

**Management of Bison in the National Wildlife Refuge System**  
**US Fish and Wildlife Service**

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## **Introduction**

### ***Bison Conservation History***

Estimates of the number of North American bison (*Bison bison*) pre-European settlement vary significantly, but bison likely occurred in the tens of millions (Shaw 1995). Similarly, a variety of theories exist as to the reasons for the rapid decline of bison, including the mid-1800's commercial slaughter, Native American hunting and trade pressures along with the introduction of horses to Native cultures, division of the plains by railroads, and newly introduced bovine diseases. However, commercial slaughter of bison in the mid-1800's likely played the most significant role in the bison population reduction of the 1800's. Estimates of remaining bison in the late 1800's vary between approximately 600 and 1300. Formation of the American Bison Society in 1905 resulted in Congressional establishment of six federally managed public bison conservation herds between 1907 and 1919. Four of these herds are currently managed by the Fish and Wildlife Service (FWS), while both Yellowstone and Wind Cave National Park herds, established in 1902 and 1913, are managed by the National Park Service (Halbert 2003, Boyd 2003).

### ***Current Status of Plains Bison***

An estimated 300,000 – 500,000 bison exist in North America today, including commercial bison operations; however, only about 19,200 bison are managed for conservation in 50 North American herds. Boyd (2003) describes those 50 conservation herds, of which only 18 are managed by the federal governments of the United States and Canada. Those federal herds contain 48% of animals managed for conservation purposes, with the remaining in state, foundation or private herds.

In the United States, almost 6,000 bison are managed in 4 National Park Service (NPS) herds, including Badlands, Theodore Roosevelt, Wind Cave and Yellowstone National Parks. Over half of this population is in Yellowstone. The Grand Teton National Park/National Elk Refuge (GRTE/NER) herd has been listed as a National Park Service managed herd in some publications (Halbert 2003), but is effectively managed through an interagency effort, and numbers approximately 1000 bison. Although Halbert (2003) and Boyd (2003) discuss 5 FWS managed bison herds, recent animal movements have resulted in redistribution of the approximately 1300 FWS managed bison into 8 herds, excluding the GRTE/NER herd (Table 1.)

All FWS and NPS bison herds are presently managed within the historic range of plains bison. Three of the 4 NPS managed herds are maintained at 500 or more bison, while only 1 FWS herd (Wichita Mountains) is currently maintained at that size.

All FWS managed bison herds are free from some specific reportable diseases for livestock, likely due to the more intense herd management practiced by FWS compared to many other conservation herds. Today, millions of visitors come to FWS bison refuges every year. Visitor Centers educate these visitors about FWS bison conservation history success, and the role that bison play in ecosystem function.

<i>Refuge and Acronym</i>	<i>Herd Founding Date</i>	<i>Herd Establishing Purpose</i>	<i>Herd Size</i>	<i>Current Culling Strategy</i>	<i>Sex Ratio (M:F)</i>	<i>Feeding</i>	<i>Vaccination, Deworming, etc.*</i>
Wichita Mountains (WM)	1907	Conservation	530	Managed in 3 subherds for breeding with yearlings moved annually, culled from captured subpopulation by age	1 : 1	none	Parasite treatment regularly
National Bison Range (NBR)	1908	Conservation	325	systematic across ages 1 - 7	1 : 1.1	none	none
Fort Niobrara (FTN)	1913	Conservation	350	Calves and older animals only	1 : 1	none	none
Sully's Hill at FTN (SUL)	1919	Conservation	39	None, transplanted 2006 to FTN to allow growth	1 : 1.2	none	?
Neal Smith (NSM)	1996	Habitat management, Education	39	To be determined, recently established new population from NBR	1 : 1.4	none	Parasite treatment regularly
Sully's Hill, ND (SH)	2006	Education	7	To be determined, recently established new population from NBR	1 : 2.5	winter	?
National Elk Refuge /Grand Teton (NER/GRTE)	1948	None	1000	Management shared with Grand Teton NP and Wyoming Game and Fish; hunting outside of park/refuge boundary	1 : 1.2	winter	none
Rocky Mountain Arsenal (RMA)	2007	Habitat management, Pilot study	16	To be determined, recently established pilot study herd in 2007	1 : 4.3	none	none
Charles M. Russell (CMR)		Education	3	1 calf per year	NA	?	?

