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From the President

I have spent considerable time pondering what I can say to our members at this time. First and foremost, I think we should appreciate our blessings being associated with a truly majestic animal. Some of us are looking for land trying to get situated, to begin the process of raising bison. Others of us are more established and have had the opportunity to raise the bison for many years. Whatever our situation is, it is a blessing to be in this land to have the opportunities we have to associate and dream about raising bison. Always remember the blessings we have.

I am personally in the later stages of finishing a house my family and I have built from scratch on our property. It is situated on the land so that we can see our bison pastures from our windows. I look forward to the times when I can sit on the porch and watch the bison in the pasture, maybe even grilling bison meat at the same time. This is a process my family and I have been going through for five years. There have been ups and downs and struggles along the way but by persevering, eventually it will all be finished.

This brings me to the second point that I would like to share. An important value the Texas Bison Association (TBA) brings is its members and their willingness to assist. In starting this adventure I have made mistakes and have relied on other's wisdom to guide me. Many people have been instrumental in helping my family and I along our journey. Being active in the TBA and attending its conferences has been pivotal in traversing this path.

This past year I was elected as president of the Texas Bison Association. A goal of mine has been to try and make sure that it provides value and support to its members. We have discussed ideas and are looking to implement some changes in 2025. Recently we have had a very successful auction that has been very useful in assisting members sell and move bison. We have also continued our Conferences in both the Spring and the Fall in 2024.

The Spring 2024 Conference was fabulous. The Hill country is always nice but we were grateful to have with us the National Bison Association (NBA) which partnered with us to prepare and conduct the conference. We also have to recognize the hospitality of ROAM Ranch for letting us use their land to gather and learn.

This conference gave us many highlights beginning with our riveting discussion of bylaws. We saw the growth of the TBA and had the fun opportunity to socialize by all who stayed to talk, listen, and interact at our Friday social. At Roam Ranch we got to see a field harvest first-hand up close and were given the opportunity to touch and see many parts of the bison as it was harvested. We even were able to eat some raw meat specially seasoned and presented for us to sample. Many classes were provided to us to learn and develop.

The 2024 Fall Conference was held in Sulphur Springs and Talco in the northeastern part of the state. At this conference we tried to provide hands on education by showing the loadout and working of animals in the squeeze chutes. For those who attended on the Friday portion, it was very exciting to see a few of the bulls break out into the crowd. This goes to show that not everything goes according to plan when working the bison.

We have begun planning for the 2025 Spring Conference. I encourage you to be active in the TBA, attend the conferences, and take time to network. I look forward to seeing all of you again and listening to your ideas and stories from the past year. May God bless all of you until then.

Jeff Williams
President, Texas Bison Association

The Texas Bison Association

works to promote and preserve Texas bison through leadership, education and building public awareness for the bison ranching and meat industry. Founded in 1994, the Texas Bison Association provides assistance in raising and producing bison among our membership. TBA also promotes the nutritional health aspects of the North American Bison to consumers. The TBA welcomes anyone with an interest in the preservation, promotion and production of the North American Bison.

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TEXAS BISON

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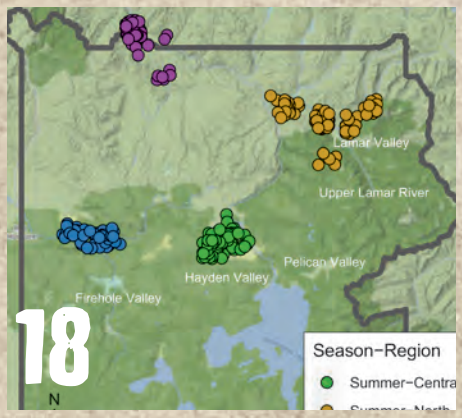

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MARKET-READY CALVES

By Dick Gehring, Sale chair, Kansas Buffalo Association

What things attract a commercial feeder to purchase your calves above others? Many answers, and questions, surround what makes a calf desirable to the commercial market. While this article isn't all-inclusive and certainly won't fit every scenario, the fundamentals are there. Hopefully the reader will be able to look hard at his program, grab what he can, and make improvements that will pay dividends.

Distance: To start with, bidding on 2 calves 100 to 1300 miles away and risking getting them bought and then no others bought to fill even a trailer load, isn't very inviting. The commercial buyer may not want to get started without at least having a partial load to begin with. Having your animals at your location by themselves can work if you have volume, if you don't have volume, you're relying on multiple opposing bidders that only want a few. They're out there but are they close enough to be interested?

Maturity: As for the calves, a calf that has the maturity to go forth in an unfamiliar environment, surrounded by multiple owner calves, eating a new diet, that gains weight and thrives, is likely of interest to a commercial buyer.

How do we get there? First, let's look at maturity. Age obviously factors in getting that animal close to that end. However, it isn't that simple. Just like other mammals, each grow at a different rate. Some of that growth is genetic potential while environment and feed source play a large role. The stronger the food sources available to the calf, the larger he'll likely grow. Along with that growth comes maturity. A six-month-old calf (October) weighing 450 lbs. is light years ahead of the disadvantaged calf that in October weighs 200 to 300 lbs. If both calves are weaned at that time, the heavier calf can go on to thrive in his new setting. His gut microbes are likely far advanced compared to the lightweight calf. His physical size and immune system are developed far beyond the lighter counterpart. Take those same calves 3 months later, the weights could easily be 550 lbs. compared to 300

This group of 22-month-old yearlings each weighed 800 pounds or better. The calves in this same group weighed between 480 and 550 pounds. These are the results of purposeful nutrition and health planning and execution.

By contrast, these 22- and 34-month-old bison are older, yet averaged 100 pounds lighter than the comparision group.

to 350 lbs., maybe. And of course, nine-month-old calves weighing 300 lbs. are going to struggle in most scenarios and likely never reach their innate potential.

Essentially, feeders tend to think the big calves have the potential to thrive and so aren't in question. Let's look at the little calves. Why are they little? Generally, when dealing with ruminants, whether it's parasites, unthrifty calves, lightweights, or illness, if you have an issue today, your cause likely started at a minimum 45 days ago, and quite possibly a year ago or longer. In the case of a 9-month-old calf that weighs 350 lbs. or less, I'm guessing the challenges that plague your calf started well before it was born. Enter the Cow into the equation.

Natives and Nutrition: If the dam isn't getting what she needs, she won't be able to produce enough quality milk to get you a weaning weight that sets that calf on a roadmap to success. If her nutrition has her shortchanged and struggling to be fat going into the fall, (enabling her to lose around 10 percent of her body weight, and rebounding quickly in the spring), she won't be able to give her calf what it needs. Look at what she had available to her. What is the nutritional profile of her feed sources? What types of grass do you have? Is it native, or has it just been prevalent in your area for so long, you think they are native species? Brome, Fescue, and old-world bluestem to name a few, are not native to North America. Scientifically manufactured or genetically modified feed sources are not native or natural. They may have feed-value, but at what cost? What does your year-round nutritional profile look like? Are the protein levels adequate for her needs? Is the mineral content available in sync? Have you done the science to find what the mineral needs are for your area? If you live in the humid southeast and are using the same mineral that a Northeastern Midwest rancher is using because his calves are big boned, slick and huge, that may be a clue. Get with a nutritionist in your area and figure out what stocking rate should be used year-round, for your grass, climate, content, and, most of all, for your animal. Bison needs aren't the same as cattle. Don't listen to the "local authority" who thinks he knows but has never done the science to find out what he really has available to get his program lined out. If he doesn't know his own, he certainly won't know what it will take to mitigate your specific scenario. Find the resources available to you that will allow your overall nutritional profile to give that cow <u>what she needs when she needs it</u>.

Regional Challenges: We all have challenges in our own region. Wetter is not always better. Lots of rain can mean washy grass that can be difficult for nutrient retention. It's green, lush, looks great, and there's lots of it. Accordingly, the <u>*assumed*</u> stocking

A conscious effort to do what is necessary to ensure adequate nutrition will pay-off at the sale and in the pasture.

"Green" grass does not necessarilty equal "nutritious" grass. Animals, like the 440-pound 22-month-old depicted here can starve on a full stomach. A lack of focus on forage and water quality will put put your animals at a disadvantage in the market and can spell disaster for your production rates and long-term returns.

rate is much denser than the arid locations. You may be able to run more numbers on less acres, but should you? More rainfall and heavier stocking rates often equate to grass being grazed too short. Shorter grass height and more animals per square foot equate to too much grass growth taken off repeatedly which keeps the pasture from thriving. It also encourages a larger parasite load. Couple those two variables together and you have a potential disaster. Arid climates require more land mass and that requires more fencing. It also typically comes with a short grass prairie and doesn't have the volume of forage the wetter climates do. But, that arid short grass packs a punch. That grass is also usually an actual native species this animal co-evolved with. Native grasses with strong nutrient content that carry good nutrient levels into the fall, generate fat cows, at the right times of the year. Those cows in turn can generate big robust calves that grow to their potential. When those building blocks are set in place early and the calf obtains a weaning weight of 450 to 550 lbs., the calf goes on feed quickly and ramps up to gain efficiently throughout the course. A disadvantaged calf that is underweight and/or immature, needs to be given nutrition and time to catch up, or it will always be behind. Competition in a feed setting doesn't usually lend itself well to those smaller calves. The commercial feeder will need to keep them separate for those little ones to not compete with another calf one-and-a-half to two times their size. Not every feeder has that space, capacity, or inclination. Consequently, many will pass on the smaller calves.

Optimize Where You Can: All that said, you can't fix everything. Rainfall, vegetation, and mineral content when you inherit, purchase, lease, or rent land, grass or ground are examples of things you can't dictate. However, overall nutrition levels, mineral availability, and water quality, are things you can dictate or, at a minimum, impact. Find those feed sources that are affordable, sustainable, and obtainable. Be sure your cows are receiving the nutrition they need when they need it (e.g. what protein at what time of the year), and how they need it. Control your parasites by learning which ones they are, how many are present, what they respond to, and when to treat. Texas A&M has a great program right there in the middle of your country, use it as it should be used. Just as importantly, use stocking rate and level of grass height after grazing, to limit the uptake of parasites and thereby impacting the amount of reingestion, the spread, and concentration of your parasite load. I can't stress the importance of all these different parts and how proper stocking rates play into the success of your herd. Miscommunication, i.e., misunderstanding with NRCS or whomever you get advice from, can be disastrous.

