some similarities. Results reported by Lukefahr and Jacobson (1998) and Lukefahr (1997) suggest that maternal effects should not be ignored. Ignoring maternal effects, as was done by Williams (1994), when there is evidence that maternal effects are important is expected to result in biased heritability estimates. Without a data set that has a structure more suitable for estimation of maternal effects, any conclusions about whether the maternal effects are genetic or environmental are speculative. Neither the TPWD data set nor the MSU data set have a structure suitable for estimation of maternal genetic and maternal environmental effects. For reliable estimates of these effects, the data set must have more animals and/or a structure more suited to estimation of maternal effects. For a more thorough discussion of maternal effects and maternal effects models see Willham (1963; 1972).

Animal models allow for more accurate heritability estimates than sire models because more relationships among animals are taken into account. If the sires are not related to one another, are not related to their mates, are not inbred, are a representative random sample of the population, and maternal effects are not a factor, then one would expect the results from sire model analyses and animal model analyses to be in agreement.

Evidently, not all of these assumptions were valid. Because several of these assumptions are rarely met in livestock breeding, the animal model has become preferred over sire models, for heritability estimation and genetic evaluation, because violation of these assumptions is less of a factor when all known relationships are taken into account. Heritability estimates calculated from restricted maximum likelihood (REML) methods are less subject to selection bias than previously used methods.

The interpretation of results from the two conference papers that address Question #2, vary widely. Harmel et al. interpret the data to suggest that expected progress from selection is substantial. The conclusion of Jacobson and Lukefahr from this proceedings is that little or no progress should be expected in yearling traits, but that selection on mature antler traits is expected to result in changes. Neither data set would be considered 'strong' relative to the genetics research that has been conducted with domestic livestock species. But, both data sets contain a considerable amount of information for which significant resources have been invested. Lukefahr (1997) used different models on the same data to provide evidence about the consequences of the assumptions made by Williams (1994). The last paragraph of Harmel's paper suggests the authors are confident about their conclusions. Based on my evaluation of the data presented, the confidence is not justified.

Origin of herds

Heritability estimates may not be the same for different populations and the origin of the populations used may be a factor in the differences in the results. Deer from several Texas sources were used to establish the TPWD population. No animals have been introduced into the herd since 1974. Lukefahr (1997) reported that 70% of the animals used in his analysis were inbred and many of the deer were related to one buck named "Big Charlie". The average level of inbreeding in the bucks born in the TPWD herd was near 10% from 1988 to 1995 (Lukefahr, 1997). These two factors are cause for concern about the applicability of the heritability estimates from this population to other populations. If one sire, or sire-family, makes up a large proportion of the data set, there is cause for concern when making inferences to a larger population. If "Big Charlie" was an unusual individual, with respect to his ability to sire sons with superior antler traits, the results may be applicable to "Big Charlie" more than deer in general. One way to determine how much of an effect "Big Charlie" had on the estimates, would be to

analyze the data without "Big Charlie" and his progeny. If the results differ substantially, then it is clear that his family is not representative.

The original animals in the MSU herd were obtained from sources in seven states in the Midwest, East and South. This population is not representative of any one population and therefore, I am also concerned about the applicability of the heritability estimates from this population to other populations.

Neither the TPWD nor the MSU population is ideal for genetic parameter estimation. An ideal population for the purpose of answering Question #2 would have a larger number of original animals that were from one population. A mating plan that would provide a more meaningful answer to Question #2 would minimize inbreeding. In order to partition variance into direct and maternal genetic effects and thereby obtain heritability estimates unbiased by maternal environmental effects, future mating plans should be to assemble data sets that will include several offspring/dam by different sires.

Conclusions

The results of the analyses reviewed do not support strong conclusions in any direction. Question #2 has not been answered definitively. The data sets are better than any others I am aware of, but they are limited as far as being able to answer Question #2. Isolated examples of a single spike-antlered yearling that produced a superior set of antlers at maturity are interesting, but without taking other effects into account (age of doe, day of birth, environmental effects which can be estimated as a function of the average of antler traits in the year of measurement) these isolated examples are not useful for making conclusions about the heritability of antler traits, except as one animal in a larger data set. Heritability is not estimated from a few animals, but a larger population. Likewise, isolated analyses of factors that affect antler traits (age of doe, day of birth, genetic variation) are not meaningful if they are subject to bias from other factors known to affect antler traits.

The most informative research projects begin with a clearly defined question. There are too many questions about genetics of antlers to be answered with one project. The conclusions which appear to conflict are partially due to the researchers asking different questions of their data. A question that wasn't addressed in these papers is: "Which question is the most important to answer?" Deer managers should also ask: "Can one choose the parents of the next generation

to an extent that will make a difference if antler traits are heritable?" Or in other words: "In a free ranging herd, might migration negate the effects of selection?" Animal breeding research is too expensive to risk conducting without starting with a well planned mating scheme and data collection procedure that has a good chance of answering an important question. Statistical analyses are relatively inexpensive, compared to the costs of maintaining a herd for several generations and data collection. Therefore, the most powerful statistical tools available should be used in order to obtain the most useful information possible.

There is more than one unanswered question.

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RANCH-LEVEL EXPERIENCE: AN OVERVIEW OF GENETICS FROM A DEER MANAGER'S POSITION

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The deer manager who desires to improve the genetics of his herd should attempt to answer or at least consider the following questions *before* embarking on any program of genetic manipulation.

The first and foremost question concerning the management of a deer herd is *do I have a problem with genetics* and/or how do I determine if there is or has been genetic degradation.

A second important question is *have I done everything possible to ensure that the deer herd in question has been allowed to reach it's inherent genetic potential?* By that question, I mean, have all the necessary management practices been instituted regarding the range (habitat), the livestock operation, water facilities and distribution, the deer herd itself, and other practices that may be vital to ensure maximum potential development of the herd?

Also, it is very important to know that if, in fact, all practices necessary to ensure maximum potential have been instituted *have these practices been in effect for at least five years?* Five years would be the time span necessary to raise a fawn crop to maturity under those improved conditions.

Another consideration is *how does one measure or separate the influence of practices* such as high protein feeding, introduction of "new or improved genetic stock", selective harvest, and any other practice that may be applied on an individual or collective basis? This question is especially important because many operations are emphasizing all or a combination of these type practices.

If improvement is desired by an individual landowner or manager, 3 other questions must be also be addressed:

offer the best chance of success?

2. Is it possible with my capabilities and facilities to accomplish those practices?

3. Is it economically feasible?

After 33 years of involvement in deer herd management, I would like to add these general observations:

1. The majority of deer ranges are supporting deer populations that are too high to furnish optimum nutritional levels from native vegetation.

2. The majority of landowners and managers will not accept reducing deer numbers to levels that would accomplish optimum nutritional levels from native vegetation.

3. The majority of individual operations have not accomplished all that is possible to improve their deer herds from the standpoint of manipulation of habitat, livestock, deer populations and other factors under their control.

4. These practices usually result in substantial improvements which are sustainable indefinitely without continually recurring costs such as the artificial practices of supplemental feeding and genetic manipulation.

5. And last, but not least, is most individuals expectations are far greater that what can actually be accomplished when "improved" management practices are applied.

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1. Which practice or combination of practices will

RANCH-LEVEL EXPERIENCE: THE QUE PASA RANCH

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Que Pasa Ranch, located here in the Brazos Valley, is 2,347 acres in size. A high fence encloses 2,200 acres of the ranch which has allowed for an intensive white-tailed deer management program. The ranch was acquired by the present owner in December of 1992 and the high fence was closed in the fall of 1993. Since that time the ranch has followed a strict management program designed to provide optimal habitat in which the deer can reach their genetic potential.

Deer genetics is 1 of 3 essential elements of deer management which must be addressed in order to effectively improve a herd. The other 2 elements are nutrition and age structure. The finest herd genetics in the country will fail to reach their potential if a deer is malnourished or is not allowed to reach maturity. It is essential that any operation pay close attention to all three elements if a superior herd is to be produced. Transporting animals with superior genetic potential to a location with inadequate nutritional opportunity will yield mediocre results at best.

We made the decision several years ago to import deer onto the ranch as well as manage the indigenous population. Prior to importing deer with good genetic potential, we believed it was very important that they would provide a superior nutritional plane. We supply supplemental feed free-choice year round. This consists of a protein pellet from antler casting in late winter through velvet loss in the fall and a high energy pellet from hard antler in the fall till antler cast. In addition, we plant 120 to 150 acres of both summer and winter food plots. Summer plots consist mainly of cow peas and clover while winter plots mix oats, wheat, and clover. We have also used annual controlled burning along with mechanical removal of yaupon mid story to promote forb production.

Additionally, prior to importation of deer, we reduced the indigenous population significantly so that the introduced animals would have a greater impact on the genetic make-up of the herd. As with many areas of the Post Oak Savannah and elsewhere, the previous owners of the ranch had shot the first buck they saw and failed to harvest many does. There was over a 4 to 1 doe/buck ratio in 1992. There were very few mature

bucks and a great number of old does. From the 1993 to the 1997 seasons, we concentrated on leveling out the sex ratio and reducing the density of animals on the ranch. In that period, we harvested over 7 antlerless deer from every cull buck. This left us with more bucks than does on the ranch. The buck herd was getting older and the doe herd was getting younger. The average dressed weight of does climbed by over 10 pounds and kidney fat indexes increased drastically.

In the spring of 1997, we released over 140 deer onto the ranch which had been imported from well managed south Texas herds. During the 1997 season we harvested a few cull bucks and no does. At this time, we want to bring the herd density back up toward carrying capacity and allow the bucks in the herd to age. We anticipate resuming a doe harvest next season to keep the density in check. Our principal genetic tool going forward will be selective harvest of cull bucks. We believe that the herd is now positioned to become outstanding over the next few years. We have the nutrition and the genetics right. All that remains is to allow the herd to age.

We have been asked to comment on the reasons for our decision to import animals. I firmly believe that it is possible to develop an outstanding herd of our own without the importation of any animals. A high fence would still be a necessity because of the size of our ranch relative to the range of a mature deer. The problem in developing a purely indigenous herd is the time involved. We aren't dealing with fruit flies. It takes at least 3 years for a buck to show what he is. Some argue that it is possible to make culling decisions on yearlings but I don't agree. Buck fawns born to yearling does which were b red as fawns are generally born late and may appear inferior as yearlings. We believe they should be given an opportunity to catch up. Additionally, summer rainfall amounts can impact the appearance of the entire herd. It is therefore important in my opinion to allow a buck to reach 3 or even 4 years of age prior to making a decision to cull the animal from the herd. By importing known genetics into the herd we believe we will end up with the herd we want after 8 to 10 years of development rather than 20+ years that it would take to shape the indigenous herd to the same level of quality.

Another factor which favors the introduction of imported animals are the quality of the does in the herd. We talk a lot about cull bucks that you don't hear much

about cull does. It is impossible to determine in a wild herd which does will contribute to superior antler development in their offspring. By importing does which have known genetic superiority, we are able to contribute greatly to the dam side of the genetic equation.

We are following essentially the same herd management principals that have been used in the cattle business for decades. You find the best brood stock you can afford then cull undesirable offspring. With the economic worth of deer skyrocketing in the past few years, it is only logical that the same principles which drive a cattle ranch should now permeate the deer industry. Deer hunting has long been a treasured sport in our state and as with most other sports in this country, it is more and more becoming a business. This may be a sad fact but is nonetheless true. The economic imperatives of this developing industry are at times in conflict with the traditional values of the sport. It is up to all of us to try to preserve the tradition while dealing with the economic realities.

RANCH-LEVEL EXPERIENCE: THE ENCINO RANCH GENETIC PROGRAM

MARSHALL BROWN and **KENNETH BARBUTTI**, P.O. Box 2690, San Angelo, TX 76902

Encino Ranch has been under a management program for 10 years with our main goal to push the native whitetail deer to there genetic potential. We have 8,000 acres under high fence which consist of live oak and cedar hills to mesquite flats. The first thing we tried to do was to provide proper nutrition along with population control. After several years of trial and error we feel that we have that under control.

Although there are several theories on culling for genetics, we started harvesting spikes, 3-point yearlings and small 4-point yearlings, along with mature deer that have undesirable characteristics. These characteristics in the mature deer were: no brow tines, 6-points, 7-points, and 8-points with short G-3s.

After a few years of this practice, we attempted to provide all the nutrition we possibly could by increasing the number of protein feeders and planting summer and winter food plots. With the proper nutrition, this enabled us to raise our culling program to a higher level. Starting with the yearlings, we culled by means of trapping and harvesting all bucks with 6 points and under. The 2, 3, and 4 year old bucks were harvested by taking out all bucks under 8 points and all 8-point buckss that we believed were not going to be 140 gross B&C type of bucks.

Our program has graduated to a point now where we feel that we have a better grasp on the genetic potential of the younger deer as well as the mature deer. We have gone to a trapping program for most of our young deer and harvesting our inferior mature deer by means of hunting. We have started by taking out all yearling bucks with 7 points or less and are now seeing more and more yearlings with 9 or 10 points. We try to take out all of our 2.5 year old bucks that score less than 100 B&C gross, 3.5 year olds that score less than 125 B&C gross, 4.5 year olds that score less than 140

B&C gross, and 5.5 year old and older bucks that do not score more than 150 B&C gross. We try not to harvest any of our potential trophy deer until they reach the age of 6 and sometimes hold them until they are 7 or 8. The 6-year old and older bucks that we hold back are main frame 12-points, drop tine bucks, and 10-pointers that are in the mid to upper 160 B&C class or better.

Encino Ranch has developed a hunting program that allows us to sell our genetically inferior bucks. We have 3 different types of hunts that cover the ranges of deer we need to harvest. Our "Management" hunts are bucks that score up to 120 B&C gross, "Classic" hunts are those that score from 130 to 140 B&C gross, and our "Trophy" hunts start at 140 B&C gross and up. We feel that this is a very effective way to control your genetics in your whitetail deer herd.

When managing your deer herd, you also have to control your doe herd. We started off by just trying to take out a wide range of does in all age classes. After discussing this with a few people, we started a new program with our does. Since the younger does should have the best genetics, because of our buck culling, we have started trying to take out our older does each year. By doing this, the younger does should have the best genetics, because our buck herd is becoming genetically stronger ever year with less chance of a inferior buck breeding.

Though there are many theories on genetics, we feel that this program best fits our country and the goal we are trying to obtain. As everyone knows, without proper nutrition and population control, your deer herd will never reach its genetic potential. With this in mind, we suggest proper nutrition and a genetic program that fits the goals you want to obtain.

RANCH-LEVEL EXPERIENCE: THE MASSER RANCH

TED MASSER, Los Cazadores, Inc., Rt. 2, Box 159, Fredericksburg, TX 78624

The Masser Ranch, consisting of 931 acres, is located in western Gillespie County in the middle of the scenic Texas Hill Country. The predominant vegetation is live oak and shin oak, but a variety of other woody plants can also be found. The ranch is a working ranch with a primary emphasis on white-tailed deer and secondary emphasis on livestock production (cattle only at this time). A devotion to hunting, fishing, bird watching, photography and other pursuits of wildlife enjoyment and appreciation are the main objectives of the ranch.

We have developed our wildlife program based on truthful information, acquired facts and a complete understanding of existing conditions on the ranch. These considerations and the knowledge necessary to formulate and implement quality deer herd management and to provide a professional hunting experience assures the hunter of our intent.

The ranch has been practicing wildlife management for over 26 years and has been high-fenced since 1990. A year-round supplemental feeding program was initiated in 1990, along with an intensive livestock management and grazing program. Supplemental feed (a combination of a private pelleted ration and split peas) is available free-choice year-round. Management practices include planting food plots, prescribed burning, and rotational grazing systems. We harvest does aggressively and strive to maintain a 1:1 buck:doe ratio.

Our philosophy on culling has essentially been that of the Kerr Wildlife Management Area's. We attempt to harvest all spike bucks as encountered. We set a harvest quota (usually 40 to 60 animals per year) and then take both does and "management" bucks (i.e., those that don't meet our criteria for "trophy" bucks). We typically harvest 12 - 14 "trophy" bucks, with the top buck for 1997 scoring 162 B&C. A "management" buck in our scheme is a mature buck that has short tines, inadequate mass, or other quality that we deem inadequate for our goals. We have not been as successful in marketing these "management" bucks (we refer to them as "classic" bucks as opposed to our top of the line "trophy" bucks).

I look forward to listening to all the comments and data presented at this symposium. My mind is open and I'm willing to take a look at different people's ideas, then try to adapt them to fit my management situation.

TO CULL OR NOT TO CULL: A REALLY GOOD QUESTION!

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"*Game management is the art of making land produce sustained annual crops of wild game for recreational use. Its nature is best understood by comparing it with the other land-cropping arts, and by viewing its present ideas and practices against a background of their own history*." (Leopold 1933:3)

Although the white-tailed deer (*Odocoileus virginianus*) for many years has enjoyed the status of being the most popular big game animal in the eastern US, recent interest in managing the species for trophy-class animals has escalated to impressive proportions. Much of this increased interest has been generated by the popular press, as well as economic pressures on private landowners to develop alternative sources of income. In Texas alone, whitetails now provide an annual economic impact of about $3 billion. No management activity has generated more controversy and misinformation than strategies to enhance trophy quality; yet, there are few scientific studies examining effectiveness of these activities.

Frankly, wildlife scientists have not kept up with consumer demand for information concerning intensive deer management. Why? Biologists are split as to the role genetic manipulation should play in deer management. Some raise ethical and public perception questions about these practices; while, others assert they have no real impact and are a waste of effort. In this presentation, we will attempt to discuss what we know about the potential for culling in management and hopefully raise some relevant questions we feel need to be addressed.

Although this session has been billed as a "debate," we do not feel a firm position can be taken at this time. Hence, our presentation should represent 1 of 2 opinions on the topic. We will attempt to proceed logically.

What is Culling?

Before we can discuss intelligently what culling is and isn't, we need a definition. Webster's dictionary provides a simple suggestion: "*to pick out from others*." Obviously, that's not much help. But, it does imply a selectivity of harvest. Hence, for the purposes of our presentation, we will interpret culling to mean the selective removal of specific individuals. Selectivity then connotes removals based on some criterion. What might these criteria be?

Culling or "The Cull" has been an accepted management practice in Europe for about 400 years. In fact, there is a patron saint devoted specifically to improving the herd by proper harvest: St. Hubertus. He is credited with saving the deer of Germany. St. Hubertus felt heavy harvest of the best males and restricted female harvest led to declines in numbers and trophy quality. Most European game keepers now consider the cull to involve both selective removals of "inferior" males and population control.

The assumed functions of culling then are to (1) control the population by removal of females, and (2) improve trophy quality by regulating who gets to breed. We do not think there is much need to justify population control among this gathering. Indeed, overpopulation is a problem common to many of our ranges. Later in this presentation, however, we will point out that culling of females may involve far more than random removals. The focus for most of our presentation will be the selective removal of males to improve antler quality. Now that we have proposed a definition of culling, we proceed to *why* one would want to change antler characteristics.

What is a Trophy?

For years, it has been bandied about in the popular and technical literature whether "trophy" is like beauty, i.e. in the eye of the beholder. The implication is a buck scoring 150 inches by the Boone and Crockett System may be the minimum criterion to a south Texas hunter, while a 2.5 year old, 8 point buck would be a memorable achievement to an east Texas sportsman. There probably is a great deal of truth in this. However, Kroll and Whittington (1994) asserted that "big" was synonymous with "old." They felt any mature (4.5 years or older) buck should be given trophy status. Their reason was such an animal was a challenging adversary, equal to the abilities of the most experienced hunter. A younger buck (a yearling in particular) should be considered as less than challenging. Jacobson and

Kroll (In press) raised questions about the biological implications of harvesting young bucks; recommending changes in regulations to provide more protection to immature bucks. Indeed, Leopold (1933) questioned the soundness of shooting young bucks on biological grounds.

