

## Genetic Management

### Background

The GYE supports the southernmost population of grizzly bears remaining in North America. Areas of human occupation, development, and transportation networks separate the Yellowstone grizzly bear from its nearest neighboring population in the Northern Continental Divide Ecosystem (NCDE) of northwestern Montana. Currently, physical distance and relatively high mortality risk due to anthropogenic influences inhibits gene flow between these two grizzly bear populations. As with any isolated population, genetic issues can potentially be of concern for the Yellowstone grizzly bear population because of inbreeding effects due to the loss of genetic diversity. The question of concern is whether genetic factors pose a risk of compromising the long-term viability of the Yellowstone population.

DNA analyses conducted on museum specimens by Miller and Waits (2003) indicated a slight decline in genetic variability in the Yellowstone population since the early 20<sup>th</sup> century; however, this loss of variability was less severe than previously hypothesized. Indeed, a more recent study by Kamath *et al.* (2015) using recent advances in genetic analysis techniques with molecular markers (Luikart *et al.* 2010) indicate that despite isolation, genetic diversity in the contemporary population has stabilized. Kamath *et al.* (2015) found that the current rate of inbreeding in the Yellowstone grizzly bear population is very low (0.2%). Likewise, the effective population size ( $N_e$ ), which reflects the number of reproducing individuals in a population, has increased from 102 to 469 during the 25-year period of 1982–2007. This positive trend is important because  $N_e$  serves as a surrogate measure for a population's evolutionary potential and risk of inbreeding (Franklin and Frankham 1998). The most current  $N_e$  estimate of 469 based on Kamath *et al.* (2015) approaches the minimum threshold criterion of 500 required for a threatened population to retain long-term evolutionary potential and maintain adequate genetic variation necessary for adaptation to environmental change. It also exceeds the requisite minimum threshold ( $N_e > 50$  individuals) needed to avoid risk of inbreeding (Franklin 1980). The recent findings that 1) genetic diversity is stable, 2) rate of inbreeding since 1985 is very low, and 3) effective population size has increased nearly 4-fold since 1982, collectively indicate that, at current population levels and under the current environmental conditions, genetic factors do not pose a substantial risk to the viability of the Yellowstone grizzly bear population. Because of this, the need for intervening genetic management of the population (i.e., translocation of grizzly bears from other populations) as previously specified in the 2007 Conservation Strategy document is considered unwarranted at this point in time (2015).

Given that the Yellowstone grizzly bear is an isolated population, it is inevitable that sometime in the future there will be loss of genetic variation in the population if no natural movement between neighboring population(s) and no artificial transplants occur. Although in the short term the urgency of this scenario is reduced (Kamath *et al.* 2015), the genetic diversity of Yellowstone grizzly bears remains low relative to other interior grizzly bear populations. Therefore, it is imperative that monitoring for flow of new genetic material via natural immigration and assessment of genetic diversity is continued. In recent decades, as the NCDE and Yellowstone populations have both increased in numbers and expanded in range, the prospect for re-establishing natural connectivity has been improved (Haroldson *et al.* 2010; Proctor *et al.* 2012). Although current methods yield a very high probability (0.96) for detecting a first-generation hybrid if one is to occur, no evidence of recent immigration from neighboring populations has been observed (Haroldson *et al.* 2010). If genetic connectivity between the Yellowstone and other (e.g., NCDE, Selkirks) populations is not evident and genetic monitoring

indicates a decline in genetic diversity such that an introduction of new genetic material into the GYE population is warranted, translocations will be conducted as needed. Miller and Waits (2003) suggest that one to two effective migrants per generation from the genetically diverse NCDE population would be an appropriate level of gene flow to maintain or increase current levels of genetic diversity in the Yellowstone population. Monitoring of transplants would be conducted to ensure that any new population members successfully breed and that resulting hybrid progeny survive to successfully introduce new genetic material into the Yellowstone population.

#### **Genetic Monitoring Protocol**

Genetic samples will be collected from all grizzly bear captures and mortalities in the GYE for analysis via cooperative efforts between the IGBST and recognized genetic experts. Genetic analyses of these samples will be conducted and evaluated for potential evidence of grizzly bears from other populations immigrating into the Yellowstone population and producing offspring. Monitoring of radio-collared grizzly bears will be used to document potential movements between other ecosystems and the GYE.

## Literature Cited

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