If you have your stocking rate and feed sources tuned in and your cows are working for you instead of simply trying to survive, then the protocols, shots, freight, etc. will have value and mean something to the discerning buyer.

Vaccinations and Worming: A good respiratory protocol such as Pyramid 5 with Presponse and a booster at 30 to 45 days later is what I like to see. A blackleg such as Vision 7 Somnus with spur boostered at 4 weeks, is helpful in my operation. I look for a good worming protocol that includes Injectables like Ivomec, Dectomax, or Cydectin. Depending on where you are located, possibly a white wormer, such as Valbazen, is good to have in the mix, or very likely, both an injectable and a white wormer are of value. This is all dependent on your findings from the testing you're doing with Texas A&M, K-State, or any other lab that will culture the samples to find what parasites you're dealing with and advise what wormer to use, when, and how.

The Pay-off: This may sound like a lot, especially if your calves are small and you aren't receiving very much money for them. If you're weaning heavy calves that are bringing you good money, it's just a cost of doing business. Enabling your cows to stand a chance at thriving and delivering you a product that is salable, valuable, and sustainable is paramount to the success of the calf. Giving all the shots, having all the protocols, keeping them for the right amount of time, and delivering them to my front door, won't mean a thing if they aren't able to thrive because they have been disadvantaged by poor nutrition in their formative years, so to speak. Get your cows straight, your nutrition adequate, your protocols up to speed, and have enough animals in one location that it pays to travel to get them, and the price will take care of itself. .

More Than an Animal: The Enduring Connection Between Buffalo and Native Communities

By Jenice Johnson, Tanka Fund

To Native peoples, the Buffalo is more than an animal — it is a relative, a living connection to ancestors and the land. For generations, it has provided not just sustenance but a way of life, shaping traditions, ceremonies, and the spirit of resilience that defines Indigenous identity. This sacred bond is woven into history, sustaining Native communities physically, culturally, and spiritually.

While the species is scientifically known as bison, Native communities have long referred to them as Buffalo, a name passed down for generations, carrying cultural and historical significance. To many, it is more than a name; it represents the deep ties between land, people, and tradition.

Because of this profound connection, many Native ranchers are returning to Buffalo as a way to restore both the land and cultural traditions. One such rancher is Brendan Siers (Sicangu Lakota Oyate) on

Feeding Bison

the Rosebud Reservation in South Dakota. Brendan also herds cattle, and he said non-Native voices have often suggested that cattle are more profitable. Yet, he remains committed to making Buffalo his primary focus and continues to serve his community through their presence.

"It's like how a spider knows how to spin a web without being taught. Maybe this connection to Buffalo is bred into us over generations," he said. "When this animal holds a significant place in your life, it isn't something you have to learn, it's just there. I've never had a tribal member work with us who didn't want to come back. Anyone with that bloodline has an instinctive bond to the Buffalo. It's hard to describe."

In years past, and even today through cultural efforts, events, and programs focused on reconnecting to Native heritage, Buffalo have provided everything a community needs. Beyond food, they offer tools, clothing, land stewardship, shelter, and more. As Theda Pogue (Seminole and Creek) of GP Ranch in Sulphur Springs, TX, explains, "We are interconnected to bison in completing the circle of life by using every part of the animal."

"Spiritually, Buffalo is a sign of strength and respect. Most animals turn their backs to a storm, but Buffalo face it head-on and walk through it. That is how Native Americans were," she continued. "They fought for their beliefs, their land, and their culture. We must remember this and what we are fighting for today. We must continue to face the storms head-on and push through our trials."

More than just a source of nourishment, the Buffalo harvest is an important event, one of reverence, gratitude, and community. The designated shooter and the community carry a great responsibility, ensuring that the Buffalo is honored in its passing. Every step of the process, from butchering to cooking, is steeped in teachings passed down through generations. The harvest is not just about sustenance; it is about gathering as relatives, celebrating milestones, and reaffirming traditions that have endured despite centuries of hardship.

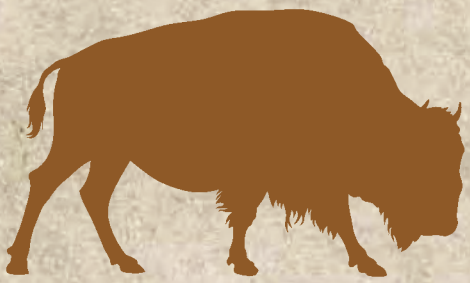
Like many ranchers, Ed Iron Cloud (Oglala Lakota) of the Pine Ridge Reservation in South Dakota participates in many of these cultural harvests and has provided his own Buffalo for them. He said he is proud to do so and shared the importance of prayer around these relatives.

Bison in Pasture Double S ranch

Bison w Rainbow

Harvesting Bison

Running Bison



Bison in Pasture

Bison along fence line

"The Buffalo is going to give its life, and we are going to eat the animal, gain strength, and continue to live because we have food. With everything, there is spirit to it… the land, air, water, and the animals. We acknowledge that and honor it," he said. "I don't consider myself a rancher; I consider myself a caretaker. We aren't taking care of them, they are taking care of us."

As a keystone species, Buffalo shape the land in ways that cattle cannot—nourishing the soil, encouraging native grasses to grow, and restoring balance to ecosystems that have suffered in their absence. Their return to Native lands is not just cultural renewal, but ecological healing. With each step, graze, and wallow, their presence is restorative to the land they inhabit. And as Theda said, "We don't own any of this land; we are mere caretakers for our grandchildren's grandchildren."

"Like our ancestors, the Buffalo were here before everyone else. Their lives and our lives now are connected in a circle," she said. "The cultural relationship we have with them is a spiritual and emotional one. Our relationship is one of respect — respect for other cultures, other creatures on Earth, and respect for Mother Earth for the next seven generations."

Wet Bison Eating

Texas A&M Study: After 120 Years Of Conservation Efforts, Yellowstone Bison Are A Single Breeding Population

Once consisting of two unique herds, researchers believe the Yellowstone bison herds should now be managed as one interbreeding population.

By Courtney Price

Researchers from the Texas A&M College of Veterinary Medicine & Biomedical Sciences (VMBS) have discovered that bison in Yellowstone National Park — the only group of American bison that has continually existed as wildlife in the United States — now consist of a single large, interbreeding population derived from multiple historic bison herds.

Population genetic studies completed just 20 years ago found that Yellowstone bison populations still retained much of their historic breeding patterns and were, in fact, two unique herds living within the national park. However, in a recent study published in the **Journal of Heredity**, VMBS researchers found a change in breeding behavior in the park and now recommend that Yellowstone bison should be managed as one large interbreeding herd.

"This finding certainly has a direct impact on the long-term conservation and management of this iconic bison population," said Dr. James Derr, a professor in the VMBS' Department of Veterinary Pathobiology (VTPB).

Bison like those in Yellowstone once suffered a population crisis that conservationists call the 'population bottleneck' of the 19th century. By the early 1900s, American bison numbers had been reduced by 99.9% across North America and only 23 wild bison were known to have survived poaching in Yellowstone.

"In one of the greatest wildlife conservation success stories of all time, a small number of domestic bison from western Montana and the Texas Panhandle were introduced in 1902 to existing animals in Yellowstone in the hopes that they would create a stable and thriving population in the world's first national park," Derr said.

Today, the Texas A&M researchers report that the Yellowstone bison population appears to be functioning as a single and genetically healthy population that fluctuates between 4,000 and 6,000 individuals.

"There has long been a debate among conservationists about how to best manage genetic diversity in Yellowstone bison," said Dr. Sam Stroupe, a VTPB postdoctoral researcher.

"To get a clearer picture, we examined samples from the two major summer breeding groups and two major winter ranges," he said. "These are where we would expect to see examples of genetic difference and overlap; however, Yellowstone bison today are clearly one interbreeding herd."

With the completion of this study, management decisions can be based on accurate information about the breeding structure and overall genetic health of the population to ensure the long-term stability of this iconic bison herd.

The researchers hope that this new information will prove useful to Yellowstone's bison conservation experts as they continue to manage and monitor this flagship population of the U.S. national mammal.

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Original Article

Original Article

Genetic reassessment of population subdivision in Yellowstone National Park bison

Sam Stroupe[1,*], Chris Geremia[2], Rick L. Wallen[2], P.J. White[2] and James N. Derr[1,*]

[1]Department of Veterinary Pathobiology, Texas A&M University College of Veterinary Medicine and Biomedical Science, College Station, TX, United States,
[2]Yellowstone Center for Resources, Yellowstone National Park, Mammoth Hot Springs, WY, United States

*Corresponding author: Department of Veterinary Pathobiology, Texas A&M University College of Veterinary Medicine and Biomedical Science, College Station, Texas, USA. Email: samstroupe@tamu.edu, jderr@tamu.edu

Corresponding Editor: Alfred Roca

Abstract

Yellowstone National Park is home to the only plains bison population that has continually existed as wildlife, on the same landscape, through the population bottleneck of the late 19th century. Nevertheless, by the early 1900s, only 23 wild bison were known to have survived poaching. Salvation efforts included the addition of 18 females from Montana and 3 bulls from Texas to augment this population. A century later, nuclear microsatellite-based population-level assessment revealed two genetically distinct bison subpopulations. However, in 2016, an analysis of mitochondrial haplotypes showed the two founding lineages were distributed throughout the park. This study is designed to delineate any current substructure in the Yellowstone bison population by strategically sampling the two major summer breeding herds and the two major winter ranges. Population-level metrics were derived using the same microsatellite loci as the original study along with a newly developed set of highly informative bison-specific single nucleotide polymorphisms. Our analyses reveal that the modern bison in Yellowstone National Park currently consists of one interbreeding population, composed of two subunits.