But, this does not provide an answer to the basic question: What is a trophy? As often happens, scientists tend to seek answers hypothetico-deductively. The true answer lies with the consumer. After about 2 decades of popular press, the consumer (hunter) fully knows what a trophy is; albeit a qualitative assessment. The Boone and Crockett System has emerged as the recognized authority on trophies. Although there have been numerous attempts to circumvent Boone and Crockett with new systems (viz., Burkett or Buckhorn, Buck Masters Full Credit, etc.) they have not met with much public acceptance. Even though a hunter may not understand what it takes to measure 170 inches B&C, he knows full well the significance of the number: it's obviously a trophy! So, even if a hunter would never consider letting a 100-inch buck pass, given a choice he will shoot the buck with an anticipated higher score. That is the nature of modern society; perhaps even historic society.

Hence, trophy status and, inherently the hunter's status with his or her peers, is a function of the B&C score. Trophy status translates, in a consumer society, to economics. A buck with a higher B&C score is worth more economically to the landowner than a lower scoring individual. It is a function of the consumer's willingness-to-pay. Anyone who has attempted to market so-called "management" or "cull" buck hunts will attest to the difficulty in selling such packages. Economists for many years have used willingness-to-pay as an indirect measure of the true value of some commodity to the public. [We will deal with the ethical ramifications of this mentality later.] So, the general hunting public has come to equate trophy quality with Boone and Crockett score, whether we as professionals like it or not!

Understanding the Boone and Crockett System

As most of you know, the Boone and Crockett System has evolved over the years, but the consistent theme of scoring is *symmetry*: one side is compared to the other. Side to side deviations are deducted from the total inches of antler to yield a "net" score. In contradiction to our earlier statement that no new system will supplant the B&C System, there has emerged a consumer-originated new method: gross B&C. Rarely does anyone use the net score to describe

a buck. When a rancher advertises he has 150-class bucks available on his property, he is referring to gross rather than net score; and, the consumer is fully aware of this. It is not considered a deceptive trade practice.

Kroll and Whittington (1994) reported what they referred to as the "10-20-30-40" rule. If we examine the Boone and Crockett record books, in general the relationship of four measures of antler quality (viz., spread, mass, beam lengths and tine lengths) conform to their rule. That is, spread accounts, on average, for about 10% of the score; circumferences (= mass) 20%, beam lengths 30% and tine lengths 40%. Armed with this information and using a computer simulation package, we constructed the four bucks shown in Fig. 1. Note they all score exactly the same thing: *207*. Yet, they differ in 1 main parameter: number of main frame points. A "main frame point" is 1 emerging typically from the top of the beam in a "normal" position, rather than drop tines or other points emerging from the sides of the beams or tines. We do not consider non-typical or extra-typical points in this analysis, as in most cases they result in deductions from the total score.

Some interesting comparisons can be made. First, the 14-point version is much smaller overall than the bucks with fewer points. The 8-point buck has the largest set of antlers; in other words, it takes a larger box to contain them. As the number of main frame points are reduced, other measurements have to increase to make up for the loss. Hence, it probably will never happen that an 8-point buck will break the world typical record. That is why there are so few 8-point bucks in the record books. It is easier for a buck with multiple points to score higher in the record book.

Main Frame Points and the Population

Although we fully admit the above discussion does not take into account the non-typical classification, the final score of any buck, typical or non-typical, is greatly influenced by number of main frame points. Therefore, if the management goal is to produce large numbers of trophy-class animals (say 150 B&C or higher), the manager will have to implement a strategy to enhance the proportion of mature bucks in the population with 10 or more main frame points. Irrespective of genetics, examining the distribution of main frame points in the "average" deer herd often will yield a *normal distribution*, peaking on 8 points. In fact, Kroll and Whittington (1994) asserted a whitetail buck "wants" to be 8 points and about 130 inches B&C. In other words, the normal standard for the species is this antler configuration. In mature bucks, individuals with less or more than 8 points are increasingly rare as you move away from the median. Hence, it is very unusual to find

a mature buck either with 2 points (spikes) or 14 points on most properties. This certainly is no real revelation, as many biological traits conform to a normal distribution.

Therefore, the question arises as to the genetic implications of this observed distribution. The unanswered question is what we see antler-wise in bucks correlated directly to the genetics of the animal or some environmental manifestation? We all know, for example, nutritional plane greatly affects antler size. Other factors include social status, previous reproductive demand and stress. However, although we make no claim to being geneticists (our genetics training ended long ago), it is obvious many of the characteristics of modern livestock were derived by selective removals and breeding of animals with perceived rather than actual genetic superiority.

What Do We Know About Heritability of Antler Traits?

The simple answer to this question is: *nothing*! However, there are some who would dispute this. It is our assertion not enough is known about heritability of antler traits to make definitive statements. The spike buck controversy is a notable example. There are 2 "camps" represented here today, each strongly supporting an entirely different position. One says spikes are inferior, the other says they are not. One claims high statistical correlation between yearling antler quality and subsequent antler develop, the other little. Yet, there *is* some anecdotal and experiential evidence that some antler traits are indeed passed on to offspring. Later, we will discuss the Ft. Perry Project. What we have seen at Fort Perry is the same antler characters and combinations of characters continually emerging from generation to generation. Clearly, there appear to be some heritable traits. Kroll (1991) proposed that points and conformation are strongly influenced by the male, while the actual size of antlers is more influenced by the female. We currently are conducting a long-term study on these relationships; primarily looking at the female contribution to the antler "equation."

The Ft. Perry Project. In 1987, we began a long-term project at Ft. Perry, near Columbus, Georgia. We added property in 500-acre, fenced segments until we reached a total of 2,000 acres. Each segment was cleared of all resident deer. This was accomplished by still hunting, followed by intensive hunting with hounds. A complex road network was used to determine whether all deer were removed by searching for tracks. Therefore, we could be reasonably sure all deer were removed before Phase Two of the project.

Phase Two involved selecting animals from breeding programs whose sires were qualifying Boone and Crockett bucks. A total of 37 deer were released. All but 1 of the founding bucks had 10 or more main frame points as 2½ year olds. The one exception was a buck that had been a 10-pointer up to 6.5 years, but had declined to 8 points at time of release. We also initiated an intensive nutrition program, involving year-round plantings of 15-20% of the area to forage crops. These plantings included: rye, rye grass, oats, arrowleaf and crimson clovers, alyceclover and cowpeas. We also installed feeders at a rate of 1 per 40 acres which supplied 16% pelleted ration and mineral ad libitum.

The current whitetail population is more than 500 animals. Tissue samples were obtained from all founder animals for later DNA analyses. The long-term goal of this project is to answer some basic questions about, (1) heterozygosity, (2) gene flow, (3) success of founding stocks, and (4) long-term effects on antler quality. Sources of founders, with the exception of a single male from Mississippi (*O. v. virginianus)*, included only northern races (viz., *O. v. borealis* and *O. v. macrourus*), obtained from breeders in Illinois, Indiana, Wisconsin, Michigan and Kansas. Over the last 5 years, we annually have used infrared-triggered camera technology developed by Jacobson, et al. (1997) to obtain photographs of all bucks on Ft. Perry and on several other study areas. We also are monitoring herd production, antler quality, nutritional plane and behavior. The Ft. Perry buck population has been culled selectively since the beginning of the project. We annually remove all 2.5 or older bucks with 8 or less main frame points.

A Comparison of 3 Herds

The real problem in answering the primary questions regarding effectiveness of culling lies in the fact there are no published studies on the subject. The harsh reality is the cost of a controlled, scientific study is staggering. The study initiated at Ft. Perry alone has cost more than $2 million to date, and we are just beginning to see results some 10 years into the project. Another problem which exacerbates the situation is often there are "apples to oranges" comparisons made in the popular, and even some scientific, literature about impacts of various management practices. Again, we return to the spike buck situation.

One individual at a well-publicized debate, hosted by the Texas Wildlife Association, on spike bucks asserted: "*I'll have you know I've killed every spike I've seen now for 10 years, and the number of trophy bucks*

has increased!" That may be a true statement, *but* under questioning, he also had implemented an intensive feeding program, an improved grazing program and a significant herd reduction program. Which 1, or combination of, these practices provided the positive results?

Although we have conducted demographic analyses of many herds over the range of the species, we decided to make comparisons among 3 study areas: Ft. Perry (Georgia), Mustang Creek Ranch (Texas) and Longleaf Farms (Mississippi). These 3 areas were selected because they represent similar levels of management; viz., annual food plot plantings, herd control, etc. In other words, we are not concerned about the nutritional plane of these herds, nor the population density. However, the management strategies for these 3 areas in regard to buck harvest were quite different. Each maintained the population below "K-carrying capacity." As noted above, the Ft. Perry strategy involved intensive removal of all bucks 2.5 years or older with 8 or fewer points. The Longleaf Farms herd, however, was managed for mature bucks, without culling. The Mustang Creek Ranch had not been hunted for bucks for 5 years at the time of our study.

We conducted infrared-triggered camera studies (Jacobson et al. 1997) on the 3 study areas. Several thousand photographs were obtained from these studies. We feel most, if not all, bucks were photographed at least once. Figure 2 presents frequency distributions of main frame antler points for bucks 3.5 years or older for each area. Note the striking dissimilarity between areas. Bucks on the unhunted Mustang Creek Ranch generally followed the theoretical, normal distribution, with the median number of points being 8. Note also there are bucks with abnormally few and many points in the herd, as well. But, they are very rare. The Longleaf Farms herd, on the other hand, has been managed for mature bucks, without culling. The origins of the animals originally stocked is not totally clear, but it is thought most came from South Carolina. In this herd, the points distribution is skewed toward the lower end, with 10 points being very rare. We feel this probably is a function of some genetic drift phenomenon, rather than historical harvest strategy. It does suggest, however, to significantly change the phenotypic appearance of the herd, it would be necessary to allow only a few individuals to breed. That precisely is the strategy imposed at Ft. Perry.

We decided *a priori* to impose a system of artificial genetic drift, in which we hand-picked sires and dams presumably with desirable traits. This was followed by 10 years of intense culling; sometimes as much as 80% of the 2.5+ year old buck population. Clearly, we have

indeed made an impact on the quality of antlers at Ft. Perry.

A Proposed Culling Strategy

As we noted above, the term "culling" connotes more than merely removing males with undesirable traits. It also includes removal of females, either to control the population, manipulate age structure or remove less productive females. We offer this caveat: given what we do not know about genetics of whitetails, implementing a culling strategy may in the long haul turn out to be a wasted effort. However, we offer 2 points to consider: (1) the success we have experienced at Ft. Perry suggests that a severe culling program might change buck appearance; and (2) at best we can see no long-term detrimental effect of culling should it turn out to be a neutral management practice. Lastly, although it may elicit the ire of some, we know of no herd in North America other than the Ft. Perry herd where culling has been imposed sufficiently to effect a change. In light of these points, we currently are imposing the following culling strategies on the herds we manage.

The female segment should be harvested by a strategy allowing control of reproduction. The vast majority of herds have too many females, even those where the landowner honestly believes he has achieved population control. There only is a need for enough females to produce an annual crop of bucks and replacement females. This implies significant control over the herd, which few managers can demonstrate. Who among you has not attempted to control the population only to be exasperated with inability to shoot females once they "smell DuPont?" Few of the Herd Control Permittees in Texas have achieved their stated harvest goal.

As with bucks, however, there is importance to which females are removed. The age and type of female removed depends on the management goal. Early on, we feel you should remove all older females. This accomplishes 2 things. First, it helps reduce total fawn production as younger does tend to produce fewer fawns. Second, it permits you to take advantage of improving nutritional conditions and genetic makeup; i.e., it "stirs the genetic pot." Once the herd is under control, however, you may want to implement a different strategy that employs removal of doe fawns primarily, leaving only those necessary for annual recruitment. In both cases, this requires a very good handle on production and mortality rates of your herd. Each year at Ft. Perry we have walked out the entire property with volunteers and students to find all

carcasses. We age and sex all dead deer and have a good estimate of annual mortality by age and sex.

Culling of bucks is another thing. It is intriguing to us that most ranchers in south Texas limit their lessees to about one buck per 500 to 1,000 acres. We feel this is a serious mistake! Returning to our assessment earlier, if the average hunter is selective in harvest which bucks will be harvested under this scenario? Obviously, the larger antlered individuals will be taken. Since bucks with more antler points are rare, a few removals could have serious implications. We feel it is fully possible to *high grade* a herd on as large as 100,000 acres in only a short time.

There are 2 strategies available. First, you could repeat the Ft. Perry experiment, fencing and removing all native deer. Then, restock with animals assumed to carry superior genetics. This would be followed by intensive culling of all bucks that do not meet minimum criteria as we have at Ft. Perry. A second approach would be to implement an intensive culling of all animals that do not fit a strict criterion for several years. Lukefahr and Jacobson (1995) analyzed Jacobson's data from Mississippi State, concluding that given the observed heritabilities of antler traits, it would take about 100 generations to change the genetics of the herd. If we assume a generation time of 3.5 years, that means it would take some 350 years to accomplish our task. But, that is under normal harvest. We could accelerate this change by limiting the number and quality of bucks reaching maturity. Again, we know of no property being managed at this level of harvest intensity. It may require harvests of 90% of the mature bucks. All being equal, we would opt for the former strategy.

As noted earlier, no issue has created more controversy than the culling of spikes. Unfortunately, we still do not have the definitive answer. However, we maintain the culling of yearling bucks is too risky to implement. A more important consideration, however, is what age above yearling to harvest. We are in agreement with Jacobson's point that many bucks eventually become trophies. But, to allow a buck as long as he needs to reach trophy class is to ignore basic economics. We often work with landowners who have all the time and money needed to wait out the results of any practice. For most landowners, however, their whitetail crop has to be harvested as quickly as economically feasible.

We have observed 3 basic growth strategies in bucks. First, some bucks have antler growth strategies which improve linearly with age. Another group have relatively poor antler quality until 4 or 5 years, then *explode* into trophy bucks at some future age. Finally, there are bucks that become trophies at 3.5, but do not add much antler growth thereafter. Our cullling strategy at Ft. Perry has been to favor the last group. And, it appears to be paying off, as we have a large proportion of that age class as 170-190 inch animals. The cost of carrying a buck to older age classes, both economically and biologically, is too great. Finally, to adhere to the concept, harvest no buck before his time, is to negate any cullling effort.

Summary

We know very little about the genetics of whitetails. It is our opinion there is a place for culling *both bucks and does* in whitetail management, but only in a few herds. Most of the concerns of biologists about genetic manipulation revolve around perceived ethical considerations. Yet, Leopold's (1933) admonition that wildlife is a crop often is ignored. We cannot have it both ways. If we want the landowner to favor wildlife over other crops, we have to work with him to improve the quality and yield of his crop. One prominent biologist recently chided trophy management with: *"Is it easier to kill a mature 8-point buck than a mature 10-point, 170 class buck?"* The implication is that the hunter should be happy just harvesting a mature buck. It does indeed have its merits, but it ignores human behavior and economics. The consumer has already spoken and the demand is for higher quality bucks.

We turn the question backward: *Is it easier to kill a mature 10-point buck than a mature 8-point buck?* We feel trophy quality can be improved without sacrificing the quality of the experience. The same individuals who criticize trophy management are those who support wholesale mining and rape of the buck segment! We feel the ethical issues in deer management lie in the areas of fair chase and the role of the hunter in the 21st century. Our studies have shown the public is willing to accept hunting, provided they feel the hunter is vital to the health and well-being of the resource. We would like to see the hunter make the transition from consumer to hunter/manager. The whole idea behind culling (effective or not) is to improve the herd. That certainly is in line with this new ethic.

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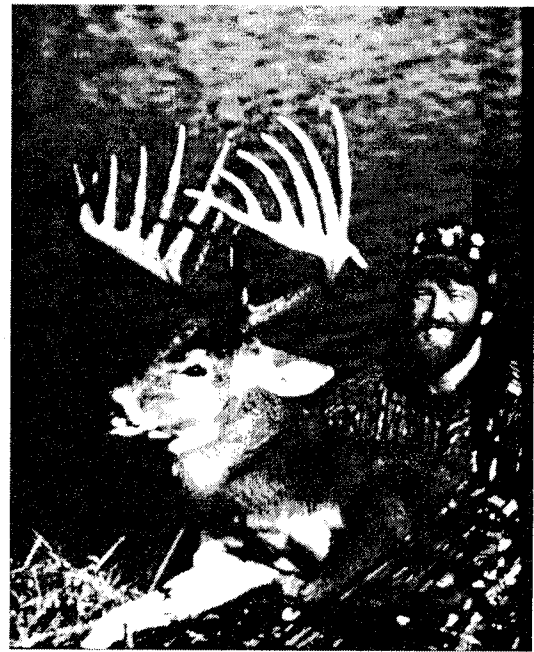
Figure 1. Using a computer simulation, the authors created 4 bucks, each scoring the same 207 inches (Boone and Crockett). Total tine lengths account for approximately 40% of the gross score. Therefore, an 8-point main frame buck must compensate by adding inches to the other scoring parameters, e.g., beam circumferences, beam lengths and inside spread. Notice the size of the "box" it would take to store each set. The probability of an 8-point buck that will break the world record typical score is quite remote.
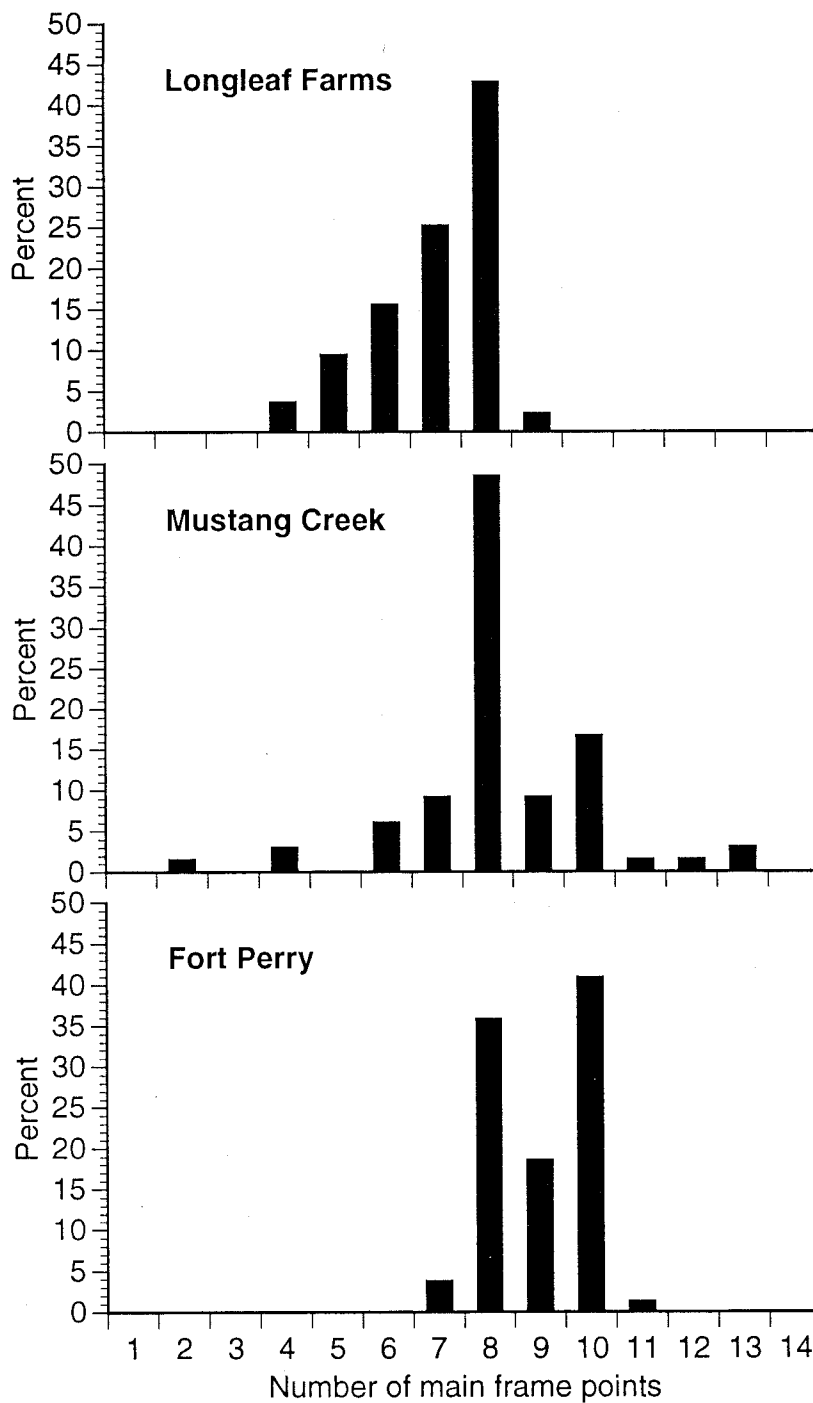
Figure 2. Distribution of main frame antler points of adult white-tailed bucks on 3 study areas under different management regimes.

