



A Metapopulation Strategy to Support Long Term Conservation of Genetic Diversity in Department of the Interior Bison



Bison at Rocky Mountain Arsenal National Wildlife Refuge in Commerce City, Colorado
USFWS / J. CARR

A metapopulation strategy to support long term conservation of genetic diversity in Department of the Interior bison

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Abstract

Once numbering in the tens of millions, plains bison (*Bison bison bison*) were nearly driven to extinction with only a few hundred individuals remaining by the late 19th century. Plains bison have since recovered to approximately 20,000 animals managed in conservation herds throughout North America, yet substantial challenges to their recovery remain.

The Department of the Interior (DOI) is working with diverse partners to steward approximately 11,000 bison in 18 conservation herds across 12 states. Most herds exist in areas without native predators, and removals are required to keep herd sizes at or below carrying capacity. The loss of genetic diversity within bison, and the fact that most DOI herds are relatively small and isolated from each other with no opportunity for natural gene flow, raises concerns about maintaining genetic diversity over the long term. Connecting populations through gene flow (i.e., creating a metapopulation) can minimize loss of genetic diversity, both within and across populations.

Management of DOI bison conservation herds has historically varied across bureaus and conservation units. Adopting a national perspective on bison conservation was identified as a priority in the [2008 Department of the Interior Bison Conservation Initiative \(BCI\)](#). The concept of metapopulation management as a potential tool to maximize the conservation of genetic diversity among DOI herds was first described in this 2008 Initiative and was specifically encouraged in the 2010 DOI Bison Conservation Genetics Workshop report (Dratch and Gogan 2010). In the [2020 BCI](#), the DOI re-affirmed its commitment to conserving bison as native, North American wildlife.

This document establishes a framework for a nationally coordinated strategy for bison managed by the DOI to support the genetic conservation goals outlined in the 2020 BCI. This is a decision-making framework that guides managers through the process of determining when and how to consider translocations. Decisions and actions within the framework are informed by analysis and interpretation of data housed in an integrated, relational database that will be initially populated with the most current data and updated annually thereafter. It provides science-based guidance on how to conserve DOI bison genetic diversity through strategic translocations, while also considering cattle introgression and bison health. We illustrate how this Strategy can be used to guide the establishment of new conservation herds and discuss what it means to be a DOI partner. Finally, this is intended to be used as a living document that will evolve as needs and technologies change.

1 Introduction

Bison (*Bison bison*) are the largest land mammal to survive the late Pleistocene collapse of megafaunal species assemblages in the Western Hemisphere (Reynolds et al. 2003; Barnosky et al. 2004). They once numbered in the tens of millions in North America, with two subspecies, plains bison (*Bison bison bison*) and wood bison (*Bison bison athabasca*) occupying a range that extended from modern day northern Mexico to Alaska, and from the Great Basin to Appalachia (Hedrick 2009; List et al. 2007; Shaw 1995). Bison contributed to healthy grassland ecosystems as their grazing and wallowing behaviors created a variety of habitats that supported high biodiversity (Freese et al. 2007; Knapp et al. 1999; Sanderson et al. 2008).

By the late 1800s the species was nearly extirpated by humans, with fewer than 1,000 animals remaining. Through the efforts of conservationists over a century ago, the species survived and began to recover. Today there are approximately 20,000 plains bison and 11,000 wood bison managed in more than 60 conservation herds across North America (Aune et al. 2017), all descendants from small remnant groups of wild bison, most of which were brought into captivity in the late 1800s.

Continued stewardship by government agencies, Tribes, non-profit organizations, and private conservationists has brought this species back from the brink of extinction, but considerable conservation challenges remain. Most conservation herds are small, geographically dispersed, and remain largely isolated from one another. This isolation is enforced by the perceived incompatibility of wild bison herds with current land uses, differences in the legal status of bison across jurisdictional and political boundaries, and concerns over disease transmission between bison and livestock. Additionally, bison were crossbred with cattle in the early stages of recovery, resulting in the introduction of some cattle genetic material in bison during the establishment of many conservation herds (Halbert and Derr 2007; Stroupe et al. 2022). Further, all extant bison are reported to originate from fewer than 1,000 plains and wood bison representing only a small fraction of historical populations, likely with loss to global genetic diversity (Ball et al. 2016; Coder 1975). Wood bison occur primarily in Canada, are not currently managed by the Department of the Interior (DOI) and are therefore not included in this Metapopulation Strategy (also referred to as the “Strategy”).

In the United States, DOI is currently working with diverse partners such as Tribes and states to steward approximately 11,000 plains bison across 12 states in 18 “conservation herds” (Appendix A). Most DOI plains bison herds are relatively small (fewer than 1,000 with some herds less than 100) with little or no natural connectivity among them. All DOI plains bison likely descend from fewer than 100 individual founders protected in the original captive herds, along with roughly 25 plains bison remaining in Yellowstone National Park (Coder 1975). As such, maximizing retention of the remaining genetic diversity for plains bison is essential for conservation efforts. Small populations lose genetic diversity much faster than large populations (Lacy 1987) and isolation makes matters worse as genetic drift (i.e., random loss of genetic diversity in small populations) can be a strong driver of genetic diversity loss (Allendorf et al. 2022). Connecting populations through gene flow can minimize loss of genetic diversity, both within populations and across groups of populations. The concept of a metapopulation—or a group of populations that are connected by occasional gene flow

(Hanski and Gilpin 1991)—has been explored and validated in natural systems (Carroll et al. 2020; Wendt et al. 2021) and serves as an excellent model for actively managed species like plains bison with a need to retain genetic diversity.

Management of DOI bison conservation herds has historically varied across bureaus and conservation units over time, with a national perspective on species conservation identified as a priority in the 2008 DOI Bison Conservation Initiative (BCI). One of the key actions recommended in the 2008 BCI was to explore the concept of metapopulation management as a tool to maximize genetic diversity among DOI bison herds, supporting evolutionary potential for this species. Here, we use the term “DOI bison metapopulation” to refer to the concept of a collection of bison conservation herds (local populations) managed by the DOI for the primary purpose of bison genetic conservation, within which some degree of animal movement among herds is facilitated by managers to enable gene flow to improve or maintain genetic diversity of local populations and the overall metapopulation (i.e., to minimize inbreeding and loss of genetic diversity due to drift). Based on a review of DOI bison conservation genetic resources (Dratch and Gogan 2010), followed by research demonstrating the conservation benefits of managing DOI bison across bureaus (Hartway et al. 2020), the Secretary of the Interior reaffirmed and expanded the Department’s commitment to a national strategy for bison conservation through the 2020 BCI. Key tenets of the 2020 BCI included 1) conserving bison as healthy, native North American wildlife, 2) employing an interagency, science-based approach to genetic management, 3) engaging in shared stewardship with states, Tribes, and other stakeholders, 4) establishing and maintaining large, wide-ranging bison herds to shape healthy and diverse ecological communities through processes of natural selection, and 5) providing opportunities to restore cultural connections to bison for all people.

Here, we establish a framework for a nationally coordinated strategy for bison managed under the authority of the DOI to support the genetic conservation goals outlined in the 2020 BCI. This Metapopulation Strategy provides science-based guidance on how to conserve DOI bison genetic diversity through strategic translocations, while also considering cattle introgression and bison health. We acknowledge that molecular technologies continue to change, and we developed this Metapopulation Strategy to be an adaptable, living document. Here, we use the best tools currently available to provide information about each herd. This Strategy is flexible and will be updated in the future to incorporate new information and types of data as they emerge.

2 Genetic Diversity

Loss of genetic diversity is a primary threat to the viability of species such as bison, who have undergone a bottleneck event and whose range has become increasingly fragmented (Halbert and Derr 2008; Wilson et al. 2023). Considered to be the raw material of evolution, genetic diversity influences fitness, extinction risk, and evolutionary potential (Hoffmann and Sgró 2011; Lacy 1997; Lande 1988). The genetic diversity of a population increases through the gain of alleles (i.e., genetic variants) through mutation or immigration and decreases due to the loss of alleles through genetic drift (Wright 1931). Genetic diversity of a species or population is typically measured by quantifying allele frequency distributions (frequency of unique genetic variants at a certain location or across multiple locations in the genome), allelic diversity (average number of alleles at one or across multiple locations), or heterozygosity (H_e ; proportion of individuals with two variants instead of one at a location or averaged across locations). Changes in the demographics of a population, such as a change in abundance or a skewing of the sex ratio, are first reflected in allele frequency distribution, then by allelic diversity (e.g., allelic richness [A_r] or allelic diversity for a standardized sample size), and finally by changes in H_e (e.g., expected H_e ; Schwartz et al. 2007; Spencer et al. 2000). Thus, while genetic monitoring systems tend to use both A_r and H_e as measures of genetic diversity (e.g., Zimmerman et al. 2023), A_r is a more sensitive metric and can provide an earlier warning of diversity loss.

2.1. Population Viability Analysis

In 2020, the DOI published the results of a population viability analysis (PVA) that evaluated and projected the effects of several management scenarios on the genetic diversity and population viability of DOI bison herds (Hartway et al. 2020). This PVA built upon the work of previous studies of empirical measures of nuclear and mitochondrial genetic diversity, herd relatedness, and cattle introgression for DOI bison (Halbert et al. 2005; Halbert and Derr 2007; Halbert and Derr 2008; Ward et al. 1999). The PVA study had three primary objectives:

1. To collect standardized, up-to-date genetic, demographic, and management data on 16 DOI and two Parks Canada herds (collectively simplified and hereafter referred to in this section as “federal herds”), to assess existing genetic variation within and between herds;
2. To use the genetic, demographic, and management data to develop and parameterize individual-based simulation models to project the long-term viability of each bison herd under current management practices; and
3. To use these simulation models to evaluate the effects of alternate metapopulation management strategies with varying levels of genetic exchange (translocations) between herds to ensure the long-term viability of federal bison.

The PVA identified considerable variation in the level of genetic diversity within, and significant genetic differentiation among, existing federal bison herds. Genetic diversity within herds generally corresponded with known herd foundation and augmentation histories, combined with the expected effects of genetic drift. The PVA also confirmed that all federal bison herds would lose genetic

diversity under current management conditions without additional gene flow. Herd size was the most important driver of genetic diversity loss, though the effect of herd size was modulated by the effect of the removal strategy used to manage herd abundances. Overall, herds with greater than 500 animals lost modest amounts of genetic diversity (3–7% decrease) over the 200-year modeled timeframe, while smaller herds (<100 animals) lost considerable diversity (34–81% decrease) over that time, with correspondingly large increases in mean inbreeding levels.

Small, isolated herds lose genetic diversity more quickly than larger herds through the process of genetic drift, which in turn can decrease the viability of populations through an accumulation of negative traits from inbreeding and loss of evolutionary potential. While all federal bison herds are at risk of genetic diversity loss, the smallest herds are also particularly vulnerable to extirpation due to random catastrophic events such as disease outbreaks or extreme weather events. In addition to managing herd size, the PVA found that removal strategies that maintain even sex ratios, target younger age classes instead of adults during removals, or target genetically overrepresented animals (e.g., bison most closely related to the rest of the herd) can also reduce the rate of genetic diversity loss.

A metapopulation approach to restore gene flow through strategic animal translocations among herds has been shown to mitigate genetic diversity loss in all federal bison herds. The results of the PVA study indicated that translocation strategies vary considerably in their efficacy among federal bison herds managed as a metapopulation, with criteria used to select potential source herds for translocations driving the genetic diversity benefit to recipient herds. Using genetically least-related herds as sources for translocations resulted in the largest gains in genetic diversity for almost all herds, and the PVA identified an optimum translocation frequency (i.e., moving animals into a herd) of 2–3 bison every 7–10 years for larger herds and 2–3 bison every 5–7 years for smaller herds.

In summary, the PVA found that adopting a metapopulation approach through facilitated periodic translocation of small numbers of bison among federal herds can substantially mitigate the negative effects of herd size and geographic isolation. By restoring gene flow, federal managers can promote effective conservation by allowing as many of the forces of natural selection as possible to operate across large populations and geographic scales to support evolutionary processes and adaptation at an ecologically appropriate scale for bison.