Key words: conservation genetics, North American bison, population structure, wildlife management

Introduction

Yellowstone National Park is home to arguably the most iconic bison population. Since its establishment in 1872 as the first National Park in the United States and the world, significant and unwavering efforts have been dedicated to the preservation of the bison population residing there. Not only has this population played a part in bison becoming a national icon but they are also a true testament to the resilience, hope, and strength bison symbolize. Yellowstone bison are the largest free-roaming bison population in the United States and the only plains bison to have continually existed in the wild and on same the landscape since prehistoric times.

The history of this population is a tale of near tragedy turned conservation success story. During the population bottleneck of the late 19th century, the Greater Yellowstone Area bison population narrowly avoided extinction, with an estimated 23 individuals remaining in 1902 (American Bison Society 1908). To preserve this population, additional bison were brought in from private ranches. Eighteen females from the Pablo-Allard herd in Montana, three males from the Goodnight herd in Texas, and four calves from the indigenous herd were used to establish a secondary "introduced" population (Meagher, 1973; Coder 1975). The introduced herd was moved to the Lamar Valley in 1907 and closely day herded or corralled through at least 1915 (Meagher 1973). Meanwhile the indigenous herd was isolated, wintering in the Pelican Valley and summering in the high-elevation grasslands of the Upper Lamar River.

The subsequent recovery of Yellowstone bison is well documented (Meagher 1973; White et al. 2015). Intermingling of the native and introduced herds increased after 1921, when managers fenced the introduced herd out of the Lamar Valley and moved them to areas used by the indigenous herd during summer. Managers also preferentially removed adult males from the introduced herd to increase the indigenous lineage. The annual report of Superintendent Toll in 1929 indicated "[t]here seems to be a gradual intermingling of the wild [Pelican] and tame [Lamar] herd. It has reached a point where it is difficult to distinguish the buffalo of the wild herd from those of the Lamar Valley herd" (Toll 1929). Therefore, it is likely the bison formed a single "Northern Herd" by the 1930s summering together and separating into two wintering units called the "Lamar" and "Pelican" bison (Meagher 1973). In 1936, managers relocated 71 bison from the Lamar bison to the Firehole and Hayden Valleys (Skinner and Alcorn 1942). The animals formed the "Mary Mountain Bison" or "Central Herd." Population reductions and subsequent recovery likely kept the Northern and

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Central Herds separated through the 1970s. Movements between the herds were believed to increase through the 1980s when Northern Herd animals wintering in the Pelican Valley began moving to the Hayden Valley and integrating into the Central Herd (Meagher 1993, 1998). By the 1990s, the animals from the Central Herd began moving to wintering areas of the Northern Herd (Meagher 1989, 1993, 1998). Today, all Yellowstone bison roam relatively freely within Yellowstone National Park, with limitations on their distribution into areas outside the park boundaries. During the past decade, the population has fluctuated between 4,000 and 6,000 animals. Modern GPS technology confirms that bison congregate into two main herds (Northern, Central) during the breeding season, some animals from each herd share wintering areas, and some individuals switch breeding areas over time.

In a study by Halbert et al. (2012a), evaluating 661 Yellowstone bison sampled between 1997 and 2003, Yellowstone bison appeared to split into two genetically distinct subpopulations defined by microsatellite genotype diversity and allelic distributions. At that time, a concern raised by Halbert et al. (2012a) involved unequal culling across these two bison populations and the impact this could have on long-term genetic diversity. Subsequently, White and Wallen (2012) suggested "managers should be promoting the conservation of wildness and natural selection to retain adaptive capabilities, rather than preconceived notions of 'natural' genetic or population structures that were likely created or exacerbated by human actions." As this discussion continued, (Halbert et al. 2012a) pointed out that because all modern bison populations are due to anthropogenic activities, it may be best to error on the side of caution and focus Yellowstone bison management to preserve genetic diversity in its, at the time, current state (Halbert et al. 2012a) . Although no definitive conclusion was reached at the time, it was agreed that there should be continued monitoring of genetic variation in Yellowstone bison and use the best available scientific data as a foundation for future bison management.

Following the study by Halbert et al. (2012a), a mitochondrial genome study was conducted to analyze haplotype diversity among Yellowstone bison (Forgacs et al. 2016). In this study, 25 mitochondrial genomes of Yellowstone bison were evaluated and compared to an additional 20 bison from diverse populations. This study revealed two distinct mitochondrial haplotype clades found within Yellowstone and the overall population of bison. This evidence was consistent with historical documentation of a second maternal lineage brought in from the Pablo-Allard herd in the early 1900s (Meagher 1973; Coder 1975). Unlike the previous study (Halbert et al. 2012b), there was no evidence, based on mtDNA haplotypes, to support population subdivision among the Yellowstone bison. In fact, this study was able to identify that bison of both mitochondrial haplotype clades, and therefore maternal lineages, were present in both present-day breeding areas (Forgacs et al. 2016).

However, both studies had limitations to their scope. Namely, neither study included Yellowstone bison sampled from both breeding populations during the same breeding season. In the study conducted by Halbert et al. (2012a), although a portion of the samples were collected within the park boundaries, over 90% of the samples were collected during the winter migration when bison were leaving the park. Considering the northern and central groups have an overlapping winter range in the Gardiner Basin, it was not possible to confidently assign home ranges without associated individual movement data such as radio telemetry (Meagher 1989; Halbert et al. 2012b). Therefore, no definitive conclusions could be drawn as to whether the identified genetic population substructure extended to the breeding groups. In the work of Forgacs et al. (2016), the mitochondrial DNA only portrays a portion of the genetic story. Although able to assign bison to maternal lineages and compare life histories, it failed to characterize levels of admixture within these individuals.

The current study was designed to evaluate population substructure in Yellowstone bison by strategically sampling the two major summer breeding populations, where one would expect to see genetic differentiation in ongoing population subdivision, and the two major winter ranges, where migration patterns of both breeding herds can overlap. Metrics used to evaluate population dynamics were determined using a set of 24 microsatellite loci (Halbert 2003), previously characterized in Yellowstone bison (Halbert et al. 2012), as well as a newly developed set of highly informative bison-specific single nucleotide polymorphisms (SNPs) (Stroupe and Derr 2024). Identifying current structure of the Yellowstone bison population is important to understanding the history of this iconic population, as well as developing strategies for its future conservation.

Methods

Biological material

Tissue biopsy samples were collected from 282 Yellowstone National Park bison. These samples were collected during the summer of 2019 and winter of 2021 in two major ranges within the park, Central and Northern (Fig. 1). The summer collection included 154 samples, 62 from the Central breeding area and 92 from the Northern breeding area. The winter collection included 128 samples, 44 from the Central wintering area and 84 from the Northern wintering area. Within each geographic area, Northern or Central, bison groups were opportunistically located during sample collection periods with up to 30% of the bison within a group randomly sampled. Tissue samples were collected using a Type P Pneu-Dart Biopsy RDD. Tissue samples were extracted from the dart using forceps cleaned in ethanol. Tissue samples were suspended in an ethanol solution and refrigerated prior to lab analysis. Biopsy tissue samples were collected according to the NPS IACUC IMR_YELL_White_Ungulates_2022.A3.

Tissue samples were cut into smaller portions in an isolation hood and divided for microsatellite or SNP genotyping. Of the 282 samples, eight were identified as duplicates with SNP data using Sequoia v2.5.3 (Huisman 2017) and confirmed with microsatellite data. Duplicates were removed from final data analysis.

Microsatellites

DNA was extracted from a portion of each biopsy tissue sample using the Gentra Puregene kit (Qiagen) according to manufacture protocols. A set of 24 autosomal microsatellite markers were used in this study including the core set of loci used for parentage determination (Supplementary Table 1) (Schnabel et al. 2000; Halbert 2003). Microsatellite samples were genotyped according to established lab protocol (Halbert 2003) using an ABI 3730 Genetic Analyzer and STRand

