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What Do Genetics Tell Us About Eastern Wild Turkeys in The Pineywoods?

Article by **SABRINA SEIDEL**, *Research Associate* and **CHRISTOPHER E. COMER**, *Associate Professor of Wildlife Management*

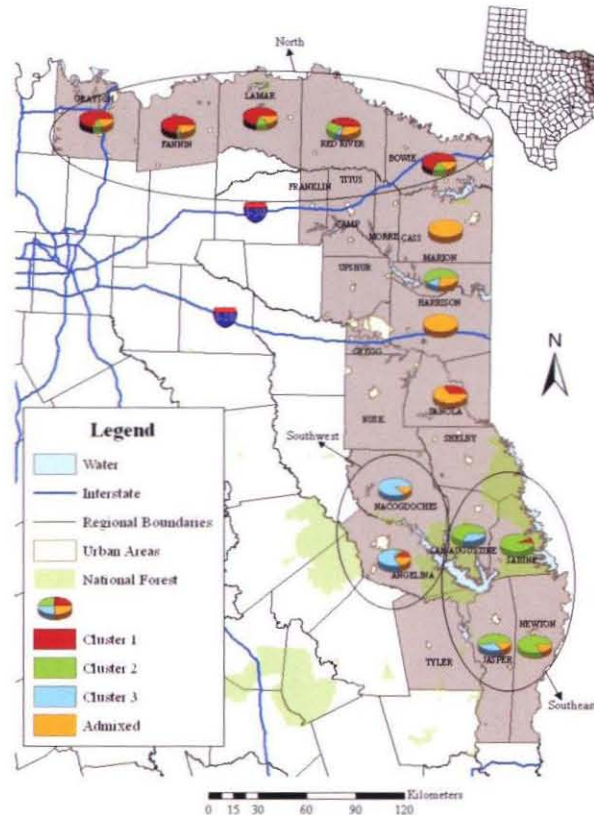
Translocation has been an important management and restoration technique for wildlife managers since the early part of the twentieth century. Capture and movement of animals has been used to restore species to native range, supplement native populations, and even introduce species outside of their normal range. In some cases, translocations have been very successful, leading to some of the greatest success stories in modern wildlife management. These success stories include the restoration of white-tailed deer to much of the eastern United States, reintroduction of black bears to Arkansas and other southeastern states, and the restoration of Eastern Wild Turkeys to much of the east.

Because of the efforts of the National Wild Turkey Federation, various state agencies across the country, and many private landowners, the capture and movement of Eastern Wild Turkeys across much of the eastern U.S. stands as one of those triumphs of wildlife management, with a population that expanded from less than 500,000 birds in the mid-1900s to well over 5 million birds today. As part of this program, over 7,000 Eastern Wild Turkeys were translocated to eastern Texas between 1979 and 2010. In contrast to most locations in the east and southeast, the turkey population of East Texas never took off. To be sure, there have been many successful turkey hunts in the Pineywoods, but harvest numbers and population estimates have fallen in recent years, and Texas Parks and Wildlife Department recently closed spring turkey season in 15 counties.

Translocations can have unanticipated impacts on the restored populations, including dramatic reductions in genetic diversity and loss of adaptations to local conditions. Characteristics of the source populations can persist for many generations following release. Consider that in some parts of the southeast, white-tailed deer in adjacent counties have peak rut dates that vary by two months or more, because translocated populations have maintained breeding synchrony from their source populations in south Texas or Florida. Particularly in the early days of wildlife translocations, managers paid little attention to the diversity or local adaptations of source populations – they took animals from wherever they could get them. With the advent of modern genetics analysis, we can now unravel the impacts of translocations on current wildlife populations and how that history may affect population health and growth.

As part of a larger research project examining the reasons behind slow population growth in Texas Eastern Wild Turkeys, Stephen F. Austin State University used DNA analyses to look at how the translocation history is evident in the current Eastern Wild Turkey population. Furthermore,

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The genetic structure in East Texas wild turkeys, as from 294 hunter-harvested and wild captured turkey tissue samples from East Texas (2007-2009) Photo by Sabrina Seidel



Removing blood sample from wild captured Eastern Wild Turkey in East Texas. Photo by Jason Isabelle

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Rocket nets used to capture Eastern Wild Turkeys in East Texas.
Photo by Ryan Bass

harvest records and gobbler counts in East Texas suggested that while some areas have consistently supported stable turkey populations, these areas appear to be isolated and separated by areas of apparently suitable habitat that are only sparsely populated. In 2008 and 2009, we began collecting tissue samples from