2.2 Types of Genetic Data

Genetic data typically consist of characterizations of small stretches of DNA for an individual at certain locations in the genome. Some genetic data are comprised of actual DNA sequences (i.e., reading the series of four nucleotides that make up DNA: adenine, cytosine, thymine, and guanine, frequently referred to as A, C, T, and G) either from the nuclear or the mitochondrial genome. Other types of genetic data (e.g., microsatellites) explore nucleotide variation indirectly by comparing the length of DNA fragments. To date, most genetic data from DOI bison herds used to inform management decisions has been collected from 52 microsatellite loci (i.e., particular locations in the genome) or by sequencing sections of the mitochondrial genome.

Microsatellites are comprised of tandemly repeated sections of nuclear DNA consisting of short sequences of one to six nucleotides, repeated between approximately five and 100 times (e.g., TGA repeated 10 times) at a particular position in the genome (locus). Differences among individuals are measured by the number of times a short nucleotide sequence is repeated at that locus (e.g., a region with TGA repeated 10 versus 11 times will differ in size by 3 bases), resulting in variation in the total length of that repetitive DNA section (i.e., the allele), which can be observed when DNA at a locus is amplified (Tautz 1980; Selkoe and Toonen 2006). Microsatellites have a relatively high but variable mutation rate (Schlötterer 2000), and as a result, a single population may have many different alleles at a given locus. The relatively large number of possible alleles (typically 2–20) per locus allows accurate estimation of population genetic parameters by genotyping 10s of microsatellite loci. Although microsatellites are generally not under selection (i.e., not subject to the mechanisms of evolution), they do provide an estimate of genetic diversity and differentiation across the genome.

On the other hand, mitochondrial sequences are data resulting from DNA amplified and sequenced from the genome housed in the mitochondria, a cellular organelle. The mitochondrial genome is maternally inherited and thus only represents information passed down from mother to offspring. Each unique sequence is considered a haplotype (DNA sequence that contains one or many variants) and is only passed down from one parent (only one copy instead of two). Although much of the previous research conducted using mitochondrial DNA (mtDNA) has focused on introgression of cattle DNA (Halbert and Derr 2007; Polziehn et al. 1995; Vogel et al. 2007; Ward et al. 1999), additional studies have revealed evolutionary history and relationships among herds that may contribute to improved understanding of how historical management affected mtDNA distribution and diversity within and among contemporary bison herds (Davies et al. 2022; Douglas et al. 2011; Ovchinnikov and McCann 2023; Verkaar et al. 2004). Whereas mtDNA is maternally inherited, the Y chromosome is paternally inherited and any variation that may be present is not well characterized in bison. It appears unlikely that the Y chromosome has been introgressed with cattle DNA due to limited reproductive success during early hybridization experiments primarily between female cows and male bison (Hedrick 2009; Ward et al. 2001). Regardless, further understanding of the Y chromosome may yield insights on this topic in the future.

Technological advancements have made sampling larger portions of the genome more accessible for non-model organisms and wildlife (Ellegren 2014; Hohenlohe et al. 2021; Oyler-McCance et al. 2020), leading to a shift in the types of molecular markers used to characterize and monitor some species in support of conservation plans. These new molecular markers involve measuring variation at single nucleotides (i.e., single nucleotide polymorphisms or SNPs) spread throughout the genome. We explored alternatives to microsatellite technology in developing this Metapopulation Strategy and identified several current obstacles to successfully transitioning from using microsatellite-based genetic data to newer methods such as using SNP-based data (e.g., Osborne et al. 2023; Zimmerman et al. 2020). Although details on the challenges and benefits of transitioning to newer technologies in the future are offered in sections below, this Metapopulation Strategy will be initiated with the current panel of microsatellite loci. We anticipate that a shift to more advanced technologies, such as SNPs or whole genome sequencing, will happen in the near future, and we have built the Metapopulation Strategy to be flexible and capable of incorporating this shift.

3 Cattle Introgression

Intentional crossbreeding of bison and cattle in the late 1800s resulted in the presence of cattle DNA in bison herds today. Successful crossbreeding between cattle and bison was difficult to accomplish and is not known to have occurred in free ranging environments (Hedrick 2009). As managers implement the Metapopulation Strategy, it will be important to understand the status of cattle introgression in source and recipient herds, to consider potential consequences of translocations, and to prevent the exacerbation of legacy cattle introgression in DOI bison, both within herds and across the metapopulation. Current tools to inform decisions regarding cattle introgression include microsatellite genotyping at 15 loci with diagnostic cattle alleles (separate from the 52 microsatellite loci used to characterize levels of diversity within bison) and sequencing of a diagnostic region of mtDNA (Derr et al. 2012; Halbert 2003; Halbert and Derr 2008). These current tools can reliably detect cattle mtDNA, yet the absence of cattle-origin alleles at sampled microsatellite loci does not preclude presence of cattle genetics elsewhere in the nuclear genome (Stroupe et al. 2022). Further, the limited number of microsatellite loci ($n = 15$) currently available provide insufficient coverage of the genome to determine that nuclear cattle alleles are absent. Emerging technological advancements, such as high-density SNP assays or whole genome sequencing, may provide better options for the definitive evaluation of nuclear genetics relative to cattle introgression in the future.

Despite the lack of sensitivity of the microsatellite loci in accurately quantifying levels of nuclear cattle introgression, the frequency of detection in wild herds managed by DOI has been reported to be significantly less than in domestic herds (Dratch and Gogan 2010; Halbert and Derr 2007; Hartway et al. 2020; Stroupe et al. 2022). Likewise, cattle mtDNA exist or have existed in only a few DOI bison herds (Derr et al. 2012; Halbert et al. 2005; Halbert and Derr 2007; Hedrick 2009; Ward et al. 1999). The implications of nuclear genetic introgression from cattle, in terms of phenotype, fitness, and ecological interactions, are not well understood, but the presence of cattle mtDNA in bison may cause physiological differences in the animals relative to metabolism, ecology and reproductive success (Douglas et al. 2011; Hedrick 2009).

Until more sensitive diagnostic techniques are available, a conservative approach to addressing cattle introgression in bison could be to utilize the existing molecular tools to inform gene flow with a specific aim of increasing genetic diversity while not increasing the occurrence of identifiable cattle genetics within herds and across the metapopulation. That is, regardless of the selection techniques for transferring animals (e.g., random, targeted), managers would genotype prospective animals to screen for known cattle genetic markers (microsatellite alleles, mtDNA haplotypes) prior to moving those animals to ensure that the translocation would not introduce known cattle variants that are novel to the recipient herd. Application of this simple principle would allow for the advancement of gene flow toward metapopulation management objectives using best-available current tools, while allowing for incorporation of more sensitive quantitative nuclear genomic techniques as they become available in the future.

4 Bison Health

Restoring gene flow among DOI bison herds may be accomplished in different ways, with translocation of live, healthy bison historically considered one of the most efficient and effective approaches. Live animal translocation may preserve multiple aspects of the processes of natural selection, including the ability of the translocated animal to integrate socially and reproductively into the recipient herd to realize the conservation benefit of genetic augmentation. However, translocation of live bison among DOI herds risks the movement of pathogens and parasites from the donor to the recipient herd, as well as possible exposure of the translocated individuals to pathogens, stress, or injury. Some level of pathogen pressure is part of a healthy ecosystem, but risks from the presence of emerging infectious diseases and introduced livestock diseases require strategic health assessments and risk mitigation protocols to facilitate translocation of bison. Comprehensive herd health surveillance programs and knowledge of key diseases and parasites for the donor and recipient herds and surrounding areas are critical components for assessing and mitigating health risks during translocation and can enable more effective and efficient decision-making. Additionally, establishing and maintaining communication among all partners and agency wildlife health programs is essential for continued effective conservation of DOI bison herds.

The DOI Bison Health History and Status Report (Jones et al. 2020) discussed overarching principles affecting bison health decisions in DOI herds and provided detailed baseline information on herd health history and management. This report provides a foundation upon which bison health is considered to successfully meet the goals outlined in the 2020 BCI for DOI bison conservation and restoration. Key points identified in the report include:

1. DOI bison are managed to ensure healthy (i.e., resilient and sustainable populations that have the capacity to cope with disease threats), though not necessarily disease-free, herds of bison that contribute to the conservation of bison across North America;
2. Tools for managing healthy DOI bison may vary with location and across time to ensure that bison health management practices employed by DOI also protect public health and the health of neighboring livestock;
3. Under the authority for wildlife management, the U.S. Fish and Wildlife Service (FWS) and National Park Service (NPS) maintain primary responsibility for management of bison herds on Refuges and NPS Units, with bison managed on other federal lands (e.g., Bureau of Land Management [BLM] or U.S. Forest Service) under delegated authority to respective state wildlife agencies with which those bureaus partner; and
4. The U.S. Department of Agriculture's Animal and Plant Health Inspection Service (APHIS) manages federally reportable diseases of livestock and administers federal eradication and control programs under the authority of the Animal Health Protection Act (7 U.S. Code § 8301). Federal legislation sets minimum standards for disease control, and interstate translocation of bison may be regulated by APHIS to prevent movement and spread of reportable diseases. Federally regulated diseases of bison currently include bovine brucellosis and bovine tuberculosis.

5. State and Tribal departments of agriculture, through their state (state Animal Health Official) or Tribal veterinarians, regulate import of animals into and transport within their states and Tribal lands. State disease testing and reporting requirements may be more stringent than federal requirements.
6. State and Tribal wildlife management agencies may also have importation or intrastate translocation requirements for bison.

The process of disease risk analysis may vary in structure and formality, depending on the needs of bureau health teams to protect donor and recipient bison herds. DOI bureaus are committed to using the best available science through a team approach to develop appropriate bison health surveillance and disease risk analysis strategies to support prioritization of potential source and recipient populations to meet the genetic, demographic, and ecological conservation goals as outlined in the 2020 BCI. We developed a bison health strategy with a specific disease risk analysis framework (refer to section 5.3.6.2 below) to help guide health aspects of bison translocation as they relate to the Metapopulation Strategy. The objectives of the bison health strategy are to: 1) minimize health risks for translocated individuals during capture, holding, transport, and release into recipient herds, thereby maximizing the potential for social integration and reproduction in the new herd; 2) minimize risks of introducing pathogens or parasites into recipient herds that could affect bison population health and conservation; and 3) minimize risks of translocating pathogens or parasites that could affect the health of humans, other wildlife, domestic animals, or the environment.

Conventional animal health tools such as vaccination, treatment, quarantine, and test-and-slaughter may not always be an appropriate or acceptable part of conserving bison as native North American wildlife. Furthermore, many of these conventional health tools rely on disease tests originally developed for use in cattle that have limited sensitivity and specificity for use in bison, creating uncertainty in disease status at both the individual animal and herd levels. To minimize the risk of introducing new or exacerbating existing diseases of concern, strategic and longer-term herd health surveillance programs are needed. Herd health monitoring of both source and recipient herds should be conducted prior to and following translocation, and individuals used to establish new herds or augment existing herds should be carefully selected and evaluated for diseases using appropriate diagnostic tools.

5 Metapopulation Strategy

5.1 Goals

Natural dispersal among DOI bison herds is not possible in most cases due to population isolation and human landscape use. Human-assisted translocation of bison to establish gene flow among herds is therefore required to maximize overall genetic diversity within the metapopulation. This Metapopulation Strategy describes a framework for deciding when, how many, and where bison could be moved to maximize levels of genetic diversity within herds and across the DOI Metapopulation. Specifically, the goals of the Metapopulation Strategy are to: 1) maintain genetic diversity at the metapopulation level, 2) maintain or increase genetic diversity at the herd level, 3) develop monitoring recommendations such that translocations of bison between herds are embedded within an adaptive management framework from the outset, and 4) as possible with current technical limitations, ensure that bison translocations do not exacerbate existing levels of legacy cattle introgression.

5.2 Herd Dashboard

To organize information fundamental to the Metapopulation Strategy, we have developed a bison herd dashboard that is a visual display providing a distilled, snapshot summary of relevant information about each herd in the DOI Metapopulation (Figure 1). Information on the herd dashboard includes measures of genetic diversity, demographics, and cattle introgression, as well as information about translocation history and the status of known federally regulated diseases in each herd.

