January 17, 2022

MEMORANDUM

To: Administrative files

From: P. J. White, Chief, Wildlife & Aquatic Resources Branch, Yellowstone National Park

Subject: Maintenance of Genetic Diversity and Population Viability in Yellowstone Bison

Background

Yellowstone bison have relatively high genetic diversity (Halbert and Derr 2007, Hedrick 2009). The introduction of bison during the early 1900s into the Lamar Valley in the northern portion of Yellowstone National Park (YNP) from different genetic lineages than the native bison that spent winter in the Pelican Valley in central YNP contributed to this diversity and, at least initially, created genetic differences between bison living in these herds. Bison spending winter in the Pelican (indigenous) and Lamar (introduced) valleys used the same areas during summer beginning in the 1920s and, in the mid-1930s, the National Park Service (NPS) relocated descendants from the introduced Lamar lineage in northern YNP to the Hayden Valley and Firehole River area in central YNP. Bison from this so-called Mary Mountain herd began mixing and breeding with bison from the Pelican Valley with the native lineage during the 1980s (Meagher 1998).

Bison sampled near the western and northern boundaries of the park during winters from 1997 to 2003 had somewhat different genetic make-ups (nuclear microsatellite allele frequencies; Halbert et al. 2012). These differences were surprising given the mixing of descendants from the native and introduced lineages for several decades. In addition, since the mid-2000s bison movements between central and northern YNP have increased, which further mixed descendants of the introduced and native lineages throughout the central and northern regions of the park (Wallen and White 2015). This finding is supported by a genetic study during 2011-2012 that sampled bison (mitochondria DNA haplotypes) in central and northern YNP and found descendants from the native and introduced female lineages in both areas in about equal proportions (Forgacs et al. 2016). It would be impossible to recreate genetically distinct herds of the indigenous and introduced genetic lineages given this mixing and undesirable to prevent bison from moving between the central and northern portions of the park. Park biologists recommended allowing ecological processes such as natural selection, migration, and dispersal to prevail and influence future population and genetic substructure, rather than actively managing to try and maintain or restore a genetic substructure initially created by human relocations of bison in the early 1900s (White and Wallen 2012).

Summer counts of Yellowstone bison have increased from about 2,700 in 2000 to 5,459 in 2016, which is the largest number in recent history and far larger than any other wild, unfenced population of plains bison. As a result, Yellowstone bison are one of a few populations that meet the viability guidelines recommended by scientists (Freese et al. 2007, Sanderson et al. 2008, Hedrick 2009, Dratch and Gogan 2010, Gross et al. 2010). Geneticist Dr. Philip Hedrick at the University of Arizona indicated “[i]ndividual herds or clusters [of bison] should have an effective population size of 1000 (census number of 2000-3000) to avoid inbreeding depression and maintain genetic variation. If it is not possible to have this primary herd in 1 location, then it could be in 2 or 3 locations with significant genetic exchange between them. Note that this is larger than any of the plains bison herds except for Yellowstone NP [National Park] and any of the wood bison herds except for Wood Buffalo NP and Mackenzie Bison Sanctuary in Canada” (Hedrick 2009:419).

NPS biologists counted 5,394 bison in YNP during summer 2021, including 3,830 in the northern portion and 1,564 in the central portion. Although there is evidence of genetic differences between bison sampled in the central and northern breeding herds (Halbert et al. 2012), monitoring of radio-collared bison and an additional genetic study suggest Yellowstone bison are a single intermixing population during recent decades, with substantial movements, breeding, and gene flow between bison originating from central and northern Yellowstone (White and Wallen 2012, Wallen and White 2015, Forgacs et al. 2016). Thus, Yellowstone bison meet Dr. Hedrick’s criteria for sustaining an effective population size. Another genetic study indicated the Yellowstone population should retain existing genetic diversity (viability) for centuries with a total combined population size averaging at least 3,000 to 3,500 bison, provided there is intermixing and gene flow between bison from the two breeding herds (Pérez-Figueroa et al. 2012).

