

Genomic analyses of prairie chickens cast doubt on species classifications

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Lesser prairie chicken (<u>Tympanuchus pallidicinctus</u>). Credit: USFWS/Ryan Hagerty Public Domain

Biologists originally classified the lesser and greater prairie chickens of the Great Plains as two different species. Difficult to distinguish by their



physical appearance alone, some scientists have wondered for decades if these grouse consist of only one species.

An accurate understanding of <u>prairie chicken</u> speciation gained new urgency in 2022, when the U.S. Fish and Wildlife Service <u>listed the</u> <u>lesser prairie chicken as endangered</u> in the southern portion of its range.

Now, a rigorous genomics study of prairie chickens in Colorado, Kansas, Oklahoma, New Mexico and Texas led by Purdue University scientists has found evidence of hybridization between species with no clear indication of genetic problems such as inbreeding.

The scientists **published** their findings in *PNAS Nexus*.

Using technology that study co-author Zachary Lowe likens to "GPS for genetics," the results show the power of genomics to document which animals are a mix of closely related species and which ones genetically qualify as unique lineages.

"With this type of genetic work, we are more informed and more able to get to where we're going accurately and quickly because this is the best available science," said Lowe, a Purdue adjunct faculty member and executive director of the Western Association of Fish and Wildlife Agencies. "When we rely on the best available science, we are more likely to make the best decision and to get the best outcome."

The Endangered Species Act of 1973 provides no clear guidelines about how to address hybrids between two presumptive species that breed with one another. That presents challenges to wildlife managers whose lands include hybrid animals, said study co-author Andrew Black, a former Purdue postdoctoral scientist now at Oregon State University.

The two species began diverging between 600,000 and 900,000 years



ago—a short time by biological standards. "These species will breed easily together, so it's important to take a study like this and figure out the best way to manage and protect the remaining diversity that we see," Black said.

The preexisting data came from 433 greater and lesser prairie chickens, mostly the latter, spanning 10 years and collected by researchers in Colorado, Kansas, Oklahoma, New Mexico and Texas. The research team sequenced the entire genome of each bird an average of four times. Each genome consisted of about a billion nucleotides, the small molecules that make larger DNA molecules.

The team needed supercomputers at Purdue's Rosen Center for Advanced Computing and the Pittsburgh Supercomputing Center to process more than a trillion nucleotides of data.

"This is a massive dataset that allows us to assess the genetic health of these populations across the range and to evaluate gene flow between the lesser and greater prairie chicken species," Black said. The data revealed little cause for concern with respect to genetic diversity. "Of course, these things can change quickly if they have population declines or disease outbreaks," he cautioned.





Artist rendering of lesser prairie chickens. Male (left) and female in a prairie setting. Biologists originally classified lesser and greater prairie chickens as two species. New research indicates they may belong to the same species. Credit: Purdue University/Gabriela Sincich

Although the study analyzed the genetics of prairie chickens in five states, the methods are relevant to the nationwide jurisdictional management of endangered and threatened species. When a species becomes formally listed, management passes from the relevant states to the federal government. Such jurisdictional changes can impact the



agricultural and natural resources industries operating in the affected local economies.

Senior author J. Andrew DeWoody, professor of genetics in Purdue's Department of Forestry and Natural Resources, and Black published a <u>similar study</u> earlier this year regarding an endangered species of pupfish in New Mexico. The genomics data from that study indicated what had previously appeared to be one species was actually two.

"This is a tool that will be implemented more and more in conservation," Lowe predicted.

The Fish and Wildlife Service listing designated two distinct populations of lesser prairie chickens—northern and southern. Species labels aside, the main genetic differences—which were quite small—were between the northern and southern populations.

The genomics data identify the southern population, recently listed as endangered and consisting entirely of lesser prairie chickens, as distinct from the northern population. The northern population comprises a mix of lesser and greater prairie chickens.

"A distinct population segment doesn't necessarily make it a different species. It just means separation by geography," Lowe said.

The problem facing prairie chickens is one of <u>habitat fragmentation</u> rather than genetics. Fragmentation results from land-use changes such as converting short native prairie to row crop agriculture and human development. Even the seemingly low-impact change of placing wind farms in high-quality prairie chicken habitat will affect their behavior.

"They will just quit using that habitat because they avoid tall structures," Lowe said.



"The vast majority of the prairie chickens depend on privately owned agricultural working lands. This speaks to the importance of practical wildlife conservation efforts that support sustainable grasslands, cattle production and private landowner incentives."

More information: Andrew N Black et al, Discordance between taxonomy and population genomic data: An avian example relevant to the United States Endangered Species Act, *PNAS Nexus* (2024). DOI: 10.1093/pnasnexus/pgae298

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