Table 1. FWS bison management stations and current status.

\*Parasite treatment is accomplished through therapeutic blocks placed in the environment.

### ***Plains Bison Restoration Movement***

In the late 1980's, the "Buffalo Commons" concept was promoted by Drs. Deborah and Frank Popper. They proposed that species could be restored at a landscape level, by allowing large herds of free-roaming bison to range across the Great Plains area. Although this project never became reality, several similar projects have been initiated since that time (Boyd 2003). Regardless of the project name, there is a distinction between conservation of bison as a species and restoration of free-ranging bison at an ecosystem level.

In 2003, Boyd published a thesis describing the current status of North American bison and provided conservation recommendations for the World Conservation Union (formerly International Union for the Conservation of Nature, or IUCN). The mission of the IUCN is to "influence, encourage and assist societies throughout the world to conserve the integrity and diversity of nature and to ensure that any use of natural resources is equitable and ecologically sustainable" (IUCN website). Within the IUCN is the Species Survival Commission (SSC), that contains Specialist Groups based on taxon. These Specialist Groups create Action Plans, which are conservation plans that are published for use by managers, agencies, academia, NGOs, and generally anyone capable of implementing the conservation action.

Boyd's conservation status summary contains information on 50 conservation herds in North America, and discusses factors that influence the definition of a "restored" population. These factors include, but are not limited to, population size, genetic diversity, hybridization, grazing rotation, fencing, disease status, location within historic range, associated predator populations, and handling. Generally, these factors contribute to a discussion of what defines a "wild" bison, and what defines a "restored" bison population. However, restrictive definitions exclude many sources of unique and valuable genetics, increasing the potential that some may be lost.

There are only a limited number of areas where landscape-level restoration of free-ranging bison is possible in the United States. The obstacles are immense, including land ownership, disease transmission, genetics, forage depredation, hunting concerns, etc. In 2005 the American Prairie Foundation (APF), an organization devoted to creating and managing a prairie-based wildlife reserve, in cooperation with the World Wildlife Fund, released 16 bison from Wind Cave National Park onto private land in Montana, near the CMR. Only local FWS involvement occurred in this project. Thirty eight animals are now reported onsite (APF website).

The Nature Conservancy has two major efforts, one in Canada and the second involving land in South Dakota also using Wind Cave National Park bison. The Nature Conservancy also manages a free-roaming herd of around 2,500 bison on their Oklahoma Tall Grass Prairie Preserve (The Nature Conservancy 2007).

In 2005, the American Bison Society (ABS) was revitalized with several meetings, including one that FWS was invited to in October 2006. This organization is working within the Wildlife Conservation Society, and has been facilitating the IUCN project and meetings.

Although these projects are devoted to bison restoration, the FWS has played a minimal role in development or implementation of these projects to date.

## **Future Management Strategy Issues**

### ***FWS Bison Management Goals***

During the FWS Bison Management meeting in 2005, FWS bison management staff identified 6 “purposes” for having bison on National Wildlife Refuges (NWR). Each Refuge has a locally unique role with bison management and any one to all 6 purposes may apply. Those 6 purposes are:

1. Legal mandate as part of establishing purpose(s)
2. Conservation of bison
3. Education and recreation for the public
4. Habitat management tool
5. Cultural or historic significance
6. Research

From a national perspective, it is bison conservation that integrates bison into national FWS conservation goals. Bison conservation then becomes a National Wildlife Refuge System priority, even if most refuges are unable to maintain population numbers high enough to accomplish that goal independently. One method for achieving this goal is through meta-population management. Though not biologically significant for bison conservation, even very small bison herds may contribute to long-term conservation of bison through education and outreach efforts to the public thereby strengthening public support for refuges capable of supporting larger herds.