Ongoing Research

Though Forgacs et al. (2016:10) concluded “Yellowstone bison can be managed” for mitochondrial diversity “as a single population with multiple breeding segments,” the authors recommended “additional studies involving population structure and genetic diversity based on both [mitochondrial DNA] and nuclear genetic diversity assessments need to be conducted.” The NPS is collaborating with biologists at the University of Wyoming to analyze bison spatial data (Global Positioning System [GPS] locations) and determine if there is spatial clustering on smaller scales within the northern and central portions of their range during the summer and winter. These results will enable biologists to sample relevant use areas appropriately for future genetic analyses. The NPS is also continuing to develop tools and conduct research with geneticists to evaluate (1) if extant diversity is relatively high and stable, (2) the extent of differentiation between primary breeding herds/areas, (3) the degree of inbreeding, and (4) population viability. The NPS is collaborating with Dr. James Derr, Texas A&M University (advisor to Halbert and Forgacs), to develop a long-term monitoring tool to track genetic diversity in Yellowstone bison and then re-sample the genetic diversity to assess how management actions could affect the conservation of genetic diversity indices. Dr. Derr and his partners are developing a Single Nucleotide Polymorphism (SNP; pronounced “snip”) genotyping platform to determine the mitochondrial DNA haplotype of unknown bison, the probability of genetic introgression from the cattle genome in the past, and parentage (relatedness).

Once this genotyping platform is available, geneticists will resample diversity in Yellowstone bison to investigate if allele frequencies (microsatellite markers and SNPs) show any significant changes in the distribution of genetic clusters from those reported in the population two bison generations ago (1997-2003; Halbert et al. 2012). Biologists in YNP have collected tissue samples from bison in their summer breeding areas (central, northern) and winter distribution (north boundary, west boundary). DNA extracted from each sample will be genotyped to determine the haplotype of mitochondrial DNA and a 200-SNP genotype for nuclear DNA. Geneticists will estimate typical diversity values by sample group, along with a comparative analysis to estimate genetic distance between each of the sample groups. Assignment tests will be conducted to identify unique genetic clusters within the samples collected during summer and winter. This will enable biologists to evaluate the genetic diversity of Yellowstone bison based on their summer (breeding) distribution and determine if there are significant differences in diversity indices compared to where bison migrate in the winter months. In addition, the Metapopulation Subgroup of the Bison Working Group is developing a strategy for managing genetic diversity among Department of Interior populations. Biologists at YNP have provided samples from bison tested during quarantine for analyses of microsatellite DNA markers to assess diversity measures and identify genetic clusters among populations.

Bison Management

Genetic samples collected from Yellowstone bison near the northern and western boundaries of YNP during 1997 to 2003 indicated “clear evidence for genetically distinct subpopulations among Yellowstone bison,” including a “[n]orthern subpopulation and [a] [c]entral subpopulation (Halbert et al. 2012:367). These authors warned “[t]hese observations warrant serious reconsideration of current management practices. The continued practice of culling bison without regard to possible subpopulation structure has the potentially negative longterm consequences of reducing genetic diversity and permanently changing the genetic constitution within subpopulations and across the Yellowstone metapopulation” (Halbert et al. 2012:368). NPS biologists noted “[t]he data and findings of Halbert et al. (2012) are significant and useful for managers charged with conserving these iconic wildlife. However, their article provides information regarding the behavior and management of Yellowstone bison that does not accurately portray historic or current conditions [after Halbert’s sampling ended in 2003]” (White and Wallen 2012:1).

