
SUBSPECIFIC IDENTIFICATION OF SHARP-TAILED GROUSE SAMPLES FROM MONTANA

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Columbian sharp-tailed grouse (*Tympanuchus phasianellus columbianus*) historically occupied much of the shrub-steppe habitat of the intermountain west, ranging from interior British Columbia south to California and Colorado. The subspecies has been extirpated from most of its range and currently exists in only scattered isolated populations. The last remnant populations in western Montana were located in the Tobacco Valley near Eureka and the Blackfoot Valley near Helmville. However, those populations were extirpated during the previous decade and the subspecies can no longer be confirmed in the state. A rangewide genetic analysis of sharp-tailed grouse in 2006 documented restricted gene flow based on an analysis of 45 tissue samples taken from Montana birds east of the continental divide. We extended that earlier analysis with a total of 133 tissue samples, including samples from western Montana birds extracted from museum skins collected in 1897, and compared these

samples to other genetic profiles reported from across the species range. We compared these samples to test for genetic differences in an area where the reported distribution of the Columbian subspecies is geographically near populations from the plains subspecies (*T. p. jamesi*). We were able to assign subspecies classification to 126 of the 133 Montana samples, including all samples from west of the Continental Divide. All Montana samples conclusively typed out to the Plains subspecies. Our analysis identified 3 similar genetic clusters across sharptail populations: (1) Alberta, Colorado, Montana, North Dakota, South Dakota and Nebraska, (2) Washington, British Columbia and western Idaho, and (3) Utah and southern Idaho. Both microsatellite and control region sequence data indicate that sharp-tailed grouse from all localities in Montana are molecularly most similar to populations from the plains regions of Alberta to Nebraska, indicating that Montana birds share a relatively recent molecular history. It does not appear that the Continental Divide is a current or historical barrier to gene flow in sharp-tailed grouse.