

- Columnists
- Markets
- Hindsight
- Weather
- Cartoon
- Buyer's Dir.
- Hotlinks
- Archives
- Classifieds
- Advertise
- Web Traffic
- Subscribe
- Contact Us
- Home

## Researchers Map Deer Genome; Management Possibilities Great

By Colleen Schreiber

SAN ANTONIO — Researchers at the Baylor College of Medicine have teamed up with deer researchers at the Caesar Kleberg Wildlife Research Institute. It is not a common alliance, for sure, but it is an interesting one.

Specifically, the Baylor scientists are studying deer antlers. Their interest stems from the fact that deer antlers are essentially bones that regenerate year after year. They want to see if they can learn more about antler regeneration, how that process works at the molecular level, and then use that knowledge to help them in their work with human bone injuries and bone diseases.

Matthew Grol and Mahim Jain shared some of the basics of the project with those attending the recent Deer Associates annual gathering here.

“The deer antler is really the only mammalian appendage capable of regeneration after being cast off,” Grol told listeners. “It’s very interesting from a perspective of basic biology and medicine, as we hope by studying it we can gain insight into possibly how to heal fractured bone and possibly understand why regeneration of mammalian appendages is limited to the deer antler.”

The antler, an innovative and vascularized structure unique to deer, is composed of skin, fibrous tissue, cartilage, and bone. A growing antler, he told listeners, shows some resemblance to the structure of the long bone in the appendicular skeleton. Long bones in humans support the weight of the body and facilitate movement.

“The antler is still somewhat unique, but it is very similar to what we know about growth plates.”

Growth plates are zones of cartilage at each end of the long bones.

Antler regeneration is highly regulated by the rising and falling of testosterone levels. The rise in testosterone in the fall signals end of growth, hardening of the antlers, and the shedding of velvet.

In spring, the drop in testosterone signals beginning of antler growth. This drop stimulates the periosteum to initiate pedicel development. The onset of the antler formation also coincides with the appearance of the velvet skin covering the deer antlers.

“We see increased resorption of the pedicel bone during the antler casting, and it coincides with a drop in testosterone,” said Grol. “Once the antler has fallen off, there is an injured site and it undergoes a wound healing response typical of what we might see with a skin wound or a bone fracture.”

To fully understand antler growth at the tissue level, the Baylor team needed to know what genes control antler development and how they are switched on and off. Therefore, the Baylor researchers first needed to sequence the white-tailed deer genome.

The process began by sampling growing antlers from two sibling bucks in the CKWRI’s Alkek captive deer research facility. Both bucks were four years of age. Antler tissue was taken from the siblings. The DNA was isolated to perform the genomic sequencing. They also isolated the messenger RNA from the antlers. This enables them to ultimately determine which genes are being expressed. They can then map this back to the DNA regions and ultimately learn where a specific gene is physically located on the genome map. Primarily they are interested in learning how the antler growth is switched on and off, what genes are involved in this, where they are located in the genome, and finally, how they may have been modified from the “normal” bone growth process to produce antlers.

Deer, he said, have 70 chromosomes. In addition to having more chromosomes than humans, the deer genome is also slightly larger compared to the human genome, and there are slightly more protein coding genes. The scientists are interested in better understanding what is happening molecularly in the different regions of the antler.

At the histological level the researchers could see differences between the two brothers. The antler tissue of the buck with the larger antlers, for example, was less differentiated compared to his brother with the smaller antlers. They then looked at a molecular test to see if they could understand what’s causing those differences.

All of this work is ongoing, as is the genome work. While the sequencing has been completed, the genome now has to be annotated. That process essentially entails taking all the DNA information gathered in the sequencing to figure out where the genes are located and what protein or RNA is produced by each gene. This process, which is done by the Center for Biological Technology, takes considerably more time.

Dr. Randy DeYoung is an associate professor and research scientist at the CKWRI. His expertise is in molecular ecology, the science of using genetic markers to investigate aspects of wildlife ecology and behavior. DeYoung followed with a presentation on how the deer genome may be used in management of the deer population. First, though, he summed up and simplified what the Baylor scientists are trying to do.

“As kids, our bones are growing, but at some point that growth stops,” said DeYoung. “That means, then, bone regrowth can’t happen as easily in older people when a bone is broken. The Baylor scientists think they’ve found out how deer regulate antler growth. If they know how the deer is able to flip the switch off and on, they might be able to give a human an injection to stimulate bone growth.”

So what does this new technology, having the deer genome mapped, really mean for wildlife managers? DeYoung and others have been using genetic markers in deer for quite some time, but this is not the same thing. Genetic markers have enabled deer scientists and managers to learn a lot about differences among subspecies and deer mating behavior via genetic parentage. Now, however, with the deer genome scientists will be able to figure out at the DNA level, for example, what makes some of these deer subspecies different, what makes some more adapted to some environments, and why some deer are better at surviving some diseases than others.

The deer story, DeYoung told listeners, begins about four million years ago when the first deer crossed the Bering Land Bridge from Europe. These early-day ancestors to the present-day deer diversified and adapted to different environments, from the tropics and mountains to the desert, plains, and the forest.

