

Mountain Lion Ecological Genetics



Sarah K. Brown, M.S.

Graduate Research Assistant

Holly Ernest, DVM, PhD.

Assistant Professor in Residence
Wildlife and Ecology Unit
Veterinary Genetics Laboratory
University of California at Davis

Illusive animals by nature, mountain lions (*Puma concolor*) inspire a sense of wonder and curiosity. Their inherent secrecy results in a complex management issue for wildlife biologists and managers. Obtaining accurate data on population dynamics and species habits on such a wide-

ranging carnivore now involves a merging of tools in ecology and molecular biology. New molecular techniques allow wildlife geneticists to discern population structure and the movements of animals.

Mountain lions are widely distributed throughout western North America, coinciding with the availability of prey and suitable cover. An estimated 2,000 to 5,000 mountain lions inhabit California, occupying more than half of the state in varying bioregions. Carnivores are in a tenuous ecological position throughout most of the West with habitat fragmentation and loss

being the most severe threat. The diminished habitat results in small separate populations that have little connectivity to other remaining populations. Reduced “gene flow” is the term that ecological geneticists use to describe the reduced ability of an animal to mate with others outside its local region. Inbreeding is a problem that occurs when habitat is degraded or lost so that there are fewer animals in the breeding pool. Inbred animal populations have lower amounts of variation in their DNA, leading to a reduced ability to respond to changes in their environment. Knowledge of the genetic structure of populations is

important to aid in the management of the species and the habitat it occupies. Dr. Holly Ernest, wildlife geneticist and veterinarian, at the University of California at Davis, has been applying genetic tools to aid mountain lion management since the mid 1990s. Her work has helped the understanding of how mountain lions move across the landscape and identified whether they might be at risk for inbreeding.

Population genetic structure of California and Nevada mountain lions was surveyed by Dr. Ernest in the 1990's working in the UC Davis

laboratories of Dr. Walter Boyce and the Veterinary Genetics Laboratory. Samples were obtained from lions killed on depredation permits (issued for animals causing harm to livestock, pets, or humans), those captured for radio-telemetry, and non-invasively by scat (feces) collection. A suite of 12 DNA markers ("microsatellites"), developed from domestic cats were used to estimate relatedness among individuals, gene flow, and population subdivision. Microsatellite markers are neutral (not under selection), evolve quickly, and are often better

able to reveal fine-scale population structure than mitochondrial DNA. The results from this study revealed that distinct populations are present in California, particularly highlighting the major barriers on the landscape scale. The North coast and central coast populations are most genetically different from each other, likely due to the presence of the San Francisco Bay and delta. The Los Angeles basin was associated as a barrier to dispersal, whereas the San Gabriel and San Bernardino mountains appeared to function as movement corridors. The

Study Location



research indicated that the California Central Valley, with more than 95% of land converted for agriculture and housing during the past century, is a barrier to dispersal as well.

This study showed the composition of mountain lion populations during the 1990s. To obtain an assessment of trends in genetic diversity and population structure, it is key to examine samples collected from multiple points in time. Dr. Ernest is conducting research to include a comparison between the samples from the 1990s, 2000s and museum samples from as far back as the 1800s. Genetic analysis of museum samples allows us to peer into the past and observe how mountain lion populations have changed over time in response to