CULLING AS A MANAGEMENT PRACTICE FOR WHITE-TAILED DEER: THE DARK SIDE

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Culling can be defined as removal of animals from the breeding population (S. D. Lukefahr, Dept.of Animal and Wildlife Science, Texas A&M, Kingsville, pers. commun.).   However, managers also use the concept of culling as a means to shift the phenotypic quality of a deer herd for economic or esthetic returns. In the latter case, the emphasis is to remove "inferior quality" animals to increase the probability that remaining animals would achieve higher quality than they otherwise would if the low quality animals were still present. The practice of culling deer for the purpose of improving herd quality gained emphasis as a management practice after the publication of Brothers and Ray's (1975) book, *Producing Quality Whitetails*.

Undoubtedly, private landowners and some deer managers practiced culling before this, but Brothers and Ray's book identified undesirable antler traits which could be targeted for elimination by the deer manager. Herein, I will explore perceived and real values to be obtained from both the concept of culling for genetic improvement and culling for phenotypic improvement of a deer herd.

Any animal can be targeted for removal from a breeding population. However, with wild populations, culling is generally limited to yearling and mature animals. This is because, unless age is known, it is extremely difficult to identify if an animal is an exceptional 2 year old, an average 3 year-old or a poor quality 4 year-old.

Although any number of traits could be selected for or against, most managers who have practiced culling have used 2 strategies, (1) removal of spike yearling bucks and (2) removal of middle age to mature males with "inferior" antler quality. In the latter case, bucks with average to below average (usually with 9 or less points) are targeted for removal.   In the common vernacular these are usually referred to as "management bucks".

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Spike Removal

Probably the most controversial practice has been the elimination of spike bucks. It has been common for some managers to eliminate spikes, with the thought that selection against these animals would improve the remaining gene pool. However as discussed elsewhere in this conference (see Jacobson and Lukefahr), we now know spike antlers show low heritability and that the prevalence of this trait is more likely linked to maternal and non-maternal environmental influences than to heritability.   Further, in captive deer research at Mississippi State University, I found the number of antler points yearling bucks had was not significantly associated with any antler traits by the time they reach 5-7 year age classes (Jacobson 1995*a,b*).   This relationship is shown by Figures 1-6. However, for some measurements, such as Boone and Crockett score, there were significant differences between some yearling antler point classes through the 5-year age class. Yearling bucks with 9 or more points also had better antler qualities in older age classes than bucks with 8 points or less.   At the 5-year age class, bucks with 9 points or more as yearlings had significantly greater gross Boone and Crockett scores than did 2-point, 5-point, 6-point, and 8-point yearlings, but did not differ significantly from 3-point or 5-point yearling bucks (Table 1). With larger sample size, this class of buck may prove to demonstrate significantly better antler qualities in latter life than other yearling bucks.

Since the 5-year old class is the age when white-tailed bucks are generally considered mature, I have provided comparisons of 5 year-old bucks from the captive deer herd at Mississippi State University on the basis of the number of points they had as yearlings. With the exception of Boone and Crockett score and antler weight of bucks with 9+ points as yearlings, spike yearling bucks were not significantly different from bucks of any other antler class by the time they reached 5 years-old.   While not significant, spike yearling bucks did show lower average quality than bucks of other classes for beam length, Boone and Crockett Scores, and antler weight through the 5-year antler class (Table 1). However, as shown in Figures 1-6, by 7 years of age, bucks with spikes as yearlings were equal to or exceeded other yearling antler classes.

For the manager, the question to be asked is what is to be gained by culling yearling spikes. Certainly,

nothing is to be gained from the view of improving genetics of the deer herd. It could be argued, that if an overpopulation of bucks were present, then harvest of spikes would allow average antler qualities of the remaining younger age class bucks to show improvement. However, we know harvest of bucks does not control overpopulated deer herds. Deer herd reduction can ultimately only be accomplished by reducing the number of females in the population. I personally have never encountered a management situation where hunters thought there were too many bucks in a deer population!

If instead of asking what is to be gained, the reverse question, what is to be lost from culling spikes is asked, the answer is obvious. It would be the opportunity to harvest that spike yearling buck at maturity. On the basis of the Mississippi captive deer data, this deer would be a buck which averages more than 10 antler points and a Boone and Crockett score of from 132-142. This exceeds the quality of bucks that most hunters would consider a true trophy.

Culling Mature Bucks

Culling of mature bucks can be expected to result in genetic improvement, if animals with inferior antler qualities can be selectively removed, and, as a result, animals with exceptional antler qualities have higher probability of breeding. Unfortunately, most management programs that practice culling of inferior quality bucks also remove trophy animals with exceptional antler qualities. Therefore, the management emphasis has been to remove the poorest and the best animals. The end result is predictable: *the average*!

Additionally, there is the question of how to identify an animal with superior breeding value. When examining the progeny of breeding bucks from the captive deer herd at Mississippi State University, several bucks which would have high enough scores to meet the Boone and Crockett record book have been produced. Most of these record book bucks were produced by bucks which themselves had Boone and Crockett scores well below record book quality. One buck that has produced 4 sons with record book qualities (>170 gross Boone and Crockett score) was, at 6 years of age, a very below average buck with 7 antler points and a gross Boone and Crockett score of 124. In a culling program, this animal would have most certainly been on the "hit" list. Incidently, this buck was a spike as a yearling.

Case Histories

The last consideration in culling as a management strategy is simply this: *does it work*? I am personally familiar with 2 high-fenced Texas ranches that have a history of over 20 years of intensive deer management. From the time of enclosure of the deer populations on these ranches with high fences, the owners engaged in intensive culling programs of spikes and mature bucks with poor antler qualities. One of these ranches, the Rondado ranch, was managed, from the beginning, by famed biologist Al Brothers. When asked if there was any difference in antler qualities of mature bucks harvested early in the management program versus the present day, Brother's response was *"there is no significant difference."* Similarly, the Lochridge ranch in East Texas, is an 11,000 acre high-fenced ranch that engaged in an intensive culling program since the inception of a high fence in 1976. In spite of a documented much reduced deer population, agricultural improvements, supplemental feeding, and the intensive culling program, there is no noticeable improvement in quality of bucks harvested or seen on Lochridge today than 20 years ago. In fact, the best deer taken on Lochridge were harvested or found dead on the ranch in the first 5 years after fence construction.

Conclusion

Culling can have a place in deer management. Managers can be selective in harvest to improve average phenotypic quality of antler traits in a deer population. If culling is to result in significant genetic progress, the culling process would have to exert selection for desired antler qualities as well as selection against undesirable traits. In general, this would require managers not harvest trophy class deer with exceptional antler traits they desire and that these animals have a better than average chance of producing progeny.

Culling of yearling bucks can improve overall average quality of younger age bucks remaining in a population. However, the result cannot be expected to provide improvement of genetic quality of a deer population. Rather, culling of yearling bucks can be expected to result in a reduction of the total numbers of mature bucks produced with antler qualities that most hunters would consider trophies. Culling of mature deer can be expected to result in some genetic progress, provided animals with highest antler qualities are allowed to remain in the breeding population and do not themselves receive selective harvest pressure. Otherwise, the result is to produce the average. To be realistic, culling should not be expected to result in

more than marginal genetic gains in free ranging deer populations within the lifetime of the manager.

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Table 1. Comparison of selected antler traits and body weights of 5-year-old white-tailed deer, in Mississippi State University captive animal facilities, on the basis of their yearling antler points.

Yearling antler points	N	Points	Beam Circum.. (Inches)	Beam Length (Inches)	Spread (inches)	Boone & Crockett Gross Score	Antler Weight (Grams)	Body Weight (lbs)
					Mean 5-year-old traits (± 2 SE)			
2	20	10.4(1.6)	4.68(.21)[a]	20.6(0.8)	17.6(1.2)	132(9)	1142(153)[b]	198(12)[c]
3	13	10.6(2.7)	5.43(.18)	21.6(1.2)[a]	16.1(1.6)	143(21)	1494(489)[c]	194(7)[a]
4	11	10.2(2.2)	5.12(.51)[a]	22.0(1.2)	16.5(2.1)	145(16)	1356(436)	200(11)[a]
5	12	10.3(1.4)	5.22(.52)	22.0(1.1)	15.8(1.2)	138(5)	1559(286)[b]	187(15)
6	15	9.6(0.8)	4.89(.30)[a]	21.8(1.1)	16.6(1.1)	137(10)	1295(147)[b]	201(16)[d]
7	9	11.0(1.7)	5.67(1.02)[a]	22.6(1.5)[a]	18.0(1.5)[a]	152(11)[a]	1587(442)[a]	192(15)[b]
8	9	10.3(1.7)	4.67(.56)[e]	21.3(2.6)[a]	16.7(1.4)[a]	139(12)[a]	1342(299)[c]	206(53)[b]
9+	6	13.2(1.7)	5.74(.39)	23.3(2.7)	15.4(1.2)	165(5)	2017(126)[c]	209(26)[e]

[a] One less sample than indicated.
[b] Three less samples than indicated
[c] Four less samples than indicated
[d] Five less samples than indicated
[e] Two less samples than indicated

NUMBER OF POINTS

	1.5	2.5	3.5	4.5	5.5	6.5	7.5
2 PTS ●	2	7.9	8.9	9.6	10.4	10.2	11.3
3 PTS +	3	9.1	9.5	9.9	10.6	11.7	8.9
4 PTS ☼	4	8.4	8.9	10	10.2	12.5	10.5
5 PTS ■	5	9.1	9.9	10.3	10.3	11.2	12
6 PTS ✕	6	8.3	9.7	9.3	9.6	10.6	10.4
7 PTS ◆	7	8.9	9.7	10.5	11	11.3	8
8 PTS ▲	8	10.1	10.9	11.1	10.3	10.2	9.7
9+ PTS ⬠	9.8	10.5	10.8	14.3	13.2	14.5	18

AGE
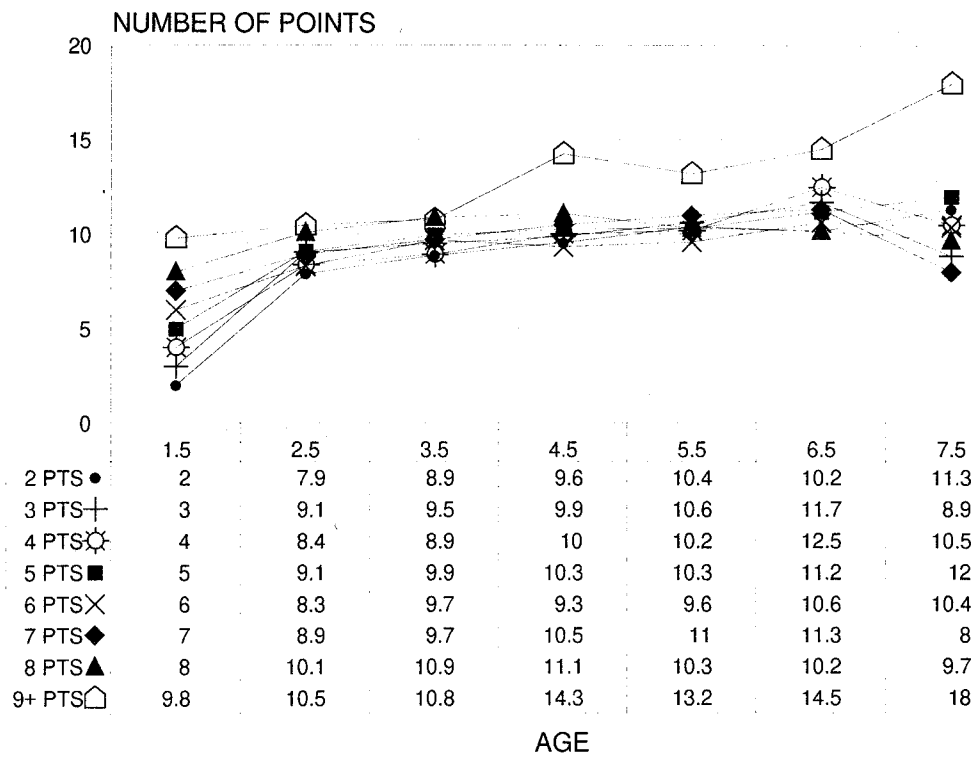
Figure 1. Average number antler points of bucks at different ages based on number of yearling antler points.

BOONE & CROCKETT SCORE

	1.5	2.5	3.5	4.5	5.5	6.5	7.5
2 PTS ●	18	86	114	128	132	140	142
3 PTS +	31	95	120	131	143	153	125
4 PTS ☼	35	97	126	140	145	162	141
5 PTS ■	40	98	123	133	138	140	145
6 PTS ✕	53	101	127	130	137	145	138
7 PTS ◆	60	110	133	145	152	150	136
8 PTS ▲	75	117	133	145	139	151	124
9+ PTS ⬠	81	127	146	160	165	170	183

AGE
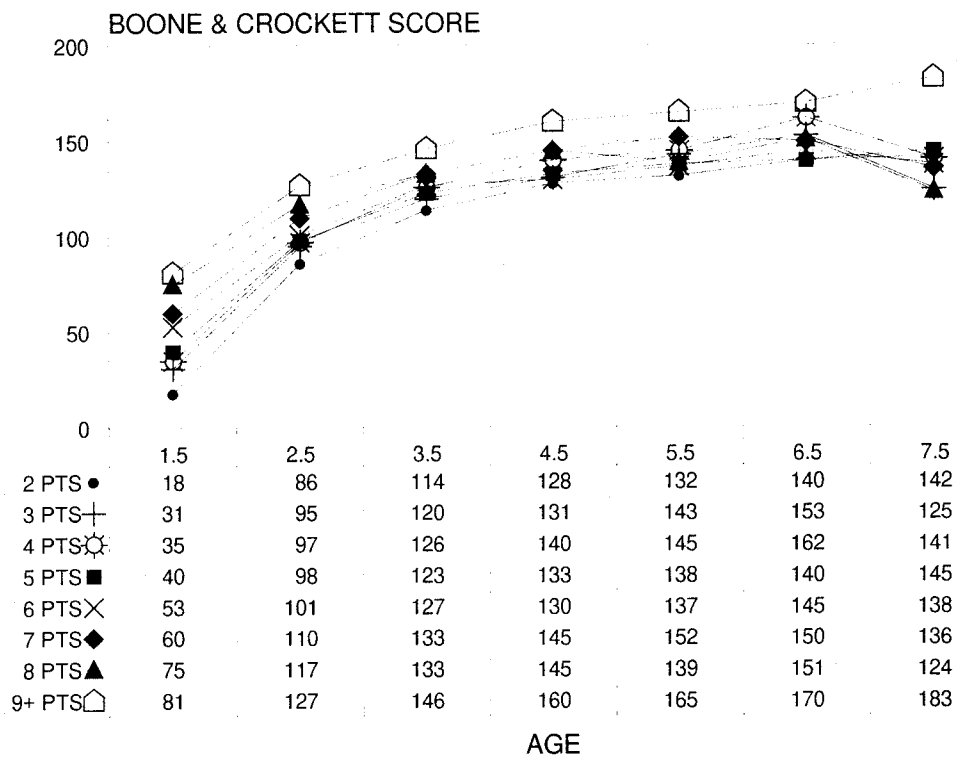
Figure 2. Average Boone & Crockett score of bucks at different ages based on yearling antler points.

	1.5	2.5	3.5	4.5	5.5	6.5	7.5
2 PTS ●	4.6	12.5	15.4	16.5	17.6	18.3	18.1
3 PTS +	7.1	12.9	15.8	16.3	16.1	16.7	17
4 PTS ☼	6.3	13.3	15.3	16.4	16.5	16.4	15.5
5 PTS ■	7.4	13.4	15.6	16.5	15.8	16.7	17.4
6 PTS ✕	8.7	13.7	16.2	15.9	16.6	17.2	16
7 PTS ◆	8.5	14.9	16.6	17.6	18	17.2	22
8 PTS ▲	10.1	15.3	16.4	16.4	16.7	17.2	18
9+ PTS ⌂	10.2	15.5	16.6	16.1	15.4	15.1	14.9

AGE
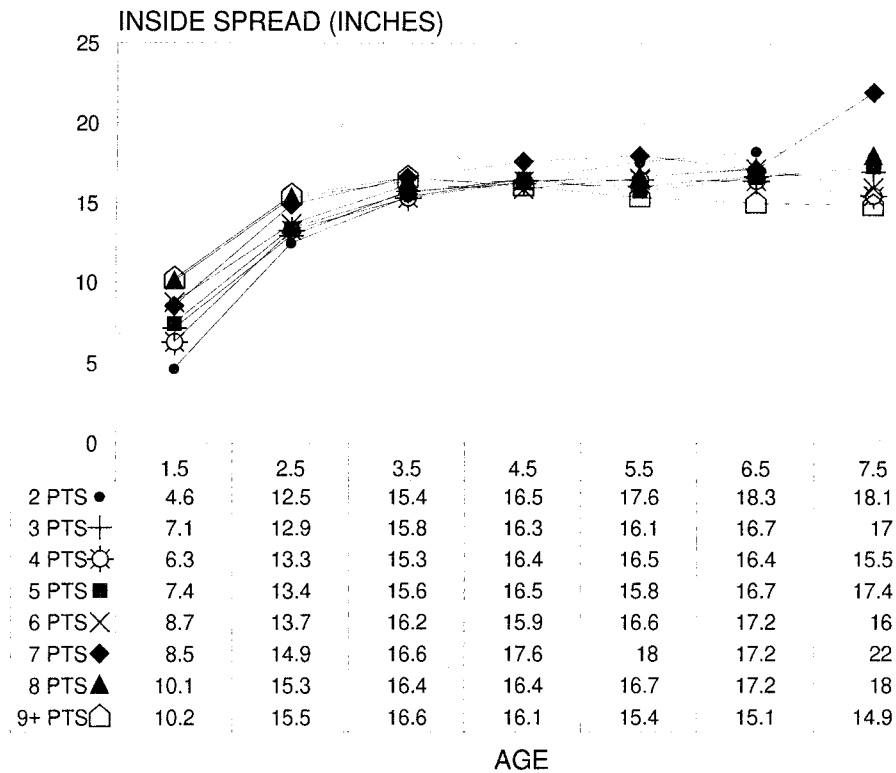
Figure 3. Average antler spread of bucks at different ages based on yearling antler points.