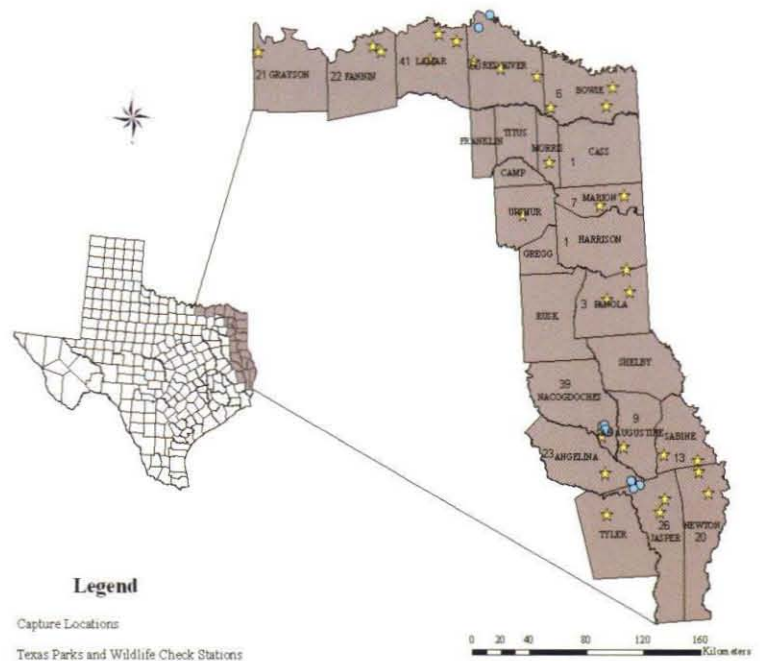
Eastern Wild Turkey blood sample stored in buffer for use in molecular analyses of Eastern Wild Turkey population genetic structuring.
Photo by Jason Isabelle

wild turkeys across the region. Although we obtained blood samples from 50 wild turkeys captured as part of a radiotelemetry study, we relied on the turkey hunters of East Texas to do most of our sample collection. Graduate student Sabrina Seidel and Texas Parks and Wildlife employees placed feather collection kits (including a tube of ethanol, disposable scissors, gloves, and a data card) at 28 mandatory check stations in 24 counties. The NWTTF offered a shotgun raffle to encourage participation, and the East Texas hunters came through for us. In all, we received 244 samples from 19 counties, representing 45 percent of all Eastern Wild Turkeys legally harvested in 2008 and 2009.

Of course, to identify the influence of the translocations on today's turkeys, we needed to know where those turkeys came from. This was a more difficult task than one might imagine, and it involved going through boxes of paper records with TPWD wild turkey specialist Jason Hardin. Some records literally consisted of dots on a paper map, with hand-written notations of release numbers and source state. Nonetheless, we determined that Eastern Wild Turkeys came to Texas from at least 16 states. Thankfully, five states (Iowa, Wisconsin, South Carolina, Missouri, and Georgia) accounted for nearly 80 percent of the turkeys translocated here, and we were able to obtain reference DNA samples from a tissue repository at Utah State University from all of these states. Ms. Seidel performed all



Translocation of eastern wild turkeys has been a successful technique to restore turkeys throughout its geographic range.
Photo by Jason Isabelle



Capture locations and Texas Parks and Wildlife Department check stations in East Texas, where blood and feather samples were obtained from Eastern Wild Turkeys from 2007 to 2009. Numbers indicate the total number of samples per county. Photo by Sabrina Seidel

of the genetic analyses, working in the lab of Dr. Randy DeYoung at the Caesar Kleberg Wildlife Research Institute at Texas A&M University-Kingsville.

Our results suggest that translocation history remains the most important influence on the genetics of Texas Eastern Wild Turkeys. Even down to the county level, the genetic influence on the turkeys reflected the source states for translocations. Across the region, about 65 percent of translocated turkeys came from the Midwest (Missouri, Wisconsin, and Iowa), and 10 percent came from Georgia and South Carolina. Similarly, we found that our current wild turkey population is influenced about six times as much by midwestern turkeys as it is by southeastern turkeys. We also found that little genetic exchange is occurring among turkeys in various regions of East Texas, with isolated populations occurring in northern counties along the Red River (north of I-20), in the Nacogdoches and Angelina counties area, and along the border with Louisiana (Newton and Sabine counties).

One unexpected finding in our study was the persistence of Rio Grande Turkey genetics in deep East Texas. We documented a strong influence of Rio Grande Turkeys in individual wild turkeys from Angelina, Newton, and Sabine counties, despite records indicating that Rios had not been translocated to those counties in more than 50 years. The origins of these turkeys are unclear, but it may be that translocations can have an even more far-reaching influence than we think.

These population genetics studies are only one piece of information in determining the status and future of these popular and challenging game birds for eastern Texas. If new habitat management and stocking techniques work out as we hope, the next version of this story will show us a healthy and self-sustaining turkey population that occupies all available habitat in the region. 🐾

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