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Background:

Based on the then prevailing science of bison genetics, and a review specific to minimum viable population dynamics of Yellowstone bison (Wilson and Kyle 1999), the Final Environmental Impact Statement for Bison Management for Montana and Yellowstone National Park (2000) and the Interagency Bison Management Plan Record of Decision (2000, p. 51) provide for the conservation of Yellowstone bison genetics by balancing a minimum late-spring, pre-parturition population of 3,000 animals with brucellosis risk management objectives. The agencies also acknowledged uncertainty around this finding and committed to conducting additional research on genetics in Yellowstone bison, and adjusting management based on research and management experience.

During 2000 to present, the National Park Service provided leadership with substantial financial and operational support to initiate cooperative bison genetics research programs at Texas A&M University and University of Montana, resulting in scientific publications by Halbert (2003), Gross et al. (2006), and Gardipee (2007).

In April 2008, the Animal Welfare Institute et al. petitioned the DOI and NPS to promulgate emergency regulations that would protect the genetic diversity and viability of Yellowstone bison by ceasing brucellosis risk management removals, translating the findings of Halbert (2003), Gross et al. (2006), and Freese et al. (2007) to suggest that a minimum of 4,000 bison was necessary to preserve 95% of allelic diversity for 200 years in both the central and northern herds.

In August 2008, the National Park Service provided continuing (2008-2010) funding to scientists at the University of Montana to conduct further research to estimate genetic diversity and gene flow between the central and northern breeding herds; quantitatively model the potential effects of risk management removals on the genetic diversity of Yellowstone bison; assess the numbers of bison necessary in each breeding herd and the entire population to preserve 90-95% of existing levels of genetic diversity; and recommend long-term genetic surveillance objectives and methodologies to ensure adequate data is collected to detect any significant changes in genetic diversity.

In September 2008, James Bailey, Belgrade, MT, provided the IBMP agencies with a recommendation that 2000-4000 Yellowstone bison are necessary to maintain acceptable levels of genetic diversity, citing Gross et al. (2006) and prevailing uncertainty of male breeding success, generation times, population substructure, herd interchange, and the effects of non-random mortality from brucellosis risk-management and hunting.

Current State of Knowledge:

Prevailing science suggests that Yellowstone bison consist of a single population, with 2-3 distinct, but not fully segregated; breeding herds (Halbert 2003, Gardipee 2007). This likely reflects the population bottleneck and subsequent isolation of endemic and reintroduced bison herds during the late 1880s through the 1970s (Meagher 1973), and strong female fidelity to breeding areas.

Retaining adequate levels of genetic diversity (i.e., alleles) is necessary for bison to adapt to a changing environment (Allendorf and Luikart 2007, Freese et al. 2007). While studies indicate a high level of genetic variation in Yellowstone bison relative to other North American bison populations (Wilson and Strobeck 1999, Halbert 2003), the northern herd may also have some genetic characteristics rarely found in the central herd (Gardipee 2007).

Gross et al. (2006) suggested that a minimum breeding population size of 1,000 bison was required to retain at least 90% of prevailing allelic diversity over 200 years. A minimum herd size of 1,000 was adopted in the Draft North American Bison Conservation Strategy by the International Union for the Conservation of Nature (C. Gates 2008, University of Alberta, personal communication). Freese et al. (2007) reviewed existing science and suggested that 2,000 bison per breeding herd was a more prudent goal to retain 95% of allelic diversity. These recommendations assumed no immigration (i.e., gene flow) from other herds.

Gene flow through immigration may reduce the population size necessary to maintain genetic diversity. Despite the findings of Halbert (2003) and Gardipee (2007), there is compelling scientific evidence that bison from the central herd began immigrating into the northern herd beginning in the 1980s, continuing to present (Taper et al. 2000, Coughenour 2005, and Fuller et al. 2007). During 2006-2008, approximately 10% of radio-collared female bison naturally immigrated from the central herd into the northern herd (3 out of 30 per year, NPS 2008 unpublished data). There is no evidence of substantial bison immigration from the northern herd into the central herd.

Increased loss of genetic diversity can also occur due to non-random mating, large variations in population size, skewed sex ratios, and non-random removals of animals. The ratio of mature bulls to adult females in the Yellowstone population and evident active competition between bulls for mates should preclude heightened concern about non-random mating effects (i.e., only a few bulls siring most calves).