White and Wallen (2012) conveyed three main points in their response. First, the human relocation of plains bison from northwestern Montana into the Lamar Valley and Mary Mountain area of Yellowstone (circa 1909 and 1936), with a different genetic lineage than the indigenous bison that spent winter in the Pelican Valley of Yellowstone, created population substructure and regional genetic differentiation in Yellowstone bison. Second, bison movements have changed since 2005, with substantial dispersal of bison from central to northern Yellowstone. As a result, there is increasing evidence Yellowstone bison now conformed to a single intermixing population with breeding and gene flow between bison originating in central and northern Yellowstone (Wallen and White 2015). Third, these biologists recommended the NPS allow ecological processes such as natural selection, migration, and dispersal to prevail and influence population and genetic substructure in the future, rather than actively managing to perpetuate a substructure artificially created by humans.

Furthermore, NPS biologists indicated they had not continued to cull bison without regard to possible subpopulation structure. To the contrary, they had cautioned in 2011 that large culls could affect the demography of the population because they “differentially affected breeding herds and altered gender structure, created reduced female cohorts, and dampened productivity” (White et al. 2011:1322). In addition, other geneticists indicated large removals could reduce generation time, which is how rapidly individuals produce surviving offspring, and competition among males for breeding opportunities (Pérez-Figueroa et al. 2012). As a result, NPS biologists recommended several adaptive management adjustments that could be implemented to enhance the conservation of Yellowstone bison, including the avoidance of frequent large culls greater than 1,000 animals. This recommendation has continued to date with an annual objective of removing fewer than 25% of the population and less than 1,000 animals per winter, focusing on the northern breeding herd which had grown substantially since 2005. Biologists also recommended maintaining more than 1,000 bison in the central and northern breeding areas to help protect any existing unique diversity or rare alleles (genes) within each area (Geremia 2021; see also the *Adaptive Management* section of *Actions Common to All Alternatives*).

In response to these cautions (White et al. 2011, Halbert et al. 2012, Pérez-Figueroa et al. 2012), the IBMP partners adjusted adaptive management and operations plans to reduce the shipment of large numbers of bison to slaughter and use other tools such as hunting and quarantine to regulate bison numbers and conflicts with cattle and humans. NPS biologists intensively track the demographic status of bison in the central and northern portions of YNP and provide annual updates to the IBMP partners, treaty hunting tribes, and the public (see <http://ibmp.info/library.php>). They track the movements of bison through the year using GPS radio collars and aerial and ground surveys and try to limit the capture of bison from central YNP based on this information. Hazing of bison near the northern and western boundaries of YNP has decreased substantially since 2015 when the Governor of Montana increased tolerance for bison in the state (Table 3, Bullock 2015). Since 2017, NPS biologists have recommended no management removals or state and tribal harvests of bison in the western management area in Montana. Bison migrating west of the park during winter are almost entirely from the central breeding herd which has decreased in abundance. Management captures and removals have not occurred along the western boundary since 2010, but state and tribal harvests continue in nearby areas of Montana. Captures for shipment to slaughter near the northern boundary of YNP (which can include some bison from the central breeding herd) did not occur during winters in 2009 through 2013 or 2021. Captures of bison for slaughter near the northern boundary during 2014 through 2020 ranged between 100 and 700 bison.

Continuing current management in this manner should not reduce genetic diversity or change the genetic constitution of the population. During 2011-2012, geneticists identified 10 different mitochondrial DNA haplotypes in Yellowstone bison and an overall haplotype diversity of 0.78, indicating a healthy diverse population (Forgacs et al. 2016). Yellowstone bison should retain this diversity for centuries if numbers average at least 3,000 to 3,500 and there is intermixing and gene flow between bison from the two breeding herds (Pérez-Figueroa et al. 2012). More than 1,000 bison congregate in both the central and northern regions of YNP during the breeding season, where hundreds of mature males compete for breeding opportunities. Also, male bison are much more mobile on the landscape than females and it is possible they attend multiple breeding areas during the same season. In addition, studies indicate a high portion of adults produce offspring during their lifetimes (Herman et al. 2014). The NPS will continue to collaborate with geneticists to develop tools and conduct research as described above. They also will continue to monitor the demographic and genetic status of bison in the central and northern portions of YNP and recommend adaptive management adjustments as necessary.