Reassessment of Genetic Diversity in Yellowstone bison: A study plan for 2018 to 2020

Introduction: Advancement in technology allows the park to consider new methods for collecting a sample of tissues from Yellowstone bison to describe the genetic characteristics of the population. Many species now require benign human interventions to improve the management and ensure their survival (Frankham et al. 2002). Genetic monitoring allows the NPS to evaluate the evolutionary potential of the population and judge how past and current management practices may affect long term persistence. Monitoring is best if implemented every one or two generations of the species of interest. The purpose of this project is to inform managers of current status, provide good information to defend the agency against litigation, and help the American public prevent the listing of this population as threatened or endangered.

Debate: Is there two populations of Yellowstone bison or just one, and if there are two should you protect 3000 bison in each population? Should the distribution of northern vs central area bison be allowed to overlap and allow management actions to affect both groups at the same time?

Halbert et al. (2012) suggested evidence of cryptic population subdivision, e.g. multiple genetic groups embedded within the two genetic clusters her data describes. Additionally, Olexa and Gogan (2007) argued that the population was spatially structured in to two groups based on their radio marking data and very little overlap existed between northern and central area bison. Plaintiffs in WWP et al. vs. DOI/NPS et al. (2009) argued two populations means you have to manage each under separate guidelines and protect each from emigration to the other distribution. Plaintiffs lost this litigation and subsequently petitioned the U.S. Fish and Wildlife Service to list Yellowstone bison as Threatened under the protection of the Endangered Species Act based on the above genetic and spatial evidence that suggests two separate and distinct clusters of bison.

Objective: Determine 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 to in the winter months.

Previous Findings: Four primary genetics based studies have been done to describe the state of genetic diversity and the conservation issues surrounding long term preservation of Yellowstone bison. Natalie Halbert published her Phd Dissertation in 2003 having collected tissue samples from bison during winter months from 1997 to 2003 and determined microsatellite allele frequencies for all of the animals she sampled. She reported that Yellowstone bison have high diversity values (He, Ho And Ar) compared to other public herds of bison. She subsequently published additional results from her sample collections in 2012 to describe the differences in genetic diversity values between the northern and central herds of Yellowstone bison. Her results note two distinct genetic clusters each focused on the unique breeding areas of the northern and central ranges of Yellowstone with a relatively small proportion of individuals exhibiting intermediate allele frequencies compared to those identified for northern and central Yellowstone bison. Florence Gardipee published her Master’s Degree in 2006 having collected fecal samples to determine the mtDNA haplotype frequencies for the animals sampled on the central and northern ranges during the summers of 2005 and 2006. She reported distinctly separate haplotype frequencies for each of the two ranges she sampled. Andres Pérez-Figueroa published the results of a model to investigate how effective population size estimates are affected by fluctuations in population abundance and male reproductive success. He reported that maintenance of a population of 2000 to 3000 bison should preserve genetic diversity values in the bison population for 2 centuries. David Forgacs published a paper describing new information about the mtDNA haplotype distribution within Yellowstone bison. He reported a total of 9 haplotypes in a sample of 25 Yellowstone bison by sequencing all 16,700 base pairs of the mtDNA genome, and found that 68 % of the animals he collected samples from could be grouped in to two haplotypes, similar to previous studies. However, his data set acknowledges that there is roughly equal distribution of those two haplotypes on both the northern and central ranges of Yellowstone.

There are other findings from these previous studies but these are the pertinent details to inform the background and justification for the objectives of this current study. Halbert and Gardipee both suggest there were significant differences in genetic indices calculated for the northern vs the central range bison in the time period prior to 2007. Some interpret that to mean there could be two distinct populations of bison in the headwaters of the Yellowstone River and those distinctions should be protected from change. White and Wallen (2012) noted that there were indications in ongoing studies of bison movements and migration that suggested the Yellowstone bison population may be changing habits from being more stationary regarding occupation of central vs northern ranges (Olexa and Gogan 2007) to being more mobile on the landscape than previously known (Geremia et al. 2014). They noted strong evidence of routine migration to the northern range from the central range during winter months and return migration during the spring, and early evidence of emigration between ranges and successful reproduction of individuals on both breeding areas. Finally, the NPS perspective considers Yellowstone bison as representing a single population with multiple breeding areas and easy opportunity for individual bison to move about between breeding areas at their own choosing, especially males that are much more mobile on the landscape. We can not dismiss the possibility that males may attend multiple breeding areas in the same breeding season. Changes in population level genetic diversity indices due to genetic drift, natural selection and gene flow are all ecological processes important to NPS preservation values.

