

Pioneers in Veterinary Genetics

Genetics testing and research are vibrant, cutting-edge components of the UC Davis School of Veterinary Medicine. Genes, environment, and their interaction play critical roles in animal health and disease, and our scientists are continuously breaking new ground and deepening our understanding of the animal world through advancements in this exciting field.

Genetics research not only furthers understanding of which animals are at risk for particular diseases, but ongoing discoveries can also lead to the development of diagnostic tests and potential gene therapies, resulting in earlier disease intervention and improved health outcomes.

The recent mapping of horse, dog, and cat genomes has made available powerful tools for the investigation of inherited diseases; it also empowers researchers to apply this vast new knowledge toward correcting genetic defects and disease susceptibilities. Each research discovery accelerates our understanding of animal diseases, which in turn can provide vital information about related human diseases.

[Yellow Fever in Bolivian Howler Monkeys](#): Veterinary scientists helped identify and respond to a Yellow Fever outbreak in 2012 after five howler monkey carcasses were found near a wildlife sanctuary in eastern Bolivia. PCR tests revealed that the monkeys were infected by a flavivirus. The Ministry of Public Health was immediately notified and cDNA sequencing confirmed that the infections had been caused by two Yellow Fever viral strains, both of which were related to human cases. Only eight days passed between the onset of outbreak and notification of the Bolivian government. Preventive measures were promptly implemented in the affected area, including vaccination campaigns, public outreach and mosquito control. Thanks in part to the fast response, no human cases occurred during the outbreak.

Discovering a new virus - UC veterinary wildlife epidemiologists, with a team of international researchers, discovered a new SARS-like coronavirus in Chinese horseshoe bats that can be directly transmitted to humans. The virus is closely related to the SARS coronavirus that erupted in Asia in 2002 and 2003 and caused a global pandemic crisis. These findings open doors for scientists to conduct detailed studies to create control measures to thwart outbreaks and provide opportunities for vaccine development; and highlight the importance of research programs such as UC Davis' PREDICT, which is actively building a global surveillance system to detect and prevent spillover of pathogens of pandemic potential that can move between wildlife and people.

Heart disease in cats - Veterinary cardiologists [identified the gene mutation responsible for hypertrophic cardiomyopathy](#), the most common cause of heart disease in cats. This inherited disease is also important in humans and is frequently responsible for sudden cardiac death. The discovery marks the first report of an identified spontaneous genetic mutation causing heart disease in a cat or dog. The findings paved the way for development of a screening test that identifies cats carrying this genetic mutation so that they can be identified before they are bred, thus reducing or eliminating the incidence of the disease. As they continue to study this disease and mutation in cats, researchers are also hopeful that the discovery will provide a valuable model for investigators in human medicine who are studying the disease.

[Gene mutation in dogs offers clues for neural tube defects in humans](#) – Veterinary scientists identified a gene related to neural tube defects in dogs. The researchers also found evidence that the gene may be an important risk factor for human neural tube defects, which affect more than 300,000 babies born each year around the world.

[Cleft palate discovery](#) – Veterinary geneticists identified the genetic mutation responsible for a form of cleft palate in the dog breed Nova Scotia Duck Tolling Retrievers. They hope that the discovery, which provides the first dog model for the craniofacial defect, will lead to a better understanding of cleft palate in humans.

Avian Responses to West Nile Virus - Veterinary pathologists have [a number of studies under way](#) to assess the effects of West Nile virus on certain species of birds. The team has developed molecular tools specific for yellow-billed magpies and is comparing magpie DNA collected before West Nile virus entered California with samples collected recently. They are also examining whether the virus is changing the population structure of crows, Swainson's hawks and red-tailed hawks statewide. Knowledge gained from these studies benefits human health, as these birds are particularly susceptible to the disease and are excellent early-warning sentinels for virus activity.

Raccoons may provide cancer clues - Scientists at the School of Veterinary Medicine and the California Animal Health and Food Safety Laboratory [discovered a previously unidentified virus](#) found in rare brain tumors emerging among raccoons in Northern California and Oregon. Dubbed raccoon polyomavirus, researchers suspect this virus contributes to tumor formation. Their findings could lead to a better understanding of how viruses can cause cancer in animals and humans.

[Advances in Dalmatian health](#) - A gene mutation that causes high levels of uric acid in all Dalmatian dogs and bladder stones in some Dalmatians has been identified by a team of researchers. The discovery equips dog breeders with the tools to eliminate that trait from the Dalmatian breed and yields clues to the cause of similar problems in humans.

[Goats' milk a treatment for diarrhea](#) - -- a veterinary professor led a study whose results showed that milk from goats that were genetically modified to produce higher levels of a human antimicrobial protein proved effective in treating diarrhea in young pigs. The study offers hope that such milk may eventually help prevent human diarrheal diseases that each year claim the lives of 1.8 million children around the world and impair the physical and mental development of millions more. It also demonstrates the potential for food products from transgenic animals to one day benefit human health.

