*The Condor* 103:657–660


# OCCURRENCE OF GREATER SAGE-GROUSE × SHARP-TAILED GROUSE HYBRIDS IN ALBERTA

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*Abstract.* Two distinct grouse were regularly observed at two Greater Sage-Grouse (*Centrocercus urophasianus*) leks in both 1999 and 2000 in southeastern Alberta. Physically and behaviorally, the birds exhibited characteristics of both Greater Sage-Grouse and Sharp-tailed Grouse (*Tympanuchus phasianellus*), suggesting they were hybrids. DNA analyses of blood and feather samples indicated that both birds were males with Greater Sage-Grouse mothers and thus, fathers that were likely Sharp-tailed Grouse.

*Key words: Alberta, DNA, Greater Sage-Grouse, hybrid, Sharp-tailed Grouse.*

## Ocurrencia de Híbridos entre *Centrocercus urophasianus* y *Tympanuchus phasianellus* en Alberta

*Resumen.* Dos aves distintivas fueron observadas con regularidad en dos asambleas de cortejo de *Centrocercus urophasianus* en el sureste de Alberta tanto en 1999 como en 2000. Las aves presentaban características físicas y de comportamiento tanto de *C. urophasianus* como de *Tympanuchus phasianellus,* lo que sugiere que se trataba de individuos híbridos. Análisis de ADN extraído de muestras de sangre y plumas indicaron que ambos individuos eran machos hijos de hembras de *C. urophasianus.* Por tanto, sus padres probablemente eran *T. phasianellus.*

Greater Sage-Grouse (*Centrocercus urophasianus*) and Sharp-tailed Grouse (*Tympanuchus phasianellus*) are sympatric throughout much of their range in western North America (Aldrich 1963). Both species gather at traditional mating sites (leks) in the early spring (Johnsgard 1983). In Canada, Greater Sage-Grouse occur only in southeastern Alberta and southwestern Saskatchewan (Aldridge 1998) and are sympatric with Plains Sharp-tailed Grouse (*T. p. jamesi*).

Sage-grouse populations throughout North America have declined by 45% to 80% since the 1950s (Braun 1998). Based on the current range only, Canadian Greater Sage-Grouse have declined by 66–92% from pre-1965 levels (Aldridge 2000). In 1999, the spring population was estimated at 813–1204 individuals spread over about 10 000 km$^2$ (Aldridge 2000). This suggests a density of less than 1 bird km$^{-2}$ (Aldridge 2000), which is low when compared to density estimates as high as 15 birds km$^{-2}$ for sage-grouse in other areas (Patterson 1952, Wallestad 1975, Schroeder et al. 1999). Surveys in 1987 and 1997 for a Sharp-tailed Grouse population approximately 260 km north of the current Canadian Greater Sage-Grouse range suggest that Sharp-tailed Grouse populations in the region have remained relatively stable (R. F. Russell, pers. comm.).

Since 1971, there have been two records of Greater Sage-Grouse × Sharp-tailed Grouse hybrids. Eng (1971) collected two individuals in Montana, and Kohn and Kobriger (1986) observed one individual displaying on a Greater Sage-Grouse lek in North Dakota. There are four anecdotal records of suspected hybrids, including an observation of a bird on a Sharp-tailed Grouse lek in Wyoming (Williams 1979), two observations of birds on both Greater Sage-Grouse and Sharp-tailed Grouse leks in Saskatchewan (Hjertaas 1995), and one bird collected in southern Alberta in 1986 (T. S. Sadler, pers. comm.). Thus, hybridization may be fairly common. No genetic analyses have been performed on any collected specimens and, thus, the nature of the breeding events is unknown. In this manuscript, we describe two Greater Sage-Grouse × Sharp-tailed Grouse hybrids, including their genetic complement.

## METHODS

This study took place on the mixed-grass prairie of southeastern Alberta (49°24′N, 110°42′W, ca. 900 m elevation). Silver sagebrush (*Artemisia cana*) is the dominant shrub and pasture sage (*A. frigida*) is the dominant forb (Aldridge 2000). Common grasses include needle-and-thread grass (*Stipa comata*), June grass (*Koeleria macrantha*), blue grama (*Bouteloua gracilis*), and western wheatgrass (*Agropyron smithii*) (Aldridge 2000).