BEAM CIRCUMFERENCE (INCHES)

	1.5	2.5	3.5	4.5	5.5	6.5	7.5
2 PTS ●	2.3	3.5	4.1	4.4	4.7	4.8	4.9
3 PTS +	2.7	4	4.7	4.9	5.4	5.2	4.8
4 PTS ☼	2.6	3.7	4.4	5	5.1	5.5	5.4
5 PTS ■	2.9	3.8	4.5	4.9	5.2	5.2	5.2
6 PTS ✕	2.9	3.9	4.6	4.8	4.9	5	4.9
7 PTS ◆	3.1	4	4.6	5	5.7	4.9	4.8
8 PTS ▲	3.2	4.1	4.5	4.7	4.7	5	5.8
9+ PTS ⌂	3.4	4.4	4.9	5.7	5.7	5.5	6.1

AGE
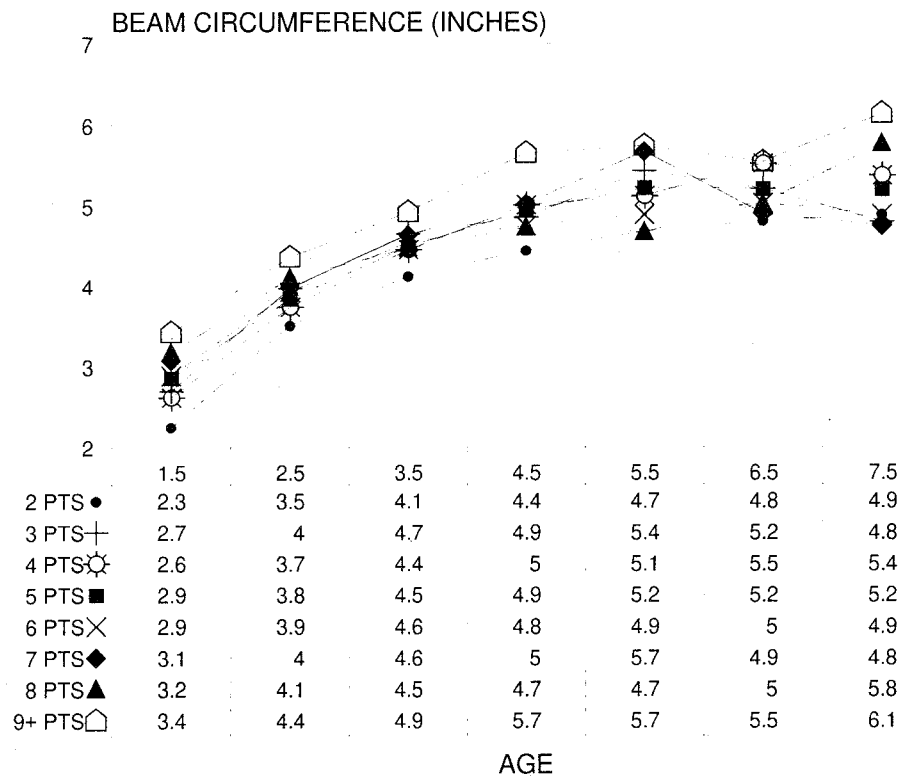
Figure 4. Average antler circumference of bucks at different ages based on yearling antler points.

WEIGHT (GRAMS)

	1.5	2.5	3.5	4.5	5.5	6.5	7.5
2 PTS ●	49	467	828	1,056	1,143	1,163	1,533
3 PTS +	101	630	1,133	1,350	1,451	1,640	1,807
4 PTS ☼	114	622	1,093	1,429	1,611	1,508	1,846
5 PTS ■	150	604	1,047	1,271	1,416	1,390	1,412
6 PTS ✕	224	673	1,054	1,235	1,347	1,399	1,371
7 PTS ◆	230	729	1,171	1,417	1,631	1,762	
8 PTS ▲	328	832	1,238	1,412	1,342	1,437	1,719
9+ PTS ⬠	400	1,033	1,376	1,756	1,995	2,172	1,879

AGE
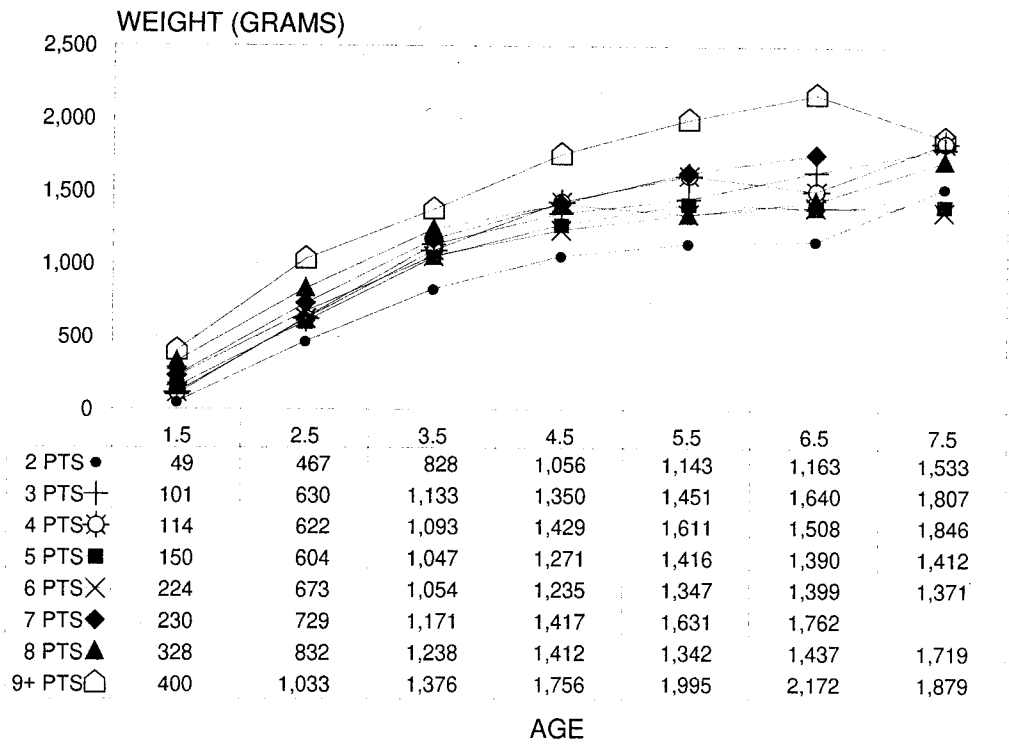
Figure 5. Average antler weight of bucks at different ages based on yearling antler points.

WEIGHT (LBS)

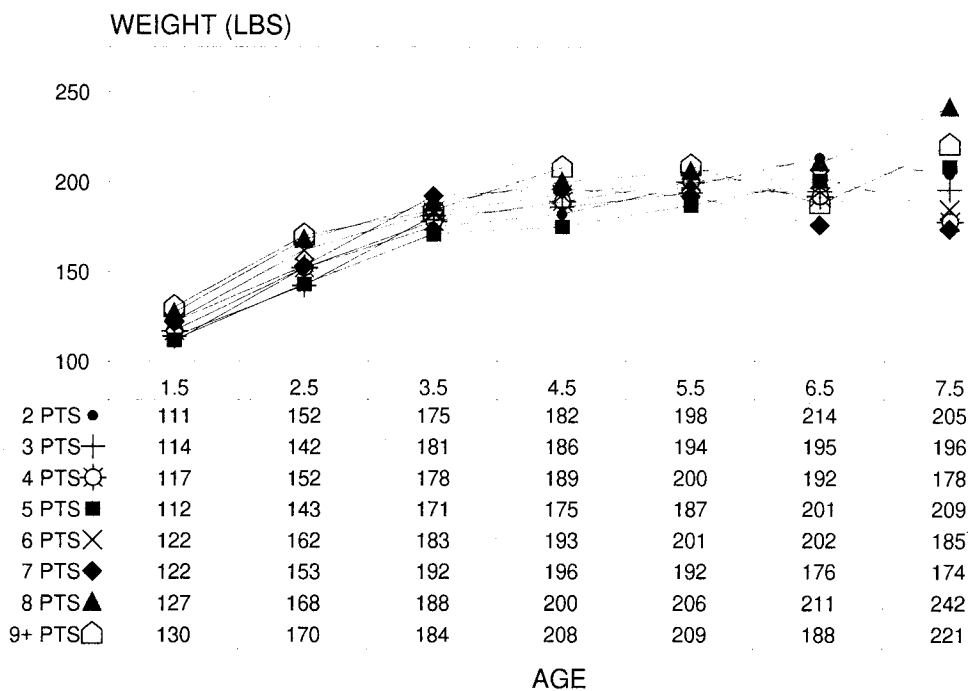|	1.5	2.5	3.5	4.5	5.5	6.5	7.5
2 PTS ●	111	152	175	182	198	214	205
3 PTS +	114	142	181	186	194	195	196
4 PTS ☼	117	152	178	189	200	192	178
5 PTS ■	112	143	171	175	187	201	209
6 PTS ✕	122	162	183	193	201	202	185
7 PTS ◆	122	153	192	196	192	176	174
8 PTS ▲	127	168	188	200	206	211	242
9+ PTS ⬠	130	170	184	208	209	188	221

AGE

Figure 6. Average body weight of bucks at different ages based on yearling antler points.

THE ROLE OF GENETICS IN WHITE-TAILED DEER MANAGEMENT

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Loren Skow asked me to present this talk. He said, "I want you to talk specifically about selection for antler characteristics in deer." And I said, "Well, OK, I'll do that if that's what you really want." And the next thing I see in the program is that we have a title of, "Assessing Management Strategies in Free-Ranging and Enclosed deer." What I really want to talk to you about is some of the things that are associated with selection in natural populations. And, so that requires that we come back and cover Genetics 101 again.

I know that Loren talked to you a little about the fundamental genetic concepts, but it is not going to hurt for us to revisit some of the issues. The points that I am going to touch on briefly in this presentation include:

1) Defining the trait that we are interested in selecting. This sounds a little trite, but it actually is critically important. What do we know about the way that the trait of interest is inherited? How many genes are involved in the inheritance of this trait? This defines very much how we will go about selecting the trait. Is it quantitative and multiple genes are involved in the expression of the trait? Or is it qualitative, like horns in cattle, where essentially there is a single gene that switches horns on and off?

2) The difference between what it is we measure in the field and what geneticists call a phenotype.

3) The components that define a phenotype. This is necessary in order that we can define the term heritability.

4) Response and correlated response to selection.

5) An example of selection response for antler characteristics that we developed from data provided by Texas Parks and Wildlife.

Let's define the trait. What is it that you are trying to improve? What is the characteristic that you are trying to change in the population? Is that characteristic sex-limited? If it is sex-limited, then obviously it is going to influence the proportion of individuals in a population that you can measure. If

you can't measure the characteristic in females, then, it is going to be very difficult to apply selection to the female side of the pedigree. However, even if you can't measure a trait in one gender, it is possible to select among those individuals, but it requires information on related males and pedigree information.

At what age do we measure the trait if, for example, we are interested in improving antler characteristics in 4.5 year old bucks? Are we going to measure the trait at 4.5 years? Because if selection is occurring in the population at 1.5 years of age and we are not measuring the characteristic until 4.5 years of age, life will be a little complicated! The breeding has already occurred before we could measure the phenotype that we are trying to change.

What percentage of individuals in the population do we actually have measurements on? If we are measuring characteristics such as Boone and Crockett (B&C) scores, do we have measurements on all the bucks that are available to us in the population? Or, on only some small proportion of the individuals in the population? All of these issues have an impact on the effectiveness of selection.

By defining the trait, we must consider the qualitative or quantitative basis for the inheritance of the trait. Are we talking about changing a characteristic that is determined by a single gene or by multiple genes? If only a single gene is involved, how is the trait inherited? For example, the presence or absence of horns in cattle is primarily dictated by a single gene. However, among cattle that have horns, horn size is inherited as a quantitative trait. So there are multiple genes that dictate horn size, but there is only one gene that switches them on and off. Further, the presence of horns is inherited as a recessive. So animals that do not have horns may carry the version of the gene that produces horns, but they do not express the gene. If two such carrier animals, without horns, are mated one quarter of their progeny will have horns.

Next, what is the difference between what we observe or measure on individuals and what geneticists call phenotype? What we measure is a combination of two things: 1) the phenotype of the individual, which is

comprised of additive gene effects (how genes additively influence a characteristic), non-additive gene effects (which is when specific combinations of genes behave differently than you would expect from simply adding their individual effects together), and individual environmental effects; and 2) systematic environmental effects that affect all individuals that are exposed to the same environments such as year, season or region effects.

Thus, what we call a phenotype is, in general, not what we obtain when we take field measurements on individuals because phenotypes are modified by the gross environment, the general environment in which those animals lived. When individuals are born in different years, the specific year and season effects influence the phenotype of an animal and modify it into the field data that we measure. Age effects are another example of a systematic environmental effect. If we measure antler characteristics on an individual at two different ages, clearly they are going to be different from each other. Hence age also modifies an individual's phenotype, as also do nutrition effects.

The whole point of differentiating between a phenotype and an observation is that, simply, if you identify a buck with a big rack, then it may have a big rack for a lot of different reasons. One of the reasons, clearly, is management, preferential treatment and nutritional effects provided during the rearing of that individual. The individual may be older than you think. It may have a good non-additive genetic combinations of genes. Or, finally, what we really want this individual to have is a good additive genetic combination of genes. That is, the genes that are influencing antler characteristics are all positive in this individual, because the important thing is that it is only these additive gene effects that are transmitted predictably between generations. If you want to genetically influence a population, it is only the additive gene effects that are transmitted predictably between generations. This concept is what is measured by heritability.

Heritability defines that part of the phenotype that is determined by the additive effect of genes. It measures the proportion of differences among individuals' phenotypes that are due to the additive effects of genes. Heritability lies between zero and one. If heritability is zero, that says that the best buck, or in fact, any buck in the population is going to produce average progeny, because there are no additive genetic differences among individuals. There are other differences that cause differences in antler characteristics, but there are no additive genetic differences between individuals in a population. And

so, essentially, you cannot change the trait by selection. If heritability and the amount of variation among individuals is very low, you will not be able to change a trait a great deal by selection. On the other hand, if heritability is very high, most of the differences between individuals in a population are direct reflections of the differences in their genes. This is the way that heritability should be interpreted. If heritability is one, then the best buck you identify in a population is going to produce progeny that are simply the average of his measured phenotype plus those of the females to whom he was mated. Half of the genes are transmitted from the buck to his progeny and the other half are from the does to whom he was mated. His progeny will be the average of the buck's genetic value and those of the females to whom he was mated. Thus, when you select breeding stock based on their phenotypes, what heritability is telling you is how well you can identify the underlying genetic values of those individuals. When heritability is zero, selecting individuals based on antler characteristics, those with the largest antlers do not have additive genetic differences causing differences in antler size. The difference is due to nonadditive genetic or environmental effects and these are not transmitted predictably between generations. If heritability is one, then all of the differences in antler characteristics are due to additive gene effects and all of these will be transmitted to the progeny.

What are the factors that define the rate at which you can change a population by selection? In essence, there are four things that define the rate at which you can change a population by selective breeding. These four things are: 1) heritability, 2) the amount of variation you have in the population, 3) the intensity with which you select individuals, and 4) the generation interval, which is primarily determined by the culling rate. A very important thing to note at this point is that heritability is not the only factor that dictates the rate at which you can change a population by selection. Even if the heritability is very high, it doesn't mean that you can necessarily change a population very rapidly, because of the importance of the other factors. In fact, estimates of heritability for antler characteristics are fairly modest, somewhere in the vicinity of twenty percent. However, this does not necessarily mean that you cannot change the antler characteristics of a population, because the second critical component is the amount of variation that exists among individuals in the population. If there is a great deal of variation among individuals in antler characteristics, it will still be possible to make genetic changes in the population even though the heritability may be relatively small. Intensity of selection also impacts the rate at which we can change a population

by selection. If you select the best bucks in the population to breed to the females, selection intensity is determined by the proportion of bucks selected. Do you take the best one percent, the best five percent, the best ten percent of bucks, or the best fifty percent- the top half? Clearly, the higher the intensity of selection, the faster you are going to be able to change the population. But it requires that the intensity of selection be greater than zero on both the male and female sides of the pedigree. If you are only selecting on the male side of the pedigree, then clearly, that is going to reduce the rate at which you are going to make changes from selection, because the intensity on the female side is zero. The final factor that influences response to selection is the generation interval, which is the average time that an animal stays in a population. It measures just how quickly the population is turning over. So, if you use a selected group of bucks to produce a group of progeny, the next thing you have got to do is to get those progeny back into the population. If you are making a selection response, if you are improving the population, you have to be getting rid of the older animals in the population and replacing them with the younger, genetically improved animals coming into the population. So do not fall into the trap of simply thinking about the magnitude of the heritability as being the single most important factor that will determine how quickly you can improve a population through selection. Heritability is not the only factor that determines selection response. It's how much variation you've got, it's how much pressure you are putting on selection on the male and female side of the pedigrees, and it's how quickly you are incorporating the progeny that you produce back into the population as the next generation of breeders.

The next thing of importance is correlated response to selection. We have talked about the factors that determine the rate at which you can change a population when you directly select for a trait, such as, Boone and Crockett score. However, you should be aware that many genes influence more than one trait. Geneticists call this pleiotrophy. For example, there are a lot of genes in humans, in mice, and in cattle that influence growth rate. Genetic research has also demonstrated that some of these genes turn on at different points in development. Some genes turn on early after conception, very early in the life-cycle of the individual; while other genes turn on later in life, after weaning for example. So it is not always the same genes that influence growth at any point in the animal's life. However, if we select for the versions of the genes that confirm increased weights at yearling or later in life, invariably what we find is that we increase weights all the way through development. This is what we mean by a correlated response. And the same thing is true in deer. Dorian Garrick, a friend of mine in New Zealand, has recently published two papers where they looked at genetic correlations in deer which determine whether or not you will see correlated responses. Some of these are interesting. For example, in farm bred deer in New Zealand, they found that the genetic correlation between two and five year old weights was about 93%, which is about what I would expect. If you look at this genetic correlation at the equivalent stages of maturity in mice, humans, cattle, it would be right up there at about 90%. So, most of the genes that are influencing five year old weight are also turned on at two years of age and are responsible for differences among animals in their weight at two years of age. The New Zealanders also found a genetic correlation of about 73% between male and female weights. This is interesting because the correlation is not one. What does this mean? It may mean that there are genes located on the sex chromosomes that also influence weight. They also found a genetic correlation of 73% between velvet yield and live weights, which is again what I would expect. When you select for larger animals, you get larger antlers, so you get more velvet. Unfortunately, not all genetic correlations are favorable. If we were to select for larger antler size, we would end up producing animals with the genetic potential for larger mature weights. Now, if we were stocking animals at, or near, the limit of our forage availability, it is likely that these animals with a larger genetic potential for growth may have a reduced fertility due to nutritional challenge. In any selective breeding program, it is very important that a good record keeping program be in place in order that the breeder can monitor the overall performance of the herd and look for undesirable correlated responses to the practiced selection.

