Mountain Sheep Conservation and Restoration Project

How large must populations be for a given species to persist in the long term? How much habitat does this number imply? Where on the landscape can this amount of habitat be found or restored? Last, but not least, how do we maintain ecological connections between populations?

These are pivotal questions for conservation science. Unfortunately, for many species of interest, they are also largely unanswered. Such uncertainty limits the role of science in forging environmental policy and philosophy, and jeopardizes effective conservation in North America and points beyond.

In this project, we combine old-fashioned, mud-and-boots field biology with cutting-edge technologies in molecular genetics and remote sensing to establish population and habitat targets for *Rocky Mountain bighorn sheep* in the Northern Rockies eco-region. We address all four "big" questions and work at all levels of scale—molecular, individual, population and ecosystem—that conservation must consider in providing for viable populations of large mammals.

IMAGES: J. Hogg

THE PROBLEM:
Habitat Loss and the Tug of Extinction

Habitat may be lost and fragmented as a direct, or indirect, effect of human activity. Agricultural conversion is an example of *direct loss*, whereas forest encroachment into grassland habitats following fire suppression is an example of *indirect loss*.

The demographic consequences of habitat loss are smaller populations, each more isolated in space, and each at greater risk of extinction from normal variation in environmental conditions. (Demography is the mathematics of reproduction and mortality at the population level.)

The genetic consequences of fragmentation include increased inbreeding, reduced genetic variation, and, because genetic diversity is necessary for continued ecological adaptation, reduced reproduction and increased mortality.

IMAGE: J. Hogg

But this genetic depression of birth and survival may further reduce population size, which further increases adverse inbreeding effects, and so on. The escalating interaction between genetics and demography may pull a population into an "extinction vortex" from which there is little hope of escape.

Why Mountain Sheep?

Large-bodied mammals, like bighorn, are at special risk of extinction. Sparsely distributed even in undisturbed habitat, populations of these species are more likely to be isolated at vulnerable sizes by loss of habitat. And, because large mammals often fill key ecological roles in natural communities, their extinction or rarification may be followed by a cascade of change in ecosystem structure and function.

The bighorn is North America's most threatened ungulate. One hundred and twenty-five years ago, perhaps two million bighorn roamed vast and largely contiguous areas of our western mountains. Today, only 50,000 remain, often in small herds restricted to isolated remnants of former habitat. It is an ideal species in which to better understand the challenges of conservation in fragmented landscapes.

Worldwide, there are over 100 species and distinct subspecies of wild sheep and goats. Almost three-quarters of these are considered threatened (one-third endangered or critical) by the International Union for the Conservation of Nature. Because many of these species have life histories broadly similar to that of the bighorn, our results will often be relevant to the conservation of this larger group.