From late March to late May of 1999 and 2000, we performed weekly lek counts at all eight active Greater Sage-Grouse leks in Alberta. Counts were performed within one hour of sunrise and a maximum count of males attending each lek was obtained (Jenni and Hartzler 1978, Beck and Braun 1980). In both years, two distinctive males were observed displaying at two different leks. Both birds were intermediate in size between Greater Sage-Grouse and Sharp-tailed Grouse and displayed physical and behavioral characteristics of both species, suggesting these birds were Greater Sage-Grouse × Sharp-tailed Grouse hybrids. The

Manuscript received 31 July 2000; accepted 19 April 2001.

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courtship behavior and attendance of the two suspected hybrids (hereafter hybrids) were recorded and compared with that of male Greater Sage-Grouse on each lek. We monitored interactions with other male and female Greater Sage-Grouse at the lek and noted the general locations of these individuals in relation to other males. The hybrids were captured with walk-in traps placed on leks (Schroeder and Braun 1991) or by nightlighting on and around leks with handheld spotlights and a long-handled hoop net (Giesen et al. 1982). Each captured individual received an individually numbered aluminum leg band and a colored split-ring leg band coded for the year of capture. Morphometric measurements were recorded, including mass, tarsal length, number of tail rectrices, and the shape of the primaries. Age (yearlings $<2$ years old or adults $\geq 2$ years old) was determined based on the shape of the outermost primaries (Eng 1955, Crunden 1963). For genetic analyses, three to five feathers were plucked from the body of each bird, and approximately 1 ml of blood was collected by clipping the outer toenail. Blood samples were placed in plastic microcentrifuge tubes lined with 15% EDTA and kept frozen until they could be processed.

To determine if the mother of each hybrid was a Greater Sage-Grouse or a Sharp-tailed Grouse, we extracted DNA from blood and feather samples and sequenced a rapidly evolving portion of the control region of the maternally inherited mitochondrial DNA. This region has been well characterized in sage-grouse (Kahn et al. 1999, Oyler-McCance et al. 1999). The same region was also sequenced for two male Plains Sharp-tailed Grouse captured in the area. All new haplotypes were submitted to GenBank (accession numbers AY030408 and AY030409). We determined the sex of the hybrids using a polymerase-chain-reaction-based avian sexing technique (Kahn et al. 1998). We report data as means $\pm$ SE.

## RESULTS

The hybrids were observed on two leks, approximately 50 km apart. One individual was observed with seven male Greater Sage-Grouse on each of 21 visits to that lek in 1999. In 2000, this individual was observed at the same lek with nine male Greater Sage-Grouse on 7 of 9 visits. The second individual was observed with eight male Greater Sage-Grouse on all eight lek visits in 1999. At the same lek in 2000, a hybrid was observed with nine male Greater Sage-Grouse on 6 of 8 visits. Even though the hybrid on this lek was not captured until 2000, it was likely the same individual as in 1999.

The courtship displays of the hybrids were characteristic of both Greater Sage-Grouse and Sharp-tailed Grouse. They began in a manner similar to the Greater Sage-Grouse strut, with the tail fanned and cocked vertically, head raised, and neck plumage erect. They then stepped forward while producing vocalizations from the esophageal pouches (Wiley 1973, Schroeder et al. 1999). Air sacs were not visible in display, as they were covered by a black collar reminiscent of the pinnae of Ruffed Grouse (*Bonasa umbellus*) or prairie-chickens (*Tympanuchus* spp.). Vocalizations were a high frequency hoot, and did not sound like the characteristic ''plops'' produced by sage-grouse (Wiley 1973).

Male Greater Sage-Grouse on the lek treated these birds like yearling male Greater Sage-Grouse and chased them from the center of the lek. When females were present on the lek, the hybrids initially stood tall and sometimes briefly exhibited the Face-Past display (Schroeder et al. 1999) with a male Greater Sage-Grouse, but proceeded to dance in front of the females like a Sharp-tailed Grouse. The hybrids displayed toward females from the fringe of the lek, while male Greater Sage-Grouse remained on their territories. No copulations by hybrids were observed.

