

KNOWLEDGE BASE

Camp Fire, Pope & Young, B&C Team Up for New Bighorn Research



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My last column described Dr. Karen Fox's new study on paranasal tumors in bighorn sheep, supported by a grant from the B&C Conservation Research Grants Program. This column introduces the

second new wildlife disease study, also on bighorn sheep, getting underway by Dr. Marjorie Matocq at the University of Nevada, Reno. As with Karen's study, Marjorie's proposal rose to the top following a rigorous peer review and additional consideration by the Conservation Research Grants Committee. However, in this case it would take a joint effort to fund the study at the required level. The Camp Fire Fund, Inc., generously matched the amount that B&C had available for the study, and the Pope & Young Club stepped up to fill the remaining shortfall. All three partners see the study as an important one for addressing disease problems and population declines of bighorn sheep. I wish to thank Camp Fire Club, and Pope & Young Club for their contributions.

Marjorie Matocq was born in San Francisco to parents who had recently emigrated from France. She moved to Lake Tahoe at age 3 and soon went to work as a bus girl in the family's restaurant. Marjorie and her brother were the first in their family to attend college. She completed her undergraduate degree in biological sciences at California Polytechnic State University at San Luis Obispo. This was followed by a master's degree in conservation biology at San Francisco State University, and doctorate in the museum of vertebrate zoology at the University of California, Berkeley. She completed

The study will investigate the relationship between reintroduction history, genetic diversity, and susceptibility to disease in bighorn sheep. INSET: Marjorie working in the field.



a post-doctoral position in the Conservation Genetics lab at the Smithsonian Institution's National Zoo, and spent six years as an assistant and then associate professor of genetics at Idaho State University. In 2008, she commenced her current position as associate professor of wildlife genetics at the University of Nevada. She lives in Reno with husband Chris Feldman, 5-year-old son Rowan, and baby daughter Morgan. Marjorie's research is broadly focused on identifying processes that contribute to both the generation and maintenance of genetic and morphological diversity in vertebrates. Her work combines traditional field studies with molecular genetics analyses, which allows conservation biologists to gain the most insight possible into the ecology of the populations they seek to conserve.

Bighorn sheep are an icon of the West and are central to what big-game hunters and all outdoor enthusiasts regard as a healthy and intact ecosystem. Despite the efforts of state wildlife agencies and others to restore bighorn populations to former ranges, many populations continue to experience catastrophic disease-related die-offs. The disease process undoubtedly is the result of many interacting factors, but relatively little is known of the role that genetic diversity plays in the overall health and persistence of populations. Growing evidence points to the importance of genetic variation in immune response and other aspects of disease resistance that are critical to bighorn conservation and management.

The study focuses on four populations of bighorn sheep in Utah (Mount Timpanogos, Rock Canyon, Mount Nebo, and Antelope Island) that have a particularly well-documented recent history of establishment, augmentation, and disease-related die-off. Three of these populations have had recent contact with domestic sheep, after

which two declined dramatically while one continues to thrive. The isolated population with no known domestic contact also continues to thrive. The ecology and demography of these populations have been well-documented through censusing and collection of samples for genetic analysis.

In 2008 the Rock Canyon and Mount Nebo populations dropped precipitously after exposure to domestic sheep. Because these were reintroduced populations, the possibility exists that they lacked overall genetic diversity and/or specific genetic profiles to resist diseases. This study will be one of the first to investigate the relationship between reintroduction history, genetic diversity, and susceptibility to disease in bighorn sheep. The specific questions are: (1) How genetically distinct are the reintroduced populations, given that some share original source populations while others have more distinct histories? 2) What is the genetic profile of persisting populations that are in contact with domestic sheep, versus populations in contact with domestic sheep and experiencing die-offs? 3) How does the genetic profile of individuals that succumbed to disease differ from that of individuals that have survived?

The answers will be sought through genetic analysis of field-collected hair and fecal samples, with emphasis on microsatellites linked to genes that play a role in disease resistance. This will be a first step in determining the complex relationship of population history, genetics, and disease in bighorn sheep. The aim is for wildlife managers to use the findings to modify translocation and management strategies in order to improve the success of their bighorn conservation efforts.

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