

Story by Kyle Orr

# New Way of Counting

## Scientists Utilize New DNA Analysis of Deer Feces to Estimate Population of Pacific Herd

**E**nvironmental scientists with the California Department of Fish and Wildlife and researchers from the University of California Davis are testing a new way of determining the abundance of key deer populations. The method, which was first tested in Alaska, involves the collection and analysis of DNA contained in deer fecal samples.

The shift in survey methods should lead to more accurate estimates and correct some of the inherent inaccuracies that occur from roadside surveys, as well as spare the animal the stress from hovering helicopters during aerial counts.

Mule deer (*Odocoileus hemionus*) abundance has fluctuated significantly over the past century in the western United States, and understanding the complex reasons for such fluctuations is vital. Management of deer herds in California requires knowledge of population parameters in order to effectively determine hunting quotas, season dates and direct activities that will ensure population viability. However, few existing methods of determining abundance are equally effective across all habitat types, so over the years the need has grown to develop alternative methods.

Estimating populations of mule deer by

aircraft over dense forests is not practical due to poor visibility through the natural canopies. Road surveys have their own drawbacks and are considered unreliable in forested environments because of the limitation to accessible roads.

Consequently, CDFW wanted a cost analysis of implementing a long-term monitoring program for mule deer using recent developments in non-invasive fecal DNA technology. A research paper, “Noninvasive Genetic Spatial Capture-Recapture for Estimating Deer Population Abundance,” provided a detailed explanation of the process.

CDFW environmental scientist Terri Weist was one of three authors of the research paper on a migratory herd of black-tailed mule deer along the western slope of the central Sierra Nevada. The research involved DNA sampling of deer pellets to provide a genetic “fingerprint” with enough information to eliminate the need to capture animals. CDFW funded the research and UC Davis conducted the laboratory work and statistical analysis. Similar field work has been conducted elsewhere in the state to estimate the population of other herds.

“This method provides us with another tool in the toolbox for obtaining accurate information on the population health of our

Photo © Toshimi Kristof



Estimating the population abundance of deer herds along the western slope of the central Sierra Nevada has been challenging for researchers because of the animals' natural habitat of dense forests and heavy vegetation. A new method being tested by the California Department of Fish and Wildlife and UC Davis promises to provide better estimates in herd counts through DNA extracted from pellets. The innovative procedure will eventually free researchers from reliance upon the more costly and less reliable aerial and roadside surveys.



A researcher with the UC Davis uses a plastic vial to collect pellets left by a migrating deer herd along the western slope of the central Sierra Nevada. Through information collected through the extracted DNA, researchers will identify individual bucks and does. Biologists will follow up with field samples, and through the matching of DNA information, will be able to better estimate ungulate abundance, size, health and migration patterns.

deer herds,” Weist said. “It has proven to be effective and provides reliable estimates of wildlife species that may be elusive, low in numbers or otherwise difficult to detect.”

California researchers based the process on a precursor study of Sitka black-tailed deer undertaken over the last decade in Alaska. There, scientists extracted DNA from deer pellets rather than the traditional means (hair or tissue samples). The research served as the source for a seminal study, “Estimating Abundance of Sitka Black-Tailed Deer Using DNA from Fecal Pellets,” by Todd J. Brinkman, an assistant professor in the Human Dimensions of Wildlife Laboratory at the University of Alaska Fairbanks. Brinkman, who has a doctorate in wildlife ecology, published the article in 2011 for the *Journal of Wildlife Management*.

The study was conducted on Prince of Wales Island, one of the islands of the Alexander Archipelago in the Alaska Panhandle. Brinkman called the study the first in the nation to precisely estimate ungulate abundance using DNA from fecal pellets. According to Brinkman, Sitka black-tailed deer (*Odocoileus hemionus sitkensis*) is a subspecies of mule deer and serves as the most important big game species both on the island and in southeast Alaska. The

species is hunted for subsistence by local residents, as well as for sport.

At 2,577 square miles, Prince of Wales Island is considered the fourth-largest island in the United States and is among the 100 largest islands in the world. Even with all the open land, by the late 1990s, hunters on the island struggled to harvest sufficient deer to meet their needs. State wildlife management authorities offered up three possibilities for the decline: overhunting, predators or a decline in deer habitat quality due to past logging operations. Wildlife experts concluded that they needed to better understand the current status and emerging trends of the population to determine whether the problem arose from inadequate deer numbers or other factors.

“Previous to this work we had no idea what the deer densities were in south Alaska or the entire range of Sitka deer,” Brinkman said. “The approach was born of necessity.”

For three years, from 2006 to 2009, Brinkman and his colleagues collected deer dung along identified trails, marking and re-surveying numerous times. They identified 10,569 pellet groups and retrieved pellets from 2,248 of them for DNA extraction. Pellets were preserved in plastic vials filled

with ethanol. Researchers then extracted DNA from 1,156 samples and genetic markers specific to deer were used to identify 737 individuals.

The evidence helped researchers discover potential causes for the difficulty hunters had encountered in harvesting deer. Brinkman determined “the most plausible cause of the deer hunting dilemma is habitat change stemming from the boom and bust of the logging industry. Those changes have dramatically altered hunter access to preferred hunting habitats, with negative consequences for hunter success.”

Brinkman subsequently was contacted by numerous wildlife departments, including CDFW, about his study and has offered encouragement and advice to wildlife agencies that face situations similar to those highlighted in the Alaska study. CDFW began to test its version of the process in 2011 in Mendocino County before beginning the Pacific deer herd study in 2013.