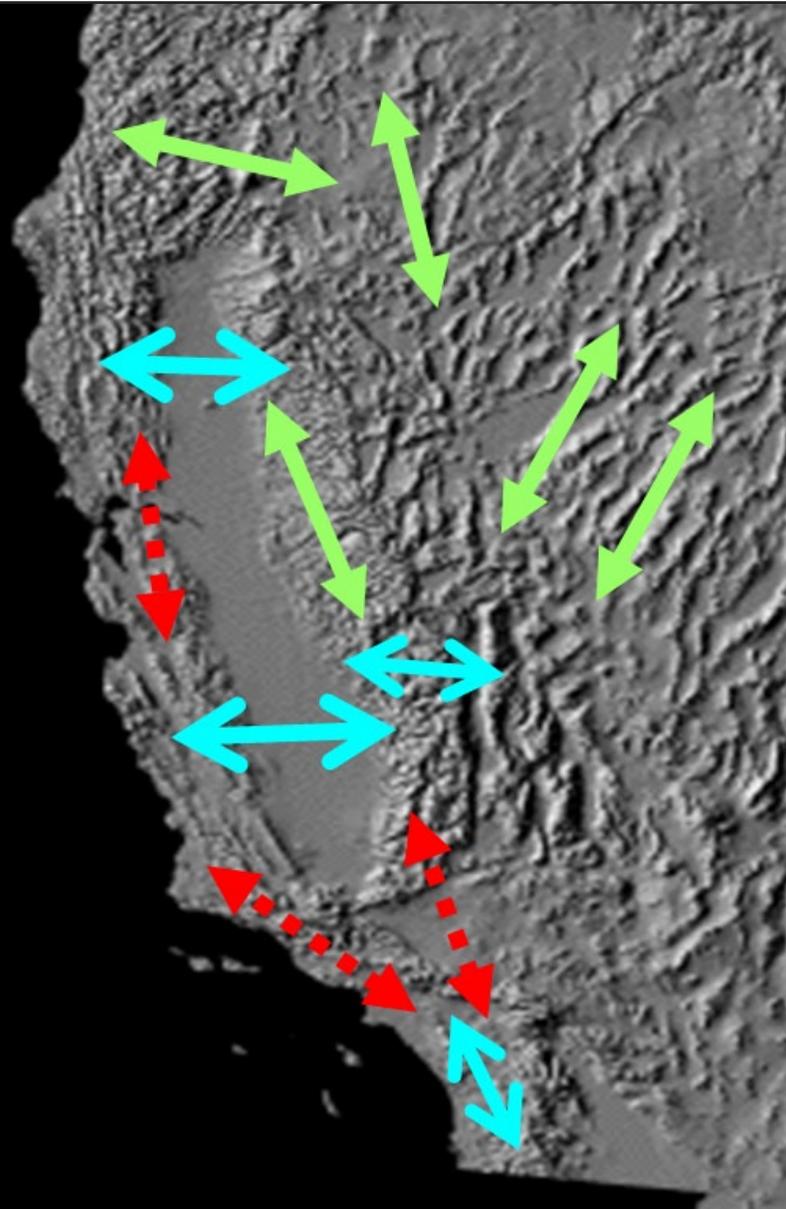
increased human population and habitat degradation. For example, while the Central Valley appeared as a barrier to dispersal for lions in the 1990s, the region was not greatly developed for agriculture until the early 1900s and riparian corridors present before that time might have allowed movement between the Sierra Nevada and Coast mountain ranges. Data from this study will be used to compare mountain lion genetics from the past to present and will aid in determining future population viability of California mountain lions.

Human activities and developments are encroaching on wildlife habitat, resulting in an increased threat of wildlife-human attacks. During the past 100 years, there have been 14 documented

mountain lion attacks on humans. Another aspect of the increasing wildlife-urban interface is livestock and pet predation by mountain lions, with an average annual report of more than 1,000 cases. In instances of human and animal attacks, forensic identification of the predator in question is important. Ensuring which species, and even in some cases which individual, caused the attack are vital tools for species management. Work done by Dr. Ernest and coworkers revealed that DNA analyzed from bite-wounds on prey animals could identify individual mountain lions and bobcats that were suspected to have preyed upon livestock. Recently, work conducted in Dr. Ernest's laboratory (published in the journal *Molecular Ecology*

F_{ST} Summary

-  Low gene flow
($F_{ST} > 0.15$)
-  Moderate gene flow
($F_{ST} 0.05-0.15$)
-  High gene flow
($F_{ST} 0-0.04$)