### ***Genetics Techniques and Research***

Historically, studies of bison genetics have been conducted using mitochondrial DNA (mtDNA). This DNA is maternally inherited, such that all offspring inherit their mtDNA from their mothers. Male animals who inherit their mother’s mtDNA do not pass it on to their offspring. MtDNA is also highly conserved, meaning its consistency across herds makes it not useful for detecting subtle differences between populations. However, mtDNA can detect hybridization events, but is limited to detecting only maternally inherited genes.

A newer technology, involving examination of selective-neutral marker genes in the nucleus, was applied by Texas A&M University to 10 federally managed bison herds. Nuclear DNA markers can be used to assess both hybridization and genetic diversity. These selective-neutral markers are microsatellites, sections of nuclear DNA that contain repeated nucleotide sequences. These sections are highly variable in the number of repeats that occur, and are therefore useful for assessing relatively subtle differences across populations. Microsatellites are believed to be neutral markers because they are not involved in protein coding, and therefore should not be subject to selection pressures. Units of measure for microsatellite analysis are the length of the nucleotides in that section of DNA. Since DNA is double stranded, this is frequently called “base pair length” (bpl). Because microsatellites occur in nuclear DNA, they are passed from both male and female animals to their offspring.

The Texas study used 15 loci for hybridization testing. An allele was suspected to be cattle origin if its bpl was the same as that found in cattle and an allele with that same length was not found in “gold standard” bison (Yellowstone National Park, Wind Cave National Park and Wood Buffalo National Park bison). Confirmatory loci were examined when suspect marker

alleles were found. Confirmatory loci are known genes well described for cattle that are close to the microsatellite marker. Based on the expectation that two very close genes would sort together over generations, the confirmatory locus would be expected to show a cattle allele bpl if the microsatellite marker was truly a cattle allele. In this manner, hybridization was detected, and Texas ultimately confirmed the hybrid alleles through sequencing and comparison to published cattle sequences. The research was designed on the assumption that if historical (generations ago) cattle genes were introduced to the population, those alleles would be widely distributed across the genome of currently extant bison. The use of markers presumes that some of these cattle alleles would end up at marker sites and could be detected if enough of the population was sampled. Implicit in that design is that if hybrid markers are detected, the herd is characterized as “hybridized”. In a known hybridized herd other areas of the genome, not analyzed, also likely contain some cattle alleles. Thus the microsatellite marker panel detects hybridization at a herd level, and has significant limitations for detecting hybridization at an individual animal level.

The model assumptions for sampling may or may not prove true. For example, alleles found in rare prevalence are highly susceptible to genetic drift (loss of alleles) due to stochastic events. Selective pressures on protein producing genes may cause some alleles to be conserved and others to decrease or be eliminated. If an F1 cattle-bison hybrid was introduced into the population decades ago, it is highly unlikely the entire haploid genome of that domestic bovine still exists distributed in the bison herd today.

In addition to hybridization, Texas also used a set of 54 microsatellite markers to assess genetic diversity. These markers were selected from the USDA bovine gene map based on high polymorphism (many alleles) in bison from the literature (Schnabel 2001). Measures of diversity include heterozygosity, allelic richness and number of private alleles. In addition, the relative genetic contribution of each herd to the overall federal herd gene pool was calculated (Halbert 2003). This latter figure is frequently confused to infer “herds lacking in diversity” when no such estimate can be made from the statistic.

The original Sully’s Hill NGP herd (SUL; now at FTN) was not included in the above study, but the hybridization data were provided by Texas after the study was completed. SUL diversity and hybridization data were also obtained independently through the University of California Davis genetics laboratory using many of the same markers as Texas.

Results from the Texas study have been published and presented to the FWS bison managers during past meetings. Generally, the Texas and UC Davis data show that all FWS herds had a sufficient genetic diversity within each herd. Given the dramatic population bottleneck of bison, the federal herds had high levels of variation, both within herd and between herds. Each FWS herd had uniquenesses when compared to other bison herds both within and outside of the FWS. As expected, herds derived from other herds were similar to their parent herd source.