Next, I want to talk a little about selection for antler characteristics. We decided to develop a model to get some sort of feeling for how much we could change antler characteristics in a farm population through the introduction of improved bucks. In our hypothetical population we had two-thousand individuals with a two/one ratio of females/males maintained by hunting. So this gives us approximately 1,334 females and 666 males in the population. Let's start out by assuming that we had a mean B&C score of 140 in this population. We assume a heritability of 50% for B&C score and this is quite optimistic because some of the published estimates of heritability are considerably less than this, in the vicinity of 20%-30%. We assumed that we are able to select a proportion of the males through the introduction of elite bucks. We assumed that in the introduced males we had a mean B&C score of 185. The easiest way to think about this is that you are just going to buy a group of males with a mean B&C score of 185 which are going to be

integrated into the farm population. These animals will then define a proportion of the males used in the farm population, and the original population, of course, has a mean of 140. The objective was to figure out, if we did this, how long would it take us to get to a mean B&C score of 165, i.e. to change the population mean from 140 to 165. If you brought in 100 males that had a mean B&C score of 185, they would define 15% of the total males that were in that population. So, remember that we were dealing with a population of about 666 males, and of those, 100 would now be brought in with a mean B&C score of 185. If you brought in 200, 300, or 400 males, then the proportion of elite bucks would increase to 30%, 45% and 60% with the introduced breeders having a mean B&C score of 185. In this strategy, selection is not operating on the female side of the population, it is only operating on the males that are being introduced into the population. And the question is how long will it take to move the mean B&C score in the population to 165? If only 15% of your males are introduced males, it takes 43 years to get to a mean B&C score of 165. If 30% of your males are introduced, you can get there in 22 years. If 45% of your males are introduced, you get there in 15 years and if 60% of your males are introduced, you get there in 11 years.

One of the points that I really need to strongly emphasize is that the genetic potential of these introduced males is not changing in time. Our calculations assumed that for the entire 43 years that you ran this breeding program, that the males that are introduced always have a mean B&C score of 185. This may be a little unrealistic because if you really are trying to change the mean of a population, then the introduced males may be getting genetically better each year. You ought to, in fact, be able to breed your own males that will, fairly soon, be better that the males that are being introduced. So we looked at what would happen if we could source improved bucks over the course of the breeding program. In the first four years, we assumed the males that were introduced to this population had a mean B&C score of 185. In the next four years, it would be 190. The next four years it would be 195, and in years fifteen to nineteen, it would be 200. So, in other words, we were making genetic improvements in the males that were being brought into this population. Again, no selection occurs on the female side of the pedigree. In this case, with only 15% of the males being introduced you get to your target B&C score of 165 in 29 years with this strategy. If 30 % of the males are introduced, you get there in 17 years. If 45% of the males are introduced you get there in 12 years. Clearly, genetic improvement is a long term process.

Let me conclude with a few observations. The literature seems to indicate that the heritability of antler characteristics in white-tailed deer is low. There have been a couple of studies, and I know that these studies have been reported and discussed extensively during this meeting. My impression is that both were fairly small-scale studies. Relative to some of the things we do in quantitative genetics in beef cattle or dairy cattle populations, the number of individuals that were involved in both of the studies where heritability has been estimated and reported is very, very small. So, these estimates, even though they were analyzed by the best statistical methods that were available, may not be very precise. That is to say, they may be accurate, but there may be a lot of uncertainty in how well they are estimated. So it seems to me that getting good, clear estimates of what the heritabilities are is a pretty important objective.

What is really critical, if you are not buying in huge numbers of individuals into a population to try and achieve genetic progress, which is what we just did in the example, is that you have to select your own males from within the population. The real problem here is that if your breeding objective is to improve B&C score in individuals that are 4.5 to 5 years of age, do you have to wait until individuals are 4.5 to 5 years of age before you can measure the characteristic and decide which individuals you want to use in breeding? Because if you have to do that, you have a big problem on your hands because they are at the end of their reproductive life, they have already done the breeding before you can decide which animals to select. Young bucks are already coming along behind them and are breeding the females in the population. However, it doesn't matter if the genetic correlation between B&C score in 1.5 year-old bucks and in 4.5 year-old bucks is not one. As long as this genetic correlation is positive and is moderate, then you are going to be able to make selection decisions in young individuals. And that's pretty much what you are going to have to do to be able to improve the population. You are going to want to hunt the older animals and you will want to make the selection decisions in the younger individuals in the population. But, again, there certainly is some uncertainty about what is the heritability of antler characteristics in young individuals and what the genetic relationship is between antler characteristics in young and older animals.

Selection response is going to be driven by the male side of the pedigree, because the females are not selected. It is really important to try and figure out what the optimum sex ratio is in a natural mating population because this is going to dictate how strenuously you can select the population. If you need

a 1:1 sex ratio in a natural mating population to be able to produce the maximum number of progeny, you can't select the population. The only way you are going to be able to select the population is by minimizing the number of males you need to breed the females. And the optimum sex ratio determines how intensely you can select the males in that population.

The more genetic progress you are making, the better are the younger individuals in the population. Even though these individuals have small antlers because they are young, genetically they have the potential to have much larger antlers when they are 4.5 years of age, than do the 4.5 year old males that are currently in the population. Consequently, hunting the existing 4.5 year old bucks in the population is desirable in the sense that it allows the genetically superior and younger males to breed the females. This strategy will help maximize the intensity of selection in males and therefore increase response to selection.

Finally, let me conclude by saying that selection doesn't change a population overnight. Selection operates slowly, though it accumulates in time, which is the important thing. For example, in dairy cattle, milk production is a sex limited trait, we only measure performance in females, not in males. We have to progeny test males to determine the best bulls in a population. The heritability of milk production is quite low, only about 25% in most dairy cattle populations in the world. However, the amount that breeders have changed milk production in dairy cows in the last fifty years is staggering. Production has increased from an average of about four thousand pounds of milk produced in a 305 day lactation to about twenty thousand pounds of milk produced per lactation. That is a five-fold increase in the last fifty years. Now this has not all been due to genetics, since the production environment has also been improved, but about one-third of this increase has been due to selection. So genetic improvement accumulates, and we can accomplish our goals in the long-term if we just get started. In a deer population, if you are going to apply selection to the female side of the pedigree it is going to require pedigree information and individual identification. This may require a technology such as DNA typing in order to be able to establish pedigree relationships in a population. It will also require that we produce accurate phenotypes on a large percentage of the males that are available for selection. If we only have records on a small proportion of the available males, then we can only select the best from among the small proportion on which we have information. We need to decide at what age we are going to make selection decisions, then obtain measurements on a large percentage of the males in the population in the appropriate age groups in order to make effective selection decisions.

HOW GOOD IS OUR AGING TECHNIQUE USING TOOTH REPLACEMENT AND WEAR?

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Abstract: Aging white-tailed deer using the tooth replacement and wear aging technique is widely used and accepted. We established a reference collection of known-age free-ranging deer from south central Oklahoma to evaluate the accuracy of the technique. Results from that study indicate that the technique allows us to confidently place deer into 3 age-classes only, i.e. fawn, yearling, and adult. Attempts to place adult deer into specific year age-classes using traditional methods were very inaccurate. Management or research programs requiring accurate and precise age determination of adult white-tailed deer should carefully review and critique the method.

If you are serious about managing white-tailed deer, chances are that estimating the ages of harvested deer, and perhaps even deer in the field, is an important part of your management and record- keeping programs. Age information is used to group deer into specific age-classes which in turn facilitates evaluation of management practices and herd health, and is sometimes used to evaluate growth potentials of certain individuals.

If management decisions are made based on age information, how those estimates are made and the accuracy of those estimates is of great importance. The most widely used and accepted aging technique is the tooth replacement and wear aging technique that was described by Severinghaus (1949). This technique is based on the theory that tooth eruption, replacement, and wear take place in predictable patterns and increments. Most wildlife professionals learned this technique while completing a wildlife curriculum at a university. These people in turn have passed it on to the general public as "the" way to age deer. Some believe that slight modifications are necessary to adapt the technique to a particular area or deer herd, but most practitioners use the technique as they perceive it was originally described. If other aging techniques are used, the tooth replacement and wear technique is generally used to verify the ages assigned using the other techniques.

How accurate is the technique? This is a valid question in light of the fact that few studies have tested the model and very little field testing has been done on free-ranging deer, especially deer in older age-classes. However, most people still believe the technique is fairly accurate. The general belief is that deer can be aged accurately a large percentage of the time using the tooth replacement and wear aging technique, and that a confidence interval of ±1 year includes the few that are aged incorrectly.

There is also a belief that the technique may require some "fine tuning" to improve its accuracy for particular areas. For example, it is theorized that tooth wear is greater on areas with sandy soils than on areas with finer textured soils. The thought being that the coarser-textured soils are more abrasive and result in greater tooth wear. There is a similar theory for areas that exhibit poor deer range condition versus good deer range condition. The rationale being that under poor conditions, deer have to eat closer to the ground, thereby picking up more soil particles with their food which results in greater tooth wear.

While these theories attempt to identify sources of error, they have not been tested. Furthermore, the overriding assumptions are that the differences result in only slightly different wear patterns than those originally described by Severinghaus (1949), and the amount of annual wear is consistent for deer within a given population.

A Case Study

Early in my professional career, I embraced many of these same theories and assumptions. The case study that I am going to relay was in fact designed initially to establish a reference collection of jaws from our management area that, over time, would allow us to fine tune the existing aging technique for our area. The study was conducted on the 2,947-acre Noble Foundation Wildlife Unit (NFWU) in south-central Oklahoma. Beginning in March 1983, free-ranging white-tailed deer were trapped, aged, tagged, released and subsequently harvested and/or recaptured in order to establish a known-age population of deer from which we established a known-age reference collection of jawbones. In 1992, we began to supplement the jawbone collection by constructing dental casts (Clawson and Causey 1991) of captured deer. In

December 1996, all of the jawbones and dental casts in the reference collection that were useful in evaluating the tooth replacement and wear aging technique ($N = 88$) were selected and used to construct a test which was administered to 34 southeastern United States deer biologists that routinely used Severinghaus' technique. The age-class distribution of jaws and casts used to construct the test are given in Fig. 1.

Jawbones and dental casts used in the test were classified as being either (1) known-age or (2) those whose ages were estimated conservatively. Known-age jaws or casts were designated as such if they were collected from deer initially captured and tagged as fawns, or from deer initially captured and tagged as yearlings (1-2 year age-class) and a dental cast made verifying them as such. For a deer to be verified as a yearling, all molars on the lower jaw were at least partially erupted and at least 1 of the following additional conditions existed:

1. the third premolar was 3-cusped and showed signs of wear;

2. the third premolar was 2-cusped but not fully erupted (this was sometimes verified by comparing with jawbones or casts taken from the same deer at later dates);

3. the first 2 deciduous premolars had been replaced but the permanent premolars were not fully erupted, or;

4. the third molar was not fully erupted.

These criteria were established based on review of the jawbones and casts of deer initially captured as fawns and subsequently captured or harvested as yearlings.

Jaws and casts were classified as conservative estimates if they were collected from deer initially captured as adults (> 2-3 year age-class) or from deer initially captured as yearlings without a verifying dental cast. If a deer was classified as an adult and a dental cast was made verifying them as such, the conservative age estimate was calculated using the 2-3 year age-class as the age-class at the initial capture. If however a deer was classified as a yearling or an adult at the initial capture, but a dental cast was not made verifying them as such, the conservative age estimate was calculated using the 1-2 year age-class as the starting point. In all cases, the only possible error was to assign deer to an age-class that underestimated the actual age, thus resulting in a conservative age estimate.

The results of the test were very interesting. Out of 88 jaws and casts, the average number assigned to incorrect age-classes was 41 (range 27-53). The percentage of jawbones and dental casts that were aged correctly by age-class were: 85% of the 1-2 year age-class, 73% of the 2-3 year age-class, 40% of the 3-4 year age-class, 22% of the 4-5 year age-class, 19% of the 5-6 year age-class, 1% of the 6-7 year age-class, and 0% for the older age-classes represented. These data certainly indicate a problem with the technique, especially in the older age-classes. However, they do not represent the entire picture.

Another way to evaluate accuracy of the technique, and perhaps the most informative one, is to calculate the percentage of jaws or casts that were estimated to be in a specific age-class that actually were in that age-class (Fig. 2). This procedure factors in estimates that assign jaws or casts in the specified age-class incorrectly. For example, 91% of the jaws or casts estimated to be in the 1-2 year age-class were in the 1-2 year age-class, but only 55% of those estimated to be in the 2-3 year age-class were actually in that age-class.

In summary, for deer estimated to be in the 2-3 year age-class or older, almost half, and in most cases, more than half were placed in the wrong age-classes. There were no accurate assignments for deer in the 9-10 year age-class and older.

Our conclusions were that using the traditional tooth replacement and wear aging technique for NFWU deer allowed us to confidently place them into 3 age-classes only: fawn, yearling, and adult. Attempts to place adult deer into specific year age-classes were very inaccurate. At best, we feel confident in placing adult deer into young/middle age adult and older age adult (based on excessive wear) categories. Additionally, there was a tendency to underestimate the ages of NFWU deer, however, a consistent error pattern was not evident in the adult age-classes that would facilitate calibration of the technique.

Management Implications

The fact that the tooth replacement and wear aging technique is not applicable to NFWU deer demonstrates the technique is not universally accurate. In other words, if it doesn't work for us, how can we assume it works elsewhere. The only way to know is to establish reference collections of known-age jawbones from areas, or at least regions, in question. Secondly, management or research programs not requiring a high level of accuracy in age determination are probably not greatly affected. This is especially true if primarily yearling age-class information is being utilized. The accuracy level for aging yearlings was quite acceptable.

However, if management or research programs require accurate and precise age determination of adult white-tailed deer, there is cause for concern. Without establishing an appropriate reference collection of known-age jawbones, there is no way of knowing how age estimates for a particular animal compares to its actual age.

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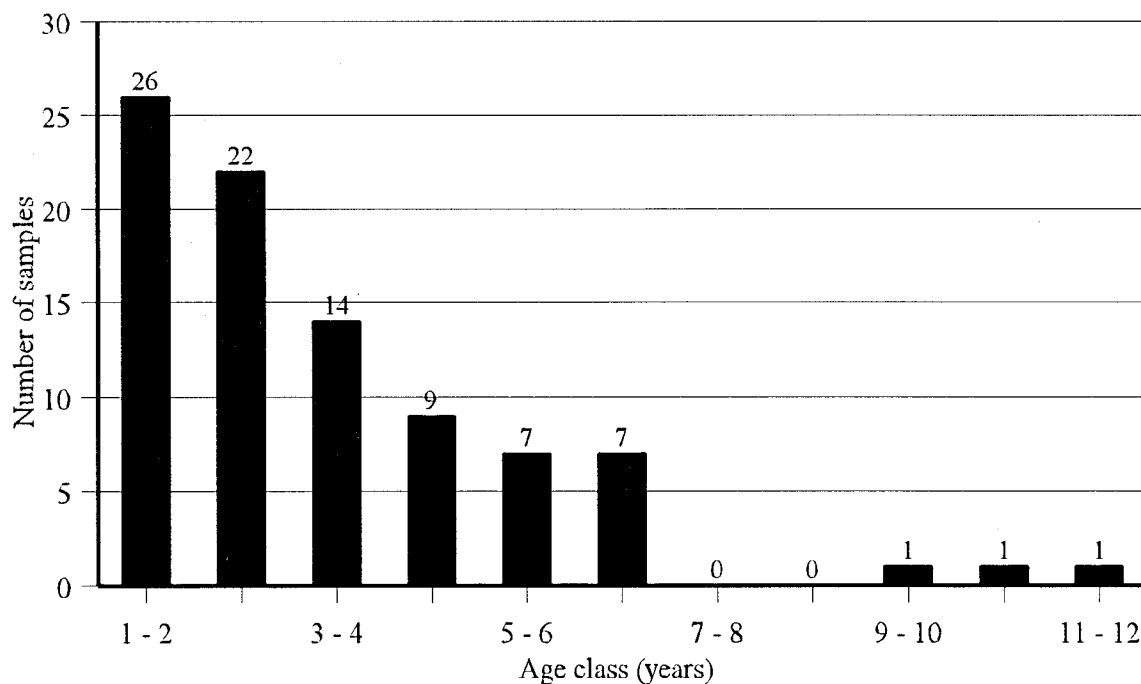
Figure 1. Age class distribution of jaws and dental casts from white-tailed deer at the Noble Foundation Wildlife Unit.
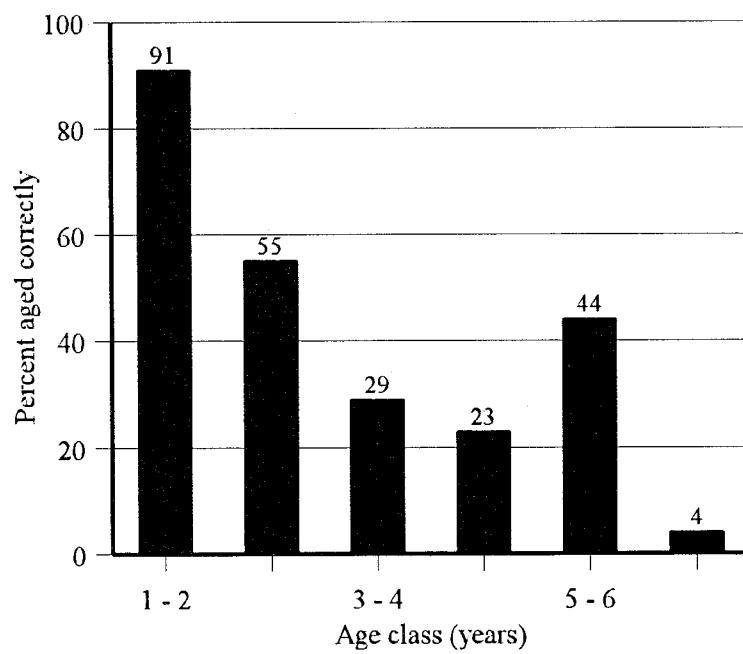
Figure 2. Percent of jaws and casts estimated correctly in specified age classes of white-tailed deer at the Noble
Foundation Wildlife Unit.

HOW GOOD ARE OUR AGING TECHNIQUES "ON THE HOOF ?"

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Abstract: Aging live deer has been an increasing interest of managers with the goal of managing for mature age in bucks. This generally requires limited harvest of younger deer, and requires the ability to distinguish between bucks of different age "on the hoof". I summarized 3 scientific papers on the subject published in recent years. The accuracy of replacement and wear aging versus cementum annuli aging was evaluated on live-caught and restrained deer. The methods did not differ significantly, although replacement and wear aging tended to overage young deer and underage old deer. Aging deer solely by antler size was evaluated in another study. Antler overlap among age classes was significant such that it was not possible to readily distinguish bucks 3.5 years and older. A third study involved classifying bucks by age from a helicopter. Bucks were separated into those 1.5-3.5 years old and those 4.5 years and older with 90% accuracy on about 60% of the 28 helicopter surveys. Managers should use buck classification data as trends through time and avoid reliance on data from a single flight. Aging deer "in hand" by the replacement and wear method is correct about two-thirds of the time. Aging deer "on the hoof" may be less accurate, but data are lacking.

