Endangered animals can be identified by rate of genetic diversity loss

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Purdue wildlife geneticist Janna Willoughby developed a statistical approach to estimating genetic diversity in an animal population, an improved way for conservationists to identify and track the threat of extinction in species like this Galapagos giant tortoise. Credit: Purdue University / Tom Campbell

A Purdue University study presents a novel approach for identifying vertebrate populations at risk of extinction by estimating the rate of genetic diversity loss, a measurement that could help researchers and conservationists better identify and rank species that are threatened or endangered.

Populations with low genetic diversity may not be able to adapt to challenges such as changing environmental conditions, shrinking habitats or new diseases, which could put them at risk of disappearing. But a study by genetic researchers shows that the criteria currently used to identify at-risk species are not correlated with genetic diversity, suggesting that many threatened species could be overlooked.

Janna Willoughby, a then-doctoral student in wildlife genetics, and Andrew DeWoody, professor of genetics, developed a statistical approach conservationists can use to estimate the number of generations remaining before a population reaches a threshold of low genetic variation.

"Genetic diversity is a key component to the long-term survival of a population," Willoughby said. "The approach we developed identifies populations with limited genetic diversity that isn't going to be enough to allow the population to persist over time. We found that this method performs significantly better than current methods for identifying species in need of conservation efforts."

Threatened or endangered populations are identified and ranked by varying methods across states, countries and organizations, but criteria typically are based on demographics.

The International Union for Conservation of Nature, for example, identifies species of conservation concern based on the number of mature adults in a population, range size and evidence of population

decline. Animal species on IUCN's Red List, the most comprehensive record of threatened species worldwide, are ranked by estimates of how close to extinction they are. The black rhinoceros, for instance, is considered critically endangered while the cheetah is listed as vulnerable.

"Conservation is complicated," DeWoody said. "But the Red List is internationally respected. It's not perfect, but it's as good as we've got."

Willoughby, DeWoody and fellow researchers conducted a review of vertebrate genetic data published since 1990 to investigate the relationship between genetic diversity and the at-risk status of animal species. The team used datasets from 5,164 studies spanning 17,988 loci - that is, positions of a gene on a chromosome - to estimate genetic diversity across wild populations of birds, fish, reptiles, amphibians and mammals. They found that threatened species had reduced genetic variation, likely due to inbreeding and the random loss of variation that occurs when population sizes are small.

The team then examined IUCN's criteria for classifying threatened species to determine how effective the criteria were at identifying genetically poor species. If genetic diversity estimates correlated with the Red List criteria, then IUCN would be systematically selecting for populations or species that have declining diversity, the researchers reasoned. Unexpectedly, they found that IUCN's criteria were not closely linked to genetic diversity.

"Unless a population with poor genetic diversity has undergone a dramatic decrease in size, it could be overlooked with our current methodology," Willoughby said. "We should consider genetic diversity in conservation rankings so a species doesn't go extinct simply because it wasn't on our radar."

The team developed an approach to estimate how fast a population is

losing genetic diversity. They then tested their approach by mining the genetic database for species with two separate estimates of genetic diversity, using one estimate to calculate their statistic and the other as an independent measure. The values were correlated.

The team's method is a feasible way for organizations such as IUCN, U.S. Fish and Wildlife and state programs to identify species of conservation concern, DeWoody said.

"The criteria of many conservation organizations were formulated before the availability of genetic data we have today," he said. "But genetic methodology has advanced so rapidly that factoring in genetic diversity is now pretty straightforward."

More information: The paper is forthcoming in the November issue of *Biological Conservation*. An early online version is available for journal subscribers and on-campus readers at www.sciencedirect.com/science/ … ii/S000632071530032X

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