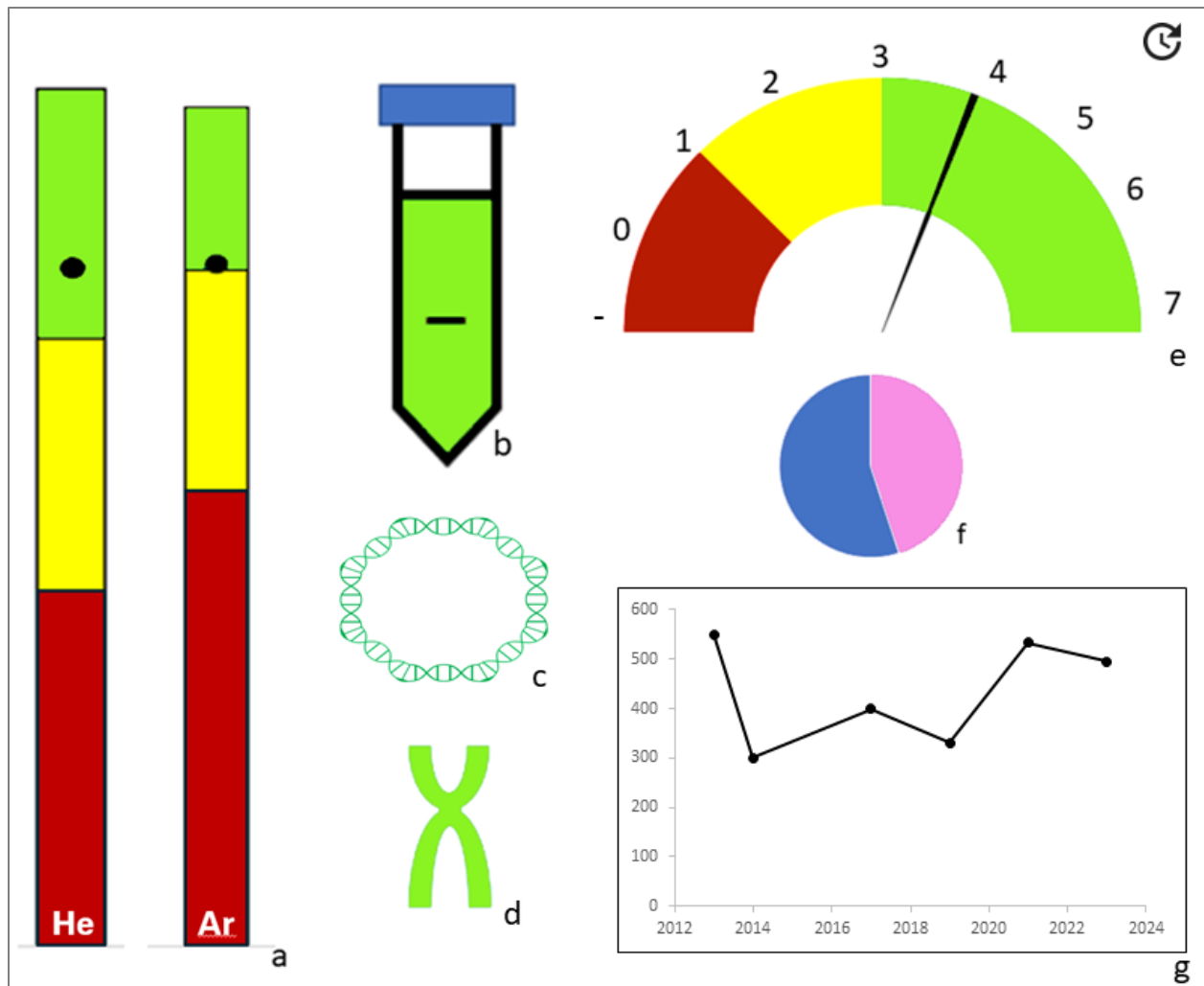


Figure 1. Example herd dashboard displaying current information for a hypothetical Department of the Interior (DOI) bison herd including genetic, demographic, and disease metrics that guide the Metapopulation Strategy decision making framework. The graphics represent (a) estimated metrics of genetic diversity, expected heterozygosity (He) and allelic richness (Ar), with green, yellow, and red representing high, medium and low levels of diversity respectively, (b) presence or absence of a federal program disease with green showing the lack of such a disease, (c) presence or absence of cattle mitochondrial DNA with green representing lack of cattle mitochondrial DNA in the herd, (d) presence or absence of nuclear cattle alleles with green showing lack of cattle alleles present, (e) years remaining until next potential translocation into this herd, (f) estimated sex ratio, and (g) estimated overwintering herd size for the past decade. Clicking on the clock image in the upper right corner will provide a table showing when each of the different data types was last updated. USGS / SARA OYLER-MCCANCE

5.2.1 Measures of Genetic Diversity

We included two different genetic diversity metrics—expected He and Ar. These metrics are calculated from the most recent genetic data collected from each herd and are represented as solid black dots within the “thermometer” graphics (Figure 1a). The colors on the thermometers represent hypothetical high, medium, and low ranges of both expected He and Ar within each herd to compare to current diversity levels. The low (red) range represents very low levels of diversity that warrant

immediate concern for inbreeding depression (i.e., reduced fitness resulting from mating among relatives). For expected H_e , we set this threshold at 0.5 based on previous research (Halbert et al. 2004) and recommendations from the DOI Bison Genetics Report (Dratch and Gogan, 2010). No such threshold has been defined for A_r in bison, so we used the data from the PVA (Hartway et al. 2020) to explore the relationship between H_e and A_r within each herd, utilizing data from the beginning and end of the “status quo” scenario that included no translocations.

In empirical studies where only a subset of individuals is typically sampled, A_r is used to account for sampling effects. In the PVA, however, Hartway et al (2020) used the metric allelic diversity instead of A_r because there was a census of all individuals at the end of the simulation. We therefore converted allelic diversity values from the PVA to A_r to be used for this Metapopulation Strategy. We assumed that our sample size was 100 for this conversion (for detailed methods for this conversion refer to Appendix B). We plotted H_e versus A_r (Figure 2), and we found that all herds with H_e less than 0.5 in this “status quo” PVA scenario also had A_r values less than 3.0. We therefore set this value as a corresponding “low” threshold for A_r in our thermometer (Figure 1a).

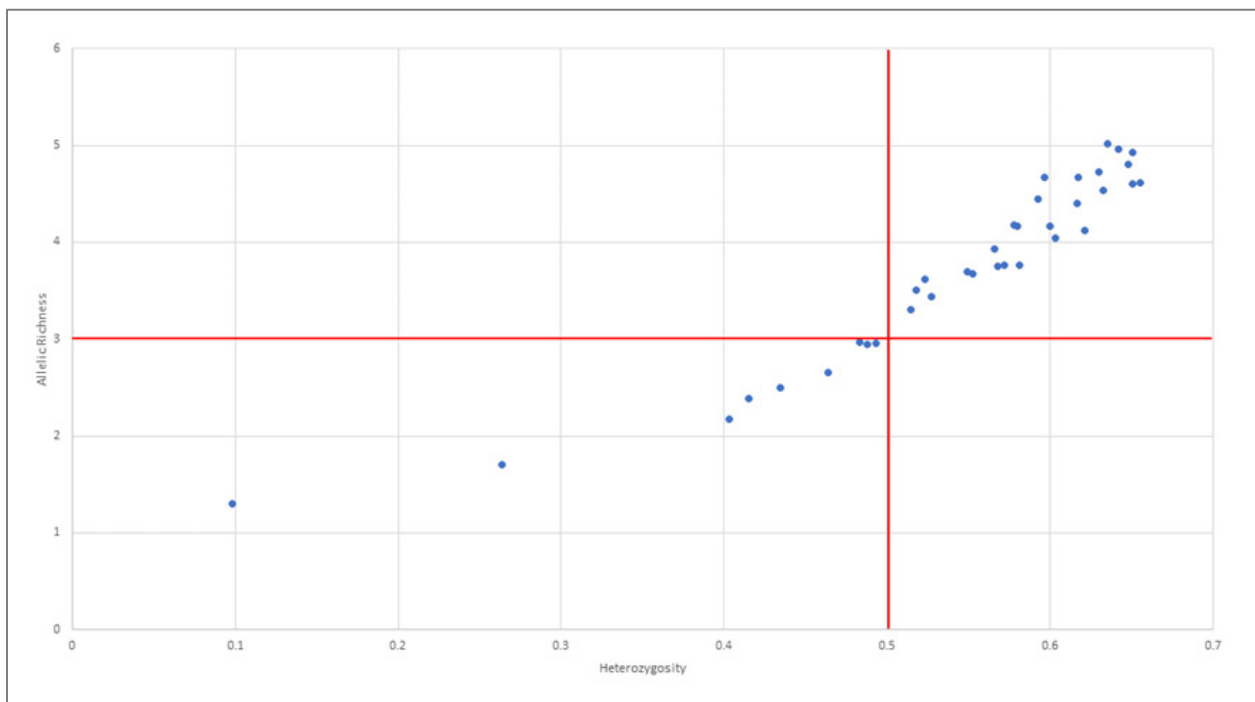


Figure 2. Relationship between heterozygosity (x-axis) and allelic richness (y-axis) in Department of the Interior (DOI) bison herds as simulated in the DOI Population Viability Analysis (PVA) (Hartway et al. 2020). The red lines show thresholds below which there are concerns about inbreeding depression (0.5 for heterozygosity and 3.0 for allelic richness). USGS / SARA OYLER-MCCANCE

The green and yellow portions of the thermometer representing high (green) and medium (yellow) levels of diversity are calculated to be specific to each herd. The highest achievable values of H_e and A_r (the very top of the thermometers) are based on the potential increase modeled in a best-case scenario from the PVA (Source Herd Scenario 1—Genetically Least Related moving 3 individuals

every 5 years). We used output from that “best case” PVA scenario to define the upper bound for He and Ar (converted from allelic diversity, Appendix B) for each herd, and then selected half of the distance to the lower bound (0.50 for He and 3.00 for Ar) to establish the upper bound for the yellow (medium) level. For example, if the highest achievable He for a particular herd was modeled as 0.64, we set the upper bound of the green level based on that 0.64 PVA best scenario modeled value. With 0.50 established as the threshold for low (lower bound of yellow transitioning to red), we then set the upper bound for the yellow level at 0.57 (half the distance between 0.64 and 0.50). We utilized the same process for Ar with the lower threshold at 3.00. Actual current herd diversity values are identified by a black dot located appropriately along the thermometer scale (Figure 1).

5.2.2 Federal Program Diseases

The status of diseases managed or administered by the APHIS under federal eradication and control programs is represented for each herd in the dashboard by a test tube symbol (Figure 1b) colored either green with a negative sign (free of federal program disease) or red with a positive sign (federal program disease present). At present, the only federal program diseases relevant to this Metapopulation Strategy are bovine brucellosis (present in elk and bison in the Greater Yellowstone Ecosystem), and bovine tuberculosis (endemic in some livestock and wildlife populations outside the Greater Yellowstone Ecosystem, with periodic introductions into other geographic areas). Details on federal program diseases and potential effects to DOI bison are found in the DOI Bison Health History and Status Report (Jones et al. 2020). Although other diseases affecting bison are important considerations when translocating animals among herds, federal program diseases present especially complex challenges for animal translocation and are considered earlier in the DOI bison translocation decision process than other diseases.

5.2.3 Cattle Introgression

As noted above (Section 3), cattle introgression is currently evaluated through use of microsatellite markers and mtDNA sequence, and the Metapopulation Strategy characterizes herds based on two metrics: 1) presence (red) or absence (green) of cattle mtDNA (represented by the circular DNA molecule in Figure 1c), and 2) presence (red chromosome) or absence (green chromosome) of nuclear cattle alleles (Figure 1d) detected in each herd. For those herds with nuclear cattle alleles present, the list of cattle alleles will be accessible by clicking the chromosome icon in the dashboard. Although many DOI bison herds have detectable nuclear cattle DNA, newer, more precise methods to quantify levels of cattle introgression are expected to become available in the near future and this metric will be revised to reflect those changes.