The scientific literature on aging white-tailed deer began with Severinghaus' (1949) landmark study on tooth replacement and wear. Since then there have been various evaluations of the Severinghaus technique, including Ryel et al. (1961), Gilbert and Stolt (1970), Brokx (1972), Lockhard (1972), and Cook and Hart (1979). Although widely used, the tooth replacement and wear technique results in a tendency to overage young deer and underage old deer. Gilbert (1966) subsequently described the cementum annuli technique that appeared at the time to be an improvement on the replacement and wear method. The cementum annuli technique involves sectioning a tooth in a laboratory and counting alternating layers of light and dark material (annuli), which are correlated with age. Unfortunately, problems with the cementum annuli technique have been encountered in southern climates, where annuli may be indistinct (Lockard 1972, Hackett et al. 1979).

Tooth replacement and wear aging and cementum annuli aging provide population structure information useful in management and research. These techniques are normally employed on dead deer harvested by hunters. Interest in aging deer "on the hoof" has increased with the growing popularity of managing for populations containing mature males. This generally involves minimizing harvest of young males so they survive long enough to grow large antlers (Brothers and Ray 1975:133, McCullough 1979:239, Weishuhn 1983:351.). Brothers and Ray (1975:134) suggested harvest concentrate on males 4.5 years old or older,

whereas Weishuhn (1983:351) suggested harvest of

those 5.5 years or older. This management strategy assumes that mature males can be distinguished "on the hoof" from younger males. At least 1 book (Kroll 1996), several video tapes, and many magazine and newspaper articles have appeared on the subject in recent years. However, there has been little scientific evaluation of aging live deer.

Along with several graduate students, I have investigated various approaches to aging live deer (DeYoung 1989a, DeYoung et al. 1989, DeYoung 1990). In addition, we have ongoing studies on the correlation with age of such characteristics as gray facial hair, "Roman" nose, various head measurements, shoulder height, and stomach girth. My objective in this paper is to briefly describe results of these investigations of aging live male white-tailed deer.

Aging Captured Wild Deer

In this study (DeYoung 1989*a*), we caught bucks by helicopter (DeYoung 1988) on the Zachry Randado Ranch and Faith Ranch. Bucks were held for a few minutes, age and other data collected, and then they were released at the capture site. I looked into each buck's mouth and aged it by the tooth replacement and wear method (Severinghaus 1949). Also, a small

incisor tooth was removed from each buck over 1.5 years. These teeth were analyzed for age by the cementum annuli method.

A number of the bucks were subsequently recaptured 1 or more years later, and the same aging was done utilizing the 2 methods. Although the buck's exact age was not known in most cases, we did know the interval between the 2 captures. We compared the interval between the 2 ages to the known interval to assess the 2 techniques.

Replacement and wear aging resulted in an interval corresponding to actual for 35% of recaptured deer versus 39% for cementum annuli aging. Wear aging resulted in 56% of the intervals being one year different from actual, versus 52% for cementum aging. For each technique, 9% of the intervals were ≥2 years different from the actual interval.

Aging Deer by Antler Size

In this study (DeYoung 1990), we captured deer by helicopter (DeYoung 1988) on the Zachry Randado Ranch and the Faith Ranch, aged them according to DeYoung (1989*a*), and took various antler measurements described by Nesbitt and Wright (1981). Using an antler index, I evaluated how well bucks could be aged based on antler size.

It was not possible to distinguish among males 3.5 years of age and older based on antler size. This was because considerable overlap in antler size occurred across age classes. It may be possible to distinguish most males 1.5 and 2.5 years old from older males, based on the sole criterion of antler size.

Classifying the Age of Bucks from a Helicopter

In this study (DeYoung et al. 1989), we evaluated how well observers in a helicopter could classify bucks into groups of 1.5 to 3.5 years versus 4.5 years and older. Study areas were the Camaron Ranch and Faith Ranch in south Texas. We used re-sightings of individually-marked and previously-aged bucks (using the replacement and wear method) during complete coverage helicopter surveys to evaluate our ability to classify. When a buck was sighted on a flight, it was classified into 1 of the 2 groups, and individual markings on the buck recorded. Later, we identified the buck based on our records of markings, and noted if it was classified correctly, based on previous aging. On the Faith Ranch, marked bucks numbered 150, and helicopter flights numbered 14. On the Camaron

Ranch, marked bucks numbered 57, and helicopter flights numbered 14. The study was conducted in 1986, 1987, and 1988.

We used 90% correctly classified as a criterion of "acceptable" accuracy. Percent aged correctly was below 90% on 3 of 14 flights on the Faith Ranch and 8 of 14 flights on the Camaron Ranch. There was no obvious reason why accuracy of classification differed between the ranches. Also, there was no clear trend across flights or ranches as to whether young males were misclassified as mature or mature misclassified as young. DeYoung (1990) found considerable overlap in antler size among various ages of south Texas bucks, so it is surprising that classifications were as good as reported above. Criteria for classifying males from a helicopter are largely subjective, and perhaps we were influenced by body musculature, as well as antler size, which may have improved accuracy.

Whereas accuracy of age classification was acceptable on many flights, classification errors were sufficient on some flights to give an incorrect indication of male composition. We recommend that managers use buck classifications from a helicopter as trend data through time and avoid calculating harvest rates of mature bucks based on any 1 flight.

Discussion

These studies indicate that aging live deer is not an "exact science". For that matter, neither is aging dead deer. The replacement and wear technique, despite its biases, is sufficiently useful for management application (DeYoung 1989*b*). However, great confidence cannot be placed in an individual age. Most studies of the accuracy of replacement and wear aging result in experienced biologists getting about 67% of the ages correct. Thus, if aging is problematic when the deer is "in hand" (either dead or alive), it seems reasonable that field aging would be even less accurate. Using antler size alone is not a good field-aging criterion, as indicated by DeYoung (1990). Antler size in combination with one or more body characteristics may improve accuracy of field aging, but controlled studies are lacking.

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SCIENTIFIC BREEDER PERMITS: STATUS, TRENDS AND IMPLICATIONS

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Abstract: The Scientific Breeder Permit (SBP) is an out-growth of a program that was originally meant to assist the State in restoration of depleted wildlife resources. This out-growth has been an evolution from a restoration focus to its current form, and is primarily the result of the notion that by-passing the environment by hand-raising white-tailed deer to be hunted following release is an appropriate management practice. Also, there are some who believe that with the proper genes, a white-tailed deer will be of trophy quality regardless of the range in which he is found or population of which he is a part. Some have a SBP because they enjoy deer; enjoy the challenge of raising quality animals; or to them it is simply a business enterprise. While the notion that "superior genes" will over-come the environment is not supported by the data, it will continue to be a distraction from more traditional habitat and population management in the foreseeable future.

The Scientific Breeder Permit (SBP) Program is an outgrowth of the much older Game Breeder's License (GBL). The original concept, back in 1939 when the GBL was created by the Texas Legislature, was to solicit the help of the private sector in the restoration/reintroduction of certain game species to Texas. Many game populations had been depleted on a national scale from unregulated market hunting, and this was particularly true in Texas. National concern for the depleted game populations in this country sparked the passage of the Pittman-Robertson Act (1937), which became the primary funding mechanism for wildlife restoration efforts in the United States. This was the context within which the GBL was created.

In Texas, a license is issued on the payment of a fee, whereas a permit is issued based on the qualifications of the applicant and many of these qualifications are defined by rule. The GBL allowed its holder to possess game species for propagation purposes and sale. The SBP allows its holder to possess and sell white-tailed deer and mule deer for propagation, management, and scientific purposes. The distinctions may seem small, but such is often the case in law.

White-tailed deer and mule deer were separated from the GBL in 1985 and incorporated into the SBP. Interest in the genetics of white-tailed deer from a management context, which began at the Savannah River National Laboratory in Georgia in the late 1960s, was pursued in earnest at the Kerr Wildlife Management Area (KWMA). The killing of spike bucks (male deer with only 2 points), which is impossible to avoid where antlerless harvest is allowed, was of great concern among hunters and landowners alike in Texas and was proving a hindrance to the expansion of antlerless deer harvest in Texas. The pen facility was built on KWMA in 1975 to allow the Department to conduct feeding and breeding trials for white-tailed deer, and to demonstrate the relative importance of genetics and environment in the development of spikes. Also, because the deer were confined, deer could grow to maturity under controlled conditions so that the growth potential for spike vs forked bucks could be evaluated. While the KWMA has been effective in researching many aspects of range and wildlife management, none have captured the imagination of the public as the studies conducted in the pen facility.

Status

As has been done with all Texas Parks and Wildlife Regulations, the SBP Proclamation has gone through a "sunset" process. The "sunset" process is aimed at removing all regulations and statutes that do not specifically address resource issues or are needed for enforcement purposes. If every deer possessed by SBP holders were to be simultaneously released into the wild, it would not represent a resource concern. From the Department's perspective, and that of the SBP holders, there are only two issues that need be addressed in the SBP regulations: (1) the right of the permit holder to possess, enjoy, and protect his/her property and (2) the right of the people of the state of Texas to possess, enjoy and protect their property. The complication comes from the fact that privately-owned, white-tailed deer look a lot like publicly-owned, white-tailed deer. This complication is the basis of marking and record keeping requirements, permitting for purchase or transportation, and the prohibition against

commingling wild and privately-owned deer. However, the resulting regulations are as user-friendly as it is possible for them to be at this time.

Trends

Each SBP holder is in the business for his/her own reasons, but most like white-tailed deer, enjoy watching them, and have an interest in breeding big ones. For others, it is simply a business venture. In the 12 years since the SBP was enacted into law, the number of permitted facilities have grown from just a few to over 270 (only 1 permitted to possess mule deer).

The fascination and appeal of claiming an association with a famous bloodline is of growing interest among SBP holders and some land managers. This interest has led to an inflating market for sire bucks. While it has long been held that high-quality, trophy-class, white-tailed deer in the wild are a product of good habitats, stable populations with well developed age structures, and cooperative rainfall patterns, some see genetics as a fast track to having big deer on their range. Some desire to raise high-quality deer to be turned out for hunters. However, assisting a deer to reach its genetic potential in a pen is a very different matter from producing quality animals on the range, regardless of their genetic background. The growing number of SBP facilities, I believe, is directly linked to the growing notion among many in the public that the offspring from a "super deer" can overcome environmental effects. This is not supported by data.

A more desirable trend would be for the public to reorient their focus back to sound management of populations and habitats. There is no silver bullet that will create a stable, high-quality, deer population.

Implications

The implications of the SBP will depend entirely on the focus of hunters and landowners in the future. If the expectations of hunters and landowners were enlightened as to the probability of ever having an impact on the genetic make-up of a wild deer herd, the SBP will go the way of the GBL; a footnote in history following a satisfied need. If the attention of hunters and landowners remains focused on genetic change as a management goal, the SBP will continue to flourish as will the continued interest in importing deer into this state and an increase confined deer herds.

Deer movement between states is the primary concern of the Texas Animal Health Commission and the U.S. Department of Agriculture because of the potential impact of tuberculosis and other diseases on the livestock industry. These concerns have already prompted action by both entities on the captive deer industry in Texas, and there are sure to be more in the future.

Fee access for hunting has a long tradition in Texas. This is not well understood by other states or national organizations. Overall, fee access has proven a boon to restoration and management of many species by providing landowners the incentive to protect and enhance critical habitats for wildlife. The development of high-fenced, intensely managed, ranches has been a natural evolution of landowner attitudes toward wildlife. However, this attitude is not well understood in traditional organizations such as Boone and Crockett Club and others who raise ethical issues about "fair chase" and scientific interference with "natural processes". Loss of support from such traditional organizations could have an impact on national issues important to Texas.

The demand for high-quality, trophy-class, white-tailed deer is perceived to have inflated the cost of hunting and placed it out of reach of many Texans. Currently, over 80% of Texans live in 6 cities, and their tie to the land is growing weaker. There could be significant political implications to a loss-of-support for hunting among the Texas public.

WHERE IS THIS ROAD TAKING US? A HUNTER'S RESPONSE

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From a hunter's viewpoint, with the overwhelming whitetail interest that is consuming Texas today, I feel that the future for the hunter far exceeds expectations of the pioneers that envisioned producing quality whitetails. This will be a win-win situation for 3 categories of participants: hunters, landowners and the breeders.

My opinion is based on the question *will the hunter, both resident and nonresident, have a better opportunity to hunt quality whitetails in Texas*. I can truly say that whitetail hunters of every economy level should enjoy much improved quality whitetail hunting for many years to come. Cooperation by all of the 3 categories previously mentioned will be the key to success.

Let me explain why I believe this. As the "Great Texas Whitetail Experiment" continues to grow and develop, new frontiers should open to all deer hunters. I put whitetail hunting opportunities into 4 general classifications.

1. Public and leased land owned and operated by the State of Texas

2. Private land owned by giant lumber industries such as Temple Inland and International Paper.

3. Private landowners that lease their land on a seasonal or annual basis.

4. Private landowners that focus on selling whitetail hunts from opening price points for management hunts to upper dollar prices for superior quality hunts. This classification operates in many different ways.

From the hunter's standpoint, all 4 of these classifications can offer improved quality whitetails. The State of Texas has been the leader in developing our whitetail herds. The State of Texas has supported improved quality whitetail programs by private land owners. The State of Texas has just instituted or is in the process of instituting new changes in whitetail breeding and whitetail stocking programs.

What all these changes mean is that Texas will continue to lead the nation for nearly 7 years as the premier developer in whitetail quality programs. By following the 4 classifications that I addressed earlier, Texas could stock its public land and leased land with quality genetically bred does by asking landowners to voluntarily donate excess does to be restocked on these 2 land categories. You could see vast improvement in 3 to 4 years due to the genetic superiority of the released does from quality ranches. This will not be an easy undertaking but it will work with the right combination of voluntary landowners, adequate education of the hunters, and tight supervision practice on all these public lands.

The very same program could be worked on vast tracts of land controlled by International Paper and Temple Inland. This would take a little more tweaking to ensure that all wildlife managers and staffs would truly cherish and appreciate the improved genetics of whitetail does donated to these properties that they manage.

The third classification will continually improve because the landowners and their whitetail specialists are committed to constantly improve their herds. This group has been improving a lifetime dream, some in excess of 40 to 50 years. Now the improvement will continue at a much more rapid pace because of the landowners being able to swap and shop. Here again is another win-win situation.

The fourth classification is similar in nature as the previous one. If profit is their game, the hunting business will prosper for this class. As their herd quality continues to improve, their income will increase because of superior whitetails. Again, another win-win deal for hunters and landowners.

Regardless of all the dreams that the pioneers of "The Great Texas Whitetail Experiment" had, it all boils down to this. For the Texas Whitetail hunters to have land to hunt, whether it be public or private, there has to be a delicate balance between the hunters and hunting places. All whitetail herds have to be continually managed and improved. We must cultivate the interest in hunting these lands that will attract new hunters, from all economic levels. The most important aspect of this entire "Hunter's Response" is that we have to grow whitetail hunters too. Everyone in this room must accept that responsibility. Not only should

we educate and convert the youth of our country, we must try and reach the non-hunting adult as well. We have to convince these

folks to try hunting as we all know it. Convince them to understand the love we have for the whitetail. Remember to share the same experiences you had in deer camp. If we do not cultivate these 2 groups, there are a bunch of us that won't be in this room in 10 to 20 years.

WHERE IS THIS ROAD TAKING US? ONE MANAGER'S PERSPECTIVE ON CULLING

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There are 2 basic issues with respect to genetics and whitetail deer:

1. As a deer manager, should I cull? And if so, what should I cull?
2. Do I build a set of deer pens?

The Emotional Appeal of Culling

Culling with the purpose of genetic manipulation of a deer herd is an emotional subject with great superficial appeal. Culling appeals to the basic human desire to DO SOMETHING. After all, management implies action. Culling satisfies this urge to action in three important groups:

1. Hunters—who love to shoot stuff. They love culling.

2. Wildlife managers. They need to feel like they're doing something. And they like to shoot stuff, too. So they are STRONG advocates of culling.
3. Anyone who has experience with breeding cattle, dogs, hamsters, or whatever. "If I can do it with my cattle, then I can certainly do it with my deer herd."

The Corral Continuum

I want to leave you with a concept that will help you think more clearly—and more unemotionally—about culling. That concept is what I call the corral continuum (Fig. 1). The corral continuum is really what Don Davis was talking about earlier today; I am just saying it in a different way.
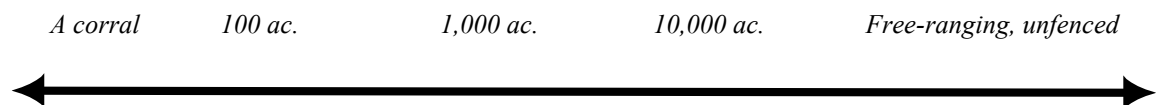

Figure 1. The "Corral Continuum.".

As you can see, at one end of the Corral Continuum is a corral full of deer—a set of deer pens. At the other end is a free-ranging, herd in a unfenced ranch. As you move along the continuum away from the free-ranging herd, you enter a high fenced environment with the size of enclosures decreasing until you enter a corral-sized pen.

The most common fallacy people make with respect to genetic manipulation of whitetail deer is this: if genetic culling works in a corral (and I think it does), then it's got to work on my place whether its 5,000 acres, 1,000 acres, a 100 acres or whether its high fenced or not. This is simply not true. You certainly cannot have any effect on deer genetics a ranch that is not high fenced; wide-ranging yearling dispersal and

buck movement during the rut is constantly mixing the genetics of a deer herd that is not fenced in. And even on a high-fenced ranch, there are great obstacles to achieving genetic change.

The problem is two-fold:

1. Without pedigreed does, you don't know anything about the does' genetics. You can't do anything about that.
2. Mother Nature's mission is to move the genetics in a population toward the averages. I love that beautiful quote: "Mother Nature abhors outliers as much as she does a vacuum."

The Culling Controversies

Culling for genetics is controversial in two senses. First, can I manipulate whitetail genetics by culling spikes versuses forked-horn yearlings? Second, can I cull older bucks to achieve genetic change?

Spikes versus Forked-horn Yearlings

We spent three-fourths of a day on the spike versus forked-horn yearling controversy. What did we learn?

We learned that yearling antler traits are somewhat correlated with mature buck antler traits. In other words, yearlings with poor antlers will more likely than not become mature deer with poop antlers. Both the Kerr County data and Jacobson's data revealed this positive relationship.

But with respect to the advisability of culling yearling to achieve genetic change, I think the most significant message was buried in the referee's desire not to offend anyone. The question is simple: are yearling antler traits heritable?
>--Bill Armstrong, citing John Williams paper in the Journal of Heridity, says YES, based on his analysis of the Kerr County data.
>--Steven Lukefahr analyzed Jacobson's data and said NO, yearling antler traits are not heritable.

But the referee said that Lukefahr's animal analysis was superior to Williams' sire analysis. So, he gave the edge to Lukefahr and the conclusion that yearling antler traits are not heritable—based on the techniques each used.

What was NOT CLEAR—though the referee mentioned it in about three sentences—is that Lukefahr DID use the superior animal analysis technique and analyzed the Kerr County data. The result: ZERO HERITABILITIES FOR YEARLING ANTLER TRAITS. Unfortunately, Lukefahr was unable to present his analysis of the Kerr County deer herd at this conference.

What is the significance of '0' heritability values for yearling antler traits?
>--If you shoot spikes, you might be killing yearlings that will produce Boone & Crockett offspring.
>--On the other hand, shooting a spike might remove an animal that will produce inferior antlered offspring.
>--More likely than not, shooting a spike will result in the killing an animal that will produce average offspring.

The bottom line is that shooting spikes is NEUTRAL with respect to genetics. You will NOT achieve genetic change by shooting spikes because of the low heritibilities of yearling antler traits.

