Genetics

Lamar Bison Ranch. COURTESY NPS

The plains bison that are presently in existence in North America are believed to have descended from fewer than 300 to 500 bison; 88 of which were captured by private citizens between 1873 and 1889—the 23 bison of Yellowstone National Park, the small herd in Texas, and some that had been maintained in various zoos (Geist, 1996; Isenberg, 1997). Although the number of bison has increased substantially, the fact that the modern population was established from a limited founder population could have a large effect on the genetic variation of present-day herds, both public and private. A number of factors have affected the genetic variability of modern bison. Bison have undergone artificial hybridization with domestic cattle, been selectively bred for certain traits in private herds, and been separated into small isolated populations (Gates et al., 2010).

The decrease of such a vast bison population to a small fraction of its original size in a relatively short time period may have caused a genetic bottleneck or founder effect. This occurs when the genetic diversity of a population is greatly reduced due to the small sample of bison, which were present in the surviving population (Geist, 1996; Boyd and Gates, 2006). Within this small population genetic variation may be reduced further due to the male dominance effect, in which there is a disproportionate genetic contribution by the most dominate bulls within the founder herds, and little to no genetic contribution of less dominant males (Geist, 1996; Isenberg, 1997). Genetic drift, which is the random fixation of genes within a population, may occur because the founder population represents only a limited selection of the genetic diversity that once occurred in the original herds (Geist, 1996; Gates et al., 2010). Another factor that could limit the genetic variability in bison is the maternal effect, in which bison captured from the same herd have a higher probability of being related through maternal descent, and would therefore have a lower amount of genetic diversity (Geist, 1996).

Recent studies have shown that reduction of the overall genetic diversity of bison may not have occurred to as great an extent as originally believed (Dratch and Gogan, 2010; Gates et al., 2010). Examination of the majority of the herds managed by the federal government has shown that the herds have retained significant amounts of genetic variation by the standard measures of heterozygosity and allelic diversity (Dratch and Gogan, 2010). Although the bison population did go through a severe bottleneck, it is believed that the population did not remain at low numbers for an extended period of time, and therefore modern populations appear to have retained a substantial amount of genetic diversity (Freese et al., 2007). The extensive movement and breeding between the historic

populations created a large amount of gene flow within the original herds (Berger and Cunningham, 1994a; Wilson and Strobeck, 1999; Dratch and Gogan, 2010). The potential that the flow of genetic information created one large gene pool within the original herd is supported by the fact that the genetic distance between current isolated herds is lower than expected (Wilson and Strobeck, 1999). It is also speculated that much of the preexisting genetic diversity may have been retained within the current herds since the bison that made up the foundation herds were collected throughout the bison's range and the herds were artificially mixed over time (Halbert, 2003; Geist, 2006). Recent studies of DNA microsatellites have shown that certain herds are genetically distinguishable from others (Wilson and Strobeck, 1999; Halbert and Derr, 2008). This raises the question of whether current conservation herds should be managed as separate populations to preserve these genetic differences, or if the herds should be managed as one large metapopulation to increase the gene flow throughout the population (Gates et al., 2010).

An important factor in the conservation of genetic diversity within a bison population is the size of the herd and the sex ratio. There is a greater loss of genetic variation when the number of breeding animals is low (Dratch and Gogan, 2010). It is recommended that in order for a population to be considered of sufficient size for genetic purposes there should be over 1,000 animals and the size of the population should remain stable over time (Dratch and Gogan, 2010). As many of the current herds reside in regions that would not allow populations of that size, it is important to develop a metapopulation structure that allows for movement of individual bison between herds, thus allowing genetic variation to flow between the herds (Dratch and Gogan, 2010). It is also important that there be a sex ratio that allows competition between breeding bulls (Dratch and Gogan, 2010).

An additional genetic concern that arises within small populations is the potential for inbreeding, which is the breeding of related individuals. Inbreeding may reduce fertility, juvenile survival, and lifespan (Frankham and Ralls, 1998). The reduction of genetic diversity that results from inbreeding increases the susceptibility of a population to extinction (Frankham, 2003). Though inbreeding can be difficult to assess, it remains a potential cause for some of the decrease in genetic variation in bison, despite the translocation of individuals among herds (Berger and Cunningham, 1994a; Gates et al., 2010).

It has been shown that most of the herds managed by the federal government do not show obvious effects of inbreeding despite having been founded with few bison and having been maintained at relatively low population sizes (Dratch and Gogan, 2010). Some herds have shown signs that are thought to be the result of inbreeding, which include high rates of physical abnormalities, reduced growth rates, and reduced fertility (Halbert et al., 2004; Halbert et al., 2005; Gates et al., 2010). The low levels of calf recruitment and high levels of calf mortality in the Texas state bison herd appear to be the result of inbreeding (Halbert et al., 2004; 2005). Inbreeding is also believed to have affected male reproductive success in a herd located in Badlands National Park in South Dakota (Berger and Cunningham, 1994b).

Extinction of a species can occur through two routes. The first is extinction brought about when the last individual of a species dies (Freese, 2007). The second is when the genetic makeup of the species is altered substantially over time either through natural evolutionary processes or through human manipulation (Freese, 2007). Human management of bison in both the public and private sector has led to the manipulation of bison genetics through hybridization and domestication.

