

Genetics research verifies purity of the Mexican wolf

June 21 2018, by Stacy Pigott



The Mexican wolf has been listed as an endangered species since 1976. Credit: U.S. Fish and Wildlife Service

In October 2015, two small minnows in the Lower Colorado River Basin—the headwater chub and the roundtail chub—were proposed for listing as threatened species under the Endangered Species Act of 1973. In April 2017, that proposal was withdrawn after new science identified the two small fish as members of the same species.

As technologies advance, genetic research is playing an increasingly important role in informing decisions about the conservation of threatened and endangered species. In addition to the roundtail chub, another recent example is the Mexican [wolf](#).

The Mexican wolf is one of 43 animals listed as endangered in Arizona, where a captive breeding program for *Canis lupus baileyi* has been underway since the late 1970s, when the population dipped as low as seven [wolves](#) in the wild. The selective breeding of a small population brings with it specific genetic concerns: Are the genetics pure, or had the Mexican wolf, on its path to near-extinction, cross-bred with domestic dogs?

"It's a question that's been brought up since before the captive breeding population started," said Bob Fitak, a University of Arizona alumnus who wrote his dissertation on the Mexican wolf while working in Melanie Culver's conservation genetics laboratory at the UA. "Are we dealing with something that is actually a Mexican wolf, or is it something a bit different?"



Genetic research was used to determine that the roundtail chub (top) and headwater chub (bottom) were part of the same species. Credit: University of Arizona

Advances in genomic technology made it possible for researchers to find out. Earlier studies that examined the genetic purity of the Mexican wolf were hindered by small numbers—fewer than 10 Mexican wolves had been analyzed, none of which came from the original three captive

lineages. Fitak and his colleagues genotyped 87 Mexican wolves representing a broad spectrum of pedigrees, including all three original captive lineages, a mixture of those lineages and wolves born in the wild.

Fitak's dissertation and subsequent research led to the recent publication of "Genome-Wide Analysis of SNPs Is Consistent With No Domestic Dog Ancestry in the Endangered Mexican Wolf" in the *Journal of Heredity*. Fitak, who now works for Duke University in the Department of Biology, was lead author on the paper that included Sarah Rinkevich, a UA alumna and endangered-species biologist with the U.S. Fish and Wildlife Service, and Culver, a U.S. Geological Survey geneticist at the Arizona Cooperative Fish and Wildlife Research Unit and an associate in the UA College of Agriculture and Life Sciences' School of Natural Resources and the Environment.

The study was the first to analyze the Mexican wolf utilizing genome enabling, which allows researchers to use genomic data from one species, such as domestic dogs, to study a similar species, such as Mexican wolves.