Increasing chicken production - Poultry experts are working in multi-disciplinary teams to [dramatically increase chicken production](#) among Africa's rural households and small farms. The new effort, called the Feed the Future Innovation Lab for Genomics to Improve Poultry, will identify genes crucial for breeding chickens that can tolerate hot climates and resist infectious diseases — specifically the devastating Newcastle disease, a global threat to food security whose economic impact is enormous.

Taking aim at foodborne diseases - [The 100K Genome Project](#) is an exciting and ambitious five-year effort to sequence the genomes of 100,000 infectious microorganisms, creating an enormous public database to reduce the typical public health response time to outbreaks from weeks to days using next-generation sequencing platforms. To date, the project has sequenced more than ___ genomes, including pathogens responsible for common and debilitating foodborne infections such as *Salmonella*, *Listeria*, *Campylobacter*, and *Vibrio*. This important project will ultimately speed outbreak investigations, reduce illness, and facilitate the development of new rapid test methods to detect pathogens.

Vaccines target Rift Valley fever- Veterinary pathologists and others have developed [two genetically engineered vaccines to combat the mosquito-borne Rift Valley fever](#), devastating to livestock in Africa and the Middle East. The virus also sickens people, who can be infected by mosquitoes or by direct contact with infected animals or their meat. Both new vaccines proved safe and produced significant immune responses in initial studies and scientists hope the new vaccines can be further developed for use in people.

Exploring insect vectors of human disease – The School’s [Vector Genetics Laboratory](#) focuses on the population and molecular genetics of insect vectors of human disease. Extensive fieldwork has been conducted in Mali, Cameroon, Brazil, Costa Rica and Nicaragua. One current project integrates vector population genomics, ecology and vector behavior with the goal of understanding the determinants of two mosquito behavioral phenotypes crucial to the transmission and control of malaria in Tanzania. Knowledge gleaned from the project will be vital for prediction of both possible downstream evolutionary responses to current vector control strategies, and also for the development of novel control strategies that improve the application of currently available vector control methods.

Human virus kills mountain gorillas - Researchers from the nonprofit Mountain Gorilla Veterinary Project and the Wildlife Health Center at UC Davis teamed up with others to discover that a virus that causes respiratory disease in humans has been linked to the deaths of wild mountain gorillas. The finding confirms that serious diseases can pass from people to these endangered animals; and that protected national parks do not provide a barrier against human diseases which can affect these primates.

Investigating Hummingbirds - Since 2010, the [Hummingbird Health and Genetic Diversity Project](#) has worked to determine levels of Hummingbird health and disease, evaluate migration ecology, and assess genetic diversity in California over large expanses of habitats. Very little is known about these small birds, and some California species are at severe risk of decline. Information gleaned from this project will help researchers to understand if populations are endangered and will assist in accurate monitoring for conservation.

Yosemite’s Great Gray Owl - Wildlife geneticists have documented [Yosemite's Great Gray Owl as genetically distinct](#) from the Great Gray Owl in other locations of western North America. DNA analysis is helping to fill significant gaps in the knowledge of the Great Gray Owl, and this genetic research has brought new attention to the species and added to the information necessary to formulate comprehensive and scientifically-defensible management and monitoring strategies for conservation.

The Mammalian Ecology and Conservation Unit, part of the Veterinary Genetics Laboratory, conducts research that advances both the persistence of wild mammal biodiversity and our basic understanding of mammal evolution and ecology. Genetic tools are a cornerstone of the unit’s methodologies, and scientists also use field- and laboratory-based approaches in their research. [Projects include](#):

- The exploration of the genetic basis and evolutionary origins of migratory behavior in black-tailed deer and Rocky Mountain mule deer
- Red fox genetics – researchers are using red fox samples to uncover the genetic relationship of red fox populations in different locations, which will answer questions such as if the population is genetically distinct and if it is relatively inbred or outbred. Results such as these can aid in understanding the evolutionary relationship between populations and how past climactic events have impacted modern populations.

Mountain Lion Health -

The Wildlife Genetics, Genomics, and Population Health lab develops and applies the science of DNA analysis, disease investigation, and ecological tools to answer key questions toward improved population health,

conservation, and management of wildlife birds and mammals.

- Using genetic tools, the lab studies the ecology and health of mountain lions as well as their populations of the past, present, and future. It has successfully developed puma-specific DNA markers and an extensive DNA data base, which allow the lab to detect and study kin relationships among mountain lions and to learn more about the mammals. These studies will help develop predictive models and project future trends for genetic diversity.
- A research team from the lab analyzed mountain lion DNA from trace samples collected at sites of livestock predation and public safety incidents. Genetic analysis was used to determine species, individual identity, and relatedness between individuals. This information will be useful to assess risk to human safety and manage human-lion interactions.

Black Bears linked to two colonies – Veterinary geneticists performed an analysis of DNA of 540 black bears across California, and discovered distinct population structure and genetic evidence of two historic colonization events. Molecular genetic techniques utilized in this study allowed historical reconstruction of anthropogenic events leading to changes in animal distributions.