IMAGE: J. Hogg

Bighorn prefer open habitats near rugged escape terrain where they browse low shrubs and graze meadow herbs and grasses. In winter, they require windblown or frequently melted slopes for movement and feeding.
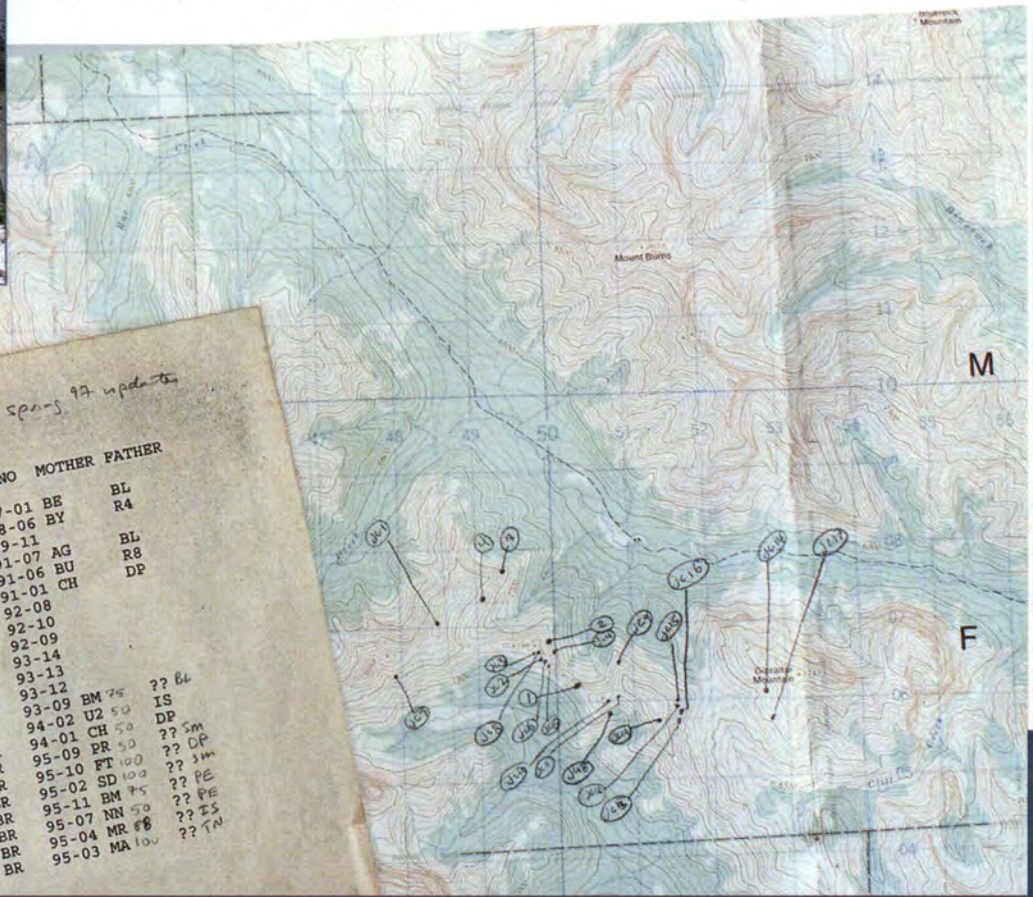
IMAGE: J. Hogg

IMAGE: G. Peat

Project leader and Institute scientist Jack Hogg searches for bighorn on summer range. The bighorn's tolerance of human observers makes our detailed study of the bighorn life history possible, and establishes the bighorn as a model species in which to address general issues in large mammal conservation.

M

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NBR POPULATION LIST
1996   w/ spr-s 97 updates

(● = with lamb)

NAME	IDLT TAG/NOTCH	SEX	AGE	HERD	IDNO	MOTHER	FATHER
FEMALES							
● BURROW	BU 50	F	9	BR	87-01 BE	BL	
● PUCKER	PR 50	F	8	BR	88-06 BY	R4	
● ORANGE K	OK 100	F	7	WB	89-11		
BALSAM	BM 75 YE/YE	F	5	BR	91-07 AG	BL	
LUNA	LA 75 BU/YE	F	5	BR	91-06 BU	R8	
● NINA	NN 50	F	5	BR	91-01 CH	DP	
MONTANA	MA 100 -/K	F	4	WH	92-08		
SUNDOWN	SD 100	F	4	WH	92-10		
SUNUP	SU 100	F	4	WH	92-09		
● ELLY	EL 100	F	4	WH	93-14		
● FLAXEN	FN 100 YE/GR	F	3	TF	93-13		
● FROST	FT 100 BU/RD	F	3	TF	93-12		
MUSHROOM	MR 88	F	3	TF	93-09 BM 75	?? BL	
ORPHAN ANNIE	AN 50 -/YE	F	3	BR	94-02 U2 50	IS	
AZUL	AZ 50 -/BU	F	2	BR	94-01 CH 50	DP	
SUMAC	SC 75	F	2	BR	95-09 PR 50	?? Sm	
MELON	ME 75	F	1	BR	95-10 FT 100	?? DP	
GERENUK	GK 100 -/N/-	F	1	BR	95-02 SD 100	?? PE	
PALOUSE	PS 50 -/N/-	F	1	BR	95-11 BM 75	?? PE	
		F	1	BR	95-07 NN 50	?? IS	
		F	1	BR	95-04 MR 88	?? TN	
		F	1	BR	95-03 MA 100		
		F	1	BR			

SOLUTIONS: Planning for the Long Term on a Regional Scale

The extinction crisis will pass if, and only if, we commit to conservation action with a long-term, ecosystem-level focus. Such an approach demands from science strategic improvements in our understanding of species that are representative or protective of a larger group of organisms (exemplar and umbrella species, respectively), play key ecological roles (keystone species), or are uniquely informative about the general causes of extinction.

