

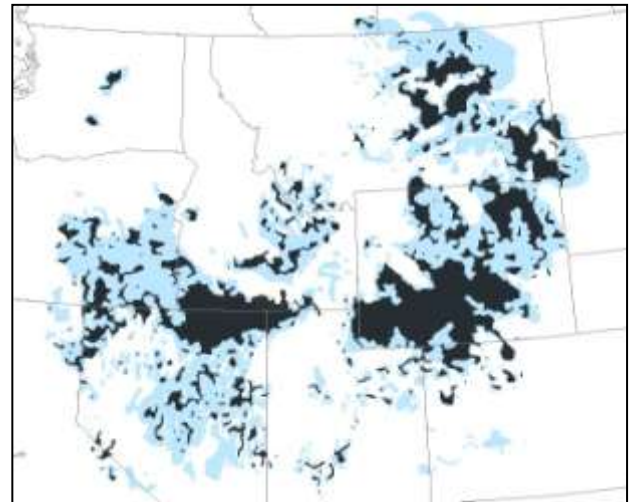
# ATTACHMENT 1.

## Range-wide Connectivity of Greater Sage-Grouse Populations: Delineating Spatial Structure from Genetic Information

**Background** Habitat and population fragmentation were considered as one of the top factors contributing to the recent US Fish and Wildlife Service decision that listing greater sage-grouse was warranted but currently precluded. This study provides an approach that combines genetic markers and landscape analyses to delineate populations, estimate fragmentation and connectivity in sage-grouse populations, and potentially identify underlying causes that limit connectivity and isolate populations.

State and federal agencies are focusing current management actions for greater sage-grouse in core areas containing the highest densities of breeding birds. The core area approach permits limited resources to be applied in regions that will have the greatest potential to benefit the largest proportion of sage-grouse. As a trade-off, energy and other development then can proceed on public lands in areas outside of the core distributions, thus impacting only a small percentage of the sage grouse in that area. This relatively simple concept of designating areas for sage-grouse conservation but permitting development in surrounding regions has the unwanted potential to fragment sagebrush habitat and increase isolation of individual sage-grouse populations. Information on gene flow and rates of genetic exchange derived from this study will be used to test the efficacy of this conservation model.

The range-wide distribution of greater sage-grouse may consist primarily of a few large core populations surrounded by numerous small populations. The viability of many of these small populations may be sustained by dispersing individuals from neighboring populations. Development that causes habitat loss or creates barriers to dispersal between core areas has the potential to restrict movements important to maintain genetic diversity, augment small populations, or recolonize extirpated populations. Thus, an analysis of movement among sage-grouse populations is needed to assess levels of connectivity among core areas, and to identify and delineate features that may act as barriers to movement. Although other methods have been used regionally (radio-tracking, banding) to assess sage-grouse movement, the most efficient and informative approach uses molecular genetic techniques. Genetic methods are less costly, allow for investigations over broader spatial extents, and measure the actual breeding consequences of animal movement. In addition to defining populations and measuring connectivity, genetic approaches also address many other relevant questions including the conservation of genetic diversity, the impacts of inbreeding, and the association among landscape and geographic characteristics, habitats, and genetics.



Greater sage-grouse population structure (black) and current species range (blue). Population structure was delineated by clustering known leks that were interconnected by an 18-km dispersal distance.

**Project Development** A major effort to examine gene flow across the range-wide distribution of greater sage-grouse is being initiated by collaboration among the Natural Resources Conservation Service through the Sage-Grouse Initiative, the Western Association of Fish and Wildlife Agencies, the USDA Forest Service, and the US Geological Survey. The project, perhaps the largest terrestrial effort ever attempted, would collect fine-scale genetic data from greater sage-grouse feathers collected at breeding locations (leks) throughout the entire range covering 11 states and 2 provinces. Over 5,000 leks are

currently mapped and visited each year for population monitoring. Large numbers of feather samples already have been collected in many states; data from these samples will be shared in the range-wide analyses.

**Output** The results from this study will provide information on levels of connectivity, characteristics of barriers, including geographic distance, topographic features, and anthropogenic land uses that influence dispersal and genetic exchange. Ultimately, the spatial and temporal dynamics of colonization derived from the study, based on rate of exchange and barriers to dispersal, can inform estimates of population viability relative to population isolation and risk of extirpation. Managers will be able to apply this understanding to focus conservation efforts in areas that will maximize benefits to greater sage-grouse populations.

**Resources** Project funding is provided through the NRCS Sage-Grouse Initiative, US Geological Survey, Bureau of Land Management, the US Department of Interior Northwest Climate Science Center, USDA Forest Service, USFWS Landscape Conservation Cooperatives, and direct and in-kind contributions from individual state agencies.

### **Contacts**

Steve Knick, US Geological Survey, 970 Lusk Street, Boise, ID 83706  
email: [steve\\_knick@usgs.gov](mailto:steve_knick@usgs.gov); Ph: 208.426.5208

Sara Oyler-McCance, US Geological Survey, Fort Collins Science Center, 2150 Centre Ave, Building C, Fort Collins, CO 80526  
email: [soyler@usgs.gov](mailto:soyler@usgs.gov); Ph. 970.226.9197

Bradley C. Fedy, NREL, Colorado State University and US Geological Survey, Fort Collins Science Center, 2150 Centre Ave, Building C, Fort Collins, CO 80526  
email: [fedyb@usgs.gov](mailto:fedyb@usgs.gov); Ph: 970.226.9456

Michael K. Schwartz, US Forest Service, Rocky Mountain Research Station, 800 E. Beckwith Ave., Missoula, MT 59801  
email: [mkschwartz@fs.fed.us](mailto:mkschwartz@fs.fed.us); Ph: 406.542.4161

Todd Cross, Wildlife Biology Program, College of Forestry and Conservation, University of Montana, 32 Campus Drive, Missoula, MT 59812  
email: [todd.cross@umconnect.umt.edu](mailto:todd.cross@umconnect.umt.edu); Ph: 406.542.4178

David E. Naugle, Wildlife Biology Program, University of Montana, Missoula, MT 59812  
email: [david.naugle@umontana.edu](mailto:david.naugle@umontana.edu); Ph: 406.243.5364

San J. Stiver, Western Association of Fish and Wildlife Agencies, 450 W. Goodwin St., Prescott, AZ 86303  
email: [stiver@cableone.net](mailto:stiver@cableone.net) ; Ph: 928.899.3732