5.2.4 Time to Next Translocation

The “gas gauge” graphic (Figure 1e) represents the time until that herd is next recommended to receive a translocation, based on simulations from the PVA (Hartway et al. 2020) that identified an optimal number of animals and an optimal translocation frequency for both small (<100) and larger (>100) DOI bison herds. This optimal strategy (moving 3 animals every 5 years for small herds and 3 animals every 7 years for larger herds) best balances the benefits to herd and metapopulation diversity from the introduction of new genetic material with the potential negative effects of low-frequency allele loss that may occur with large, frequent genetic augmentation. The “gas gauge”

counts down the number of years since the last augmentation with green representing a recent translocation, yellow representing a time to start considering another translocation and red representing a time to actively plan for translocation to genetically augment the herd. Analogous to how one might keep an eye on the fuel gauge in a vehicle, managers have flexibility in planning for translocations. The gauge for small herds ranges from 5 (full in the green zone) to - (completely empty in the red zone), while the gauge for large herds ranges from 7 (full, green) to - (completely empty, red). Note, that much like pulling over at a gas station with an especially good price, managers are encouraged to occasionally “top off the tank” earlier than necessary, and especially if unique opportunities arise that may not be available in future years.

5.2.5 Sex Ratio and Demography

The pie chart graphic represents the current sex ratio of the herd (Figure 1f). Blue represents the proportion of males in the herd and pink represents the proportion of females. Sex ratios have been demonstrated to influence loss of genetic diversity (Gross and Wang 2005) through impacts to competition for mating (i.e., number of males contributing to the next generation), social structure (affecting randomness of mating), and mitochondrial inheritance potential (relative to transmission of cattle mtDNA from females to successive generations). Sex ratio can therefore affect the molecular genetic composition of the herd over time and should be factored into the measured success of herd augmentations when animals are translocated.

Although age structure is also an important demographic consideration for managers, and the results of the PVA identified significant differences in the long-term genetic diversity loss among DOI herds associated with culling strategies of different age classes, these data are not currently included in the dashboard but will be available in the database. Age structure relative to selection of individuals for translocation, as well as to establish a new herd, are discussed in sections below.

5.2.6 Herd Size

The final graphic on the herd dashboard represents the current herd size, as well as trend in herd size for the last 10 years (Figure 1g). This information allows managers to quickly assess the rate of projected genetic diversity loss in their herds based on whether the herd is classified as “small” or “large”, as defined in the PVA and again here in this Metapopulation Strategy. This information can also be used to assess fluctuations in herd size over time that also affect the rate of genetic diversity loss (i.e., greater fluctuation is generally associated with faster rates of genetic diversity loss). The history of yearly estimated overwintering herd size (for as many years as are available) will be accessible through the database for a more comprehensive view of each herd.

5.3 Metapopulation Strategy Decision Support Framework

The Metapopulation Strategy is fundamentally a decision-making framework (Figure 3) that guides managers through the process of determining when and how to consider translocations. Decisions and actions within the framework are informed by analysis and interpretation of data housed in an integrated, relational database that will be initially populated with the most current data and updated annually thereafter. The database will be used to generate the herd dashboard (Figure 1), which graphically presents the status of core genetic, health, and demographic parameters used in the

translocation decision-making framework. This section describes the database and the steps in the decision-making framework (Figure 3).

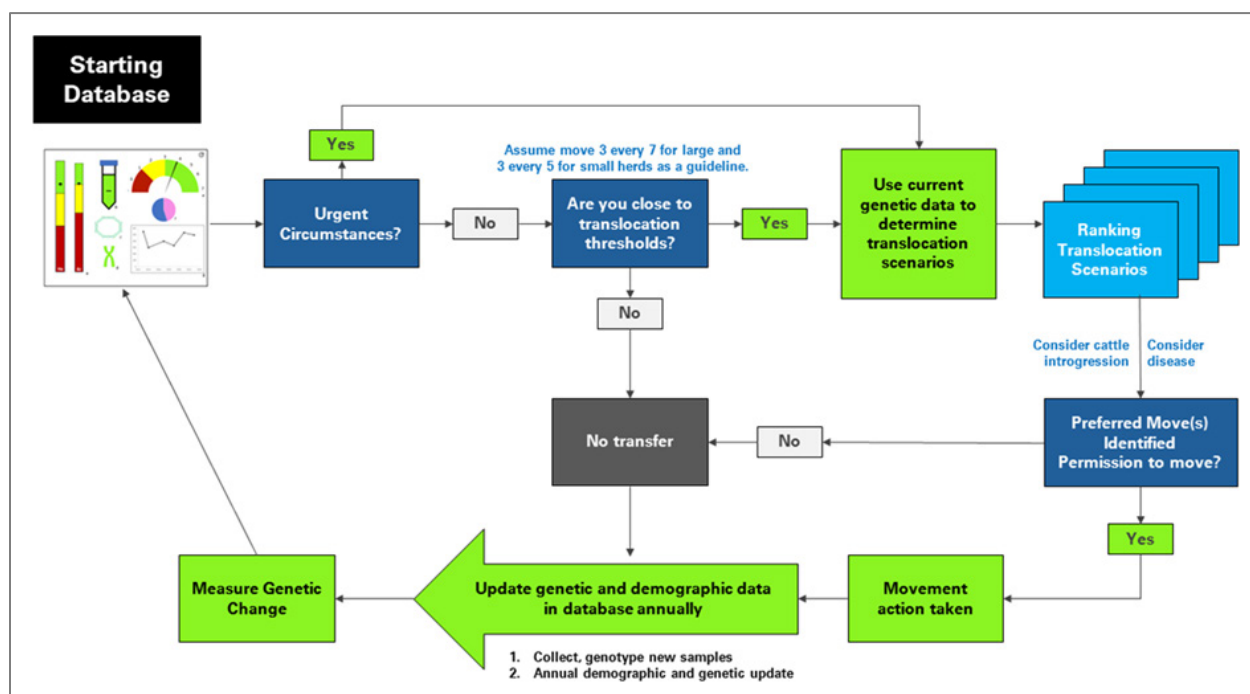


Figure 3. Metapopulation decision framework showing the series of steps and decisions that guide the process of determining when and how to consider bison translocations. USGS / SARA OYLER-MCCANCE

5.3.1 Bison Database

Although each bureau currently has different data management protocols, the five bureaus in the DOI Bison Working Group (NPS, FWS, BLM, Bureau of Indian Affairs [BIA], U.S. Geological Survey [USGS]) have committed to developing a comprehensive DOI bison metapopulation database to support this Metapopulation Strategy. The database will be developed and hosted by USGS. It will house genetic, demographic, and disease information for each herd to directly inform the herd dashboard and other analyses. The database will include both individual and herd-level information. Herd-level data will include information such as herd name/unit, managing bureau, location, and appropriate management contacts. The database will also contain herd-level information on disease, demographics, and genetic summary statistics. Herd-level genetic statistics will include the year, expected H_e , and A_r . Information associated with individual animals will include demographic information (e.g., sex and age), nuclear genotypes and mtDNA haplotype data, as well as laboratory identifiers associated with the tracking of samples and DNA. Individual bison will be referenced using a globally unique identifier to ensure appropriate linkage of samples and data collected. Disease information will vary among herds based on the herd health surveillance history. Finally, the database will hold information about transfer of bison among herds including the unique animal identifier for a bison moved, age (birth year), sex, the year of transfer, origin herd, destination herd, and fate and/or confirmed reproduction if known. In the first year of the Metapopulation Strategy

implementation, the database will be populated with the most up-to-date information (represented by the “Starting Database” rectangle in Figure 3). After the first year, the bison database will be updated on an annual basis.

5.3.2 Current Herd Dashboard

The first step in the Metapopulation Strategy is to populate the herd dashboard (Figure 1) with the most current data available for each herd in the metapopulation. We will populate the starting database with the most recent genetic, demographic, and health data, as described in Section 5.2. The dashboard will be updated annually, yet there may be some years in which a herd does not have new genetic or demographic data. The clock icon in the upper right corner of the dashboard provides a way for a herd manager to click and see when each data type was last updated.

5.3.3 Consider Urgent Circumstances

The next step is to determine whether there are any urgent circumstances affecting a herd. Urgent circumstances might include genetic diversity metrics close to inbreeding thresholds, a drastic reduction in herd size due to disease, wildfire, or other catastrophic event, or information that a previous translocation failed (e.g., death of translocated animal before having the opportunity to breed). Rare opportunities to incorporate unique or novel genetic material that may not be available for future translocations can also qualify as an urgent circumstance. The existence of urgent circumstances negates consideration for time since last translocation, such that the herd may be prioritized to receive translocations more quickly to mitigate the circumstances (Figure 3). If there are no urgent circumstances with the herd (answering “No” to this question), the process of decision-making for this herd moves on to the next node of the flow chart.

5.3.4 Consider Recommended Translocation Intervals

The next step in the decision process evaluates whether the herd is nearing recommended temporal translocation thresholds: moving 3 individuals every 7 years into large herds >100 individuals and moving 3 individuals every 5 years into small herds <100 individuals (Hartway et al. 2020). If a herd is nearing its respective temporal threshold, the herd is identified as appropriate to receive translocations (green square “Use current genetic data to determine translocation scenarios”, Figure 3). It is important to note that the recommended intervals between translocations are flexible, and that managers may consider the timing and logistics of receiving animals (e.g., when a source herd can/will capture animals). Otherwise, the decision-making process moves to the “No Transfer” black rectangle (Figure 3), with no translocation implemented and the decision process moves forward to the next annual evaluation timestep.

5.3.5 Evaluate Translocation Scenarios

Once it is determined that a herd meets the criteria to receive bison via translocations from another herd, the next step in the decision-making process evaluates each possible source herd to estimate the genetic effect of moving 3 bison from each potential source herd into the recipient herd. Information about herd relatedness and the potential genetic benefits of translocation to support this decision is presented in two different ways. Current genetic data are used to calculate relatedness values of the recipient herd to each source herd and displayed in a table from least related to most related. Herd

genetic data are also used to estimate the potential genetic effect of moving bison into the recipient herd from each source herd. To do this, we developed a simulation model (described in detail in Appendix C) to rank all possible donor herds for translocation scenarios in terms of maximum predicted genetic diversity gains. In this model, we first calculate the allele frequencies (e.g., probability of sampling an allele in a herd) for the recipient herd using its current microsatellite data. We then use those data to simulate genotypes for all individuals in the recipient herd (N_{init}) based on its current herd size, as well as 3 individuals randomly selected from a potential donor herd (N_{trans}) that are then added to the recipient herd (Figure 4). We then calculate genetic diversity for the simulated recipient herd before (gd_{before}) and after (gd_{after}) the addition of the 3 transplants and report the predicted gains in genetic diversity ($gd_{\text{after}} - gd_{\text{before}}$). The process is then repeated 1,000 times to estimate an average effect. This allows managers to understand the predicted genetic effect of moving 3 individuals from each potential source herd. This simulation model is simple and ignores population growth, and assumes sex, age-class, and environmental variation will have a negligible effect on genetic diversity change. The database will track measures of genetic diversity gains (e.g., A_r , H_e) along with mean kinship (mK) values. These values are used to identify which herds are preferable as donor herds to increase genetic diversity, before other information (i.e., disease status, cattle introgression) is considered. In a hypothetical example using the White Horse Hill (WHH) herd, we show the predicted change in H_e for WHH by moving 3 bison from any one of the 17 DOI herds in the PVA (Figure 5). In this hypothetical example, selecting pairs of herds that are the least related (smallest mK) predicted the greatest genetic gains (see Figure 5). Each manager and/or designated bureau bison conservation coordinator will be provided with the relatedness table and output from the simulation providing a list of predicted outcomes for each translocation scenario.