In this multi-disciplinary study of Rocky Mountain bighorn sheep, a keystone, exemplar, and umbrella species of large mammal, we will:

Identify population sizes at which the likelihood of extinction over a period of centuries is acceptably small.

Identify, for the Northern Rockies, the amount and location of bighorn habitat adequate to support populations that meet or exceed these population size thresholds.

Discover how individuals and genes move between bighorn populations, and provide guidelines for maintaining and restoring ecological linkages on a landscape scale.

The bighorn cannot stand apart from the habitat for which it is designed or the genetic foundation upon which continued adaptation depends. The broad goal of this study is to better identify the constraints that the bighorn's needs impose on our options in providing for its long-term persistence in the wild.

IMAGE: J. Hogg

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Population Size Targets For Long-Term Viability:

Reliable targets for population size depend upon a comprehensive understanding of bighorn reproduction and mortality (see *Population Bottlenecks*). To build this understanding, we are compiling detailed life histories for several hundred marked bighorn in our National Bison Range and Sheep River study populations. These life histories will, in turn, govern computer simulations of extinction in model populations (see *Simulating Extinction*). Population sizes associated with an acceptably small risk of extinction in cyberspace represent size targets for populations of bighorn in the real world.

Our life histories of study bighorn include records of birth date, birth weight, gestation, estrus date, mating associations, breeding migrations, social rank, genealogy, reproductive success at each age, and date of death.

IMAGE: J. Hogg

Population Bottlenecks

To establish population size targets, we require good measurements of the extent to which (i) bighorn populations fluctuate annually in size and (ii) individual bighorn differ in the number of offspring they produce during their lifetime.

The importance of fluctuation in population size is straightforward: populations more prone to changes in size are more apt to crash in an unlucky series of closely-spaced declines, or reach numbers at which genetics and demography interact to create the tug of an extinction vortex.

The connection between inequality in individual reproduction and population extinction is more subtle. Nonetheless, when individuals differ widely in lifetime reproductive success, genetic bottlenecks, and hence an extinction vortex, can develop in the absence of marked fluctuations in population size.

Genetic bottlenecks are time periods during which genetic diversity is lost. They occur whenever

IMAGE: J. Hogg

Home of the Sheep River study population: winter range along the Sheep River gorge (left) and lambing and summer habitat among the peaks of the Highwood Range in the Canadian Rockies (below). The herd belongs to a still-interconnected complex of native populations. At this location, we focus on the mechanisms and population consequences of migration and gene flow.

IMAGE: J. Hogg

IMAGE: The Ecology Center / GIS

The National Bison Range study site viewed from space and on foot. The Range is an island refuge in an agricultural landscape. Our studies here focus on the population conse-quences of 75 years of ecological and genetic isolation.

IMAGE: J. Hogg

the number of individuals contributing genes to the next generation is small. Perhaps the population itself is small. Or, the social system may permit only a fraction of those living to reproduce. In bighorn and many other large mammals, male mating opportunities are limited by social dominance.

Such "mating system bottlenecks" are difficult to detect, yet can operate year-after-year over a wide range of population sizes. We are using genetical analysis of paternity (see *Measuring Genes*) in the Sheep River and National Bison Range study populations to measure, for the first time in bighorn, the effect of male reproductive monopolies on population persistence.

Habitat Targets and Inventory:

IMAGE: J. Hogg

Regional targets for amount of habitat follow directly from our targets for population size and existing knowledge of individual habitat needs. To identify the location of suitable (or restorable) habitat, we will first search our already assembled landscape database for areas in the Northern Rockies meeting (or potentially meeting) the known habitat requirements of bighorn. From this broad-brush survey, we will then select critical areas for a more detailed, field-based inventory of landscape attributes and bighorn distribution.

