Breeding Migration, Gene Flow, and Management for Connectivity in Bighorn Sheep

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Abstract: Many bighorn sheep (*Ovis canadensis*) populations are isolated by development and habitat loss. Previous study by our group indicated marked, adverse effects of inbreeding in an insular population of bighorns deprived of migration for only 10 to 12 generations. Using life history and movement data over 17 yrs in a native complex of populations, we show that males (commonly) and females (less frequently) make temporary migrations to other populations solely to breed and these breeding migrations are likely the primary source of gene flow in the species. Ram migrations on a spatial scale encompass many populations. Eight rams fitted with GPS collars and originating in a single source population, ranged over a collective area of 1000 km^2 and together visited a total of 7 distinct matrilines during the 4 to 6 wk breeding season. Individual rams in this group visited 1 to 5 different matrilines and traveled a total of 50 to 150 km out from and back to their natal herd. We present evidence that decisions to migrate are understandable in terms of male mating strategy and suggest that managers can encourage (or discourage) connectivity by using harvest regulations to manipulate regional patterns of population sex ratio and male age structure.

BIENN. SYMP. NORTH. WILD SHEEP AND GOAT COUNC. 15: 2006

Key words: Bighorn sheep, dispersal, gene flow, genetics, *Ovis canadensis,* population structure.

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