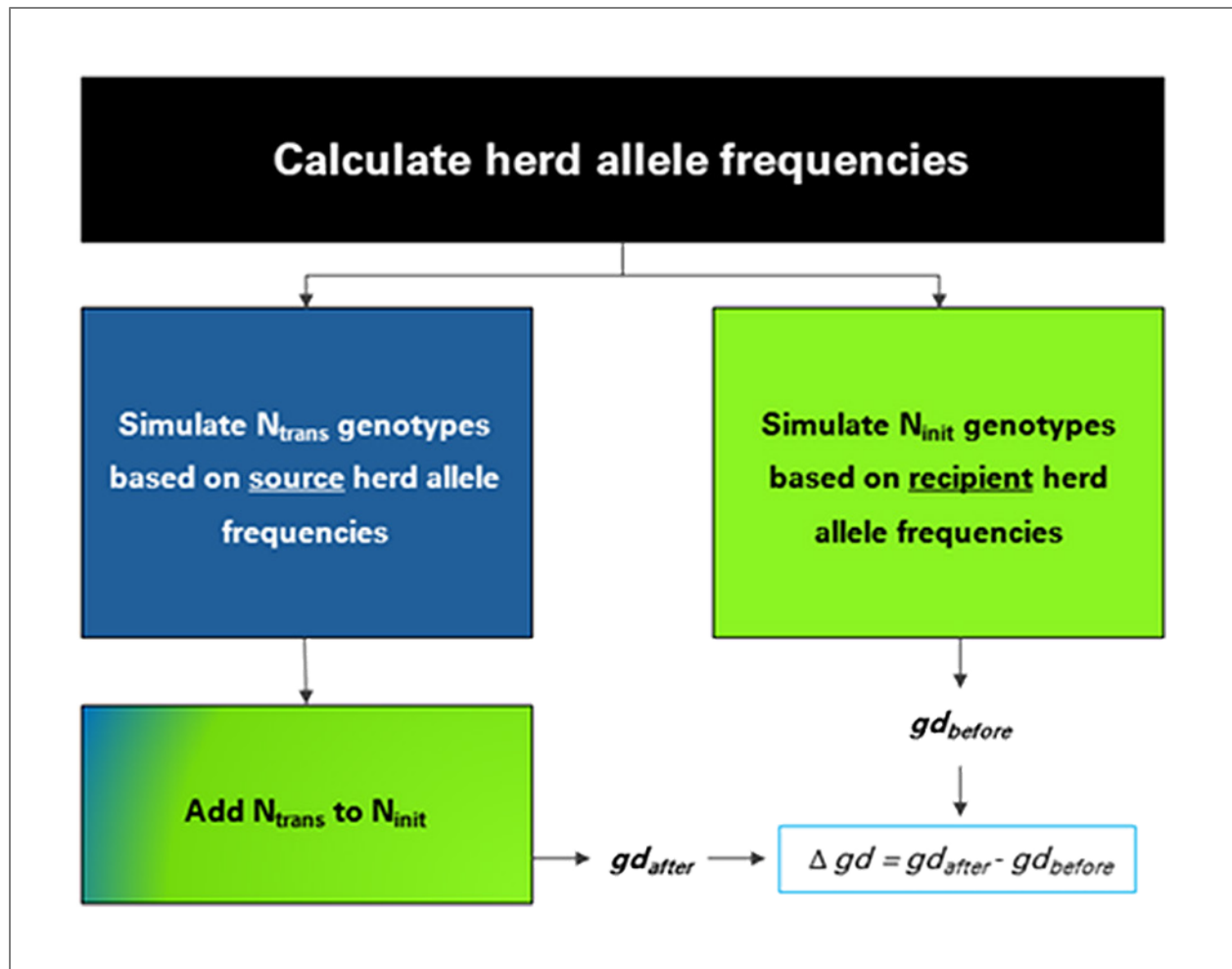


Figure 4. Schematic of our simulation model that begins with microsatellite-based bison herd specific allele frequency distributions that are used to simulate the genotypes of the recipient population (N_{init}) and of animals to be translocated from each potential source herd (N_{trans}). Genetic diversity is then estimated for the recipient herd before (gd_{before}) and after (gd_{after}) the source herd animals are added. The predicted genetic gain (Δgd) is the difference between the genetic diversity before translocation efforts (gd_{before}) and the genetic diversity after translocation (gd_{after}). USGS / SHAWNA ZIMMERMAN

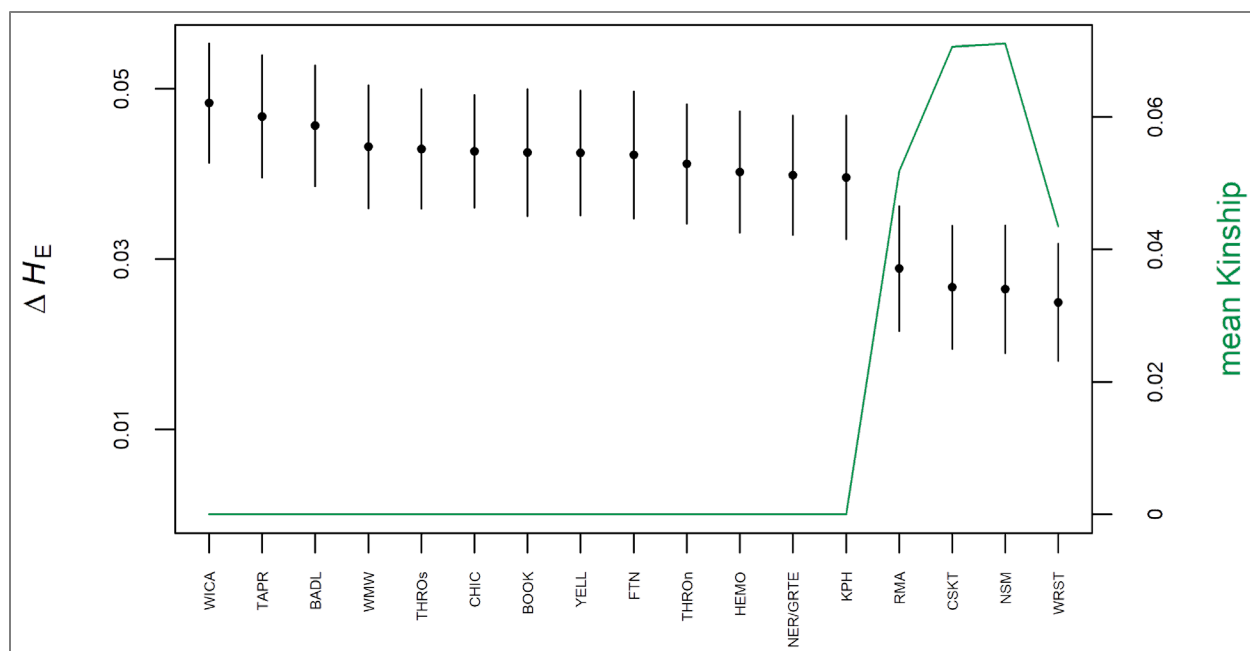


Figure 5. Simulated example showing the predicted change in expected heterozygosity (ΔH_E) for the White Horse Hill Department of the Interior (DOI) bison herd under a scenario of moving 3 animals from each possible source herd. Herds are ordered along the x-axis from those that result in the greatest (left) to the least (right) predicted change. Herds that are more closely related (larger mean Kinship, green line) are predicted to have the smallest genetic change. WICA is Wind Cave National Park, TAPR is Tallgrass Prairie National Preserve, BADL is Badlands National Park, WMW is Wichita Mountains Wildlife Refuge, THROs is the Theodore Roosevelt National Park south unit, BOOK is Book Cliffs, YELL is Yellowstone National Park, FTN is Fort Niobrara National Wildlife Refuge, THROn is the Theodore Roosevelt National Park north unit, HEMO is Henry Mountains, NER/GRTE is the National Elk Refuge and Grand Teton National Park, KPH is the Kaibab Plateau Herd at Grand Canyon National Park, RMA is Rocky Mountain Arsenal National Wildlife Refuge, CSKT is the Confederated Salish and Kootenai Tribes' Bison Range, NSM is Neal Smith National Wildlife Refuge, and WRST is Wrangell-St. Elias National Park and Preserve. USGS / SHAWNA ZIMMERMAN

5.3.6 Rank Translocation Scenarios

The previous step provided predicted outcomes of bison translocations from each source herd into the recipient herd. The next step ranks translocation scenarios by taking into account issues such as cattle introgression and bison health.

5.3.6.1 Consideration of Cattle Introgression

Acknowledging current limitations in cattle introgression detection at the herd and especially at the individual animal level, we recommend characterizing herds as to the presence or absence of nuclear cattle alleles and mtDNA using the 15-microsatellite marker introgression panel and mtDNA haplotype evaluation, which have been used consistently across DOI bureaus (Dratch and Gogan 2010; Halbert and Derr 2008). This information will be displayed in the herd dashboard (i.e., list of cattle alleles present in a herd will pop up if the user clicks on the chromosome icon) and will be available in the database. Until more sensitive techniques become available to detect cattle introgression, managers may wish to avoid introducing animals with known novel cattle DNA

segments into a recipient herd. Prior to translocation, managers would genotype prospective bison to screen for known cattle genetic markers (microsatellite alleles, mtDNA haplotypes) to ensure that the move would not introduce known cattle variants that would be novel to the recipient herd or increase the frequency of existing cattle alleles. As molecular tools advance and more accurate quantification of introgression becomes possible, these recommendations may change to include quantitative values.

5.3.6.2 Disease Risk Analysis

At this stage in the decision framework the potential translocation scenarios are assessed from a bison health perspective. Prioritized translocation recommendations will be provided to the respective bureau wildlife health branches and bison managers to support development of a disease risk analysis for each prioritized translocation scenario.

A disease risk analysis is an evidence-based process that is especially valuable for identifying, prioritizing, and minimizing potential consequences of disease on ecosystems, wildlife, domestic animals, and people in the face of uncertainty (Hartley and Sainsbury 2017; Jakob-Hoff et al. 2014; Travis and Smith 2019). A disease risk analysis for this Metapopulation Strategy seeks to optimize conservation benefit while minimizing disease and other health risks associated with bison translocation. Details on the core components of a disease risk analysis may be found in Appendix D.

5.3.7 Preferred Translocation(s) Identified

Once potential translocation scenarios have been evaluated for effects on genetics, levels of cattle introgression, and disease risk, a vetted translocation (or translocations) will be identified. Decisions significantly outside the scope of the recommendations presented here could negatively affect the conservation value of a herd. Therefore, identifying multiple good translocation options gives managers flexibility in meeting the goals of the Metapopulation Strategy.

5.3.8 Request Approval for Translocation

After consultation with managers from both source and recipient herds, authorizing and key partner agencies (including but not limited to federal, state, or Tribal animal health officials, other state or Tribal wildlife or livestock agency personnel, DOI bureau and herd managers) must approve the decision to translocate bison. While we anticipate that most translocations that have been comprehensively vetted in terms of genetics, cattle introgression, and bison health will be approved, there may be extenuating circumstances that preclude such movements. If the translocation is approved by the authorizing agencies, then it can proceed. If not, lower benefit vetted options may be considered. Alternatively, managers may decide that there will be no transfer that year and the decision framework cycle will continue to the next year.

5.3.9 Translocation Action Taken

Translocations will follow best management practices for the movement of wild, healthy DOI bison. Official identification, as required through state and federal regulatory health authorities for inter- or intrastate transport, should be used for all DOI bison translocations regardless of origin and destination. Minimum standards for official animal identification, as required by APHIS, are described in Appendix E. If more than one method of official animal identification is available, the

receiving DOI unit of translocated bison may choose the official identification method that best meets the needs of that unit, with special consideration for visibility and access by the public for viewing as native North American wildlife. Official ID may be used in addition to any implanted microchip or other methods of individual ID meeting the needs of the bison conservation units. Special tags or marks (such as tattoos, highly visible plastic dangle tags, temporary hair bleach marks, glue-on back-tags, radio-transmitters, etc.) may be required by the state or Tribal animal health authority or may be requested by the manager of the recipient herd or bureau health office. These additional tags or marks may be used to support post-release identification and monitoring of translocated animals.

Although not always required by state or Tribal animal health authorities for animal movement within certain jurisdictions, a Certificate of Veterinary Inspection (CVI) should be completed by a state, federal or accredited veterinarian and accompany bison translocated among DOI herds. CVIs serve as documentation of the final individual animal(s) loaded for transport and provide immediate information to the manager of the recipient herd regarding identification, demographics, and health status of translocated animals upon arrival. Establishing veterinary inspections prior to transport as a DOI Metapopulation standard also upholds DOI's commitment to protecting bison health, public health, the health of neighboring livestock, and to ensure effective and transparent communication among partners and stakeholders.