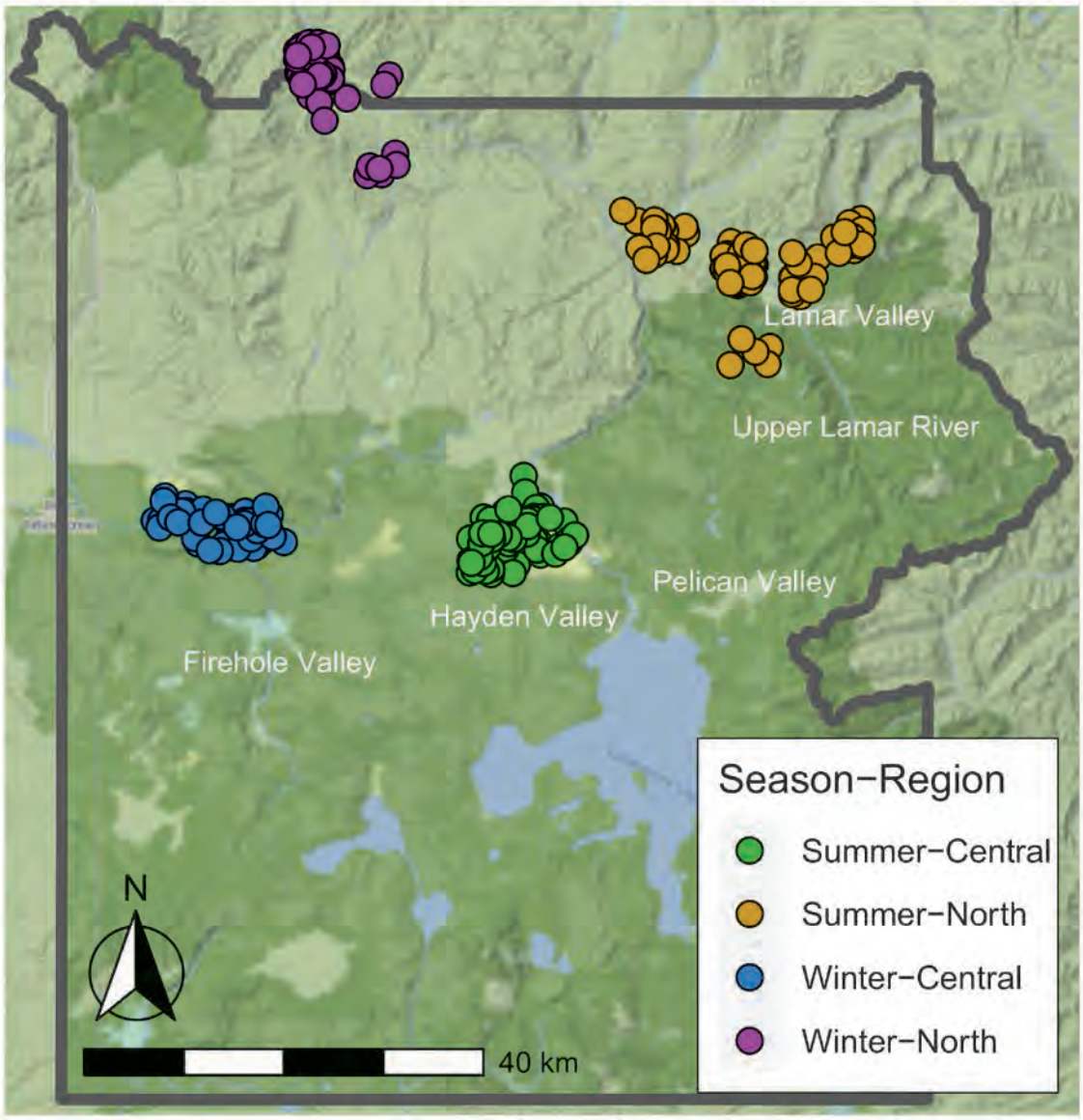

Fig. 1. Map of sample collection sites.

software (Toonen and Hughes 2001; https://vgl.ucdavis.edu/STRand). Three samples had a call rate below 90% and were removed from further analysis resulting in a final microsatellite data set of 271 samples and 24 microsatellite markers. Of those, 148 samples were collected during the summer breeding season.

Cervus v3.0.7 (Kalinowski et al. 2007) was used for initial overview of population genetic diversity and formatting data set for downstream analysis. A series of principal component analysis (PCA) were used to establish patterns in the data using collection location and time of year to group samples. Ade4 v1.7-22 (Dray and Dufour 2007) was used to calculate eigenvalues and eigenvectors on the final data set and plotted with 95% confidence level ellipses using ggplot (Wickham 2016) in R v4.1.2 (R Core Team 2022). Observed heterozygosity (H_O), expected heterozygosity within populations (H_S), allelic richness (A_R), F_{ST}, and F_{IS} with 95% confidence intervals were calculated with the Hierfstat R package (Goudet 2005). F_{ST} was calculated using the Weir and Cockerham (1984) equation. Values calculated per individual or per loci were averaged across each population. These analyses were carried out in R v4.1.2 (R Core Team 2022).

Population parameters were evaluated according to the following methods. Evidence of population structure was assessed using STRUCTURE (Pritchard et al. 2000). The data set was evaluated across 20 iterations at each K from 1 to 6. Notable changes in default program setting include a burn-in period of 40,000 replicates and 80,000 Markov chain Monte Carlo replicates. Structure Harvester was used to compile and format the resulting data (Earl and vonHoldt 2012). Results were visualized with all iterations at each K aligned and merged using the R package pophelper v2.3.1 (Francis 2017).

Single nucleotide polymorphisms

Portions of the biopsy tissue samples were sent directly to NeoGen Canada for processing, DNA extraction, and genotyping. Samples were genotyped according to standard Illumnia Infinium HD Ultra Assay protocol guideline on the GGP Equine-Bison chip (NeoGen). Initial data quality

control was done by NeoGen using Illumina's GenomeStudio with a call cutoff of 0.95. Details regarding the development of the SNP panel used in this study are described in Stroupe and Derr (2024). Briefly, a larger set of SNPs was filtered to a panel of 798 autosomal and 13 mitochondrial SNPs that was then evaluated in 995 bison across ten populations. This panel was found to be highly informative for individual identification and population distinction.

The Illumnia SNP Chip final report data was converted to plink lgen format using the script "illumina_to_lgen.R," originally written by Ryan Schubert (github@RyanSchu), with adjustments made to include metadata specific to our data set. In addition, a plink fam file was created from the sample list. Data were then converted into VCF format using Plink v1.9 (Purcell et al. 2007). Nuclear and mitochondrial SNP genotypes were analyzed separately in downstream analysis.

The nuclear SNP data set was further thinned to remove monomorphic SNPs and SNPs with a genotyping call rate below 90% among the Yellowstone samples, using VCFtools v0.1.16 (Danecek et al. 2011). Two samples had a genotyping call rate below 90% and were therefore removed resulting in a final SNP data set of 272 samples and 725 SNPs. Of those, 151 samples were collected during the summer breeding season.

A series of PCA were used to establish patterns in the data. Plink v1.9 (Purcell et al. 2007; Chang et al. 2015) was used to calculate eigenvalues and eigenvectors on the final data set and plotted with 95% confidence level ellipses using ggplot (Wickham 2016) in R v4.1.2 (R Core Team 2022). Observed heterozygosity (H_O), expected heterozygosity within populations (H_S), allelic richness (A_R), F_{ST}, and F_{IS} with 95% confidence intervals were calculated with the Hierfstat R package (Goudet 2005). F_{ST} was calculated using the Weir and Cockerham (1984) equation. Values calculated per individual or per loci were averaged across each population. These analyses were carried out in R v4.1.2 (R Core Team 2022).

fastStructure 1.0 (Raj et al. 2014) was then used to determine population structure among the samples with values of $K = 1$ to $K = 6$ and visualized using the R package pophelper v2.3.1 (Francis 2017). fastStructure chooseK.py was used to test for the most likely number of subpopulations.

Mitochondrial haplotype assignments were made according to Stroupe and Derr (2024). Briefly, mitochondrial SNPs originally identified by Forgacs et al. (2016) were used to assign interspecific haplotypes (bison or domestic cattle) and intraspecific clade haplotypes (Clade I or Clade II).

Results

Biopsy tissue samples were collected from 282 bison from Yellowstone National Park during the summer breeding season of 2019 and the winter of 2021. Collection location was used to group bison into either the Central or Northern Herd according to previous studies, migration patterns, population history, and observations (Meagher 1973, 1989; Halbert et al. 2012; Geremia et al. 2014) (Fig. 1). Collection time of year was used to distinguish samples during summer breeding season and winter migration. Of these samples, eight were identified as duplicates and removed from final analyses. All duplicate bison were sampled on the same range; however, two bison were sampled during both the summer and winter on the same range. In those cases, the sample collected during the summer breeding season was kept and the winter sample was removed from the data set. Additionally, two samples from the SNP data and three samples from the microsatellite data were removed due to a genotyping call rate below 90%. The summer breeding season samples included 151 bison in the SNP data set and 148 bison in microsatellite data set.

Samples were genotyped at 24 microsatellites (Schnabel et al. 2000; Halbert 2003), 798 autosomal SNPs, and 13 mitochondrial SNPs (Stroupe and Derr 2024). Microsatellite marker frequencies for individual loci can be found in Supplementary Table 1. The autosomal SNP data were further filtered to remove monomorphic variants and variants with a genotyping call rate below 90% resulting in a final data set of 725 autosomal SNPs. All microsatellites and mitochondrial SNPs passed the 90% call rate threshold. Genotyping call rates for the final data sets were 99.94% for microsatellites and 99.67% for SNPs.

Evidence of population structure and differentiation was evaluated using PCA, admixture analysis, and calculations of F_{ST} (Figs 2 and 3, Table 1). In the PCA of only samples collected during the summer breeding season, there is not a definitive separation between the breeding herds (Fig. 2). In the PCA based on 725 SNPs, the central herd seems to only contain a subset of the genetic diversity found within Yellowstone, whereas the northern herd has a wider distribution (Fig. 2a). In the PCA based on 24 microsatellites, there is more overlap between the two breeding herds sample distribution (Fig. 2b). The inclusion of samples collected during the winter migration did not substantially change the distribution of samples in the PCA for either herd (Supplementary Fig. 1). In fact, there are minimal differences between the PCAs of summer samples only and all samples besides the density of sample points. Additionally, admixture analyses, fastStructure, with 725 SNPs, and STRUCTURE, with 24 microsatellites, did not separate the geographically defined herds into genetically distinct subpopulations (Fig. 3, Supplementary Fig. 2). In the fastStructure analysis ran from $K = 1$ to $K = 6$ for only the samples collected during the breeding season, both the model complexity that maximizes marginal likelihood and model components used to explain the data structure were revealed to be equal, meaning the best fit for this data is one population (Fig. 3a). This was the same when including winter samples (Supplementary Fig. 2a). In the microsatellite-based STRUCTURE analysis, there was again no distinction between the two summer breeding herds (Fig. 3b). Evaluation of multiple runs revealed the best fit as $K = 3$ according to the delta K (Evanno et al. 2005), meaning there is evidence for three genetically defined clusters. However, this did not extend to geographically defined breeding herds. In fact, all samples seem to have an even representation of all clusters at all instances of K. Inclusion of samples collected during the winter migration was consistent with the summer only analysis in admixture of individuals; however, the best fit was $K = 2$ instead (Supplementary Fig. 2b).

