IBMP Briefing Statement

Agency:	**Yellowstone National Park**
Issue:	**Genetics Assessment of Effective Population Size**
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Yellowstone National Park recently collaborated with the University of Montana (Drs. Luikart, Allendorf, and Schwartz) to assess to assess population substructure and impacts of culling Yellowstone bison. Genetic differentiation between the central and northern breeding herds of Yellowstone bison based on mitochondrial DNA extraction from feces resulted in rather large differences (F_{ST} = 0.402). However, estimates of differentiation between the breeding herds based on microsatellite DNA analyses showed a much smaller difference (F_{ST} = 0.02 in 2006; F_{ST} = 0.01 in 2008). F_{ST} is the portion of total genetic variance contained in a subpopulation compared to the total genetic variance. Values can range from 0 to 1 and high F_{ST} implies considerable differentiation among subpopulations. In bison, mitochondria are normally inherited exclusively from the mother, while microsatellites, which are repeating sequences of 1-6 base pairs of DNA, result from a mixing of DNA from both parents. Thus, while the mitochondrial DNA results suggest female Yellowstone bison exhibit moderate to high fidelity to their breeding ranges, the microsatellite results suggest that there is substantial gene flow between the two breeding herds, likely facilitated more by males than by females.

We constructed an individual-based simulation model to examine how actual management strategies influence the effective population size (Ne) and allelic diversity in realistic population scenarios similar to management actions conducted with Yellowstone bison. Simulation scenarios included a population size (Nc) ranging from 250 to >3,000 bison, a wide range of variance in male reproductive success, loci with 2, 5, or 20 alleles, and several realistic population culling strategies causing fluctuations in Nc.

The resulting effective population size ranged from 746 to 1,176 with high to moderate variance in male reproductive success, respectively, for a stable population size of 2,000 bison. The Ne/Nc ratio remained stable around 0.33-0.38 for high variance in male reproductive success irrespective of the population size or the culling scenarios, but dropped to only 0.04 with extreme variance in male reproductive success. Heterozygosity was maintained at >95% over 200 years (28 bison generations) for all simulation scenarios with Nc >500 and non-extreme variance in male reproductive success.

The conservation of allelic diversity depended more on average Nc than Ne in fluctuating populations. Simulations suggest that 95% of allelic diversity will be maintained over 100 years if the Nc remains above 2,000 - 3,000 bison. However, less than 90% of alleles will be maintained at loci with more than five alleles (e.g. at immune system loci). Variance in male reproductive success had little effect on allelic diversity except under unrealistically-extreme variance in male reproductive success.

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