All of these deer, he noted, look different. Their body size is different, their coat color may be different, even some of their life history is different. On the big scale, DeYoung said, some of these differences are likely due to genetics.

But what about on a local and regional level? Why do some ranches that may only be separated by 10 or 20 miles have bigger deer than others? He used the East Ranches in South Texas, where there has been essentially no management of the deer population whatsoever as one example. What CKWRI researchers have found is there might be up to a 12-pound difference in doe body weights across the East ranches that are only 50 to 70 miles apart. There are even more pronounced differences in bucks, in some instances as much as 30 or more pounds difference in bodyweight. Boone and Crockett scores also vary by as many as 11 inches.

“Is it just habitat or nutrition, or is there something at a deeper level that we just haven’t been able to detect? Having the deer genome sequenced will enable us to get at that now,” he told listeners.

Another aspect that many managers are interested in, DeYoung noted, is the impact of selective harvest. For years, many have tried to improve their deer herd by specifically harvesting the poor-performing individuals. That culling process is typically done through antler size and by age class.

“What effect does that have? There are a whole bunch of genetic markers that go into building that antler, but right now, all we’re looking at is the size of those antlers. It might be nice to know what else is going on.”

Restoration is another management tool that has been widely used throughout the U.S., in particular in the Southeast, but no one really knows how this tool may or may not impact the overall deer herd.

“In 1900 there were hardly any deer in the Southeast,” DeYoung pointed out. “Could the mixing of genetics cause these animals to adapt differently to one environment or another? If we can learn what limitations there might be or how much flexibility there is, that might be something we could incorporate into management.”

He noted, too, that in the Southeast there are big differences in breeding dates.

“In places like southern Mississippi, southern Alabama and Florida there might be 30 to 90 days difference in peak rut in areas that may only be 50 miles apart.”

DeYoung said that some of this may be attributed to restocking, but there is no hard evidence for that theory.

“There are abnormal breeding dates in many regions and in every population, and we really don’t know why that is. We see this in livestock. For example, the timing of breeding in sheep and goats that come from the tropics shifts when they are moved to northern latitudes.”

These kinds of things, he added, can be managed relatively easily in the livestock industry using synchronization of estrus and hormonal treatments. It is not so easy to do with wildlife. It’s a problem, as any deer manager can understand, because a buck fawn born 30 to 60 days later than another just down the road gets a late start growing antlers, and in Texas it’s all about the antlers.

Another management option being used more and more in Texas that has not really been studied intensively and certainly not at a molecular level is the replacement of native deer with “better” deer, better in this case typically being bigger-bodied and bigger-antlered deer.

“How those deer mix in with the native deer and what the consequences of that might be is something that we need to better understand,” DeYoung told listeners. “This new technology will help us to do that.”

In the Southeast, there is a high incidence of mature bucks with brain abscesses.

“We don’t see this often in Texas, but in parts of Georgia it’s pretty high. So there’s probably something about those deer that causes them to be less resistant to this malady. Again, very little is known what causes it.”

Also, some deer in different parts of the U.S. are much more susceptible to bluetongue. It tends to be less of a problem in the South, and more so in the North and upper Midwest.

“Some of this resistance or nonresistance is probably do to genetic factors, but again, we don’t know what genes are involved.”

Chronic wasting disease is something deer managers in Texas are particularly concerned about these days.

“We know that there are some mutations in the prion protein gene that make it maybe a little harder for some deer to be infected by the disease, and in some cases some of the deer infected take longer to show symptoms of the disease,” DeYoung said. “Perhaps we can learn more now that we have the deer genome mapped.”

There are many deer all over the U.S. that have become “habituated” to an urban environment. The problems extend far beyond vehicle crashes and destroying manicured landscapes. In the Northeast a larger concern, DeYoung told listeners, is that these urban deer are vectors for Lyme disease and other tick-borne diseases. Perhaps, he said, “we will now be able to better understand and manage this disease.”

Another future use of this tool, DeYoung said, may be for exploring retroviruses.

“Up to eight percent of all of the human DNA originated from a virus,” he told listeners. “Scientists have explored retroviruses in mule deer, and they’ve learned that these viruses can actually insert themselves into the genome. We may be able to use this as another genetic marker. If whitetails have this kind of viral DNA and the mule deer don’t, then it had to happen after the split of whitetails and mule deer. That might help us date some of the speciation.”

He reminded listeners that overall, a lot of the differences seen in the deer population today may not be due to differences in the genes themselves.

“Some genes may be turned on at different times, or some produce a lot more of certain protein or RNA products, so the timing and the amount of proteins being produced can really influence how the deer grows, how it looks, for example.”

DeYoung wrapped up by telling listeners that it’s definitely an exciting time for deer scientists and deer managers.

“We’re now in the very first stages of making some estimates about heritability based on animal genetic models. This resource gives us the potential to do that.”

He qualified that, however, telling deer enthusiasts that they shouldn’t really expect a big payout on this in the short term.

“The human genome has been out for over 10 years now, and we are just now starting to reap some of the benefits,” DeYoung said.

“The good news is that DNA is pretty similar in a lot of organisms, even in fairly distantly related ones like people, rats and deer. All mammals share similar developmental pathways, so we’re not starting from scratch. That’s really good news,” he concluded.

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