Now the caveat to all of this was expressed by Jerry Taylor this morning. The two data sets analyzed are very small and were not designed to answer the question of heritabilities. They are only the best we have at this time.

Culling Mature Bucks to Manipulate Genetics

The second controversial issue is whether to cull older bucks to achieve genetic change. Theoretically, this can be done since mature buck antler heritabilities are moderate. But in my opinion, this is really a corral continuum issue. In fact, Jerry Taylor tackled this general problem with the model he presented in which he introduced large antlered deer into a deer herd and then predicted genetic change. Although his assumptions were speculative, this type of model is the kind of model needed to address the corral continuum problem. That is, what level of intensity of harvest (or introduction of large-antlered deer would be required to achieve genetic change for a given sized deer herd and

ranch.

In my opinion, achieving genetic change through high intensity harvest of older cull bucks would:

--take a VERY long time, and

--Require a VERY INTENSIVE mature buck harvest.

This would be very costly to implement. You would have to employ many top quality guides to achieve this level of intensity. In my opinion, this is money that is not well spent. But remember, the closer you get to a corral, the more you can effect genetic change.

My Recommendation to Achieve Genetic Change

If you really want to manipulate whitetail genetics, here's what I recommend:

·   Build yourself a set of deer pens and get a scientific breeder's permit;

·   Pay TOP DOLLAR for incredible genetics;

·   Raise a couple of 190 class bucks;

·   Release them into your high fenced pasture;

·   And then shoot 'em.

I don't have any problem with that—ethically or otherwise. But recognize where you are on the corral continuum: you are raising deer in a corral; you are not managing a deer herd.

The Certainty of Age and Nutrition

Before you spend a bunch of money on deer pens and breeder bucks and pedigreed does, let me tell you what works at any point along the Corral Continuum.

1. Focus first on age structure. But that's no fun, because it means NOT shooting animals and waiting until they grow to maturity. I call it MANAGEMENT BY RESTRAINT.

2. Add nutrition to your deer herd. You can:

   a) Shoot deer to get the numbers of deer down so that there is more food for the remaining deer. Here's where the Kerr County work is valuable. If you have a severe overpopulation problem, you can shoot spikes (in addition to mature culls and does) to get your numbers down. You might be shooting a future Boone & Crockett, but more often than not, the spike yearling would have been average or below average at maturity. But this effect is nutritional, not genetic.

   b) You can increase nutrition by feeding protein pellets.

   c) You can grow food plots.

NOW TAKE THIS TO THE BANK. INCREASING NUTRITION WORKS AND IT WORKS BIG TIME.

1. It works in the short term. When bucks first get on the increased nutrition, they grow larger antlers.

2. It works in the intermediate term. When the fawns that have been fed consistently high protein all their lives become mature, the average size of the mature bucks increase dramatically in a herd.

3. It works in the long term. There is evidence from the work Valerius Geist did on red deer in Germany in the 1920's and 1930's that sustained levels of high nutrition for long periods results in generational improvement in antler quality.

Now, adding nutrition to your deer herd is expensive stuff–but unlike culling–it is GUARANTEED to work.

Assume your herd has an old age structure and it enjoys a high plane of sustained nutrition. Then it probably makes sense to cull intensely older inferior bucks. Of course, you will have to spend the money on personnel, infrared cameras, feeders, and all that stuff. Your great grandchildren will be grateful for you culling effort. They will be grateful, provided, you haven't spent so much money on deer that there is no money left to pay estate taxes so you have to sell your ranch. In that case your great grandkids will be quite irritated, but that is an entirely different issue.

Summary

1. Keep the corral continuum in mind when analyzing management choices. What works in a corral won't necessarily work along all points along the corral continuum.

2. If you want to manipulate deer genetics, pour a bunch of money into breeder bucks and deer pens, raise big bucks, and shoot 'em when you can't stand it any longer.

3. But if you want to manage a deer herd, focus on age and nutrition and always keep in mind where your ranch falls along the corral continuum.

WHERE IS THIS ROAD TAKING US? AN OUTDOOR WRITER'S PERSPECTIVE ON WHITETAIL GENETICS

RAY SASSER, 2136 Chisholm Trail, Rockwall, TX 75087

As a writer who loves writing about white-tailed deer, I thrive on scientific research that proves or disproves popular theories. A recent example is the horn rattling study that proved some of the things we suspected and disproved others. It proved, for instance, that the hunter never sees most of the bucks that respond to rattling.

It also proved that mature bucks do not necessarily come more warily to rattling than do their less experienced counterparts. Likewise age and nutrition studies that, in my mind, have formed the cornerstone of modern whitetail management. With computerized tracking systems, we're unlocking the mysteries of whitetail movement, proving that mature bucks expose themselves less often than does or immature bucks. Soon, there will be a computer model that predicts deer movement based on range conditions, weather, calendar, hunting pressure and moon phase. Such a model may already exist.

Luckily, whitetails are such adaptable animals that they continually frustrate our most serious hunting attempts, no matter how much weird science we use. In theory, at least, genetics is the last frontier of whitetail research; the last piece of puzzle that fills in a mysterious mosaic and helps us fully understand the animals.

In theory, whitetail genetics is a great debate. In practice, we may as well debate the existence of heaven and hell. For example, I have a friend who, for 20 years, has intensely managed a large, high-fenced ranch. One of his management techniques is to cull every 8-point buck and every spike buck that he sees. He wants to remove the inferior antler genes from his deer herd. He tries to accomplish this by killing the 8-pointers before they can breed. Some scientists say that such gene manipulation cannot be done on such a large area. All I know is this particular ranch has more bucks with 10-plus points than any wild deer herd I've seen.

In fact, the popularity of high-dollar package deer hunts seems to have adversely affected the bucks on "managed" ranches across Texas. Hunters who pay $5,000 or more for a brief deer hunt are not inclined to shoot an 8-pointer. They'll shoot an immature 10-pointer before they shoot a mature 8-pointer.

The same thing is true of lease hunting where Texas hunters pay $6 to $10 per acre and are allowed one trophy buck per 1,000 acres. They selectively kill the very best animals they can find, leaving less desirable bucks to do the breeding. I've seen too many deer herds where mature 8-pointers are the most abundant bucks. I even coined a phrase to describe such undesirable bucks: *he's kinda narrow but he's got short tines*. That's like describing me kind of short, but chubby.

On the opposite end of the management spectrum, another manager I know never kills any bucks until they are 5.5 years old. He has been pleasantly surprised on more than one occasion by the unexpected antler development on mature deer that my friend with the bigger ranch would have killed in previous years as a cull. Once the deer are 5.5 years old, they're fair game. Even the biggest bucks are fair game, though the very biggest are saved until they reach 6.5 years.

Yet another deer manager I know likes to grow bucks until they are at least 6.5 years old before the harvest. He designates outstanding bucks as "brood bucks" and may never hunt them at all. Most of the truly good bucks on this particular ranch die of old age. They have plenty of breeding seasons in which to spread their genes. While there are some truly eye-popping monsters on the place, the average buck is an 8-pointer that most managers would consider a cull.

I always wonder how much breeding the super bucks accomplish in a wild deer herd where super bucks are outnumbered 5 or 6 to 1 by bucks that I

unkindly categorize as "ratheads"? Some of those ratheads, incidentally, are big-bodied, aggressive, bad-assed ratheads. They can put a big-time whipping on a buck with Boone and Crockett antlers.

The point is, the deer managers in all 3 of those scenarios are convinced their management method is the best.   Despite the difference in techniques, all 3 have produced great bucks. They mostly accomplish that goal by making sure the deer grow to maturity without ever going hungry. The food can be natural browse, planted food crops or commercial feed poured out of sack.

Can you really influence the genetics of a sizable deer herd? Sure, people are doing it all the time, mostly through deer pen breeding. They buy or capture an outstanding brood buck and put him in an enclosure with a group of does. If the breeding program is done right, the pedigrees of the does that are the brood buck's concubines indicate they have produced outstanding buck fawns in the past.

The real wild card in the genetics formula is, of course, the doe. We can look at a whitetail buck and tell whether he shows desirable antler characteristics. Just as we know that little Billy got his red hair from his maternal grandfather, we may eventually know what antler traits are passed to a buck from his mother's side of the family. We cannot look at a doe in the field, however, and determine if she's genetically inferior.

Actually, I guess people are doing that already. Unfortunately, such identification requires a written pedigree along with a freeze brand on the deer's flank or a numbered tag in its ear. The whole issue of whitetail genetics, brood bucks, brood does, artificial insemination, genetic diversity, ad infinitum comes perilously close to making a wonderful wild animal into another form of glorified livestock.

Will I write about genetics? Sure, just as I write about $15,000 trophy buck hunts or someone paying $150,000 for a brood buck. Those are "Gee Whiz!" kind of stories; the hunting fraternity's equivalent to what we see on Lifestyles of the Rich and Famous. As fodder for off-season stories, whitetail genetics is an interesting subject. From a practical standpoint, who really cares? Certainly not my readers. Many of them (I include myself in this category) come from questionable genetic backgrounds, themselves. That's what makes them interesting. That may also be part of what makes the deer so interesting.

A friend once asked what I consider to be an astute question when a landowner said he would never shoot one of the truly outstanding bucks on his property because that was his brood buck. He wanted that buck left on the place to breed does. Here's the question: "where did that brood buck come from?" It came from the ranch, of course. The genetics for outstanding bucks exist in any sizable deer herd.

Let's think about this genetics thing for a minute. The real interest in white-tailed deer is directed at bucks. We can look at a buck and tell whether we like him or not. All the does look pretty much alike. If biologists really want to do something for deer hunters, they should develop a buck that reproduces itself by splitting cells, thus eliminating does from the formula. I was stunned last year when I read about scientists in Scotland cloning a domestic sheep. Who cares about domestic sheep? If you're going to clone an animal, why not clone an interesting animal, like a big whitetail buck.

On second thought, if we eliminate does, we eliminate the rut. Without the rut, we'd probably never see the bucks, anyway!

WHERE IS THIS ROAD TAKING US? GENETIC MANIPULATION IN DEER MANAGEMENT: A WILDLIFE PROFESSIONAL'S PERSPECTIVE

DALE ROLLINS, President, Texas Chapter, The Wildlife Society, 7887 U.S. Hwy. 87 N., San Angelo, TX 76901-9714.

I am speaking today as a representative of the Texas Chapter of The Wildlife Society (TCTWS). The TCTWS is comprised of some 500 professional wildlife biologists. The TCTWS is a state affiliate of The Wildlife Society, which has some 6,000 members worldwide. On behalf of the TCTWS, we are proud to co-sponsor this symposium. One of our goals is to provide professional development opportunities to our members, and this symposium is an excellent example of that endeavor. As wildlife professionals, the TCTWS believes in the science-based management of Texas' wildlife resources to ensure a sustainable wildlife management system for recreational use. But to claim that my comments today are representative of every member's opinion would be ludicrous, as we surely have members at opposite ends of this debate, and all degrees therein. My comments today basically reflect my personal opinions as a wildlife professional, but they were routed past our Executive Board for their perusal and comment.

So, is our infatuation with genetic improvement within a deer herd "good" or "bad?" I will dissect this argument as I perceive it affecting the 3 legs of the wildlife management "triangle." My perceptions are based primarily upon 17 years of working with private landowners as an Extension specialist in both Oklahoma and Texas.

We often refer to wildlife management as a triangle with legs representing (a) habitat management, (b) population management, and (c) people management. Invariably, wildlife professionals refer to habitat management as the base for this triangle, the foundation upon which the other two aspects rest. Personally, I tend to be prioritize the legs as (1) habitat management, (2) people management, and lastly (3) population management, so consider that an admission of my bias. Surely all 3 aspects are closely interwoven when you consider deer management in Texas. While I've listed "people management" as second in priority, I choose to discuss it last here, as my arguments are largely philosophical, and less likely to be shared by the TCTWS membership as a whole.

Habitat Argument

If there's 1 tenet upon with which I think all TCTWS members will agree, it's that the habitat leg of the triangle is the foundation of any wildlife issue. If a practice is not conducive to good habitat management, I argue that it will not be sustainable nor conducive to a more diverse wildlife community. And when I say "good" for habitat, I'm asking does it promote species diversity and community stability? Relative to deer management, this argument rests more with how many deer occupy the habitat, not what their genetic makeup is. But we must examine the habitat issue not as just a function of herd dynamics per se, but also of practices that will accompany genetically "improved" deer herds.

For the immediate future, a deer manager interested in genetic improvement will most likely be in a high-fenced and nutritionally-supplemented situation. This presents 2 opportunities for mismanagement in that (1) it's tempting to try and carry too many deer (i.e., well above the habitat's "carrying capacity"), and (2) a supplemented herd may have greater opportunity to be more selective in it's browsing, which may cause long-term overuse of more desirable browse species. I stress "may" because certainly there are exceptions.

As we move towards more and more of a "registered" deer enterprise, in contrast to what I would refer to as a "commercial" herd (to use an analogy from beef production), there is a tendency for the registered herd to grow larger than a commercial herd. You feel like you have more of an investment in "your" animals, and you're a little less likely to part with them.

Economic principles tend to be less of a management force for someone who operates a "purebred" operation. Most likely if you've got a high-fence and high-feed situation, your motivation for management is more than likely recreation or "pride of ownership" than it is profit, per se.

Research at the Texas A&M University Experiment Station at Sonora (Murden and Risenhoover 1996) suggests that a supplemented deer herd can afford to be more selective in its grazing and browsing than a non-supplemented herd. In essence, this means that a browsing deer can "afford" (nutritionally) to spend more time seeking out the more desirable, and less abundant, plants. Whether or not such selective browsing would result in less plant diversity is speculative, but the vehicle for such a response is present. This tendency will be most pronounced as high-fenced properties get smaller and smaller, and supplementation becomes more and more common.

Certainly if someone is motivated enough to build a high-fence, or to work diligently on improving "his" deer herd's genetics, he should be sold on the idea of good habitat management. To that end, he is perhaps more likely to be balancing deer and livestock numbers, more interested in plant diversity, and more likely to appreciate the management tools for promoting plant diversity. Perhaps "genetics" is the appetizer upon which you sell the entree of habitat management; I hope it is (refer to the Kerr WMA example below).

Population Argument

There's something about the population leg of the triangle that captivates managers, be they deer managers or cow-calf producers. Deer hunters are eager to participate in "active" management where they presume that shooting spikes or other "culls" is benefitting a deer population. On the other hand, habitat management (range management) is perceived as a beast that moves too slowly to provide much personal satisfaction. It's difficult to market habitat management, perhaps because most people can't differentiate good from poor habitat.

I think the Kerr WMA is a good example of people's infatuation with antlers. I don't know how many groups have listened to Donnie Harmel or Bill

Armstrong over the last 20 years preach about habitat management and the respective roles of fire, brush control and livestock grazing as habitat management tools. But, if the Kerr WMA didn't have the "deer pens" and the allure of genetics experiments, would those tours have been anywhere near as popular? I don't think so. In today's fast-forward mentality, habitat management is just too darn slow to get people excited. But we as a profession should take heed of the Kerr's experience: you must hook a fish before you can land it. But we must also be cautious, lest the sex appeal of genetics supercede our emphasis on the habitat foundation.

The rationale for this symposium is to present (and professionally debate) the current state of the science relative to manipulating genetics in a deer herd. As someone involved with this symposium from its inception, I assure you that there is considerable consternation on the part of the sponsors, and the speakers, relative to the debates that have been waged here (either from the podium or in the bar last night). As professionals and scientists, "debate" should be viewed as a positive process, not a negative one. Science progresses only when peer review and skepticism force us to design experiments that will provide objective answers to the hypotheses that we test. We look to our experimental designs, statistical tests and the like to analyze how "good" the science is behind the results that are being presented. We then weigh, and if necessary mesh and reconcile, these findings with our own personal experiences on the matter. It's more of a process than a product.

There is certainly much to debate on the issue of deer genetics. Can we manage for a phenotype (i.e., large antlers) with a limited understanding of genotypes, gene flow and perhaps an even more limited understanding of how genetics interacts with other variables (e.g., nutrition, age)? How do results of deer in pens extrapolate to those on the range? Is the buck's first set of antlers a good predictor of what it will look like at 6 years of age? What is the doe's contribution and how can we select for phenotypic traits in her? Does .30-06 deer management (i.e., "culling") promote, hinder or have no effect on genetic improvement?

I assure you that I am as confused as any of you about the relative and absolute merits of culling as a tool for improving a deer herd. I've heard the arguments before, but I've never had the opportunity to hear them simultaneously with an opportunity for

rebuttal by each viewpoint's critics. Will I be convinced that 1 camp is right and the other wrong by the end of this symposium? I doubt it, but I should have additional information upon which to make an informed decision. Hopefully, I'll be more learned about some of the "new" science, i.e., DNA analyses, that will shed light on some of our techniques, if not our results.

People Management

Does genetic improvement have an effect on the "people management" leg of our triangle? It may, if it affects either overall hunter numbers (hence license sales) or public support for hunting (both in the non-hunter and hunter ranks). I submit that evolution towards a "registered" deer enterprise is not healthy for the "average" deer hunter, as it will continue to drive the costs of deer hunting upwards. However, our interest in today's topic (largely bigger antlers) is surely driven by consumer demand. Thus, I see a niche market (which already exists) where landowners seek to develop and market larger-antlered bucks for a higher-paying clientele. The appeal to the landowner is a higher price per hunter, thus fewer hunters to deal with, which appeals to most landowners.

Hunter numbers statewide, and nationally, are in a moderate decline. As hunter numbers decline, the future of deer hunting is affected both by declining revenue for license sales (which drives most state game agencies) and declining public support for hunting. Surely much of that decline is a result of demographic shifts (i.e., an aging and less populous white ethnic group that dominates the hunting clientele), but an equally powerful force in the short-term is lack of hunting opportunities. Surely, the landowner interested in deer genetics has an avenue for providing less expensive hunts (e.g., doe or "cull bucks" [however you define them]). While the opportunity is there, I am skeptical that many landowners will capitalize on that opportunity, especially when permits (e.g., the so called "kill permit") are available that allow them to control doe numbers themselves and circumvent the necessity to deal with more hunters.

And what does the trend towards "trophy management" portend for public support of hunting? Adams and Thomas (1990) reported that "hunting for trophies" received the least support of any category of deer hunting. If the interest in deer genetics progresses

towards "cloning", which seems far-fetched today but is within the capabilities of emerging technology, will it help or hurt public support for hunting? If we get to the point where we can mass-produce Boone and Crockett bucks, have we marred the very essence of what attracted us to them? I submit that the trend is not a positive one for the future of hunting in general.

Texas is in a league of its own relative to interest, and history, in trophy deer management. Surely some of Texas' hunting customs (e.g., hunting deer over corn feeders or behind high fences) tend to raise the eyebrows of both hunters and wildlife professionals from other states. The term "privatization" often comes up in such discussions, and it is one which the TCTWS has touched upon only gingerly over the years. We realize that, while the regulations say the public owns the deer, de facto possession resides with the individual landowner. And in a private lands state like Texas, any progress in wildlife habitat management and sustainability must be achieved on private lands. Earlier this year, the TCTWS issued a position statement opposing legislation (HB 3061) that we perceived as fast-forwarding the privatization issue. We believed that, even here in Texas, the landowner's ability to manipulate a public resource (i.e., a deer herd) was moving too quickly. That legislation was later attached to an omnibus bill that did indeed pass, and now the TPWD commission is debating how such legislation will be implemented.