The migratory Pacific herd roams over approximately 568 square miles of public and private land along the western slope of the Sierra Nevada in El Dorado and part of Placer counties. The herd’s summer range shrinks significantly to nearly 330 square miles, but the terrain remains steep, rising from 4,800 feet to nearly 9,900 feet in elevation. The land consists primarily of Ponderosa pine, red fir, lodgepole and white bark pine mixed with shrubs of huckleberry oak, snowberry and sagebrush. Meadows provide important grasses and forbs during fawning season.

CDFW and UC Davis researchers collected deer pellets during the summer from the range near Icehouse Reservoir and Loon

Lake. They divided the space into three subsections to ensure complete coverage. The scientists cleared the collection area of fecal pellets and then re-sampled the area three more times to determine how many of the previously identified individuals were re-encountered and how many new individuals also were present.

Testing and analysis of the pellets was performed by Dr. Benjamin N. Sacks, a UC Davis adjunct professor at the Mammalian Ecology and Conservation Unit, Veterinary Genetics Laboratory. Sacks co-authored the California study on the noninvasive estimation of deer population with Weitz and Jennifer L. Brazeal, a doctoral candidate at the university. The analysis was jointly conducted with CDFW, and Sacks said scientific advances are making the process increasingly feasible. Sacks credited Brazeal with playing a “leading role” in the study, praising his colleague for refining the data analysis.

“Genetic technology is moving fast,” Sacks said. “It is becoming more cost effec-

tive and procedures are being increasingly streamlined.”

Using statistical programs, researchers estimated the Pacific herd consisted of 2,600 animals in 2013 and 2014. In this case, DNA analysis determined the sex but not the age of the deer.

CDFW deer surveys using the fecal DNA process are underway in other parts of the state, including Tehama, Plumas, Imperial, Riverside, Sacramento and Marin counties. CDFW scientists expect to use the technique on an even larger scale, as similar studies are planned for 14 deer herds across a dozen counties in the north central portion of the state. Once baseline population data can be collected, researchers will shift to periodic monitoring to track the trends throughout the state. 🐾

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There are six subspecies of mule deer in California: Columbian black-tailed deer (*Odocoileus hemionus columbianus*), Rocky Mountain mule deer (*O.h. hemionus*), California mule deer (*O.h. californicus*), Inyo mule deer (*O.h. inyoensis*), burro deer (*O.h. eremicus*) and southern mule deer (*O.h. fuliginatus*). The natural habitat for deer is thick vegetation and heavy forest with an overhead canopy that offers concealment and protection from predators. Unfortunately for wildlife researchers, these conditions make their task nearly impossible.

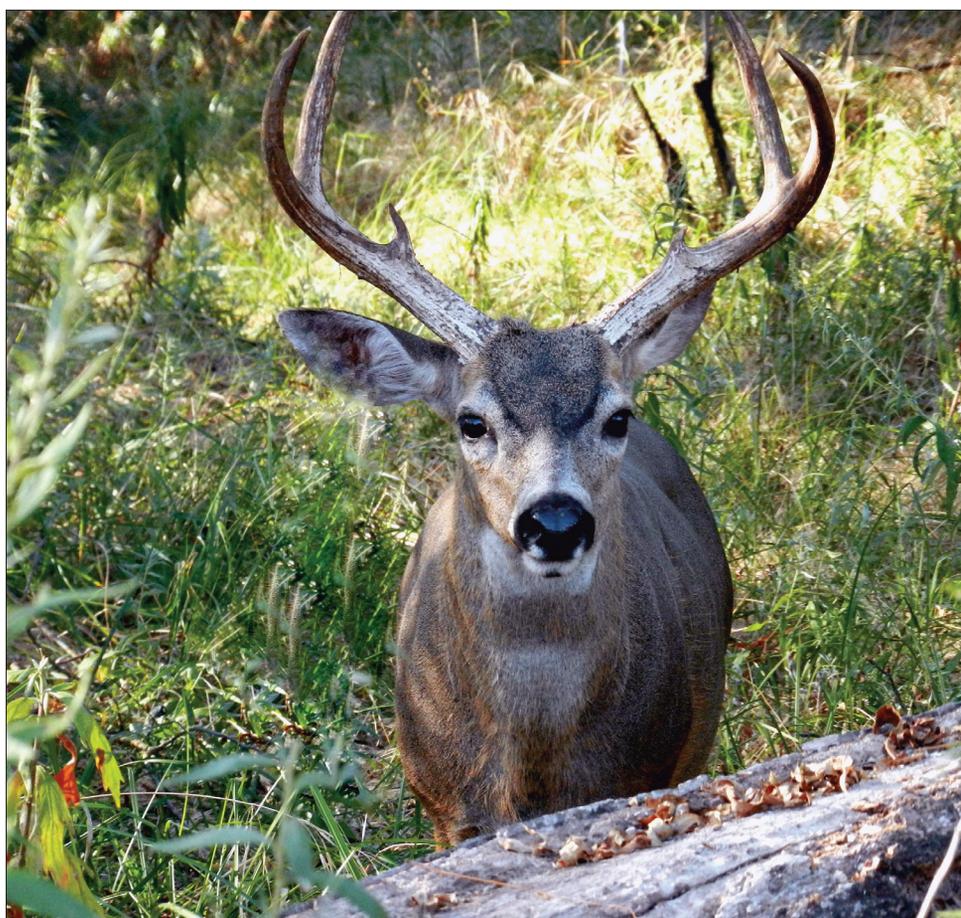


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