Project collaborators include Director Roly Redmond and staff of the Wildlife Spatial Analysis Lab, a full-service remote-sensing and GIS facility at the University of Montana. Their library of landscape data includes satellite imagery of the Northern Rockies and vegetation maps for the region based on field data collected by a variety of organizations, including our own.

Simulating Extinction

Computer simulation allows us to conduct large-scale and long-term experiments that are simply impossible to do in the real world. Our simulations are individual-based. In individual-based simulation, "virtual" individuals populate cyberspace. Virtual individuals have names and life histories just as our real-world study animals do.

Each simulation run ("experiment") proceeds by (i) creating a population of virtual individuals and then (ii) allowing them to reproduce and die according to rates measured on real-world populations. Reproduction and survival can be made conditional on age, level of inbreeding, or other individual trait. Over many runs, initial population size is varied until the persistence of model populations meets some accepted criterion (e.g., 95% likelihood of population survival after 1000 years).
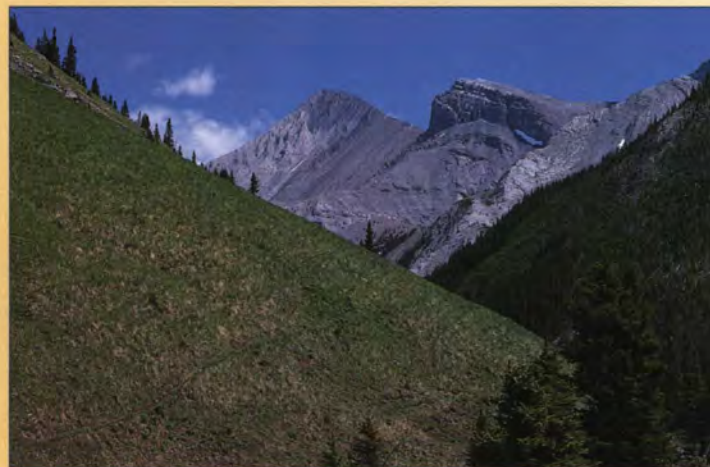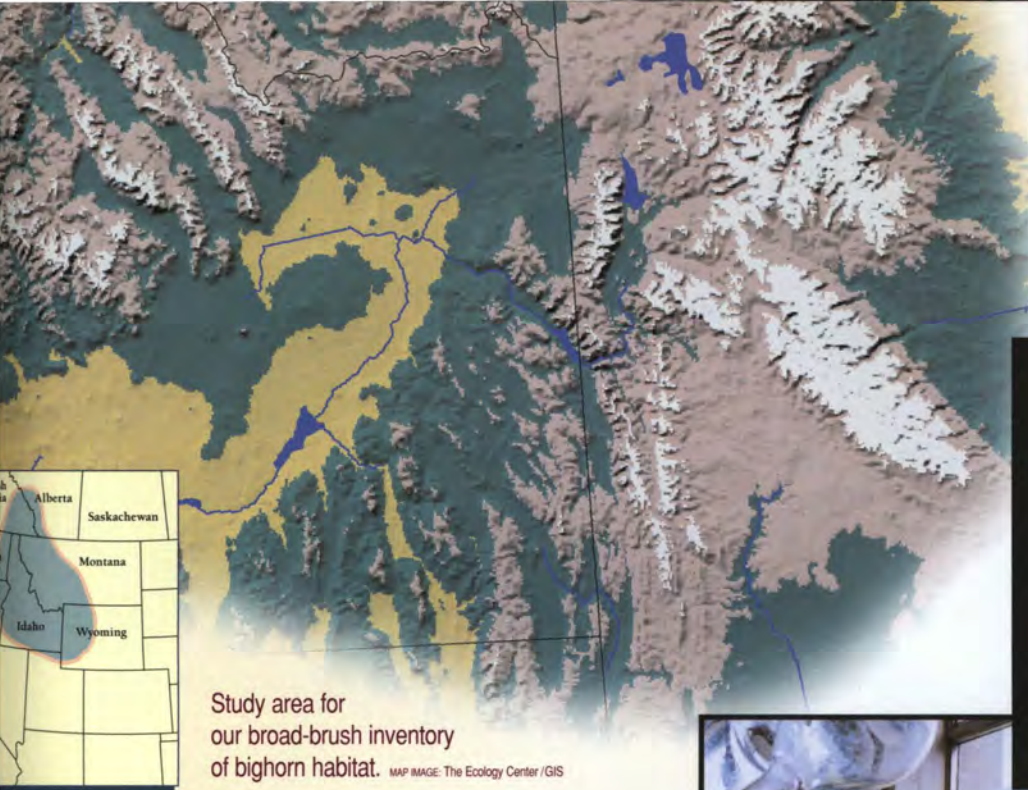