Controversy regarding management practices at Yellowstone National Park has led to critics suggesting a reduction in management related mortality from winter time boundary actions (hunting and capture/ship to slaughter). Litigation to have current management practices halted have failed and subsequently conservation groups have called for listing of Yellowstone bison as threatened under the Endangered Species Act protections. Critics on the opposite side of the debate argue that there are too many Yellowstone bison and the population should be reduced to less than half the current abundance (2000 bison). Long term monitoring of genetic diversity indices will provide data to correlate with management actions and changes in abundance and distribution of the bison population.

Proposed Methods: We propose to collect bison tissue samples and sort them in to four groups of 50 samples. Two groups will represent the summer breeding areas (northern range vs central range), and two groups will represent the winter distribution of Yellowstone bison (north boundary vs. west boundary). The proportion of each sample group, that 50 samples represents, is variable and further discussion is proposed to consider whether additional samples will be needed for northern range estimates (both summer and winter). Once samples are procured they will be shipped to Texas A&M University for processing. DNA will be extracted and each sample will be genotyped to determine the haplotype of mtDNA and a 200 SNP genotype for nuclear DNA. After genotyping each of the samples, data analyses will estimate typical genetic diversity values (He, Ho and Ar) 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 summer vs winter collected samples.

Tissue samples can be collected a variety of ways. During winter capture operations, blood can be collected on FTA blood stain cards. Additionally, this could be done by encountering hunters in the field and collecting blood on FTA cards and /or collecting a fingernail size piece of hide and hair from remnant pieces of the carcass that the hunter allows us to collect. The third method would be use of biopsy darts to collect skin and adipose tissue. Blood cards and hide tissue collections will be dried and labeled immediately after collection. Biopsy tissues will be stored in 1 or 2 ml cryovials with 90% alcohol solution immediately after collection and labled.

Final questions that need to be addressed before field implementation:

1. Is there spatial clustering of bison on smaller scales than the northern vs the central ranges during the summer and winter time periods? If so, we should sample them appropriately.
2. Thus, a cluster analysis of spatial data is being undertaken by collaborators at UWY to identify whether GPS data suggests any sub range spatial clustering in either summer or winter. Preliminary information could be available to inform our sampling strategy in summer 2018.
3. We have FTA blood cards from numerous radio marked bison that are part of our ongoing movements studies. Should we use these bison simply to inform the spatial cluster assessment or is it reasonable to include the genetic data from these individuals as part of our 50 ish samples for each study group?
4. What is the appropriate time scale to collect samples from. A period of collection from a 3 to 4 year time frame will focus data on ½ of a bison generation and most literature suggests that population level genetic data is unable to detect units of change between years and may not be able to detect units of change between successive generations. It is feasible to collect biopsy dart samples up to 5 or 6 per day, possibly up to 10 if the breeding area groups are relatively concentrated. Thus, it is likely that field sampling would take a team of 2 or 3 about 15 to 20 days to collect all of the samples. Summer range concentration occurs from early July to late August in to September in Lamar Valley, Cache Calfee Ridge Top, Mirror Plateau, and Hayden Valley. Late migrants back to Hayden Valley have sometimes not arrived until early/mid July. Thus it is not recommended to sample from Blacktail Deer Plateau earlier than late July because it is possible to have either northern or central breeders in this area at that time. There is also evidence that northern range bison can end up in Hayden Valley for short periods of time in late summer and autumn. So completion of sampling for summer distribution should be limited to the mid July to early September time period. There is no doubt that summer collections should be made in Hayden Valley, Lamar Valley, Little America, Cache Calfee and Mirror Plateau. Whether there are other locations to be sampled could be informed by the spatial clustering analysis being done by UWY.

Literature Citations

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