Since 2000, the Yellowstone bison population has varied between ~2,500 – 5,000, with removal of ~1,000 bison during winter 2005-06 (20% of extant population) and ~1,700 bison during winter 2007-08 (36% of extant population). Large-scale management removals likely remove a disproportionate level of calf-mother pairs and reduce rates of genetic recombination through non-random harvest of bison from each breeding herd leading to higher probability of lost genetic diversity (Allendorf and Luikart 2007, Allendorf et al. 2008).

Findings:

Cumulative available scientific evidence suggests that the conservation of an overall bison population of 2,500 – 4,500 (i.e., 1,000 to 2,000 bison in each of the central and northern herds) should retain 90-95% of genetic diversity and alleles in Yellowstone bison over the next 200 years.

During the past eight years, the NPS has vigorously supported new bison genetics research, and initiated new research and long-term monitoring to inform short- and long-term IBMP adaptive management for the conservation of genetic diversity.

Evidence suggests that periodic large-scale removals are the most important negative impact to the genetic diversity of the Yellowstone bison population, and that the IBMP should be adaptively adjusted to incorporate multiple, relatively low to moderated levels of random and non-random mortality (e.g. predation, winter-kill, hunting, quarantine, brucellosis risk-management, etc.).

At present, the greatest vulnerability to the genetic health of Yellowstone bison would be a near-term, large-scale removal of bison from the northern range.

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Scientific Literature Cited

- Allendorf, F., P. England, G. Luikart, P. Ritchie, and N. Ryman. 2008. Genetic effects of harvest on wild animal populations. *Trends in Ecology and Evolution* 23:327-337.
- Allendorf, F., and G. Luikart. 2007. Conservation and the genetics of populations. Blackwell Publishing, Malden, Massachusetts.
- Allendorf, F. P., and N. Ryman. 2002. The role of genetics in population viability analysis. Pages 50-85 in S. R. Beissinger and D. R. McCullough, editors. Population viability analysis. University of Chicago Press, Chicago, Illinois.
- Coughenour, M. B., 2005. Spatial-dynamic modeling of bison carrying capacity in the greater Yellowstone ecosystem: a synthesis of bison movements, population dynamics, and interactions with vegetation. Natural Resource Ecology Laboratory, Colorado State University, Fort Collins, Colorado.
- Freese, C., K. Aune, D. Boyd, J. Derr, S. Forrest, C. Gates, P. Gogan, S. Grassel, N. Halbert, K. Kunkel., K. Redford. 2007. Second chance for the plains bison. *Biological Conservation* 136:175-184.
- Fuller, J. A., R. A. Garrott, and P. J. White. 2007. Emigration and density dependence in Yellowstone bison. *Journal of Wildlife Management* 71:1924-1933.
- Gardipee, F. 2007. Development of fecal DNA sampling methods to assess genetic population structure of Greater Yellowstone Bison. Thesis. University of Montana, Missoula, Montana.
- Gross, J. E., G. Wang, N. D. Halbert, P. A. Gogan, J. N. Derr, and J. W. Templeton. 2006. Effects of population control strategies on retention of genetic diversity in National Park Service bison (*Bison bison*) herds. Revised final report submitted to U.S. Geological Survey, Biological Resources Division, Bozeman, Montana.
- Halbert, N. 2003. The utilization of genetic markers to resolve modern management issues in historic bison populations: implications for species conservation. Dissertation. Texas A&M University, College Station, Texas.
- Halbert, N., and J. Derr. 2007. A comprehensive evaluation of cattle introgression into US federal bison herds. *Journal of Heredity* 98:1-12.
- Meagher, M. 1973. The bison of Yellowstone National Park. Scientific Monograph Series Number 1. National Park Service, Washington, D.C.
- Taper, M. L., M. Meagher, and C. L. Jerde. 2000. The phenology of space: spatial aspects of bison density dependence in Yellowstone National Park. Final report to the U.S. Geological Survey, Biological Resources Division, Bozeman, Montana.
- Wilson, G. and C.J. Kyle. A review of the influences on minimum viable population estimates (MVP) in bison. Final Report to Yellowstone National Park. Department of Biological Science, University of Alberta, Edmonton, Alberta, Canada, T6G 2E9. 22pp.
- Wilson, G.A., and C. Strobeck. 1999. Genetic variation within and relatedness among wood and plains bison populations. *Genome* 42:483-496.