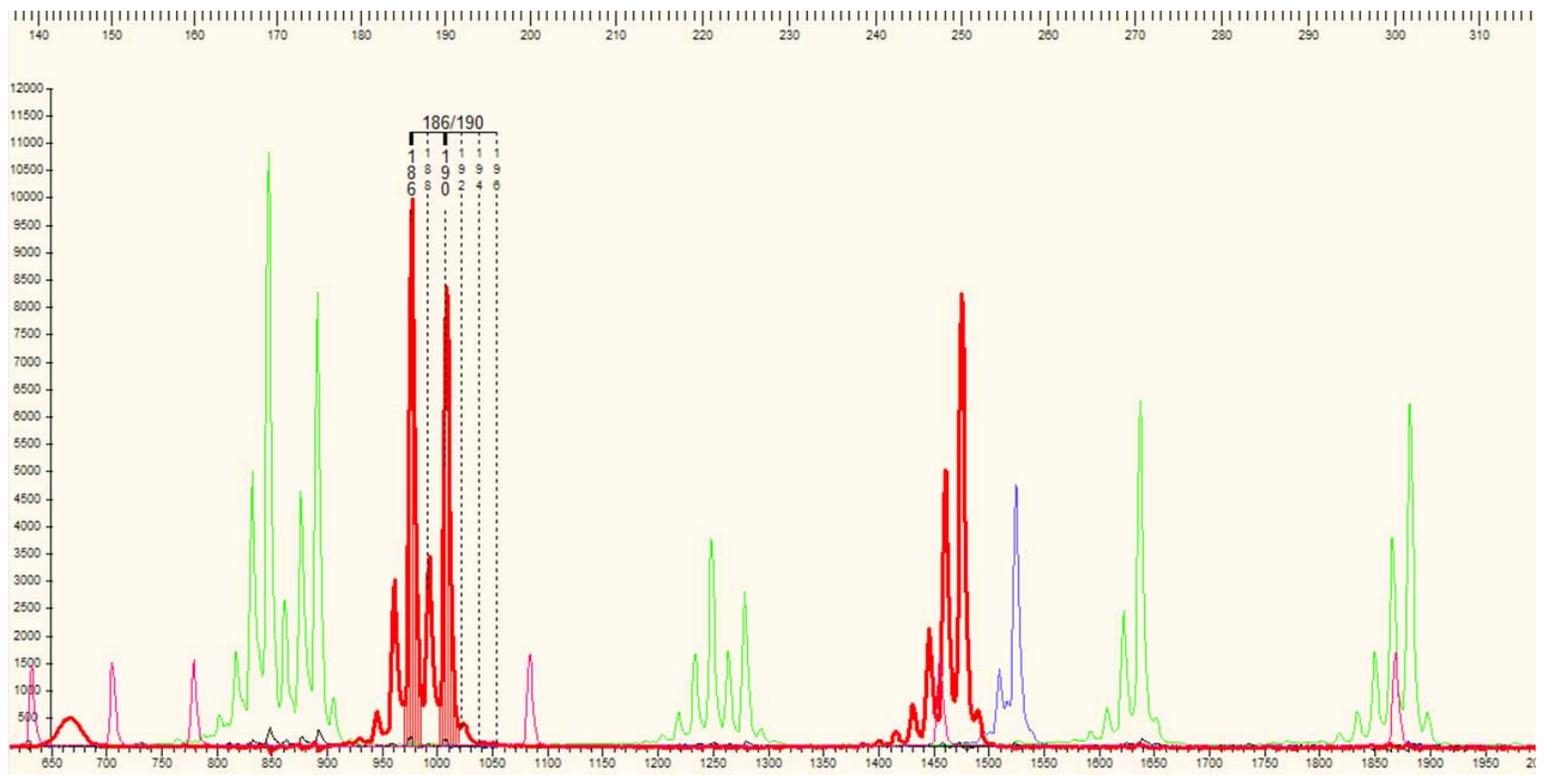


Figure 1: An example of a microsatellite chromatogram, from an individual mountain lion. A chromatogram is a graph of fluorescence signal, showing sizes of the pieces of DNA. The Y-axis denotes general strength of the markers, and the X-axis represents length in base pairs of DNA. The single pink peaks are an internal size standard placed at known base pair intervals. Markers are fluorescently labeled and in this gel appear green, red or blue. Depending on the individual, the loci are either homozygotes (a small stutter peak (not actual allele) before a taller allele peak), or a heterozygote (a small stutter peak followed by a taller allele peak, then another stutter peak and the second allele). There are 7 markers in this multiplex. The second marker from the left (in red) is a heterozygote, with base pair lengths of 186 and 190. Base pair length is recorded for each individual at all loci, and then used in further analysis.

Notes in 2006 with lead author Jennifer Kurushima) produced the first panel of microsatellites designed specifically for pumas, including forensic-quality DNA markers. The forensic-quality markers are similar to those adhering to legal standards for human forensic identification. Previous population genetic studies of pumas by geneticists Ernest utilized markers, which were developed for the domestic cat. These newly developed DNA markers will augment the quality of data collected using the domestic cat markers.

Puma-specific DNA markers may have particular application to mountain lion predation on native populations of bighorn sheep in the state of California. Bighorn sheep, particularly in the peninsular ranges of California, have been declining during the past 30 years. Threats include habitat loss, disease, and mountain

lion predation. Through fecal DNA analysis at bighorn sheep kill sites, Dr. Ernest and others have been able to identify mountain lions responsible for the kill. The recent development of fine-scale forensic DNA markers, better able to identify individuals, may aid in the management of both the bighorn sheep and the mountain lions, perhaps by reducing the chance of removing mountain lions not responsible for bighorn sheep predation.

Research by other investigators has added to the knowledge base on mountain lion population dynamics throughout western North America. Beginning in the 1990s, Dr. Melanie Culver and colleagues pioneered the then-new field of mountain lion molecular genetics. Her research changed our concepts of subspecies and provided valuable evolutionary information about the puma as a

species. Work by Dr. Brad McRae and collaborators has shown that mountain lions in Utah, Colorado, Arizona, and New Mexico show strong genetic differentiation on a longitudinal gradient, and that within each region, gene flow is limited by distance and habitat barriers. He also developed a new way to examine the movement of mountain lions and their genes across the landscape, called a circuit theory model. Dr. McRae's work will help in outlining landscape connectivity and habitat preferences to aid in management.

Disease is also a threat to mountain lions. Dr. Mary Poss, Dr. Roman Biek, and collaborators have investigated prevalence of mountain lion specific feline immune deficiency virus (FIV), and the co-evolution of host and virus. They found that occurrence of FIV is high (58%) in certain populations and occurs

mainly in older cougars. Interestingly, Biek and Poss were able to track mountain lion population structure and demographic history using viral genome information.

Mountain lions are integral to the health of ecosystems in western North America. Wildlife biologists and scientists are finding that degradation of habitat is the most immediate threat to the species. Genetic tools are helping to identify units of conservation concern, important breeding habitat, and corridors for connection between populations. As the field of ecological genetics develops, it is likely to contribute greatly to the management and preservation of habitat and species conservation.



Above: photo by Esther Rubin. Below: a cougar at a bighorn sheep kill. Photo by Esther Rubin and Charles L. Hayes.