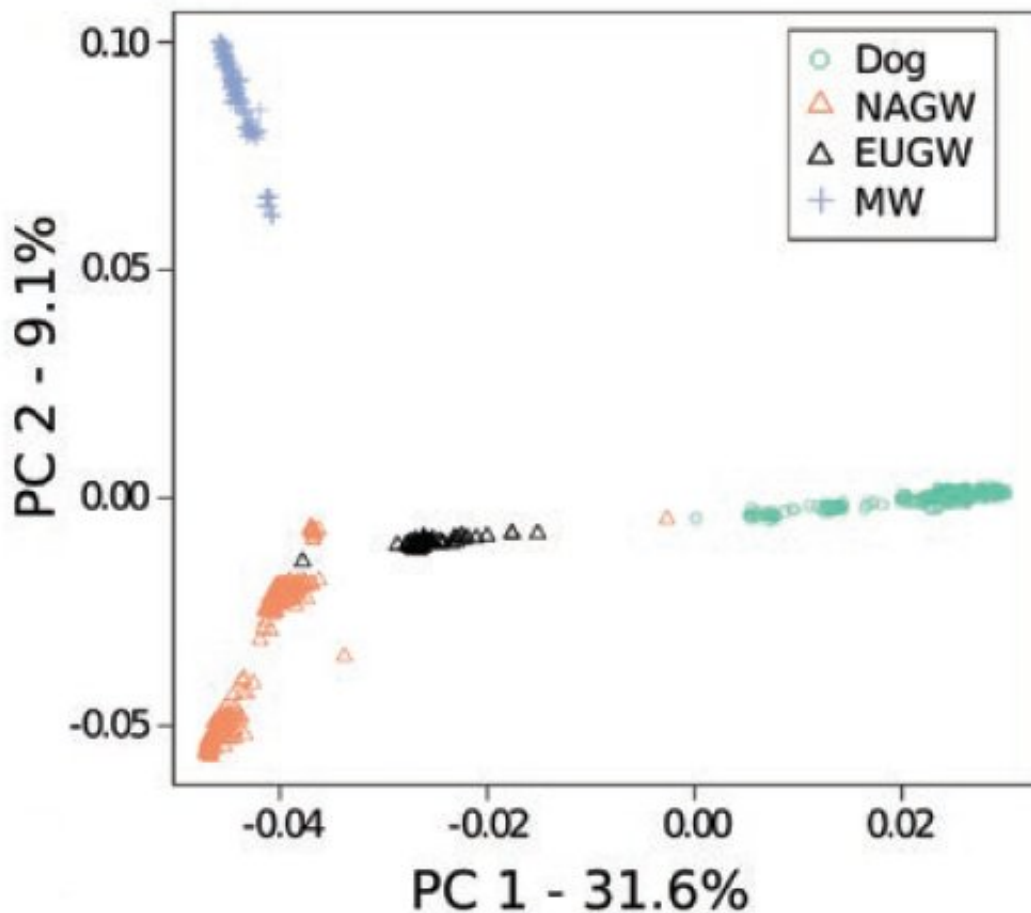


A captive breeding program has brought the Mexican wolf from the brink of extinction to current population estimates of no fewer than 114 Mexican wolves living in the wild. The breeding of such a small population brings with it genetic concerns such as the purity of the genome and outside hybridization. Credit: U.S. Fish and Wildlife Service

"I started in Melanie's lab about the time there was this growth in genomic technologies, so I was interested in those new concepts and new ways of applying things," Fitak said. "Wolves are pretty unique because we had a really interesting Mexican wolf population, and we had some new tools from dogs that we could use to study them in a way that hadn't been done before."

Fitak's analysis benefited from advances in genomic technologies such as SNP chips, which analyze single nucleotide polymorphisms, or SNPs. Each SNP represents a difference in a single DNA building block, making it useful as a biological marker.

Prior studies were able to analyze only about two dozen biological markers. SNP chips allowed Fitak to examine more than 172,000 SNPs across the whole genome.