The average number of alleles per locus is one measure of how much variation exists within a herd. NBR had the highest average number of alleles per locus of all 10 federal herds; followed by FTN, WM, NER/GRTE and then SUL. The number of fixed loci, loci that have only one allele present in the entire herd, is another measure of lack of variation within each herd. The NER/GRTE herd was the only federal herd with a fixed allele detected; however, the NER/GRTE sample size for genetic analyses was small. Private alleles, the number of alleles found only within a specific herd, are a measure of between herd differences. NBR ranked second behind Wind Cave in the study, followed by WM, FTN and SUL. The NER/GRTE herd and the Neal Smith original herd had no private alleles detected, while the NBR had 9.

Although FWS managers often went to great pains to reduce the risk of importing animals with cattle alleles into a herd, the technology simply was not available to detect hybrids with any certainty. Even today's technology has serious limitations for detecting individual hybrid animals. On a herd basis, only SUL has had no hybrid alleles detected to date. Given the small size of the herd, the number of animal introductions, and the nature of the modeling statistics used by Halbert, the confidence in SUL herd having no hybrid alleles is relatively low. However, future technology may increase our ability to detect hybrids, perhaps even at the individual level. Because the SUL herd has potential to be a non-hybridized herd, it was separated and moved to a larger suitable habitat to permit herd growth to reduce additional genetic loss.

NBR had the least amount of detected hybridization. Because animals need to be culled from this range-restricted herd, individuals with known hybrid alleles have been culled. Because this culling method may decrease diversity (by removing bison alleles along with the hybrid alleles) most of the recent culling involved comparing the bison portion of the markers to the herd at large to ensure those bison alleles were still well represented in the population. How this culling strategy has affected genetic diversity is unknown because the markers represent only a small portion of the genome.

Measures of diversity are only applicable to the time of sampling. Alleles that were unique to a particular herd are no longer unique to that herd when animals with those alleles are transferred to another refuge. For example, a number of alleles formerly unique to NBR have been moved to SH, NS and RMA. Some rare alleles detected by Halbert may no longer be present if only a few individuals contained those genes, and all of those individuals have been culled or died.

Two specific herds warrant further scrutiny because of small sample sizes which can markedly affect inferences. Sample sizes from WM and NER/GRTE were exceptionally small. Detection of 4 private alleles from a sample of 35 animals at WM suggests this herd may be quite unique from other FWS herds. Similarly, the finding of a fixed locus in the NER/GRTE herd may not be significant because alleles may be discovered with an increase in sample size.

Given the constraints of the data, we must clearly continue to monitor the genetics of our herds across time to understand how bison herd management affects genetics. Modeling can help us estimate the effects of management actions on the genetics of a herd. However, monitoring data will be essential for assessing the effects of management – did we have the effect we expected?

### ***Conservation Modeling Minimums***

The current allele frequencies observed within each herd are the result of conditions that existed at the time the herd was established, the effects of animal changes (losses through mortality or human culling, and gains through additions of outside animals), and bison mating systems. Although natural selection played a significant role in the original genetic definition of bison, humans have played a significant role in the selection of today's bison. In addition to the human-caused bottleneck of the 1800's, management of bison on federal lands has not historically been neutral from a selection perspective. Many parks and refuges alike have historically culled animals based on body size, condition, health, age, sex, etc. Some have routinely culled animals that exhibit specific behaviors, such as jumping fences, migrating outside of a boundary, or aggression. Human selection pressures, in addition to pre-historic natural selection, have created today's bison gene pool.



