

After near extinction, new genome data bodes well for condors' future

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A photo of a California condor. Credit: San Diego Zoo Wildlife Alliance

The once-abundant California condor briefly went extinct in the wild, with only 22 individuals living in captivity by 1982. Today, 300 condors live freely in the wild and another 200 are in captivity. But, despite the

condor's struggles, a new study of the California condor genome reported in the journal *Current Biology* on May 13 has found a surprising amount of genetic diversity.

The study is the first to begin quantifying diversity across the entire California [condor](#) genome, which offers researchers needed baseline information to inform future research and conservation of this iconic species, the largest species of land bird in North America. The researchers say that the quality of their genome assembly is among the highest for any bird genome sequenced to date.

"We estimated that prior to 10,000 years ago, there were tens of thousands of condors," says Jacqueline Robinson of the University of California, San Francisco. "The relatively high level of diversity in condors today is a legacy of their high historical population sizes."

She adds, "Our results accord with what we know from the fossil record, which is that the ancestors of California condors once ranged across the contiguous United States. Over time, the condor's range shrank until they only persisted along the Pacific coast, where they were able to incorporate the carcasses of large marine mammals into their diet."

The condor nearly went extinct in the 20th century from lead poisoning, poaching, and loss of habitat. But much about the bird's history remains obscure. To fill this gap and aid future management of the species in the new study, the researchers, including Robinson and Jeff Wall, also of UCSF, along with Cynthia Steiner of San Diego Zoo Wildlife Alliance, produced a high-quality chromosome-length genome assembly for the California condor. They also analyzed its genome-wide diversity.



A photo of a condor. Credit: San Diego Zoo Wildlife Alliance

For comparison, the team examined the genomes of two close relatives of the California condor: the Andean condor and the turkey vulture. They report that the genomes of all three species show evidence of historic population declines. However, the California condor genome shows a surprisingly high degree of variation from its historical abundance.

"Our study showed that the California condor's history includes a long-term decline over geologic time that predates its recent near extinction driven by human activity," Robinson said. "This isn't to say that the California condor was already doomed to extinction, because we found

historical declines in the Andean condor and turkey vulture as well, and turkey vultures are extremely abundant today. The consistent pattern of historical decline in these species may be connected with the decline and extinction of avian scavenger species in the Americas since the Pleistocene, but we need to do more research to really address this question."

Long-term evolutionary forces and recent inbreeding have shaped the California condor genome, according to their analysis. Nevertheless, outside of regions where California condors lacked variability due to inbreeding, they found relatively high genetic diversity. The researchers also found encouraging evidence that purifying selection had removed deleterious mutations from the population, which they say bodes well for future restoration of the species.

"Despite the severe bottleneck the California condor experienced in the 20th century, the genome retains a relatively high degree of genetic variation that is representative of the ancestral demographic history of the species, with a larger ancestral population size," Steiner said. "This is an extraordinary finding, observed in few other critically endangered species such as the vaquita," she says, referring to a species of porpoise that is the most endangered marine mammal. "It's very promising in terms of the recovery potential of this [species](#) in the wild if current threats are managed."

"We didn't know to what extent California condor genomes would show signs of inbreeding," Robinson added. "We now know that there was some inbreeding in the wild prior to the start of captive breeding efforts. Future sequencing of more individuals will tell us if there are regions of the [genome](#) that have completely lost variability, or if captive breeding and building up the population size over the past few decades has mitigated the effects of previous inbreeding."

Steiner says they plan to extend the genomic research on California condors at the population level to better understand levels of inbreeding and genetic erosion and to measure genetic load in the living population. An important goal is to determine the genetic basis of fitness-related traits and disease. For example, they now have the genomic tools needed to understand the genetic basis of traits such as chondrodystrophy (abnormal skeletal growth) and the fourteen-tail feather syndrome (in which condors have two extra tail feathers) and potentially manage these deleterious traits in the breeding program, she says.

More information: *Current Biology*, Robinson et al.: "Genome-wide diversity in the California condor tracks 1 its prehistoric abundance and decline" [www.cell.com/current-biology/f ... 0960-9822\(21\)00548-0](https://www.cell.com/current-biology/fulltext/S0960-9822(21)00548-0) , DOI: [10.1016/j.cub.2021.04.035](https://doi.org/10.1016/j.cub.2021.04.035)

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