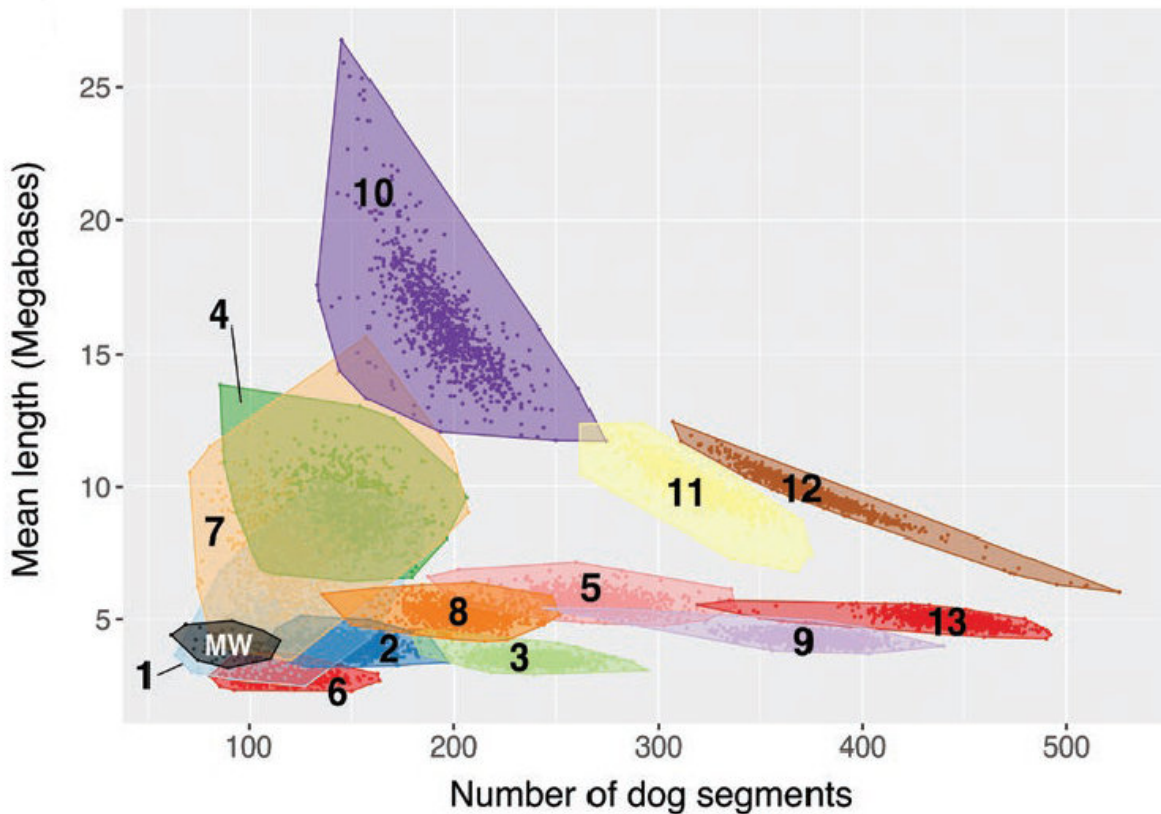


A principle component analysis, which is often used to show genetic distance and relatedness between populations, indicates distinct clusters of domestic dog, North American gray wolf, European gray wolf and Mexican wolf genetic data. Credit: Bob Fitak

The first section of Fitak's study looked at average ancestry across the genome, also known as global ancestry. The analysis showed that across the entire genome, Mexican wolves share an average of only .06 percent ancestry with domestic dogs, indicating a lack of biologically significant ancestry from domestic dogs. The Mexican wolf, which became isolated in North America prior to the domestication of dogs in Europe, shares a small amount of ancestry with the European gray wolf, while 98.9 percent of the Mexican wolf genome is specific to the subspecies.

The second section looked at local ancestry, which is ancestry at a specific chromosomal location. When individual chromosomes were analyzed, an average of 7.8 percent of the Mexican wolf genome contained fragments that could have resulted from domestic dogs.

"There are some signals of [domestic dog](#) in the Mexican wolf genome," Culver said of the 7.8 percent. "Are they just artifacts? Could that similarity be by chance because they're closely related, or could there have been some event where a domestic dog did hybridize with wolves, and if so, when was it? Was it recently or was it a long time ago, like thousands of years ago?"



Researchers simulated what the Mexican wolf genome would look like if no hybridization with domestic dogs occurred or if hybridization took place recently or many generations in the past. The observed Mexican wolf genome (MW) mostly closely matched with the model of no hybridization with domestic dogs (1). Credit: Bob Fitak

To answer the questions, Fitak and his colleagues simulated what the Mexican wolf genome would look like if no hybridization took place, or if hybridization with domestic dogs occurred two generations ago, 20 generations ago or 200 generations ago. The observed Mexican wolf data matched the predictive model of no hybridization between Mexican wolves and domestic dogs.

"This study, showing no hybridization with domestic [dogs](#) found within this population, was important because it again confirms the genetic purity of the Mexican wolf," said Rinkevich, who is often involved in the listing and delisting of endangered and threatened species in her role as an endangered-species biologist. "That genetic information is important to conservation efforts."

The study by Fitak, Rinkevich and Culver netted genetic data from the largest population of Mexican wolves that is now publicly available for all geneticists to use in future research. For Fitak, that might mean delving deeper into the amount of inbreeding in the Mexican wolf as the captive breeding program continues. Until then, an important question about one endangered species, the Mexican wolf, finally has been answered.

More information: Robert R Fitak et al. Genome-Wide Analysis of SNPs Is Consistent with No Domestic Dog Ancestry in the Endangered Mexican Wolf (*Canis lupus baileyi*), *Journal of Heredity* (2018). [DOI: 10.1093/jhered/esy009](https://doi.org/10.1093/jhered/esy009)

Provided by University of Arizona

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