DOI bison managers and bureau health teams must meet accepted professional standards of animal welfare as applicable to wildlife. In 2017, FWS launched a low-stress handling training program, resulting in a significant decrease in bison injuries associated with the gather, capture, sampling, loading, transporting and release of bison. To support movement of bison among DOI units as recommended in this Metapopulation Strategy, low-stress handling techniques should be implemented, including:

1. Use the minimum number of personnel required to capture, sample, and load bison for transport as key to minimizing bison stress prior to translocation;
2. When possible, avoid transporting animals the same day they are captured from the field as long as they can be safely held overnight in appropriate holding facilities with water and hay or natural forage;
3. Avoid using processed feeds, such as grain, pellets or cubes, which can cause significant gastrointestinal disturbance. Although processed feeds may be used in small amounts as an attractant during capture operations, they should not be used during holding or transport;
4. Hold and transport bison in segregated groups of similar age, sex, size, and behavior to minimize injury. Bison exhibiting aggressive or dominant behavior should be held and transported separately from other bison. If segregation is not possible, aggressive animals should be removed from the translocation group and returned to the herd of origin;
5. Bison transport vehicles should be clean, sturdy, well ventilated, and sufficiently enclosed to prevent bison from seeing outside the trailer during transport. A dark environment with minimal outside visual stimuli reduces stress; and

6. Transport bison directly from origin to destination whenever possible, with no overnight stops or significant delays. Upon arrival of translocated bison, the recipient unit of origin should release bison from the transport vehicle as soon as possible, providing access to fresh water and natural forage. Holding animals in a confined area as part of a “soft-release” effort is generally not recommended unless a specific holding period is required for disease or other management reasons.

In addition to official identification and CVI, state and Tribal animal health authorities may require specific disease tests for bison transport across state lines or special geographic disease surveillance areas. All translocated DOI bison must meet these minimum transport regulations, including required disease testing conducted by a state, federal, or accredited veterinarian. Additional tests for diseases of potential conservation concern, both in translocated individuals and as part of a comprehensive herd health surveillance program, may be requested by the recipient DOI conservation unit (Appendix F).

Timelines for testing and a disease risk analysis will vary depending on the sensitivity and specificity of the diagnostic tests available for the identified disease risks, changes in the risk environment (including disease and/or animal introductions into either the herd of interest or neighboring livestock and wildlife populations), and the availability of previous herd health data. Regular communication and advanced planning with bureau wildlife health programs can facilitate timely testing and selection of the most accurate and appropriate diagnostics. Bureau wildlife health program offices can also work with state and Tribal animal health officials to ensure health requirements are met while avoiding unnecessary testing and holding of animals to protect animal welfare.

Selection of individuals to translocate may vary among herds and may be discussed among managers of source and recipient herds for a translocation. While a group of animals may be set aside from the source herd during bison capture operations for evaluation and consideration for translocation, specific animals may be selected for transport based on anticipated benefit to the recipient herd. Similar to pre-transport disease testing that may be required, obtaining genotypes will allow selection of the individual animals from the source group set aside that will provide maximum benefit to the recipient herd. Young animals may be preferred as they are easier to handle, are less likely to be injured, and are more likely to socially integrate into the recipient herd and successfully reproduce. While males have traditionally been chosen for translocation based on livestock models of producing rapid integration of new genetics under bull rotation strategies, females contribute new genetic material to the recipient herd over a longer period of time, with a higher potential for breeding into older age than males. The possibility of pregnancy in individuals selected for translocation should be considered, both in terms of the benefit of additional sire-contributed genetic material (Wilson et al. 2023) but also in terms of the risk of introducing undetected cattle introgression. Most DOI herds have a low rate of pregnancy in yearling females, with much higher rates in two-year olds. Transporting males greater than two years of age may result in injury during capture and transport, or from aggressive males in the recipient herd. Overall, transporting a combination of yearling male and female bison may offer the greatest chances of successful genetic augmentation for the recipient herd.

Taking into account the considerations discussed above, a potential translocation scenario where three bison are moved might include introducing two yearling females and one yearling male. Once sexually mature, female bison have a high probability of annual reproduction (69% for prime age cows; Mooring and Penedo 2014). Male bison mating success is more variable, and males also generally have higher mortality rates than females (Brodie 2008; Hartway et al. 2020; Mooring and Penedo 2014; Wilson et al. 2002), but individual males may outpace reproductive input of individual females over short time periods when they are successful competitors for mates. Males could potentially contribute introgression-free diversity through the Y-chromosome, although this concept has not yet been clearly demonstrated. Managers introducing mixed sexes may experience lower risk and more predictable outcomes from female introductions while still pursuing higher risk, but potentially higher payoff, introductions of males.

5.3.10 Update Genetic and Demographic Data in Database

Demographic information will be collected and updated after each bison capture operation or translocation, describing which bison remain in each herd (including calves and any bison that have been transferred in) and which bison are no longer present (i.e., those that were donated, translocated out, or died/presumed dead). This information will be tracked and stored in the database. Additionally, each time bison are handled (i.e., yearly or every other year), new samples will be collected for genetic analysis. These samples can consist of whole blood, tissue, hair, and/or blood cards and will target all (or as many as possible) bison that have not previously been sampled. Samples will be sent to a centralized location (USGS Fort Collins Science Center) for storage and subsequent genotyping. All samples from small herds (<100 animals) will be genotyped. In larger herds (>100), a random sample of at least 100 new individuals will be genotyped after each sampling year. New genetic data will be uploaded into the bison database reflecting up-to-date genetic information for each herd based on the set of individuals known to be present in each herd. This information will be used to calculate current metrics of genetic diversity for each herd and will be used to populate the herd dashboard for the following decision cycle.

5.3.11 Measure Genetic Change

Each year, demographic information in the database will be used to identify bison known to be alive that year within a given herd. All genetic data associated with those individuals will be used to estimate current H_e and A_r . Not all individuals known to be alive may have genetic data associated with them, but diversity estimates will be calculated for all bison that do. These diversity estimates will be shown in the herd dashboard in the thermometer graphics. In addition, each herd will have a figure tracking genetic diversity metrics through time (Figure 6). The starting point for this figure will be values estimated by Halbert and Derr (2008) if available, followed by levels of diversity calculated at the time of the PVA (Hartway et al. 2020). Arrows indicate when translocations into that herd have occurred. The figure will also show predicted loss of diversity from the PVA with no augmentation (blue dotted line), as well as predicted optimum levels of genetic diversity (green dashed line) under the best-case scenario in the PVA (Hartway et al. 2020). This will allow managers to assess current levels of diversity compared to “do nothing” and “best-case scenario” as outlined in the PVA. Actual change in diversity will be calculated from the starting point of the PVA to the current estimate.

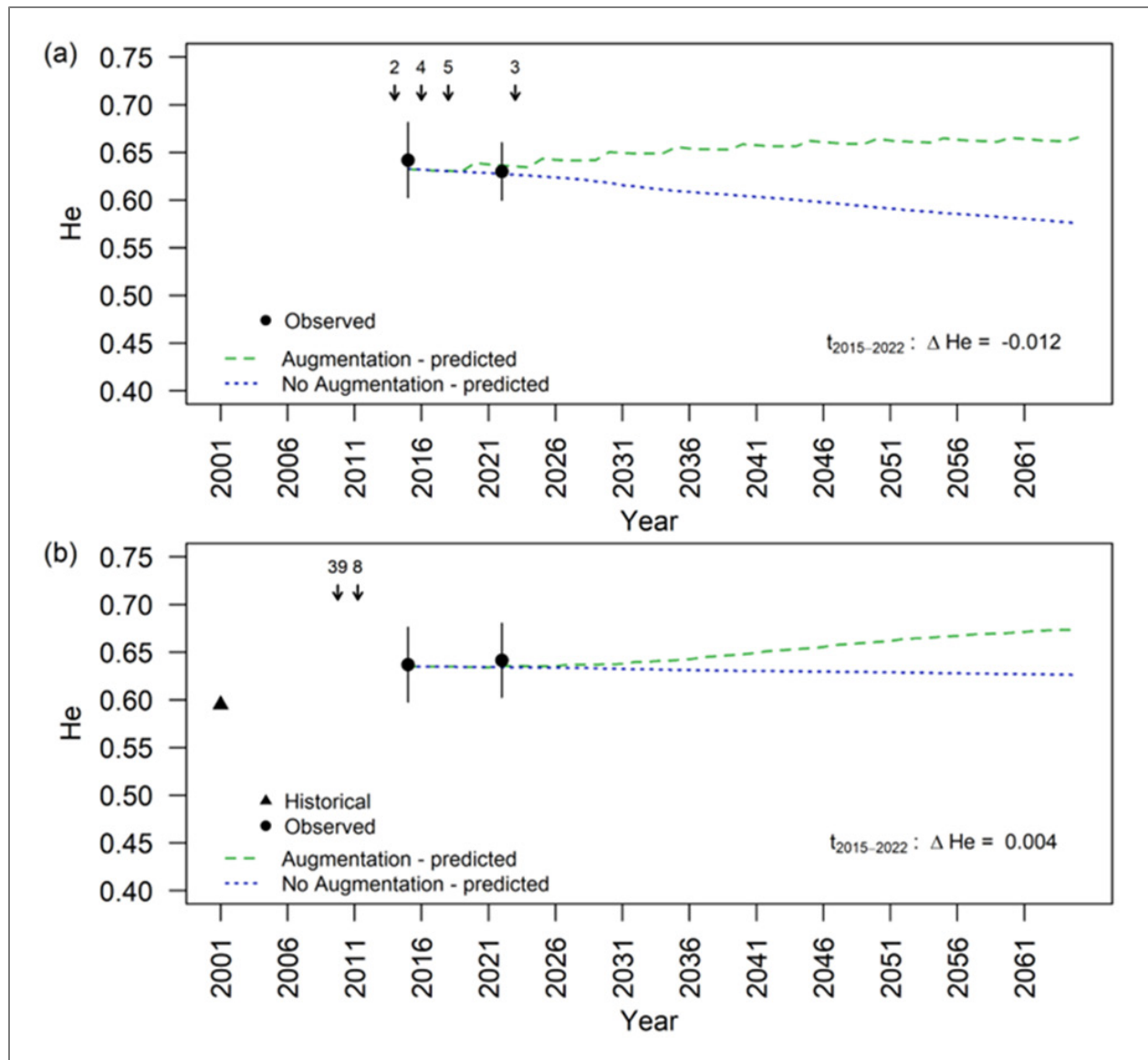


Figure 6. Genetic change in expected heterozygosity (H_e) for two Department of the Interior (DOI) bison herds through time (years): a) Neal Smith and b) Fort Niobrara. No augmentation curve (blue dotted line) is based on predicted loss of expected H_e as measured in the Population Viability Analysis (PVA) (Hartway et al. 2020) for each herd. Similarly, the augmentation curve (green dashed line) is based on the best-case scenario prediction from the PVA for each herd. The black dots with error bars represent actual estimates of expected H_e at the time of the PVA and currently. The black triangle (if present) represents historical diversity as measured in Halbert and Derr (2008), before the PVA was initiated. Arrows represent timing and number of individuals used in each augmentation. Change in H_e is also reported describing the change in expected H_e from the PVA until present. USGS / SHAWNA ZIMMERMAN

6 Standing Up a New Herd

Creating large, new bison herds has long been recognized as key to the functional conservation of bison and the ecosystems upon which they depend (Sanderson et al. 2008). With the genetic and behavioral adaptability to survive landscape change, disease, and increasing human disturbance, bison are uniquely positioned for successful restoration as native North American wildlife. The 2020 BCI emphasizes the importance of collaboration with diverse partners to achieve ecological restoration of this species, and Secretary's Order 3410 also emphasizes the benefits of such restoration efforts to healthy grassland ecosystems.

Grasslands are the most endangered ecosystem in North America (Samson et al. 2004). Numerous studies suggest that bison contribute to the health and restoration of grassland ecosystems through their grazing and wallowing behaviors that alter plant species composition, increase vegetation heterogeneity, add and redistribute critical nutrients, decrease shrub and tree encroachment, and create soil disturbance and intermittent water sources (Freese et al. 2007; Knapp et al. 1999; Sanderson et al. 2008). Returning bison to their keystone role (Knapp et al. 1999) as ecological architects to restore grassland habitat may also help support a myriad of grassland bird and mammal species that co-occurred historically with bison (Augustine et al. 2021).