The hybrids had 20 rectrices, similar to sage-grouse (Schroeder et al. 1999), as opposed to 18 in Sharp-tailed Grouse (Johnsgard 1983). Rectrices were dark like those of Greater Sage-Grouse, but about one-third the length (we did not measure them) and rounded with a white tip, resembling Sharp-tailed Grouse. Undertail coverts had a solid white tip, characteristic of male Greater Sage-Grouse. Tarsus length (60 and 66 mm) was between that reported for adult Greater Sage-Grouse (74 $\pm$ 1 mm, Hupp and Braun 1991) and Sharp-tailed Grouse (range 38–49 mm, Connelly et al. 1998). The hybrids lacked the black belly patch characteristic of sage-grouse, resembling a Sharp-tailed Grouse with a white belly and sides. The back and upper chest was mottled brown and black like Greater Sage-Grouse; however, the chest area was somewhat scaled like a Sharp-tailed Grouse. The small black cheek patch characteristic of Sharp-tailed Grouse was even more prominent in the hybrids.

Body mass of hybrids was 1766 g and 1674 g, whereas adult male Greater Sage-Grouse in Alberta average 3122 $\pm$ 30 g ($n = 48$) and yearlings average 2623 $\pm$ 77 g ($n = 12$) (Aldridge 2000). Four male Sharp-tailed Grouse captured in the same area in 1999 averaged 787 $\pm$ 13 g.

Genetic analyses confirmed that both grouse were males. Mitochondrial DNA sequences of both individuals were characteristic of Greater Sage-Grouse, suggesting their mothers were Greater Sage-Grouse. Slight differences in the sequences of the mitochondrial DNA indicated the birds had different mothers. One hybrid had haplotype AL described for Greater Sage-Grouse by Kahn et al. (1999). The second hybrid had a new haplotype that was similar to Greater Sage-Grouse haplotype B (Kahn et al. 1999) with 1 transversion (0.7% sequence difference). Overall, the two hybrids had 2.1% sequence difference. The percentage difference between the Sharp-tailed Grouse we sampled and the Greater Sage-Grouse sequences from Kahn et al. (1999) was 34%, while the sequence difference among all the Greater Sage-Grouse from Kahn et al. (1999) was only 23%.

## DISCUSSION

Sage-grouse populations across their range have decreased by 45% to 80% since the early 1950s (Braun 1998) with declines from 1985 to 1995 averaging 33% (range 17% to 47%, Connelly and Braun 1997). With decreasing numbers and reduced population densities, hybridization may become more common and pose problems for the conservation of sage-grouse. Inter-

breeding can decrease the already low genetic diversity in small populations. Production of fertile hybrids can result in the loss of co-adapted gene complexes (Triggs and Daugherty 1996) and result in the near-extinction of small populations through genetic swamping (Olsen 1996, Triggs and Daugherty 1996), as has been the case for the New Zealand Forbes's Parakeet (*Cyanoramphus auriceps forbesi*; Triggs and Daugherty 1996). Efforts have been made to prevent hybridization in order to conserve genetic diversity of threatened bird species (Olsen 1996, Triggs and Daugherty 1996, Lucking 1997) and wolves (Lehman et al. 1991, Randi et al. 2000). Greater Sage-Grouse in Canada exist at some of the lowest known densities ($<1$ bird km$^{-2}$), while Sharp-tailed Grouse populations in this area have remained at relatively stable and high densities ($\sim$71 birds km$^{-2}$; R. F. Russell pers. comm.). Of the nine recorded observations of Greater Sage-Grouse $\times$ Sharp-tailed Grouse hybrids, five have occurred in Canada over the last 13 years. If hybridization is becoming more common, the genetic diversity in sage-grouse populations could be disrupted, especially if these hybrids are able to successfully back-cross into the Greater Sage-Grouse population.

The Alberta Conservation Association, Alberta Environment, Alberta Sport Recreation Parks & Wildlife Foundation, Cactus Communications, Canada Trust Friends of the Environment, Canadian Wildlife Foundation, Endangered Species Recovery Fund (World Wildlife Fund Canada, Canadian Wildlife Service, and the Government of Canada's Millennium Partnership Program), Esso Imperial Oil, Mountain Equipment Co-op, Murray Chevrolet, Nature Saskatchewan, North American Waterfowl Management Plan, Nova/Trans Canada Pipelines Ltd., Saskatchewan Environment and Resource Management, Saskatchewan Stock Growers Association, Saskatchewan Wildlife Federation, and the University of Regina funded this research. We thank T. L. Seida, E. J. Urton, M. E. Watters, and C. A. Cullins for assistance in the field. T. S. Sadler provided information about the Alberta hybrid collected in 1986, and R. F. Russell (Alberta Environment) provided information on Sharp-tailed Grouse populations. We also thank C. E. Braun, R. G. Poulin, W. M. Iko, J. R. Young, and one anonymous reviewer for comments and discussions on early drafts of this manuscript.

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