Estimates of F_{ST} were used to measure genetic differentiation among each collection group using both the SNP and microsatellite data sets (Table 1). All F_{ST} estimates were less than or equal to 0.0050, with the confidence intervals for most comparisons overlapping and including zero. The central herd summer and winter samples had the lowest measures of differentiation in both the SNP and microsatellite comparisons, $F_{ST} = -0.007$ and -0.0043 respectively. In the

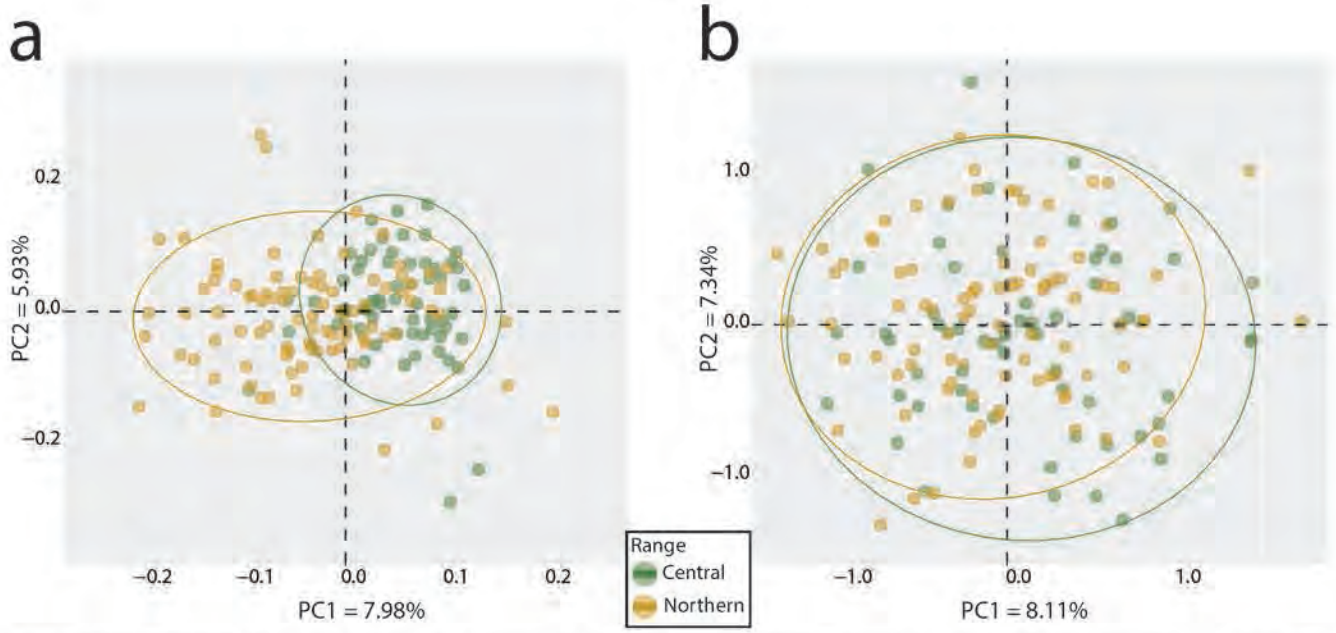

Fig. 2. Principal component analysis (PCA) plot of the summer breeding herds of Yellowstone bison using 725 SNPs (a) or 24 microsatellite markers (b). Breeding herds are identified by color with ellipses of 95% confidence intervals.

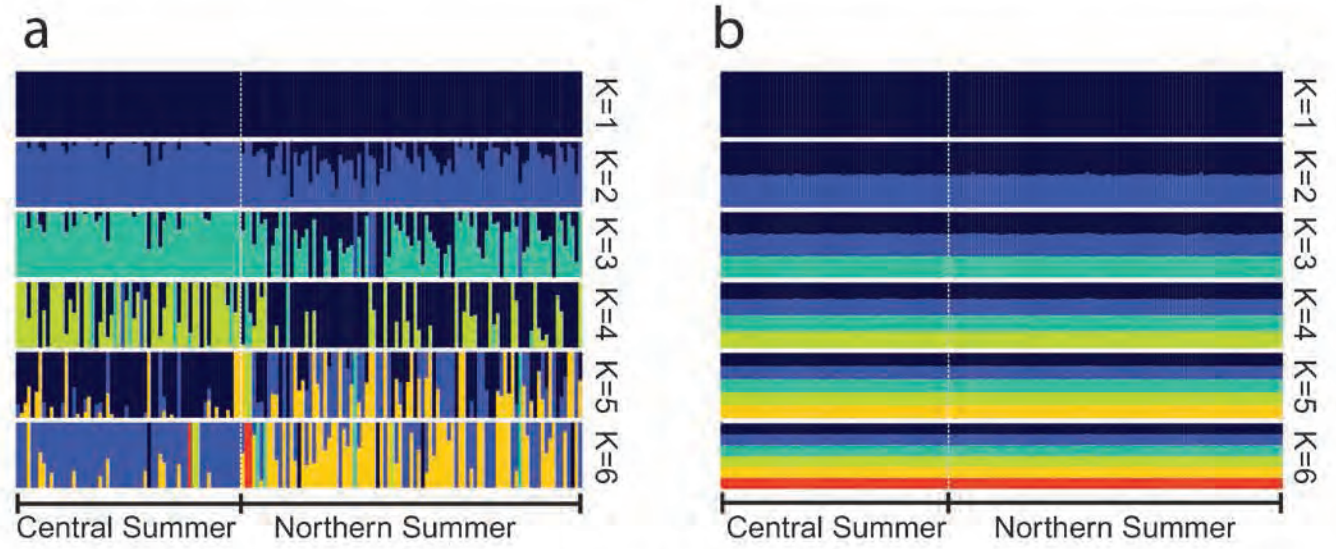

Fig. 3. Clustering plots of the Yellowstone bison breeding herds for $K = 1$ to $K = 6$ using fastStructure with 725 SNPs (a) or Structure with 24 microsatellite markers (b). Each vertical line represents an individual sample and horizontal bars represent a run for each K. Plots were generated using pophelper v2.3.1 (Francis 2017).

SNP comparison, the highest level of differentiation was between the central winter and northern summer samples (F_{ST} = 0.0050) though the 95% confidence interval overlapped with the central and northern summer comparison (F_{ST} = 0.0049). However, in the microsatellite comparison, the highest differentiation was between the central and northern summer samples (F_{ST} = 0.0044) though the 95% confidence interval overlapped with all comparisons except for the central herd summer and winter comparison.

To characterize the genetic diversity of each collection group (central herd—summer, central herd—winter, northern herd—summer, and northern herd—winter) estimates of mean observed heterozygosity (H_O), mean gene diversity within populations (H_S), mean F_{IS}, and mean allelic richness (A_R) were calculated across each group for 725 autosomal SNPs and 24 microsatellites (Supplementary Table 2). Estimates of genetic diversity had a larger range when calculated with the microsatellite data set compared to the SNP data set. In the SNP data set, the central herd had on average higher observed heterozygosity than the northern herd. Both central groups were above the overall mean (H_O = 0.4239), whereas both northern groups were below the overall mean. Though in the microsatellite data set, the central summer was above the overall mean (H_O = 0.5906) and the other groups were below the overall mean with the central winter group estimate the lowest. All 95% confidence level range estimates

Table 1. Measures of population differentiation (F_{ST}) between each grouping of Yellowstone bison defined by sample collection location and time of year. Estimates of F_{ST} are based on 725 SNPs or 24 microsatellite markers.

SNPs				
F_{ST}	Central Herd—Summer	Central Herd—Winter	Northern Herd—Summer	Northern Herd—Winter
Central Herd—Summer		−0.0007	0.0049	0.0018
Central Herd—Winter	−0.0007		0.0050	0.0011
Northern Herd—Summer	0.0049	0.0050		0.0013
Northern Herd—Winter	0.0018	0.0011	0.0013	
F_{ST} 95% CI	Central Herd—Summer	Central Herd—Winter	Northern Herd—Summer	Northern Herd—Winter
Central Herd—Summer		[−0.0019,0.0004]	[0.0039, 0.0058]	[0.0004, 0.0028]
Central Herd—Winter	[−0.0019,0.0004]		[0.0037, 0.0067]	[−0.0001, 0.0020]
Northern Herd—Summer	[0.0039, 0.0058]	[0.0037, 0.0067]		[0.0005, 0.0020]
Northern Herd—Winter	[0.0004, 0.0028]	[−0.0001, 0.0020]	[0.0005, 0.0020]	
Microsatellites				
F_{ST}	Central Herd—Summer	Central Herd—Winter	Northern Herd—Summer	Northern Herd—Winter
Central Herd—Summer		−0.0043	0.0044	0.0031
Central Herd—Winter	−0.0043		0.0008	0.0000
Northern Herd—Summer	0.0044	0.0008		0.0007
Northern Herd—Winter	0.0031	0.0000	0.0007	
F_{ST} 95% CI	Central Herd—Summer	Central Herd—Winter	Northern Herd—Summer	Northern Herd—Winter
Central Herd—Summer		[−0.0059, −0.0015]	[0.0017, 0.0077]	[−0.003, 0.0075]
Central Herd—Winter	[−0.0059, −0.0015]		[−0.0014, 0.0031]	[−0.0036, 0.0043]
Northern Herd—Summer	[0.0017, 0.0077]	[−0.0014, 0.0031]		[−0.0005, 0.0022]
Northern Herd—Winter	[−0.003, 0.0075]	[−0.0036, 0.0043]	[−0.0005, 0.0022]	

of mean F_{IS} calculations overlapped with each other and the overall mean 95% confidence interval in both data sets.

All Yellowstone animals had bison-derived mitochondrial haplotypes based on ten interspecific mtDNA SNPs (Ward et al. 1999; Forgacs et al. 2016; Forgacs 2019). No sample had evidence of domestic cattle mitochondrial DNA. Additionally, three SNPs distinguished the major intraspecific mitochondrial clades found in bison (Forgacs et al. 2016). All 272 samples in the final SNP data set were assigned a mitochondrial haplotype based on the criteria outlined in Stroupe and Derr (2024). Of the two bison-specific mitochondrial haplotype clades, Clade II had the highest frequency of 65% in overall assignment (Fig. 4). Within each group, Clade II was also the predominant mitochondrial haplotype. However, the central herd winter samples had the highest frequency of Clade II followed by central summer, northern winter, and northern summer with frequencies of 78%, 70%, 65%, and 57%, respectively.

Discussion

No evidence supports the hypothesis that the bison in Yellowstone National Park are currently composed of genetically distinct and independently breeding subpopulations. The presented genetic analyses using both microsatellite and SNP markers did not reveal substantial differentiation between bison sampled in the northern and central ranges during the summer breeding season. Moreover, analyses showed clear support for considering the bison in Yellowstone as one interbreeding population, composed of two subunits. However, there is undeniable evidence of multiple genetic lineages contributing to the current genetic diversity as can be seen from historic documentation and the presence of multiple maternal lineages.