The establishment of new bison herds has the potential to meet a variety of the cultural and ecological objectives outlined by the DOI in the 2020 BCI and the [Bison Shared Stewardship Strategy](#). Establishing new herds requires careful consideration of many social, ecological, and biological (e.g., behavioral) factors. Input from stakeholders, partners, and affected communities is critically important early in the planning process. The level of social tolerance by local communities and perspectives of adjacent landowners should be considered and may mean that starting small to demonstrate success is most appropriate in some landscapes and for some projects. Partners may also express preferences for a particular founding herd, such as a herd with historical or cultural importance, a herd with a particular geographic history, or a herd with a uniquely documented health status. The goals and objectives for a new bison herd and discussions regarding selection of a founding herd(s) may be informed by Indigenous and traditional knowledge.

Establishing new bison herds requires careful consideration of many of the same technical factors discussed in sections above covering bison translocations, including cattle introgression, genetic diversity, logistics for safe transport and animal welfare, herd demographics, herd health, and the long-term potential for regular genetic augmentation. The planning process for new herd establishment must also include forethought regarding how social structure within a new herd may facilitate the natural expression of behavior and resource selection, and how those behaviors may contribute to ecological restoration.

Establishing new herds with animals from multiple age classes can serve as a strategy to maintain natural behavioral differences across age and sex of bison, such as behaviors associated with mate competition and breeding. For example, three herds established in the FWS National Wildlife Refuge System (Rocky Mountain Arsenal National Wildlife Refuge, Neal Smith National Wildlife Refuge,

and White Horse Hill National Game Preserve) were founded from a source herd with only a small number of mature, breeding males, with subsequent augmentation of additional young males for several years to increase mate competition and reduce the potential for high variation in male reproductive success (L. Jones, unpublished data). The need to facilitate natural behaviors in a new herd, however, must be balanced with transportation effects on the welfare of bison. While adult females generally tolerate translocation well with little or no effect on survival and reproduction, adult males are more difficult to capture, handle, and transport. Even males as young as 3 years old may suffer injuries from other animals if not transported singly in individual compartments.

New herds should meet minimum genetic and health criteria described in this Metapopulation Strategy. Principles of genetic diversity outlined in the PVA (Hartway et al. 2020) and in published accounts (Wilson et al. 2005) suggest that newly established herds may be especially vulnerable to genetic diversity loss during the first few years after herd establishment, owing to variation in reproductive success (with special concerns for males with demonstrated high variation in reproductive success); unexpected loss of individual founders due to injury, disease, or emigration; and/or rapid accumulation of inbreeding due to undetected high levels of relatedness among founders. However, bison translocations to establish and augment new herds within DOI have been successful to date, with some recent examples demonstrating how high levels of genetic diversity may be achieved and maintained (Hartway et al. 2020).

Once the social, ecological, and technical goals and partner perspectives are thoroughly evaluated, an optimal strategy to establish a new conservation herd will include the selection of the founding herd. Until new genetic technologies are available to quantitatively evaluate cattle introgression in individual bison, establishing a new herd with animals selected from one founder population reduces the potential for new herds to be established with high levels of cattle gene diversity, while also potentially increasing integration of those individuals into the new, smaller social and reproductive unit. Furthermore, newly established herds are especially subject to high levels of drift due to variation in reproductive success (Wilson et al. 2005), such that the desired social and reproductive integration may not occur in the first few years. Unless limited by interstate transport regulations, disease concerns or other factors, establishing a new herd with a wide age range of adult females (e.g., pregnancy adds significant additional genetic diversity to a new herd from breeding males not transferred), along with a smaller number of younger breeding age males is likely to support appropriate social structure and behaviors within the newly established herd. Augmenting new herds with additional young males for several years after establishment may allow each cohort of males to socially integrate into the existing herd to improve probability of reproductive success.

Similar to pre-transport disease testing, a group of individuals may be segregated, sampled, and genetically evaluated prior to transport to reduce founder herd relatedness through identification and exclusion of highly related individuals (e.g., parent-offspring, half-siblings) from the founder group. After meeting health testing and regulatory transport requirements as described in other areas of this Strategy, animals should then be transported directly and released to the new location with safety and animal welfare concerns as the highest priority, including transport of breeding age males singly in separate trailer compartments.

Following the genetic and health guidance detailed in this Metapopulation Strategy will best facilitate the long-term maintenance of conservation value of the new herd to partners included in the herd restoration effort, as well as to conservation of the species. Participation in this Metapopulation Strategy will also ensure the appropriate genetic and demographic monitoring needed to mitigate natural variation in reproductive success associated with new herd establishment.

7 What it Means to be a DOI Bison Conservation Partner

Being a DOI bison conservation partner can include different kinds of collaboration. Currently many opportunities exist to partner with DOI to conserve wild bison, which may be mutually beneficial to both DOI and partners including information sharing and collaboration in scientific research; sharing of Indigenous and traditional knowledge; the sampling, evaluation, and management of genetic data; the surveillance, interpretation, and management of herd health; operational and handling training and assistance; data collection and management; funding agreements; bison donations; strategic bison translocations; shared stewardship; conservation planning; internal and external communications; cultural events and support; and conferences, symposia, and other technical outreach collaborations.

This Metapopulation Strategy does not address opportunities and requirements for non-DOI entities and organizations to partner with DOI in the Strategy. While DOI eagerly anticipates exploring partnership opportunities in the near future, the scope of this Metapopulation Strategy document is the development, compilation, and utilization of the best available science and best management practices to conserve DOI bison conservation herds. Any future expansion of this Strategy to include potential partners managing non-DOI herds will address opportunities and requirements of such partnerships. In the meantime, DOI will continue collaboration with bison conservation partners to make strategic bison translocations as appropriate.

8 Future Adaptations of the Metapopulation Strategy

Automated high throughput genotyping technologies, such as SNP panels (Hughes-Stamm et al. 2011; Jenkins and Gibson 2002; Kraus et al. 2015; Natesh et al. 2019) and whole genome sequencing (Barbarosa et al. 2020, Oyler-McCance et al. 2016; 2020) are increasingly appealing for monitoring programs, particularly given their ability to improve precision in population genetic parameters (Zimmerman et al. 2020) and potential for examining functional genetics (Hohenlohe et al. 2021). While developing this Strategy, we explored an Affymetrix (Thermo Fisher Scientific, Santa Clara, CA) genotyping array for 83,000 SNP loci (Yang et al. 2020) as a potential alternative to the current microsatellite panel. As expected from previous comparisons (Langin et al. 2018, Zimmerman et al. 2020), the SNP-based parameter estimates were more precise (Zimmerman, unpublished data). Yet despite the promise of the SNP data and the efficiency of genotyping arrays, our sample failure rate was high (i.e., many samples failed to produce usable genotypes). Significant improvements in the SNP genotyping process are necessary before adoption and application in this Metapopulation Strategy. We anticipate shifting to more precise genomic methods in the near future as the technology advances.

The potential of SNP panels to increase our ability to understand divergence and cattle introgression from genome-wide data is particularly appealing for future applications. As previously described, the current coarse genetic indicators for evaluating cattle introgression are based on either the presence of maternally inherited cattle mtDNA or a microsatellite-based identification of nuclear cattle ancestry. A SNP-based approach to obtain a genome-wide evaluation of the degree of cattle ancestry is likely to be a more accurate and consistent metric. Technological advancements are likely to continue to shift the genetic marker paradigm from SNPs to whole genome sequence data in the future. This shift could expand potential avenues for monitoring and understanding population structure and diversity among herds, and for optimization of translocation strategies and animal selection.

As advances continue to be made in new technologies, such as SNP and whole genome sequencing, these methods will be re-evaluated periodically to ensure that this Metapopulation Strategy is informed by data that provides optimal information to support management decisions, while ensuring that investments in laboratory analysis, data management and data analysis remain appropriate relative to data quality and information density of those technologies.

9 Conclusion

This Metapopulation Strategy is meant to guide strategic translocations of bison with the goal of maximizing the remaining genetic diversity within plains bison while also considering bison health and cattle introgression. The motivation for this Strategy was DOI's assessment of the genetic diversity and long-term population viability of DOI bison conservation herds, which highlighted the need for a metapopulation approach for bison conservation. This Strategy is the culmination of a collaborative effort among a diverse group of scientists and managers across the five bureaus that are represented in the DOI Bison Working Group and will continue to serve as a living document with adaptations and improvements as technology advances.

This consistent and integrated approach to managing bison genetic diversity represents a significant advancement in our efforts to conserve bison. The development of a central repository for genetic samples and a user-friendly database to house and serve bison demographic and genetic data will also provide the necessary infrastructure needed to support this Strategy. The herd dashboard provides a visual guide for managers outlining the status of each herd in relation to genetic diversity and need for future augmentations. With this Metapopulation Strategy, DOI bureaus have a strong new tool to support the ongoing cooperative, multi-scaled stewardship efforts for bison conservation.

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Appendix A: Definition of DOI “Conservation Herds”

DOI bison conservation herds (conservation herds) are native North American wild bison conserved for the long-term viability of the species *Bison bison*. They are among the last remnants of the large herds of bison that ranged across much of the North American continent prior to European colonization; are the closest extant bison to that ancient morphological, physiological, behavioral, and genetic heritage; and are an irreplaceable resource for the restoration of self-sustaining wild bison herds and naturally functioning ecosystems. Conservation herds are managed by DOI, or in cooperation between DOI and Tribes, States, or other conservation partners as wildlife through the Public Trust Doctrine, for the benefit of all Americans.

The functional definition of a conservation herd is focused on management priorities that are directly linked to the five DOI bison conservation goals established in the [2020 BCI](#). This definition and these goals pertain only to DOI and conservation herds. One, some combination, or all of these goals may be of interest to other bison managers to prioritize and adopt for their own purposes and objectives, and DOI recognizes all contributions to any of these goals as worthwhile and valuable. DOI is committed to maximizing the simultaneous pursuit of all five goals, and to anchor management of conservation herds to the long-term viability of the species and their interaction with ecological and human communities. When opportunities for establishing new conservation herds arise, DOI will prioritize the selection of bison sources that are of high genetic conservation value and managed as wildlife.

DOI aligns management and the establishment of conservation herds to these five conservation goals:

1. **Wild, Healthy Bison Herds**—Bison are conserved as wildlife. To the fullest extent possible, past and current management maintains the wild character of bison, minimizes artificial selection, and allows forces of natural selection to operate, including natural age and sex demographics, competition for breeding, and the natural expression of behavior and resource selection. Bison are generally not vaccinated or provided medical intervention outside of exceptional circumstances that threaten the conservation value of the herd. Supplemental feeding only occurs when there are urgent conservation needs due to extraordinary conditions or required holding, and only then for the shortest necessary duration. When possible, populations are regulated through natural predation, and/or human hunting, and/or removal selection practices that contribute to maintaining a natural age class demographic.
2. **Genetic Conservation**—Conservation herds are managed utilizing a science-based approach to maximize the maintenance of genetic diversity, minimize loss of diversity due to genetic drift, and preserve adaptive capacity of bison as a wildlife species. This can be facilitated through establishing large herds or managing several small populations as a metapopulation. To mitigate the loss of genetic diversity within herds and across the DOI bison metapopulation, management of gene flow across conservation herds follows the DOI Bison Metapopulation Strategy. Cattle gene introgression is monitored in conservation herds and managed to minimize cattle introgression through time, prevent the introduction or amplification of novel segments of cattle genetic material to individual herds or the

metapopulation, and to not exacerbate cattle introgression (nuclear or mitochondrial) in any individual herd or the metapopulation.

3. **Shared Stewardship**—Conservation herds promote and support diverse partnerships to address the scale, complexity, and ecological and cultural significance of conserving and restoring wild, healthy bison as native North American wildlife. Bison partnerships promote ecocultural restoration, and embrace place-based connections between bison, ecological processes, and human cultures.
4. **Ecological Restoration**—Bison are maintained or restored in historically occupied ecoregions dominated by natural habitats and, to the fullest extent possible, express their roles as ecosystem engineers and as keystone species to shape healthy and diverse ecological communities. Bison densities and other native flora and fauna are managed in support of overall ecological health, using the best available science and knowledge to inform management.
5. **Cultural Restoration**—Bison support and restore cultural connections between bison and people, support reconciliation between diverse human cultures and the natural world, and foster a reciprocal relationship between people and nature. Bison that are excess to management objectives can support Indigenous Peoples' communities, spirituality, food security, landscape restoration, and economic development through both the direct use of bison and by supporting the restoration of bison to Tribal lands. Conservation herds unite communities to honor and promote the unique status of bison as the National Mammal and as an icon for all Americans.