In a population of finite size, where a pair of parents have a limited number of offspring, even in the absence of selective pressures the gene frequency will not be exactly the same from one generation to the next because of the chance reproduction by a few more or few less of a specific genotype. The frequency of a gene “drifts” with this random process. This effect, genetic drift, is most pronounced in small populations and progressively results in the loss of alleles. The only counterbalancing random genetic process is mutation which can add new alleles. However, mutation rates are so low that in small populations genetic diversity is rapidly lost. Models suggest that 400-1000 bison are needed in a discrete population to have high confidence of retaining about 90% of the genetic diversity of the population. But because of assumptions in the model and the fact that bison breeding behavior is unlikely to match optimum assumptions, the modelers suggest the minimum population size needs to be 1000 and may actually need to be higher (2000) if ability to genetically adapt to current and new selective pressures is to be retained (Gross and Wang 2005).

Since we are unable to predict the future environment that bison must survive in, and we know so little about what each allele might actually code for in an individual animal, the most conservative bison genetic conservation strategy is to retain the most diversity possible. Thus, unless we have a population of at least 1000 to 2000 free-ranging randomly mating animals with absolutely no human intervention that are exposed to a full complement of predators, models predict that we will lose genetic diversity within our herds.

Clearly, individual FWS herds, with numbers significantly below 400 on limited landscapes, are at significant risk of genetic diversity loss. We lack the land mass to significantly expand FWS-managed bison populations. Management on a holistic basis, across multiple Refuges, with all herds considered one part of a “metapopulation”, will allow us to reduce the loss of genetic diversity in our bison.

## **Future Management Strategy Opportunities and Challenges**

### ***Metapopulations and Bison Genetic Conservation***

A metapopulation is defined as “a collection of spatially divided subpopulations that experience a certain degree of gene flow among them” (Allendorf and Luikart 2007). By selectively moving animals from one herd to another, specific genes may be moved to counter the effects of genetic drift or gene loss due to other management effects. Such actions will require monitoring pre and post animal movement to first determine what we need to move, then to assess the effects of the move.

FWS has several advantages in our traditional herd management techniques that will facilitate metapopulation management. Many of our animals are individually marked, or are in locations where individual marking and sampling are possible. FWS has experience handling bison and our animals are generally free of regulatory diseases precluding movement. However, these same advantages also present limitations to successful bison conservation, as the increased handling and ability to identify individuals means our human-induced selection pressure can have marked effects (including negative ones) on the FWS bison gene pool.

### ***The FWS Role in Bison Genetic Conservation***

Our concept of a comprehensive National Wildlife Refuge System (NWRS) bison management program is focused on the objectives of conserving what we have while not exacerbating the introgression of cattle genes into bison. Collectively our Refuges may be able to

manage a metapopulation that reaches that minimal genetically viable population level of 1000 to 1500. Our overarching goal for these objectives is to provide resource bison with innate high genetic diversity and low hybridization for landscape-level conservation and restoration efforts. These large scale efforts are designed to restore an ecologically functioning component of native North American prairie ecosystems. As articulated by Freese et al (2007), bison have been “ecologically extinct” since the late 1800s.

For FWS to play a role in bison conservation will require an adoption of guidelines to minimize genetic loss, applied across all Refuges with bison within the NWRS. Multiple management strategies will be needed to accomplish these objectives:

- Develop and maintain NWRS-wide genetics and disease data management and support capabilities.
- Develop and maintain effective communications pathways to ensure that information necessary for management decisions is effectively shared among FWS bison conservation stations.
- Pursue new research partnerships to develop genetic information useful in FWS bison management such as:
  - new genetic technologies (e.g. single nucleotide polymorphisms (SNP))
  - re-interpretation of existing datasets
  - improved hybridization detection at both the herd and individual animal levels
  - new animal identification technologies
- Manage FWS bison resources as a metapopulation to maintain the genetic complement and minimize loss of diversity through low levels of carefully planned and subsequently monitored animal movements among herds.
- Manage individual herds with a focus on maximizing genetic retention
  - Address culling strategies, sex ratio targets and animal handling and sampling protocols.
- Maintain enough individually marked animals to accomplish planned animal and gene movements between herds.
- At a minimum, maintain existing carrying capacity, and increase bison capacity where possible:
  - Address invasive species impacts on carrying capacities
  - Address land use issues by other competitive species
  - Explore additions to acreage through grazing leases, new Refuge locations for bison management, etc.
  - Develop and maintain genetic monitoring programs, including cooperative research projects focused on genetics management issues
  - Explore existing Refuge habitat monitoring programs to monitor dynamic habitat and range conditions.
  - Pursue research opportunities addressing improved habitat management strategies for bison, including use of fire, timber management, etc.
  - Develop new public outreach programs to educate and promote bison conservation as a valuable future endeavor, based on FWS past success.
  - Cooperatively pursue new funding opportunities to expand bison management capabilities.