The sets of microsatellites and SNPs used in this study have both been used in previous population genetic studies and have revealed genetic distinctions between related populations (Halbert and Derr 2008; Stroupe and Derr 2024). Therefore, it is unlikely the lack of population subdivision is due to a lack of sensitivity in the selected genetic markers. Both previous studies revealed an observational difference in multiple measures of genetic diversity between Yellowstone National Park and other federal bison populations. Based on estimates using the same set of SNP markers, the genetic differentiation between the Yellowstone National Park breeding herds is lower than between closely related federal bison populations such as Theodore Roosevelt National Park's North and South units (F_{ST} = 0.0049 vs 0.0884). Furthermore, the level of genetic differentiation in the Yellowstone breeding herds is more comparable to two Turner Enterprise Inc. bison populations, Snowcrest Ranch and Vermejo Park Ranch, that are derived from the same source and have been separated less than 8 yr (F_{ST} = 0.0049 vs 0.0030) (Stroupe and Derr 2024).

Although the SNP and microsatellite analyses both revealed the lack of subdivision among Yellowstone bison, there were some observed differences. PCA and admixture analysis using SNPs seemed to reveal a higher sensitivity of

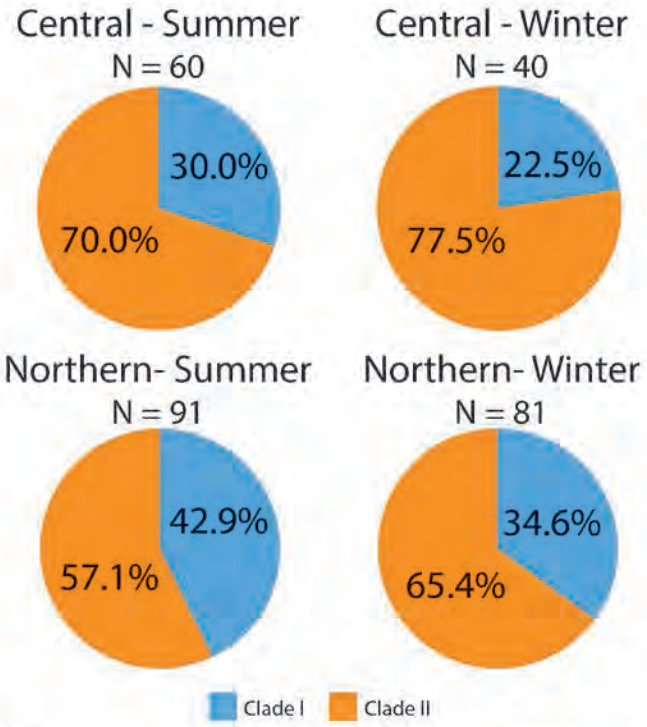

Fig. 4. Percentages of samples that were assigned to each mitochondrial haplotype, Clade I or II, for each grouping of Yellowstone bison, as defined by collection location and time of year. Bison mitochondrial clades are described by Forgacs et al. (2016).

subtle differences. PCA of SNPs exposed the central herd as a subset of the whole, whereas the microsatellite PCA showed no observable differences in the herds. Admixture analysis of the SNPs showed variable levels of admixture among samples, whereas the microsatellite data was congruent across samples. Differences could be due to the SNP data set being more sensitive to individual signals of admixture derived from multiple genetic lineages compared to microsatellites.

Due to anthropogenic movements of bison since the population bottleneck in the late 19th century, all modern bison populations are derived from multiple historic lineages, and all have evidence of domestic cattle introgression (Coder 1975; Stroupe et al. 2022). Therefore, when engaging in tasks such as gauging population divergence and migration rates, a comprehensive understanding of a population's historical trajectory is imperative for accurate interpretation of findings.

During the population bottleneck in the late 19th century, bison in the Greater Yellowstone Area consisted of a dwindling population of indigenous bison that had persisted since prehistoric times. However, when the population reached an estimated low of 23 individuals in 1902, genetically distinct animals were brought in from Montana (Pablo-Allard herd) and Texas (Goodnight herd) to form an introduced population in the northern range (Meagher 1973). Therefore, the bison in Yellowstone would be better described as initially two subpopulations of genetically distinct lineages that have become a single interbreeding population through gene flow, population growth, range expansion, response to environmental pressures, and migration instead of a historic divergence then convergence of a single source population (Meagher 1989, 2002; White and Wallen 2012).

Although previous studies provided evidence of genetic subdivision in Yellowstone bison, there is no evidence this persists in the modern population (Halbert et al. 2012b). No conclusions at the time could be drawn as to whether the identified genetic population substructure extended to the breeding groups due to limited location data during the summer breeding season. Additionally, two decades (1997–2003 vs 2019–2021) separated when the population was sampled and showed subdivision compared to the presented study, which did not. It is not clear if the observed differences represent a change in population dynamics over time, management actions, increase in apex predators, sampling strategy and study design, or a combination of these factors.

Our estimates of genetic differentiation between the central and northern breeding herds were much lower (Microsatellite $F_{ST} = 0.0044$, SNP $F_{ST} = 0.0049$) compared to previous estimates ($F_{ST} = 0.0321$) (Halbert et al. 2012b). This difference could represent a change in population structure over time or could be due to grouping samples by genetic cluster rather than geographic distribution or a combination thereof. Moreover, the previously estimated migration rate of two bison per generation between the two identified clusters is likely underestimated due to the separation of samples based on genetic clustering rather than location and lack of samples collected during the breeding season (Halbert et al. 2012b).

Throughout the years, there have been many changes in conditions and management that could alter the behavior and movement patterns of bison (White et al. 2015). Yellowstone National Park is one of the only places where bison population size and behavior freely respond to environmental changes such as predators, resource limitations, and climate. Furthermore, the Yellowstone bison population also fluctuates due to culling bison during the winter at the parks boundaries to reduce numbers and the risk of brucellosis transmission to domestic cattle (White et al. 2015; Geremia 2022). In some years, this management practice has resulted in the removal of over 1,000 animals from this population, with disproportionate removals from the central and northern herds (White et al. 2011; Geremia 2022).

In addition, we were able to evaluate maternal lineages and mitochondrial haplotype distribution within the Yellowstone bison population. Similar to the findings of Forgacs et al. (2016), mitochondrial haplotype clades I and II were distributed across the central and northern ranges in both the summer (breeding) and winter. These two mitochondrial haplotype clades likely reflect the mixed lineage history of indigenous and introduced animals that comprise the current Yellowstone National Park bison herd. Overall mitochondrial haplotypes from Clade II were found in higher frequency than Clade I haplotypes (65% for Clade II and 35% for Clade I) and Clade II was also found in higher frequency in both the Central and Northern populations in summer and winter collections (Fig. 4).

This reevaluation of the Yellowstone bison population to delineate the current population structure was able to improve upon previous studies by evaluating the two major summer breeding populations with previously used methods and new SNP-based technologies. The SNP panel has proved effective in population differentiation among closely related bison populations and estimating measures of genetic diversity (Stroupe and Derr 2024). The SNP-based evaluation of this important population provides a point-in-time observation of the Yellowstone bison. With the increased efficiency

of SNP-based platforms due to large number of loci, consistency, easier automation (Anderson and Garza 2006), lower mutation rates (Amorim and Pereira 2005), reduced influence of inbreeding (Fernández et al. 2013), ease of data sharing (Forcina and Leonard 2020), and an increase in precision and power for population genetics analyses over microsatellites (Zimmerman et al. 2020), there is more opportunity for utilization in long-term management. Moreover, samples collected during the breeding season are imperative for establishing the current structure since that is when genetic exchange between populations occurs and migration patterns can overlap in the winter ranges. Though the addition of samples collected in the winter in our analyses showed similar results.

Here we present evidence, developed from multiple analyses, that indicate bison within Yellowstone National Park represent a single interbreeding population. Even though there are multiple breeding herds and clear evidence of historical bison lineages, it appears substantial gene flow is occurring throughout the population. Thus, there is no way to confidently assign individuals outside of the summer breeding season to their respective breeding herd without tracking individual movement histories. The bison at Yellowstone National Park are an important biological resource that is essential to the long-term conservation of this species. Continued genetic monitoring is imperative to track genetic diversity indices of both nuclear and mitochondrial DNA in order to maintain stewardship of this iconic bison resource.

Supplementary Material

Supplementary material can be found at http://www.jhered.oxfordjournals.org/.

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Data Avaliability

The data underlying this article are available in the article and in its online supplementary material. Additional data will be shared on reasonable request to the corresponding author.