Appendix B: Detailed Description of Converting Allelic Diversity from the PVA Model to Allelic Richness Assuming a Sample Size of 100

The VORTEX simulation model (Lacy and Pollak 2017) that was used in the PVA (Hartway et al. 2020) reports the mean allelic diversity (A) across all animals in the herd at the end of the simulation averaged over all replicates.

In practice, changes in allelic diversity across years will be assessed on a sample of the herd (as opposed to a census of all individuals). Measures of allelic diversity are particularly sensitive to sample size, thus allelic richness (Ar ; allelic diversity rarefied to a standard sample size) is the more appropriate proxy for genetic monitoring. We therefore converted final reported A predicted in the VORTEX simulation modeling to Ar for use in the Metapopulation Strategy. We used multiple output summary statistics to accomplish the simulation of genotypes that we could use to estimate Ar for multiple sample sizes for each herd. Final VORTEX output allele frequencies are averaged over replicates and include a probability of persistence for each allele (e.g., the proportion of the replicates where each allele was not lost), but no measure of variation across replicates.

Variation across replicates is expected to be low, but any variation could result in inaccurate simulation of genotypes and an upward bias in genetic diversity measures. We therefore needed to incorporate variation across replicates to accurately simulate genotypes. Our simulation of genotypes for each herd was accomplished in multiple steps. First, we used the probability of persistence for each allele as the parameter in a Bernoulli trial to predict whether an allele went extinct or not (1 = present, 0 = absent) in 1,000 replicates. The final VORTEX mean allele frequency was multiplied by the replicate Bernoulli trial outcomes, and the frequencies were adjusted such that each locus in each replicate summed to one. This resulted in replicate allele frequencies where some alleles went extinct in some replicates. Second, we used an iterative approach to estimating the amount of variation in the adjusted replicate allele frequencies. This involved selecting two non-zero alleles per locus in each replicate allele frequency and adding a small amount of random variation from one allele while simultaneously subtracting the same amount of variation from the second allele. Frequencies < 0 were adjusted to 0.001 and the frequencies of all alleles for each locus were divided by their sums to ensure they sum to one.

We then used the updated replicate allele frequencies to calculate expected heterozygosity (He) and then calculate the log probability that the replicate He estimates came from a normal distribution with a mean and standard deviation equal to the mean and standard deviation of He reported for the VORTEX simulation replicates. If the log probability of He from the updated allele frequencies was greater than the log probability of He from the previous iteration, then the amount of variation introduced into the previous iteration's replicate allele frequencies was replaced with the updated amount of variation and a new amount of variation was drawn from a normal distribution centered on the variation from the previous iteration. We ran this algorithm for 10,000 iterations to allow

adequate searching of the parameter space and accurate estimation of the variation in the allele frequencies across replicates.

Lastly, updated allele frequencies for the final iteration were used to simulate genotypes from a multinomial distribution and calculate replicate A, H_e , and A_r for multiple sample sizes (we ultimately used a sample size of 100 for this Metapopulation Strategy). These values were compared to the final VORTEX output for accuracy. The input allele frequencies were based on observed data and so A_r for t_0 was based on simulating genotypes from the observed allele frequencies and subsampling individuals to the rarefied sample size.

Appendix C: Detailed Description of Simulating Genetic Change Under Different Translocation Scenarios

We developed a genetic simulation model to rank all possible donor herds for translocation scenarios in terms of maximum predicted genetic diversity gains. In this model, we first used the observed microsatellite-based genetic data for a recipient herd to estimate locus-specific allele frequency distributions, or the probability of sampling an allele in a herd (Figure 4). We used the allele frequencies as the parameter in a multinomial probability distribution to simulate genotypes (size = 2 for two alleles per locus) for the number of individuals in the recipient herd (N_{init}) and 3 individuals from a potential donor herd (N_{trans}). We then calculated genetic diversity (e.g., A_r , H_o , H_e) for the simulated recipient herd (gd_{before}). Next, we combine 3 randomly selected donor herd individuals with the simulated recipient herd and re-calculated genetic diversity (gd_{after}). This allows managers to see the predicted immediate effect of moving 3 individuals, yet this simulation can also explore different numbers of bison moved if desired. The predicted genetic diversity gains are measured after the addition of individuals from a different herd minus the genetic diversity before ($gd_{\text{after}} - gd_{\text{before}}$). This simulation model ignores population growth, and assumes sex, age-class, and environmental variation will have a negligible effect on genetic diversity change. This simulation will be performed using R statistical software (R Core Team 2020) in 1,000 replicates for all herd combinations, but future iterations may include other platforms or software. The database will track mean and standard deviation of the replicates along with mean kinship (mK) values calculated with the R package related (Pew et al. 2015).

Appendix D: Core Components of a Disease Risk Analysis

A Disease Risk Analysis includes identification of a problem, description of hazards, assessment of risk (probabilities and consequences associated with each hazard), and evaluation of the effectiveness of potential mitigation or management of that risk. Effective risk communication among managers, partners and stakeholders is required throughout all phases of the disease risk analysis for any wildlife management activity and is especially crucial for wildlife translocation.

Within the context and framework of creating resilient and sustainable wild bison populations, the structure and formality of disease risk analysis and health assessment protocols to support bison translocations will vary and must be implemented on a case-by-case basis. Core factors common to all analyses include the need to:

1. Identify goals and objectives of the management action, such as translocation of bison between DOI units;
2. Assess known health threats to North American bison, including emphasis on regional hazards to the health of bison, humans and domestic animals in the relevant geographic locations;
3. Compile and summarize available information on the disease history and status of both the donor herd and the recipient herd;
4. Compile and summarize available information on the disease history and status of wildlife and domestic species associated with the donor and recipient bison herds;
5. Identify current regulatory requirements for bison transport;
6. Identify information gaps and the effect of uncertainty on the assessment;
7. Evaluate mitigation measures for managing priority disease risks, including biosecurity protocols and availability of effective treatment (if applicable) for use in bison; and
8. Develop and implement post-release monitoring protocols of translocated animals and the recipient herd.

The potential for rapid and unexpected changes in the disease landscape of either the donor or recipient herd requires both a comprehensive and flexible approach to assess DOI bison herd health status. Specific disease risks and priorities for DOI bison herds and planned translocations will vary depending on a variety of factors, including the geographic location of the herds and associated transport regulations established by state, Tribal, and federal animal health authorities; known contemporary disease threats; and availability of historical disease surveillance data. Additional factors, such as the type of diagnostic tests, the sensitivity and specificity of those tests, and uncertainties in this information must also be considered.

The first step in assessing and mitigating risk is identifying hazards. Although pre-transport disease tests provide some information about disease status in individual animals at the time of testing, planned herd health surveillance programs can leverage a larger sample size within a herd over a

longer period of time. A two-pronged approach to herd health surveillance using both passive and active methods increases confidence in the health status of a herd and in the predictive value of individual animal tests. Passive surveillance methods include animal health observations recorded in association with other field activities. Active methods include testing all or a subset of individuals in a herd over time for specific diseases of concern to determine presence or prevalence of those diseases and any changes in the population. Mortality investigation may supplement both strategies through conducting necropsies on animals found dead, as well as proactively searching for and collecting samples from moribund animals and carcasses. Mortality investigation includes the use of appropriate field sampling and laboratory diagnostic tools, and significantly increases the probability of detecting disease in a herd that may otherwise be difficult to detect through periodic sampling of captured live animals during population management activities. Outcomes of this two-pronged herd health surveillance approach can be used to inform and refine a disease risk analysis for integration into the planning process for specific bison translocations to optimize health and conservation outcomes.

Appendix E: Current Minimum Standards for Official Animal Identification

Starting in November of 2024, the minimum standard for official animal identification for newly tagged bison is a visually and electronically readable eartag, imprinted with a nationally unique official animal identification number and the U.S. Official Eartag Shield, as described in [APHIS's Animal Disease Traceability Framework Official Eartags: Criteria and Options](#). Contact bureau wildlife health teams for current animal identification requirements and recommendations.

Appendix F: Current Pathogens and Parasites of Potential Concern for Bison Translocation Within the DOI Metapopulation

The following list of pathogens and parasites includes agents and diseases that are either known to affect bison health or may affect the ability of the affected herd to contribute live animals to other herds as part of this Metapopulation Strategy. *This list is not comprehensive and will change as both science and pathogens evolve.* Many other pathogens and parasites not included on this list can infect bison and may be a concern in specific translocation scenarios and locations. This appendix identifies a minimum core group of pathogens of concern from a DOI bison herd health and translocation perspective and should be reviewed in consultation with your bureau wildlife health office to incorporate local conditions and herd-specific risk factors early in the translocation process.

- Disease associated with *Mycoplasma bovis* is an emerging threat to bison causing variable disease presentation (respiratory illness, lameness, mastitis) that results in 25–60% morbidity and mortality, with significant effects most commonly observed from recent introductions into naïve herds. Research is ongoing to develop sensitive and specific tests for the presence of this pathogen in live animals. Due to the potential for significant effects of this disease, confidence gained through a comprehensive herd health surveillance program will best support translocation of healthy DOI bison.
- Johne's disease caused by *Mycobacterium avium paratuberculosis* is a chronic, sometimes fatal infection affecting the intestines. Transmission within a herd is enhanced by environmental resistance of the bacteria. Due to the insidious nature of this disease, confidence gained through a comprehensive herd health surveillance program will best support translocation of healthy DOI bison.
- Bovine brucellosis is a zoonotic disease caused by *Brucella abortus*. Introduced to wildlife by domestic livestock, this disease has been the target of a national eradication program in the United States since 1934. As one of the two federally regulated diseases with current potential to affect bison, bureau wildlife health teams can help address any testing requirements that may be appropriate in specific geographic areas.
- Bovine tuberculosis is a zoonotic disease caused by *Mycobacterium bovis*. Circulating between cattle and wildlife in some geographic areas, this disease is one of the two federally regulated diseases with current potential to affect bison. Bureau wildlife health teams can help address any testing requirements that may be appropriate in specific geographic areas.
- Bovine Viral Diarrhea (BVD) infection can result in respiratory disease, diarrhea and can also have reproductive effects. Fetuses infected in utero may become persistently infected (PI) chronic carriers that expose other animals in the herd to this disease. Periodic sero-surveys conducted as part of a comprehensive herd health surveillance program can help identify herds at high risk of exposure to this virus. For herds with high risk of exposure, consider testing for BVD PI carriers prior to translocation.

- Anaplasmosis (*Anaplasma marginale* most commonly) is a vector-borne disease primarily transmitted by ticks that is found in both domestic and wild ruminants and can cause anemia in susceptible populations. Although animals in naïve herds may experience illness upon infection, most bison herds develop immunity to the disease and exhibit no apparent signs of illness from infection. Consider testing donor and/or recipient herds or individuals prior to transport.
- Infection with *Trichostrongylus axei* is a reproductive disease of cattle carried by bulls and spread through breeding. *Trichostrongylus axei* is a single celled flagellated parasite that can cause infertility in cows. While the disease has not been reported in bison, testing of breeding age bulls is occasionally requested by state animal health officials to prevent potential movement of the parasite. Consider moving only cows or pre-pubertal virgin bulls in areas where testing is required prior to translocation.
- Recent work to better characterize internal parasites in bison has highlighted some differences among herds (Avramenko et al. 2018; Danks et al. 2022), with resistance to anthelmintics becoming an increasing concern. Wild, healthy bison with adequate range are less likely to have significant parasite burdens, but aggregation of bison in one area or confinement of bison for prolonged periods of time can increase parasite burdens and transmission with the potential to cause illness or death in susceptible individuals. Annual parasitology surveys of 30–60 fecal samples collected in the field in mid- to late summer, combined with mortality surveillance, may be able to identify differences in internal parasite communities between donor and recipient DOI bison herds or changing parasite burdens within herds over time. At the discretion of the manager for the receiving herd or bureau health team, an anthelmintic may be administered to animals selected for translocation prior to transport. However, inappropriate anthelmintic use can detrimentally affect individual and herd health, as well as contribute to anthelmintic resistance if not used judiciously as part of a comprehensive herd health strategy under the guidance of bureau wildlife health teams.

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