Preliminary Evaluation of the Genetic Structure of Dall’s Sheep Populations in Wrangell-St. Elias National Park and Preserve, Alaska

GRETCHEN ROFFLER1, USGS-Alaska Science Center, 4230 University Drive, Suite 201, Anchorage, AK 99503
LAYNE ADAMS, USGS-Alaska Science Center, 4230 University Drive, Suite 201, Anchorage, AK 99503
REBECCA KELLEYHOUSE, Alaska Department of Fish & Game/Wildlife Conservation, P.O. Box 47, Glennallen, AK 99588-0047
GORDON LUIKART, University of Montana, Division of Biological Sciences, Health Sciences Building, Rm. 105, Missoula, Montana USA 59812
GEORGE K. SAGE, USGS-Alaska Science Center, 4230 University Drive, Suite 201, Anchorage, AK 99503
MICHAEL K. SCHWARTZ, U.S. Forest Service Rocky Mountain Research Station, 800 E. Beckwith, Missoula, Montana 59801
SANDRA TALBOT, USGS-Alaska Science Center, 4230 University Drive, Suite 201, Anchorage, AK 99503
KRISTY PILGRIM, U.S. Forest Service Rocky Mountain Research Station, 800 E. Beckwith, Missoula, Montana 59801
BOB TOBEY, Alaska Department of Fish & Game/Wildlife Conservation, P.O. Box 47, Glennallen, AK 99588-0047

Abstract: Currently little is known of the genetic structure of Dall’s sheep (Ovis dalli dalli) populations within contiguous mountain ranges, such as the Wrangell and Chugach Mountains of Wrangell-St. Elias National Park and Preserve (WRST). Broad scale evaluations of sheep genetics are currently limited by the great expense of tissue acquisition from live sheep or the availability of archived samples. Furthermore, finer scale analyses have not been conducted on Dall’s sheep. We used DNA extracted from tissue samples collected form 30 hunter-killed rams to test a set of 15 microsatellite loci used in bighorn sheep (O. canadensis), and to screen and develop markers to access sequence data from three mitochondrial DNA genes, including the control region. We used these markers to test the feasibility of using DNA extracted from fresh feces collected in late summer from 47 adult male and female sheep inhabiting the Chitina River drainage of WRST, an area covering approximately 20,000 km². All markers were assessed for genotyping or sequencing error rates in both tissue and feces. Preliminary laboratory and statistical analyses suggest we have developed a suite of markers sufficiently polymorphic and reliable for use in landscape genetics studies using fecal DNA. We will use these markers during 2008-2009 to assess levels of genetic diversity and gene flow within the sheep population, and to determine the level and spatial scale of population differentiation. Increased understanding of the presence and extent of genetic partitioning of the sheep population over a large montane landscape will provide useful assessments of natural patterns of genetic variability in Dall’s sheep and the appropriate geographic scales for population monitoring and harvest management. In addition, results from analyses will provide baseline data for long-term monitoring and for comparison to sheep populations in other areas.

1Email: groffler@usgs.gov