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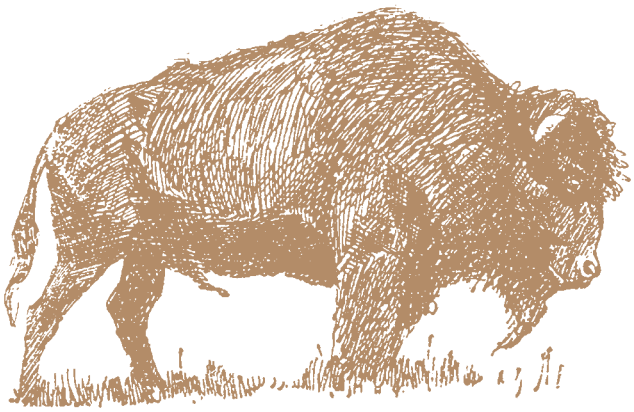
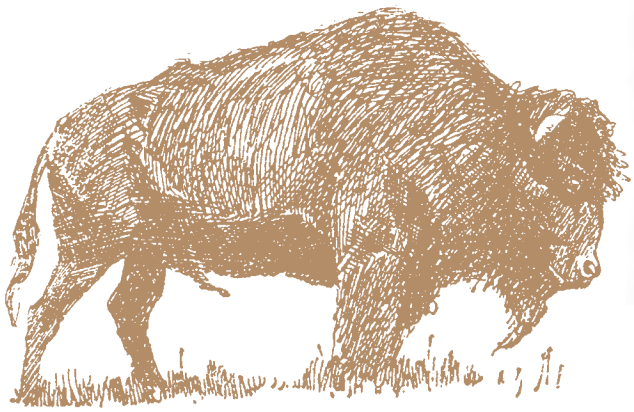
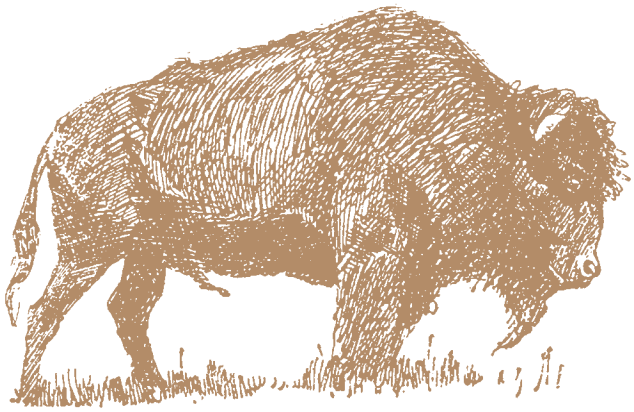
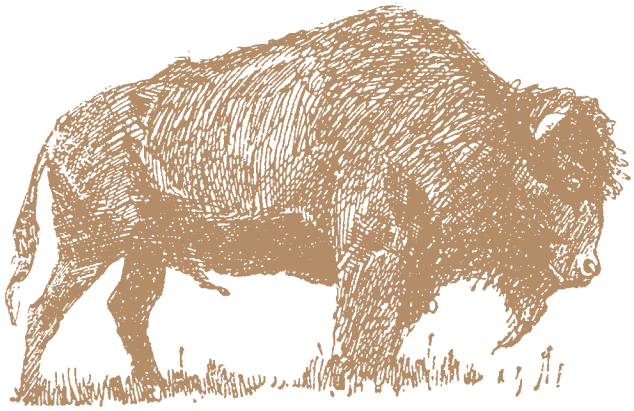








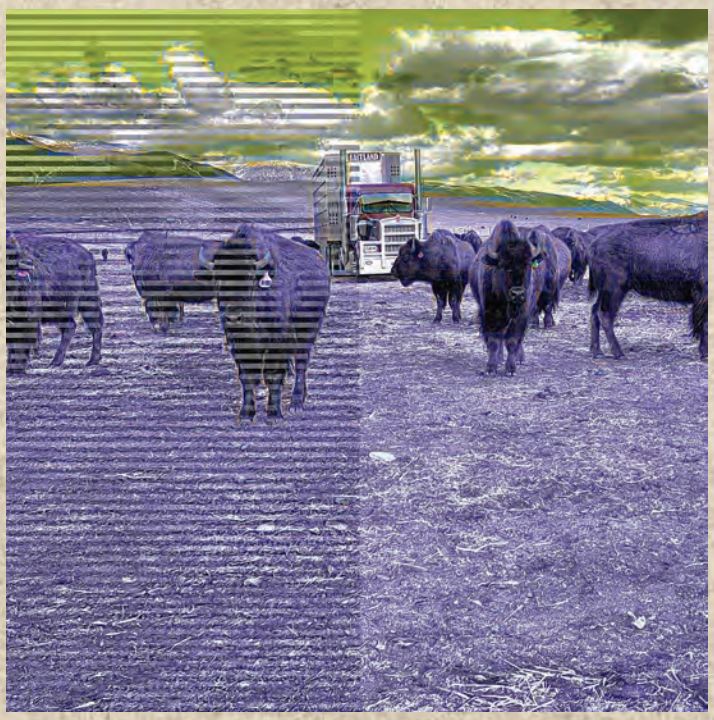
The Bison Buying Season Bison Sequestration Systems

Bison auctions abound, and private treaty sales are always afoot as folks plan to buy bison to add to their existing herd, start a new herd, or buy and sell food animals for the strongest conservation vehicle in this amazing story called North American bison. Commerce drives the conservation and preservation of the species, and, while we strive to be conscientious stewards of an ecologically important species, we all too often choose to focus on the fun stuff like show-champs, trophies, genetic diversity, conservation genetics, lineage, color, size/weight, vaccinations, grassfed, and regulatory preparedness for transit and entry. All these things are very important ethical boxes to check as buying and selling take place.

BUT, something else is also happening when buying and selling that you might not be aware of. Something right out of a sci-fi movie that is accurately identified as "alien" and "exotic," AND *we* are the transmission vehicle for it when we buy bison and bring 'em home! You guessed it: exotic parasites—parasites not originally from the grasslands where bison evolved alongside native parasite species for thousands of years.

So, OMG! Right? Yea, hold on a minute and understand that there are simple management techniques to stop the translocation-induced spread of exotic parasites in North American bison and their grasslands. That said, not very many bison stewards today understand the importance of it to the point of devising management strategies to stop it. Not even the US and Canadian Governments concern themselves with what they sell to the public, or gift to Tribal Nations. The Tribal governments, responding to federally gifted bison to ensure the culturally correct pairing of First Americans and North American bison, are also complicit in this ongoing faunal disruption causing the potential for biological problems. So, where did this all come from and who's to blame? Gotta have a villain, right?

Sorry folks, but the logical scientific surmise puts the beginning of exotic parasitism introduced by domesticated livestock to North America in about the year 1531. The worms have had a minute to build their ranks, right under our noses for the last 500-ish years. So, the biological beginnings are rooted in a lack of knowledge, concern and understanding. Today, the spread, or further faunal disruption of native ecosystems, can either be an inevitable repeat of past mistakes, or we change the way we perceive our place and responsibility as stewards to—this place. The latter is what we hope we do; the former is already done and cannot be undone. The future, our future as stewards of bison, North American grasslands, and ecosystems *can* be different.

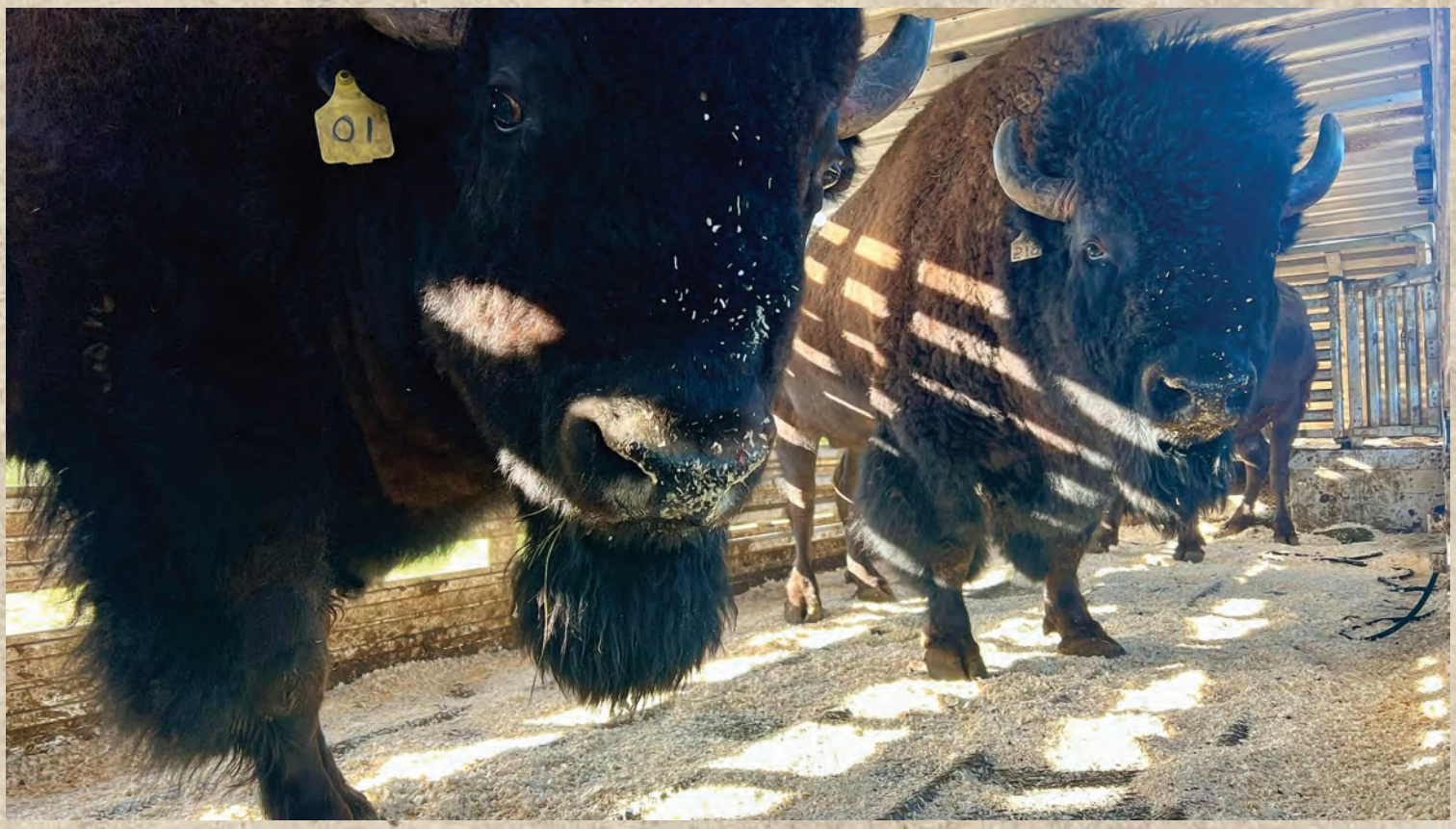


Bison Sequestration Systems are just what the name says and can be very effective. The concept of sequestration systems can also be perceived as quarantine, but we don't want what we are trying to accomplish to be confused with viral or bacterial issues in town-talk, or explanation to the public. We sequester bison for many reasons, sometimes to manage AU capacity issues on range and pasture to protect the grasslands from over grazing. A system, or strategy, to sequester new bison is very much about protecting your grassland as well. Protecting range and pasture from parasite infection. That's right! It's not just the bison that have worms, it's the grassland which becomes used by gastrointestinal nematodes (GIN) during the infective larvae stage to find a host (your bison) and begin their biological cycle to pass on their DNA to offspring. And they're good at it too! So, when your new bison bring in new variations of exotic parasites originating from exotic grazers like sheep, goats, and cattle, they immediately begin to infect the grasslands through fecal deposits and hatching eggs, which produce third stage larvae (L3), or "infective larvae." Ok, so that's the problem. Now for the solution. To actively mitigate or control the translocation of exotic parasites from across North America we need to be more aware of what we bring home ***with*** our new bison. The only way to get that information is from the bison themselves. The only way to rule out the parasites that already exist on YOUR grassland, is to sequester the new recruits in a small pasture, or a large pen. A spacious pen, with no grass, is my choice to prevent reinfection. This is also a good idea for behaviorally organizing new bison, which is also referred to as soft release.