Halbert and Derr (2007) note that "bison and domestic cattle do not naturally hybridize" (pp. 7). Hybridization of bison and domestic cattle was originally attempted by early ranchers as a means to create offspring that exhibited the ruggedness and winter forage ability of the bison and the meat production of the domestic cow (Boyd, 1914; Dary, 1989; Geist, 1996; Boyd and Gates, 2006). While free-ranging bison do not readily breed with domestic cattle, breeding can occur between the two species in captive and artificial settings. The majority of private bison producers no longer attempt to hybridize bison with cattle. Mossom Boyd, a rancher experimenting with bison hybridization in the early 1900s, found that it was possible for a male bison to mate with a female cow in captivity. However, the percent of failure when crossing a male bison with a female cow was extremely high, with an abnormal secretion of amniotic fluid occurring in every cow, which often proved fatal. Boyd's attempts to cross a male cow with a female bison were unsuccessful (Boyd, 1914). Boyd (1914) also found that almost no male calves were born during the first cross, and the females that were born were usually barren. The first generational backcross (breeding the hybrid female offspring from the male domestic cattle and the female bison back with a male bison) produced a female 75 percent of the time (Boyd, 1914; Hedrick, 2009). This was also the experience of Charles Goodnight, who was attempting to cross bison and cattle around the same time period as Boyd (Goodnight, 1914).

Hereford x bison hybrid. PHOTO CREDIT: BOB HEINONEN; FROM GATES ET AL., 2010

The breeding of bison and cattle has caused an introgression of cattle genes into bison herds, which is a gene flow between populations that results from the hybrid offspring being bred back to the parental population (Boyd and Gates, 2006). The genetic integrity and natural genetic diversity of the species is compromised, as the introgressed DNA replaces portions of the original genome (Gates et al., 2010). A significant number of both private and public herds were established or supplemented with bison that originated from herds that had a history of hybridization (Boyd and Gates, 2006).

When testing for cattle gene introgression in bison, there are two separate types of DNA that are analyzed. The first is mitochondrial DNA (mtDNA), which is located within the mitochondria and passed from the female to her offspring with little or no variation. Her female offspring then continue to pass this DNA along with little or no variation, which makes mtDNA a good source for observing ancestry. The second type of DNA that is examined is nuclear or autosomal DNA (nuclear DNA), which is DNA that is inherited equally from both parents. There is evidence of cattle gene introgression in both mtDNA and nuclear DNA within public and private plains bison herds (Polziehn et al, 1995; Ward et al., 1999; Halbert and Derr, 2007; Dratch and Gogan, 2010). However, there is a much larger amount of mtDNA, which can be partly attributed to the fact that the first crosses and the first generational backcrosses primarily produced females (Hedrick, 2009; 2010). Hedrick (2010) notes that of 22 herds surveyed there was an average of 13.9 percent mtDNA domestic cattle ancestry and 0.6 percent nuclear DNA. Hedrick (2009) notes that it is important to recognize the difference between mtDNA and nuclear domestic cattle ancestry, as the differences in inheritance could have management implications.

In herds where there are low amounts of cattle gene introgression, individual bison that have been identified as having domestic cattle ancestry through molecular markers have not been reported to be observably different than bison without domestic cattle ancestry (Hedrick, 2009). However, there are two unpublished reports that bison with cattle mtDNA show a smaller body size on average (Hedrick, 2009). Douglas et al. (2010) found that there are a large number of differences between the mtDNA genome of bison and the mtDNA genome of cattle. The study then compared the mtDNA genome of bison and of bison hybrids and found that there were numerous non-synonymous mutations. While further studies need to be completed, Douglas et al. (2010) note that "the critical nature of the mitochondria in cellular function and necessary interaction of multiple protein complexes for proper mitochondrial function suggests that the additive effects of such large numbers of non-synonymous mutations will likely affect the mitochondrial function and the overall fitness of the organism" (pp. 7).

Prior to July 2010, based on tests examining mtDNA and nuclear DNA, there were seven plains bison conservation herds that showed no evidence of the introgression of cattle DNA. These seven herds were Yellowstone National Park (Montana, Idaho, Wyoming); Grand Teton National Park (Wyoming); Henry Mountains (Utah); Sully's Hill National Game Preserve (North Dakota); Wind Cave National Park (South Dakota); Elk Island National Park (Alberta); and Mackenzie Bison Sanctuary (Northwest Territories) (Ward et al., 1999; Halbert et al., 2005; Gates et al., 2010). Only two

Captive bison in Yellowstone National Park circa 1906. COURTESY NPS

of the herds, Wind Cave and Yellowstone National Parks could be confidently considered free of cattle DNA (Halbert et al., 2005; Gates et al., 2010). Yet new technology, which uses DNA single nucleotide polymorphisms (SNPs), is changing the current base of knowledge and understanding of the extent of cattle gene introgression in bison. This new technology can provide higher resolution, detect recent hybridization, and identify individual bison within a herd that have domestic cattle ancestry (Dratch and Gogan, 2005). DNA technological advances are displaying a greater prevalence of cattle gene introgression than previously documented. Of the seven herds mentioned above, the only public herd that is currently considered free of cattle introgression is the YNP herd.

There is also a large amount of introgression of cattle genes within the private herds. Of the 100 herds tested by 2007, the only herd that had a high probability of being free of cattle genes was the Castle Rock herd on Turner Enterprise's Vermejo Park Ranch, which is a 590,823-acre property in northern New Mexico and southern Colorado (Freese et al., 2007; Turner Enterprises Inc., 2010). As of April, 2011 the Castle Rock herd is considered free of mtDNA cattle gene introgression, and further testing will be completed in the future (Turner Enterprises Inc., personal communication). The Castle Rock herd descended from bison that were translocated in the 1930s from Yellowstone National Park (Gates et al., 2010). As the only bison in existence today that are likely to be free of cattle genes, the bison in the YNP herd and the Castle Rock herd comprise only a fraction of the overall plains bison population.