

## Rangeland Connectivity



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Photo: Jeremy Roberts/Conservation Media

**C**onnectivity is a core principle for maintaining healthy wildlife populations and for keeping rangelands intact for rural grazing communities. If rangelands are increasingly fragmented, wildlife populations become more isolated. For species like sage grouse, isolation can sever the dispersal of breeding birds necessary to maintain genetic diversity. Using feather DNA, Working Lands for Wildlife (WLFW) scientists and partners are identifying spatially the ties that bind the sagebrush biome. The USDA's Natural Resources Conservation Service (NRCS) is using this information to incorporate conservation actions that facilitate sagebrush connectivity on which wildlife depend.

In the largest genetic evaluation conducted for any species, scientists extracted unique DNA signatures from feathers collected at sage grouse breeding sites (i.e., leks) to identify individual birds and then recapture them in subsequent feather collections. Surveyors conducting annual bird counts at leks collected tens of thousands of fallen grouse feathers from ~1,200 leks across the West. Genotyping feather DNA identified 5,950 individual grouse. Scientists used these data to characterize the sage grouse connectivity as a network of 458 genetic hubs that facilitate gene flow throughout the West.<sup>1</sup> Hubs are centrally located across Wyoming and in eastern Idaho, with genetic exchange most evident in Montana

and northern Wyoming, and Utah and eastern Nevada. Scientists then used feather DNA to build resistance maps classifying the landscape into “habitat” and “nonhabitat”.<sup>2</sup> Mountains and valleys that facilitate and naturally restrict movement shape genetic connectivity. Other major contributors include sagebrush availability (less than 10–30 percent), tree canopy cover (more than 10 percent), and cultivation (more than 25 percent) within parts of the range with each reducing movement beyond their respective thresholds.

In additional work across Montana, Wyoming, and Idaho, 2.5 percent of unique individuals occurred twice in feather samples, and in 41 recaptures, birds had dispersed to different leks.<sup>3</sup> These are important indicators of connectivity that should be maintained because dispersal is a rare event (less than 1 percent), and evidence of dispersal reduces the risk of genetic isolation and inbreeding. Seven grouse journeyed more than 30 miles away, and one recapture dispersed 120 miles. Across Montana, North Dakota, and South Dakota, these short-range dispersals translate to long-range connectivity.<sup>4</sup> Genetic bird groupings largely mirrored their known population strongholds.

Early investment in genetic analyses is an emerging opportunity for WLFW to further incorporate connectivity into conservation delivery. Connectivity maps are just now being used to identify where conservation actions might best facilitate movement within and between population strongholds. Early examples include woodland management within and outside priority areas of conservation (PACs) to facilitate movement between seasonal habitats and among populations. Easements too have been placed inside and outside of PACs to alleviate large-scale cultivation risk. Connectivity may inform cheatgrass-reduction strategies before it invades intact core areas.

**Feather DNA studies will soon help inform management of ways to keep population strongholds connected throughout the biome.**

## WLFW-SUPPORTED SCIENCE PUBLICATIONS:

1. Cross, T.B., M.K. Schwartz, D.E. Naugle, B.C. Fedy, J.R. Row, and S.J. Oyler-McCance. 2018. The genetic network of greater sage-grouse: Range-wide identification of keystone hubs of connectivity. *Ecology and Evolution* 8:5394–5412.
2. Row, J.R., K.E. Doherty, T.B. Cross, M.K. Schwartz, S. Oyler-McCance, D.E. Naugle, S.T. Knick, and B.C. Fedy. 2018. Quantifying functional connectivity: The role of breeding habitat, abundance, and landscape features on range-wide gene flow in sage-grouse. *Evolutionary Applications* 11:1305–1321.
3. Cross, T.B., D.E. Naugle, J.C. Carlson, and M.K. Schwartz. 2017. Genetic recapture identifies long-distance breeding dispersal in greater sage-grouse (*Centrocercus urophasianus*). *Condor* 119:155–166.
4. Cross, T.B., D.E. Naugle, J.C. Carlson and M.K. Schwartz. 2016. Hierarchical population structure in greater sage-grouse provides insight into management boundary delineation. *Conservation Genetics* 17:1417–1433.