A *system* of sequestration for parasites involves a few parts: The infrastructure to hold and care for the bison, the lab work to determine the infection type and level, the ability to treat the bison if they are infected, knowledge of how to treat the infections they have, the efficacy testing to confirm the fecal egg count reduction (FECR), the time and patience to wait on assurances that the L4's don't jump out after the initial treatment, and finally a clean report and turn out, with the confidence that the only parasites in your ecosystem come from the bison, other grazers and wildlife, from your locality.

Let's go through the process of buying bison and using a sequestration system to protect your grassland.

1.0) Purchase bison from a sale, park, or producer. Load' em up and bring' em home?
  1.1) Yes-ish. You should also try to get all available the animal information from the source.
  1.2) The information should include the deworming history including the drugs used recently on the herd and the animals you've purchased.
2.0) Unload and give them a couple of days to get over their trip physically.
  2.1) It is not unusual to see very high Eimeria and elevated EPG numbers right after a trip.
  2.1) Waiting three to five days should give you a more accurate look.
3.0) Collect fecal samples and send to a parasitology lab.
  3.1) My choice of labs is the Diagnostic Parasitology Lab at TAMU
  3.1) Whichever lab you use will need to have the ability to determine the EPG and the larvae genus from Coproculture very accurately, as well as the "Other Parasites" that also matter, but can be identified visually with certainty.
4.0) Consult accredited people about treating your newly purchased internal parasites.
  4.1) Accredited people for anything-bison may include veterinarians, parasitologists, or folks with lab report records of drug efficacy on bison.
  4.1) Accredited people on anything-bison should NEVER include anyone who has not confirmed results with certain drug types and dosages without lab work.
5.0) Organize your treatment-strategy.
  5.1) Treatment for parasites is a game of accuracy. REMEMBER: Every time you treat, you risk resistance to that drug family. That means get it right, then check on the fecal egg count reduction by testing again 10 – 14 days after treatment, *a.k.a: Efficacy Testing*.
  5.1) Treatment "strategies" absolutely include distribution. This means the method used for getting the drug into the bison. Sounds easy right? The bane of my consulting existence with worms and bison is distribution methods. Behavior is 90% of the battle, and trick. This can apply to field treatment more than chute works,



but it can also include percentages above label dosage-targets to account for dominant bison feeding behaviors, or water treatment accounting for bison-specific requirements and waste.

6.0) Treat the bison.

6.1) Check your process and treat the bison.

6.1) So, they're wormed right? HA! Stay nervous until the FECR report is in from the lab.

7.0) Do the most important test—10-14 days after treatment—Efficacy Test.

7.1) Drug Efficacy testing that hopefully results in zero/acceptable FECR's is a must if your goal is to rid the animals of parasites.

7.1) This test may cause you to (a) be frustrated /mad, (b) revisit drugs and dosages, (c) revisit drug distribution, (d) pull your hair out, (e) consult the accredited folks you lean on for guidance, (f) change which people you get advice from, and/or (g) all the above.

7.1) The efficacy test may also cause you to be satisfied that your new bison are without any translocated internal parasites.

7.1)1. If the infection level was high, or very high, then you should consider a different next step by waiting for about 5 weeks and then retesting the bison. If the infection level was low or moderate, then you might be ok to turn out with confidence. Hypobiotic 4th stage larvae (L4) cannot be killed with any drug known. They are alive, but not alive, and they often emerge after a big population is killed. It takes about 5 weeks to be sure that all the L4's have had a chance to come out and become EPG reporting adults. Sorry folks, I don't make the worm rules, but I've learned the hard way that we need to play by them.

8.0) Retest the bison in 5-ish weeks after the first treatment if 7.3)1 is your scenario.

8.1) It's a big deal to do a second round of testing when the initial EPGs are extremely high, even when after the first treatment you achieved a 0.00 EPG.

8.1) Retreat the bison using the SAME

DRUG that worked the first time.

8.1)1. Many bison stewards have been indoctrinated into a flawed perspective of switching up deworming drugs as a routine, or rule, in an effort to keep the parasites off balance and prevent resistance in the worms to drugs. That doesn't work and the parasitology community agrees. The research shows, and parasitologists will tell you, that alternating drugs was a good idea that met with a fatal fact – It Doesn't Work! Use the efficacious drug as long as it works, then switch or play around with different off-label dosages safely if a problem arises.

9.0) Guess what? Time to do another efficacy test 10 to 14 days after treatment.

9.1) I know, I know – do it to make sure. It's worth it to accomplish the management target.

10.0) TURN OUT! Yay! You've done your part as a steward of the existing herd's health and a conservationist of your ecosystem by stopping the spread of Exotic Parasitism in American bison.

So, why not just wing-it and wait until you work the existing herd on the normally planned bison work? Personally, I think that's a great question to ask. Unfortunately, I have an answer and reason for that being a very bad idea. It's all about the threat of the devil you don't know because you can't see it. Let's take this, one scenario at a time:

11.0) If you already see Nematodirus in your reports, which can be common, the pathogenic threat is low unless the visual count is very high. If you bring in Nematodirus battus with new bison, the pathogenic threat is high if they are present in any number.

12.0) If you have typical EPG's running in the 30's and 40's with Cooperia and Haemonchus, your herds pathogenic threat, or disease level concern, is very low. If you then bring in Ostertagia *ostertagi*, the same EPG's may flag a high potential for pathogenic threat.

13.0) If you buy a set of calves and they are carrying Toxocara Vitulorum, the grasslands can become a reservoir for a known calf killer for many years. If you sequester, identify, and treat the calves, the grasslands will not become infected. The producer, or source, may be unaware of the problem. This parasite operates via embryonated egg in the environment for many years waiting for a host. Its life cycle once up taken, involves passage through the mammary glands of what's known as the paratenic host, and the infective larvae are transmitted to the nursing calf. It is a known calf-killer and can be stopped in the calf once the parasite becomes an adult and reports eggs. Unfortunately, it is undetectable in the mature female host. I have successfully treated bison calf crops with field-treatment for this parasite with 100% efficacy. It's a good parasite to stop at the door when you can.

14.0) If you have streams and ponds on your property, and you bring bison in with Liver Flukes, you will have Liver Flukes from that point forward so long as the environment is suitable. You could have stopped them by testing and killing them before turning out using a sequestration system strategy.

15.0) For bison who are being fed for food animals on pasture, or even in spacious pens on dirt, the process of checking the infection levels and efficacy of treatment is a money maker.

Allowing an afront to healthy bodily functions to persist, or introducing new parasites to a growing population may cause problems.

16.0) Introducing new parasites to an existing herd that is responding well to treatment may cause a change in the response to treatment of the newly combined herd. Crossbreeding sensitive (to a drug family) parasites with resistant parasites can produce higher sensitivity to treatment, however, if you introduce new parasites that are resistant to breed with the sensitive parasites you already have, you may observe more resistance to treatment than before. If the bison you purchase have been recently treated for internal parasites and still have EPGs in the low to moderate range, you could be bringing in genetic resistance to your existing herds internal parasites. Parasite resistance to drug treatment is a global conversation.

The economics of rolling up your sleeves and taking parasites seriously when you purchase new bison can be big. I have seen disease-level parasitism take out 15 to 60 percent of a herd's population. The diagnosis can sometimes get mixed up with viral and bacterial complications. The bison may have succumbed to something like M. *bovis*, but the 'whole story' involves disease level GIN infections with low body condition scores (BCS). A low BCS flags organ damage from the parasites that can easily take 4 to 6 months to repair, which also represents an economic burden. The bison are weak and frail during this repair period and can be taken down easily by many things. For people who struggle with healing a herd while on pasture, reinfection becomes part of the problem as well. That's why we call it disease "cycle." We don't have it licked until the reinfection from a larvae laden grassland is corrected.

The buying and selling season is a critical aspect of the bison industry and our place in the restoration of the species. Through our actions in the market, we emulate nature, and by so doing, we cause the bison species to be more robust and secure. Don't be scared to purchase bison from various reputable sources. Be weary of what the seller, including governments, may say to reassure or comfort you as a buyer. They are not misleading you, but they may be unaware. Check on your newly purchased parasites for yourself when you get them home. You paid for them, so you might as well see what you got for the money.

The Texas Bison Parasitology Stakeholder Citizen Science & Observations Initiative (TXBPSCSOI), or TXBP for short, is a citizen science group that is always available to help bison stewards with Parasitology. TXBP also produces tools to help like the SVA Small Parcel Shipment program for reduced shipping costs, the TXBP TRACKER TOOL which helps keep track of your herds parasites, and the occasional Special Report when something interesting is observed and the participating collaborators give permission to share. TXBP is the first citizen science group that is all about bison parasitology. Its purpose does NOT involve dues, memberships, or donations, but relies solely on solving problems, and sharing information and data. This TXBP Citizen Science group can be found with a simple google search for Bison Parasitology or go to Frasier Bison LLC.

Preemptive management to reduce losses is the economic benefit of being conscientious. Losses can be animals, or reduced production. When we, the Buffalo People, talk conservation about our amazing animal, we should accept our responsibility to the entire ecological system. If we, as conservationists, disregard the faunal disruption of exotic parasite translocation, then we are not conserving, or tending with care, a place.

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