Cliff Creek in the Canadian Rockies.

IMAGE: J. Hogg

Mammals carry two sets of 100,000 different genes. One complete set is inherited from each parent. Many genes come in two (or more) slightly different forms called alleles.

Individual Genetic Profile

| 117 | 123 | 123 | 117 | 117 | 115 | 117 | 117 | - | 117 | 123 | 117 | 117 | 123 |
| 117 | 113 | 113 | 115 | 117 | 115 | 117 | 117 | - | 117 | 113 | 115 | 113 | 117 |

Alleles:

123

117
115
113

A B C D E F G H I J K L M

Individual Identification Label

Study area for our broad-brush inventory of bighorn habitat. MAP IMAGE: The Ecology Center /GIS

Alberta
Saskatchewan
Montana
Idaho
Wyoming

Migration, Gene Flow and Corridors:

A *detailed understanding* of the logic underlying animal movement is our best antidote to the threats posed by habitat fragmentation and population isolation: Who migrates? Why and when do they migrate? What habitats function as migration corridors? The oasis of meadows at the head of Cliff Creek (left) is year-round range for a neighbor herd of the Sheep River study population. Our back-country surveys for marked and radio-tagged bighorn in this, and adjacent, areas are designed to discover the who, why, when, and where of bighorn migration in a relatively undisturbed setting. With this knowledge, we can design and promote more effective plans to protect or restore linkages in areas that are threatened or disturbed by fragmentation. ∎
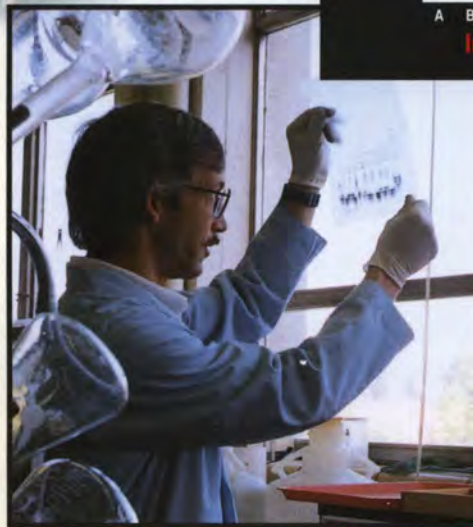
IMAGE: B. Schwan

Collaborator and population geneticist Steve Forbes employs state-of-the-art molecular techniques to study the genetics of threatened and endangered mammals, including bighorn, wolves, and grizzly bears.

This laboratory gel shows genetic profiles at one gene locus for 13 study individuals (columns A-M). Variants of this gene differ in length, hence numbers are used to label alleles. Shorter (smaller) alleles travel faster through the gel matrix and hence travel farther from the origin (top) toward the end (bottom) of the gel.

Individuals with a single dark band (e.g., A) received the same variant of the gene from each parent. Bighorn with two dark bands (e.g., B) received different alleles from mom and dad. A total of four distinct variants of this gene (113, 115, 117, and 123) are present in this "population".

Measures of genetic variation can be derived from counts of alleles made over a number of different genes and individuals. By comparing the genetic profiles of potential fathers with mothers and their lambs, we can determine paternity. For example, ram C cannot be the father of lamb K since neither allele present in the lamb (115/117) is present in this ram (113/123).