Finally, and on a mostly philosophical note, what does the trend towards ever more intensive management portend for the "essence" of deer hunting? Is the formula for finding a trophy genotype a holy grail for wildlife managers? Does the "end" (i.e., a Boone and Crockett buck) justify the "means?" Are we massaging something that we cherish as the epitome of a natural "trophy" and contriving to artificialize it? Will the deer manager 25 years from now come equipped with an animal science degree and be more conversant in AI, EPD and scrotal circumferences than he is in plant identification and prescribed burning? Are we progressing towards a feedlot syndrome where a hunter orders "options" for his buck as if he was ordering a new pickup truck? Again, this is a stretch of where we're at right now, but that is the direction in which we are traveling. I, for one, am uncomfortable with that heading.

I tend to be a romanticist; perhaps more of an artist than a scientist. But I appreciate that wildlife

management is perhaps an art based on scientific principles. I think most wildlifers are like that. Perhaps that's why issues like the role of genetics in deer management perplex, and intrigue, us. We strive for science to replace our less scientific "tads" and "sprinkles" with heritability estimates and mitochondrial DNA, but we're hesitant to relinquish the idea that the manager's skills can be replaced with artificial intelligence. I subscribe to Aldo Leopold's definition of wildlife management as "*the art and science of making the land produce a sustained, annual crop of wildlife for recreational use*."

As scientists and deer managers, we seek to dissect a Rembrandt into a "paint by number" scheme that allows us each of us to try our hand at being a Russell or a Remington. I often debate the "art vs. science" argument with fellow quail biologist Dr. Fred Guthery. Dr. Guthery is the epitome of a scientist; his quest is driven by the search for data upon which to build and test his models of habitat theory or population gyrations. I counter his logic with observations accumulated over miles of walking with my bird dogs and carrying a shotgun. While Guthery typically gets the upper hand in our debates, I claimed a moral victory about a year ago when he wrote to me with this lamentation, "*trying to write equations for perfect bobwhite habitat is like trying to write equations for pretty girls. We can recognize properties of perfect habitat and pretty girls, that is all*." I submit that some things are perhaps best left to natural processes, be they perfect habitat, pretty girls or 180-class bucks.

Conclusion

The renowned physicist Sir Isaac Newton, in his Third Law of Motion, noted that "*to every action there is an equal and opposite reaction*." As a wildlife ecologist, I argue that Newton was too simple minded. I maintain that to every action (e.g., genetic manipulation of a deer herd), there are many reactions,some very apparent, others quite transparent. As resource managers, it is incumbent upon us that we proceed cautiously and try to discern as many of the reactions as we can. This symposium is a step in the right direction.

"*The urge to comprehend must precede the urge to reform*." -- Aldo Leopold

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WHERE IS THIS ROAD TAKING US? THE ROLE OF GENETICS IN WHITE-TAILED DEER MANAGEMENT: TEXAS PARKS AND WILDLIFE DEPARTMENT PERSPECTIVE

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When you are in a position like we find ourselves in, as the Texas Parks and Wildlife Department, of having to deal with regulations on a state-wide basis, county basis, regional basis, you find that deer management on small operations (deer pens, breeding enclosures, deer management on a ranch-fenced or not) all ties together. The impact of land management, deer management, and wildlife management in general on one ranch can be felt by the neighboring ranch, the county, state, and even the whole region.

Some observations from the last few speakers and comments that went along with them:

1) If you have a lot of spikes, you have a problem. You should not have a lot of spikes. There should be practically no spikes in any age class other than the 11/2 year old. Even in the 11/2 year old age class, anything above about 20% spikes is excessive. I know a gentleman who said he remembered the first time he ever saw a spike in south Texas and what a shock it was.

2) If you have a very long, strung-out breeding season you have a problem. Long, strung-out breeding seasons indicate poor nutrition. If you hear about a long, strung-out breeding season, the first thing that comes to my mind is you've got nutrition problems. Look and see. Like Rollins said, "If you don't know your top ten deer plants, you need to go home and learn them." Habitat, habitat, habitat. We've said it so much through the years that we've had people tell us, "quit talking about habitat, we're tired of that. We want to know what to do next"or, "We want to know what else we can do. We want to know the easy way to do this." Folks, there is no easy way. It is habitat, habitat, habitat. It's food. Now, somewhere after that, as you proceed into management, as you work hard and spend money and commit your time and your family's time, etc., it is very important that you watch your age structure, watch your sex ratio. And this genetics thing is there. I believe you can impact genetics. I believe you can improve genetics. I don't know how long it will take. The gentleman this morning said it could take somewhere between ten and fifty years, but that's ok. I've got a feeling that there are going to be people coming along behind you and me with just as strong an interest as we have. They'll still be trying fifty years from now to improve; I hope and I believe that they will.

"Genetics" gets all mixed up. When you say genetics, we all throw a lot of things in the hat, but we believe at TPWD that we should allow the legal harvest of spike bucks where you have deer hunting going on. We believe that is important. At one time it was not legal and many of you who are much older than I am, which most of this audience is, remember those days. And we remember, 1) people made honest mistakes when they were harvesting a doe or harvesting a buck, and 2) just that thought of, "What is it about this deer that needs to be protected?"

But I and most of our folks, based on the findings at the Kerr Wildlife Management Area, encourage people to kill spikes. Sometimes we encourage them real strongly. We support that. We believe it. We believe it is *part* of the program. It's not for everybody, everybody doesn't have to do it, we don't make anybody do anything, but it is there, and it is available.

Regulations: Where is this road taking us? Like Rollins, I'm not sure. I am apprehensive at times about this, and I have expressed that before. If we are not doing research or doing studies that are applicable to management, then we need to be doing something else. We need to be learning things and answering questions that you people have, that you need to do a better job of habitat and wildlife management.

What we've done in regulations, particularly in recent years, is something the chairman of our commission has encouraged, and what this agency has done, and what I support 100%. And that is giving land owners lots of options, lots of flexibility to set their goals on their property and at their expense to work towards the accomplishment of those goals and objectives. We have worked hard to do that and I believe we will continue to do that. We will also continue to provide long seasons. I get a lot of people who will call me and say, "Cook, I don't want to start hunting that early in November." I say, "Don't do it. Wait 'til December. It'll be okay, it'll be alright." They say, " I don't like to hunt seven weeks." Okay, don't hunt seven weeks. My wife doesn't like me to hunt seven weeks either. Most of our hunting seasons are about as long as most marriages can stand. We can't get much longer. But we need to allow regulations (bag limits, seasons, those kinds of things) that are as liberal as this vast, renewable resource can stand, not only just for the land owner to provide those options, but to provide as much hunting opportunity as possible to the people who enjoy hunting in Texas. Folks, don't forget that. Why are we doing all this? Because people love to hunt. A lot of those people don't own land and never will own land, but they come to your property, you know them, they're friends of yours, friends of your family, some of them have been hunting with you and your family for generations and will continue to do so. We need to provide them a lot of opportunity with these wonderful resources we've got.

One thing that we (Texas Parks and Wildlife Department) have that I want to make sure you know about and tell other people about is our wildlife management plans. We say we have a lot of people that work with us on wildlife management plans. What does that mean? That doesn't mean we've gone out and told him what he ought to do. It doesn't mean that the Extension Service or other groups of folks like that who are "experts" have gone out and told him what he needs to do. Normally, it starts out that the land owner says, "I want to do better; I would like to produce bigger deer; I would like to have more quail." That's how it

starts. Then those folks, whoever they're with, (Forest Service, TPWD, USDA, Extension Service) will help that land owner design a wildlife management plan that suits him, suits his place, his family, his goals, and his ability- his financial ability. My financial plan and my wildlife management plan will look a whole lot different on my little piece of property than it will on somebody else's property. But I've got a plan and I enjoy doing it.

We have about ten million acres in Texas where land owners have come forward voluntarily and gotten into wildlife management plans with us. They are doing a better job and we're not putting a pe1nny into implementation. The landowner is paying for that improvement on his property. With those plans, wherever you are in the Texas, you can have, if you will ask for it, the most liberal regulations on white-tailed deer that there are in the state. In other words, if you are in a one buck county, your hunters can have a five deer limit. You could have a long season- a special season, under an approved Texas Parks and Wildlife Department wildlife management plan. If you don't know about that, you need to get in touch with us and find out about it. It doesn't matter if you have a high fence or not.

Future research: there are still a lot of questions. I believe that we are going to continue to do research on this topic and related topics. I want to invite you, I want to invite the universities, the other agencies, the private land owners, the hunters in this group, to participate in that with us, up front. The design on those projects, how are we going to do them? What are the questions? What are the real objectives in future research? Let's sit down together and work on that together so that we answer those questions, so we all understand what's going in, what the process is we're going to use, what the question is we're going to try to answer, and *then* move forward. And I invite you to participate in that process and know that the invitation will be specifically coming forth to a number of folks who you have heard speak in this meeting.

WHERE IS THIS ROAD TAKING US? THE ROLE OF GENETICS IN WHITE-TAILED DEER MANAGEMENT: TEXAS ANIMAL HEALTH COMMISSION PERSPECTIVE

JOE W. TEMPLETON, Professor, Department of Veterinary Pathobiology, College of Veterinary Medicine, Texas A&M University, College Station, TX 77843

I do not claim to be an expert in anything. I am a geneticist and also a commissioner in the Texas Animal Health Commission.

The only animal disease consideration that I harbor, with the patrol led be Cook, is that we don't want TB brought in by deer if TAHC feels like that's a threat. We don't, and if it does become a threat, you will be clamped down on. We will control all the imports and the breeder permits in cooperation with the Texas Parks and Wildlife when that happens. We don't want to put a bunch of test facilities on a truck and run around all over all these places, trying to trap deer and look at them. We're going to look at deer at the first point of collection just like we do cattle. We will try to make sure that disease stays contained. It's in everybody's best interests that we do that.

I am a geneticist. I am a particular geneticist, I am hyphenated. I am an immuno-geneticist. My interest is in genes that control natural resistance to disease, and the diseases that we are interested are in that category of study.

I have heard a lot of statements where someone will say, "Now I don't know anything about this, but" STOP. Listen, if you don't know anything about it, we don't need to hear from you. I think that that's the problem with this. See, everyone here thinks they're at least an armchair geneticist and, so they've got an opinion about it and they want to express that opinion. I've heard most of them express and most of them are wrong. So, I'm going to titillate you a little bit. I am going to tell you whether the Jacob study or the Harmel study is correct. I am absolutely going to tell you that. And that's the titillation. We'll get to that in just a moment.   I want you to leave here with that information.

Now, in terms of the genes that control our disease resistance, you're fighting a slightly simpler battle in increasing gene frequency in that system than you are with antlers, but not much. So it is going to follow the same rule of application that you like to have. And if you are going to do a genetic study, get a geneticist. A true geneticist will never deny that you need habitat. You've got to have it. But I'll tell you this, you can have the best habitat in the world with inferior genetics, and you will not have genetically superior deer. I don't care what you do. You have to do them together. If you do one in front of the other, you are going to string it out years down the road and waste a lot of time, and .you won't enjoy the fruits of your labor in your lifetime.   And there is not anybody here that has practiced genetics, whether a geneticist or not, that does not believe that deer antlers are determined by genes partly and the gene environment in action.

I'm going to go and finish up and tell you who's right. And then we can debate this any way you want to that both are right. But, what you don't understand is the limitations of these studies and the application of them.   You want to take those two studies and apply them generally to everything. Those two studies, and every geneticist knows this, are limited by several factors and they apply only to the area where they were conducted and to the animal they were conducted on. They don't apply to every deer, to every piece of land in the country, in Texas, West Texas, in Mississippi, or any place else. If you want to apply Harry Jacobson's study, it applies best at Harry Jacobson's setting, with the deer he collected. If you want to do Donny Harmel, it applies best at the Kerr area with the deer he started with. One of them had more profound affects than the other.   And it is clear when you look at the results of those studies that you have to know something about the composition of those animals, and if you want to try to apply them to your place, you are going to have to mimic that. If you don't, it won't apply. It just won't apply. And you're just going to waste you're time. So don't be going around thinking, "Well, I've got the

answer now. I'll just blend them both." So, what are you going to do? You're going to select half of them at one-and-a-half and half of them at two-and-a-half? And so you've got to know the limitations, you've got to know how to apply the data. You are going to have to talk to a real geneticist, because there are a whole lot of people who don't know anything about it, but it seems to them that this is the way you ought to go. Genetics works, folks. You can sit here in denial and I'll call you Cleopatra: you can be the Queen of d' Nile. Because I'm telling you genetics works. And genetics determines antlers. Now, it's interaction after that, but you will not have antlers without the genetic component in them to make them superior, no matter what you do.

Disease is something else that you need to think about, and that's the first point I was raising. You need to understand that there are diseases that really affect gene expression, and they're all over the place. Cattle and sheep are asymptomatic carriers of diseases that affect deer. So, when you have dense populations of deer and dense populations of livestock, you up the chances of having sub-clinical diseases in deer, and even a lethal outbreak of disease in your deer populations. And, so, I think what you have got to look at is to know that genetics works and to get some help in how to apply that in your particular setting. And then it will go from there. But if you try to say, "Well, I am generally going to do it this way." Well, again, I would say you're generally going to do it wrong. I know everybody wants a simple answer. The one paraphrase I always use is, "There is a simple answer for every complex question, but it is invariably wrong." You've got to understand that.

The last thing I'll leave you with is Albert Einstein's quote. Albert Einstein made a quote onetime when someone wanted him to explain the theory of relativity a little simpler. He said, "Everything should be explained as simply as possible, but never simpler than it really is." So, guys, when you want to explain gene action in five words or less, you can't do it. When they ask you to explain heritability in four words or less, you can't do it. So, you've got to understand that some of it is complicated and you will need help. And go with that and you'll get it.

Now, I was impressed with some of the roundups some of those people gave that said don't be one-eyed in your selection. Now I have a lot of experience in genetic selection. If you're one-eyed you will accomplish in a very short time, unintended problems, unintended consequences of that one-eyed selection. You may end up with a deer that has great antlers, but he's so stupid that he can't even find his way to water. So you've got to understand that when you go at this selection, you've got to do more than one-eyed selection. I will say this, and it's all well intended. And everybody says I'm a geneticist, but I'm going to say this, and it's not intended to be as harsh as it sounds. The Harmel study and the Jacobson study were set by non-geneticists. They answered some simple questions. They tried to expand it, by analysis, to answer more complex questions. It doesn't lend itself to that. They did some good studies with no geneticist in the front end. And the thing that's interesting is they did it out of desperation because the geneticists were not doing their job. So, they need to be there to help them. All I can say is the geneticists are arriving and the argument that's here, and I have a very strong opinion about it, is we need to redo those studies and do them correctly. And I don't like that. I think we need to start looking for the genes directly. That's the only way you're going to find them in the doe. There is no feature of the doe that tells you what the genetic make-up is.

The last thing: If you take a deer that comes from maternal and paternal sides where you have forked-horn one-and-a-half year olds and nine pointers and look at them, the breeding value is much greater than the same number of points on an animal that comes from a whole line of spikes. I can tell you that is true. Now, what you'd have to look at is multi-point lineages can still segregate spikes and spikes can still segregate multi-point animals. But, the rate will be higher from the multi-point line than it will from the spike line. And there's no doubt about that, it works every time. It's simple genetics, and it works. And, so, if you say, "Well, I am going to keep these spikes until they are ten points." Bless your heart, you'll never make it.

CLOSING COMMENTS

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I mentioned at the opening that this would be one of the most controversial of our series of wildlife symposia sponsored by the Texas Agricultural Extension Service. I certainly was not disappointed. We popped more people's balloons than at any meeting I have ever attended. And that is not a negative. Remember that the purpose of this meeting was to exchange information on the role of genetics in white-tailed deer management, not to come to a consensus on the accuracy of that information. Again, the information here was presented by scientists, practicing wildlife biologists, and experienced landowners. No one came here with false information, and no one came here to criticize other's work. We all came here to share our knowledge and experiences, to critique each other's science, and to challenge each other's assumptions. Knowing that, there is something here for everyone, regardless of your opinions about deer management, antler heritability, or culling spikes.

If anything became clear in this workshop, it was that deer genetics is a complex topic, and that the dangers, or at least the expenses, of making errors when trying to manipulate the genetics of a white-tail population could be great. Ken Gee's and Charlie DeYoung's data even raised questions about our ability to census deer from the ground or from the air, and our ability to age deer accurately with any common method. The issues of whether you can predict (at least accurately) the antlers of an adult from his antlers as a yearling and what, if any, the heritability of antler characteristics might be are still in question. The "MSU" and the "Kerr Area" data are largely in conflict with each other, as pointed out by our independent reviewer, Dr. D.F. Waldron, and to some extent by the field observations on the Faith Ranch. This raises serious questions about how or even whether one should try to manipulate a deer herd genetically. As Dr. Waldron pointed out, the MSU and Kerr studies were conducted differently, to answer slightly different questions. We know things now, through DNA analysis and more sophisticated statistical techniques, that we didn't know when these two major studies were begun. It is therefore not the fault of the researchers

that neither of these studies is conclusive. I agree with Dr. Waldron that it would be great if these two data sets could be combined, to get the best we can out of all of it. Even then, remember that we are working with wild critters, and we will never have the numbers of animals or years of observation that livestock producers have to accurately predict heritability.

Even more disturbing for the deer manager were the comments of Drs. Skow, Honeycutt, Templeton, Davis, and Taylor. They spoke of the dangers of selecting for a single trait (antler size) and not knowing what other traits you might be selecting for (remember double muscling in cattle?). They also spoke of the need for genetic variation (think biodiversity) to avoid genetic bottlenecks and inbreeding depression of herd fitness. During the question and answer sessions, they spoke of the dangers of bringing in herd sires from Northern states that might be genetically susceptible to Southern diseases. They also spoke of the importance of the dam in genetics, and the obvious difficulty of culling does to improve antler characteristics in bucks.

To me, one of the most economically important papers was that of Jerry Taylor. His computer model showed how many years it would take to upgrade a deer herd with a B&C average of 140 to an average of 165 by introducing sires with B&C scores of 185. The answer - 43 years - should not warm the heart of your local banker! Clearly, anyone thinking of buying and introducing breeding bucks into their herd needs to read this paper carefully.

In fact, I hope that everyone will read, highlight, underline, and reread all of the papers in this proceedings. Some of it may be hard to follow, but it will be an education. Unfortunately, I think we omitted a couple of important topics. One was deer behavior. While we discussed at length whether we should cull spikes, 8-points, or does; whether we should introduce sires; whether we should manipulate a herd's age structure; or whether we should feed or put in food plots; the fact of the matter is - we don't have a clue

which bucks are doing the breeding! Is it the big guys or the little guys - or some of both? This needs to be a topic of future research. And , although Dale Rollins touched on it in his paper and Clark Adams spoke of it during our informal session, we really have not dealt with the ethics of all of this. Do hunters really want genetically manipulated deer? Will expensive management price out the average hunter? What does the voting public think of high fences, of AI for does, of feeders and food plots, of pen-reared and released deer, or even potential cloning? And, when does a wild thing become domestic? We clearly need a grasp of the social implications of our science before we get too far into this type of management.

Finally, once the reader has read, studied, contemplated and perhaps debated the wealth of information in this proceedings, it might be wise to reread the first article, by Steve Nelle. Steve took us back to the basics, reminding us that there are no silver bullets. Perhaps we should have used this quote from his article on the cover of this text, ***"habitat management is the key to healthy, high quality, profitable deer herds."*** See you at our next symposium.

Stephen Fuchs
10/29/89

The Role of Genetics in White-tailed Deer Management- Second Edition