- Utilize existing partnerships, explore and develop new partnerships with other agencies, organizations and tribes to improve bison management within FWS herds.

Several small steps have already been taken due to specific circumstances that required immediate response. The SUL herd had no identifiable hybrid alleles suggesting it needed to be maintained isolated from outside bison introduction. Yet the extremely small size (39) on very limited habitat meant that this herd was at high risk for genetic drift and subsequent gene loss. This herd was relocated to FTN, though kept separate from the FTN herd with known hybridization, in order to allow the herd to expand. This management action will at least temporarily minimize loss of genetic diversity due to culling. Bison from the original Neal Smith herd were removed because they represented a gene pool well established in other FWS herds. Animals from the NBR were selected for transport to SUL and Neal Smith to conserve the large number of private alleles found at NBR. In addition, animals from NBR were transported to the Rocky Mountain Arsenal to expand the habitat base for this herd and provide a satellite herd where the uniquenesses of NBR are conserved.

### ***“Shaping our future”***

The Director’s recent release of the Fish and Wildlife Service Vision and Conservation Principles from the “Shaping our Future Workshop” provides an excellent reminder that the FWS cannot continue to operate status quo. Although status quo is the easiest route to choose, prioritizing objectives and goals based on past success and future needs is essential in lean budget times.

The Vision and Conservation Principles include “stewardship of lands and natural resources” across the agency. Two of the six highest priorities for the Fish and Wildlife Service are “National Wildlife Refuge System: Conserving our Lands and Resources” and “Connecting People with Nature: Ensuring the Future of Conservation”.

Within Refuges, stations managing bison have an excellent opportunity to demonstrate accomplishments within this vision by working together in a coordinated effort to maintain the quality of bison genetics that we currently protect. Development of guidelines designed to prevent loss of bison alleles will help us accomplish the first priority. In addition, by maintaining and improving our relationship with the public, including improving our focus on the future of bison management, we can educate and connect people with bison and the lands they inhabit. Developing a more comprehensive National Wildlife Refuge System bison management strategy will enable the FWS to accomplish the stewardship vision and goals we are challenged to meet in the near future.

### **References**

Allendorf, Fred and Gordon Luikart. 2007. Conservation and the genetics of populations. Blackwell Publishing. 592 pp.

American Prairie Foundation website: ([www.americanprairie.org](http://www.americanprairie.org))

Boyd, D.P. 2003. Conservation of North American bison: status and recommendations. Master's dissertation, University of Calgary. 222 pp.

Freese, CH, et al. 2007. Second chance for the plains bison. *Biological Conservation in press*

Gross, J. and G. Wang. 2005. Effects of population control strategies on retention of genetic diversity in National Park Service bison (*Bison bison*) herds. Final Report, Yellowstone Research Group, USGS-BRD. United State Geological Survey, Bozeman, Montana

Halbert, Natalie D. 2003. The utilization of genetic markers to resolve modern management issues in historic bison populations: implications for species conservation. Doctor of Philosophy dissertation, Texas A&M University. 199 pp.

IUCN website: ([www.iucn.org](http://www.iucn.org))

Shaw, James H. 1995. How many bison originally populated western rangelands? *Rangelands* 17(5):148-150

The Nature Conservancy 2007. Tallgrass Prairie Preserve website.  
(<http://www.nature.org/wherewework/northamerica/states/oklahoma/preserves/tallgrass.html>).