Bison Conservation Genetics and Disease

James Derr
Department of Veterinary Pathobiology
and the Graduate Faculty of Genetics
Texas ***Agri***LIFE – Research
Texas A&M System

TEXAS A&M
UNIVERSITY
COLLEGE OF
VETERINARY
MEDICINE

VETERINARY PATHOBIOLOGY

The Bison Genetics Program at Texas A&M University

Ph.D students: the Brains and the Brawn

Todd J. Ward, Ph.D.

"An Evaluation of the Outcome of Interspecific Hybridization Events Coincident with Dramatic Demographic Decline in North American Bison." Graduated in May of 2000 and he is employed at the USDA National Center for Agriculture Utilization Research in Peoria, IL.

Robert Schnabel, Ph.D

"Developing DNA-Based Technologies in North American Bison: Parentage Testing, Linkage Mapping and QTL Scans." He worked for 18 months for the USDA in Beltsville, MD as a research scientist and is now a Research Assistant Professor in the Department of Animal Sciences at the University of Missouri.

Natalie Halbert, Ph.D.

"The Utilization of Genetic Markers to Resolve Modern Management Issues in Historic Bison Populations: Implications for Species Conservation." She is currently employed as a Research Assistant Professor in the Department of Veterinary Pathobiology at Texas A&M University.

Christopher Seabury, Ph.D

*"Genetic Evaluation Of The Ovine And Bovine Prion Protein Genes (*PRNP*)". He is employed as a Postdoctoral Research Associate in the Department of Veterinary at Texas A&M University.*

From a Species Conservation Point of View, Bison are Ultimate Survivors

- They have survived:
  - Multiple historic climatic periods with extreme temperature, moisture and ecological changes.
  - Imported parasitic, bacterial and viral diseases from Europe and Africa.
  - Widespread habitat destruction and population fragmentation.
  - One of the most dramatic population crashes and one of the most documented population recoveries of any wildlife species.
  - Forced hybridization with another species.

My goal today is briefly discuss 3 bison genetic issues.

- Conservation genomics and the role of Yellowstone NP in these long term efforts.
- Genome integrity and why contamination of bison genomes with domestic cattle genes is important.
- Should there be more effort to investigate genetic resistance / susceptibility genes in bison brucellosis research?

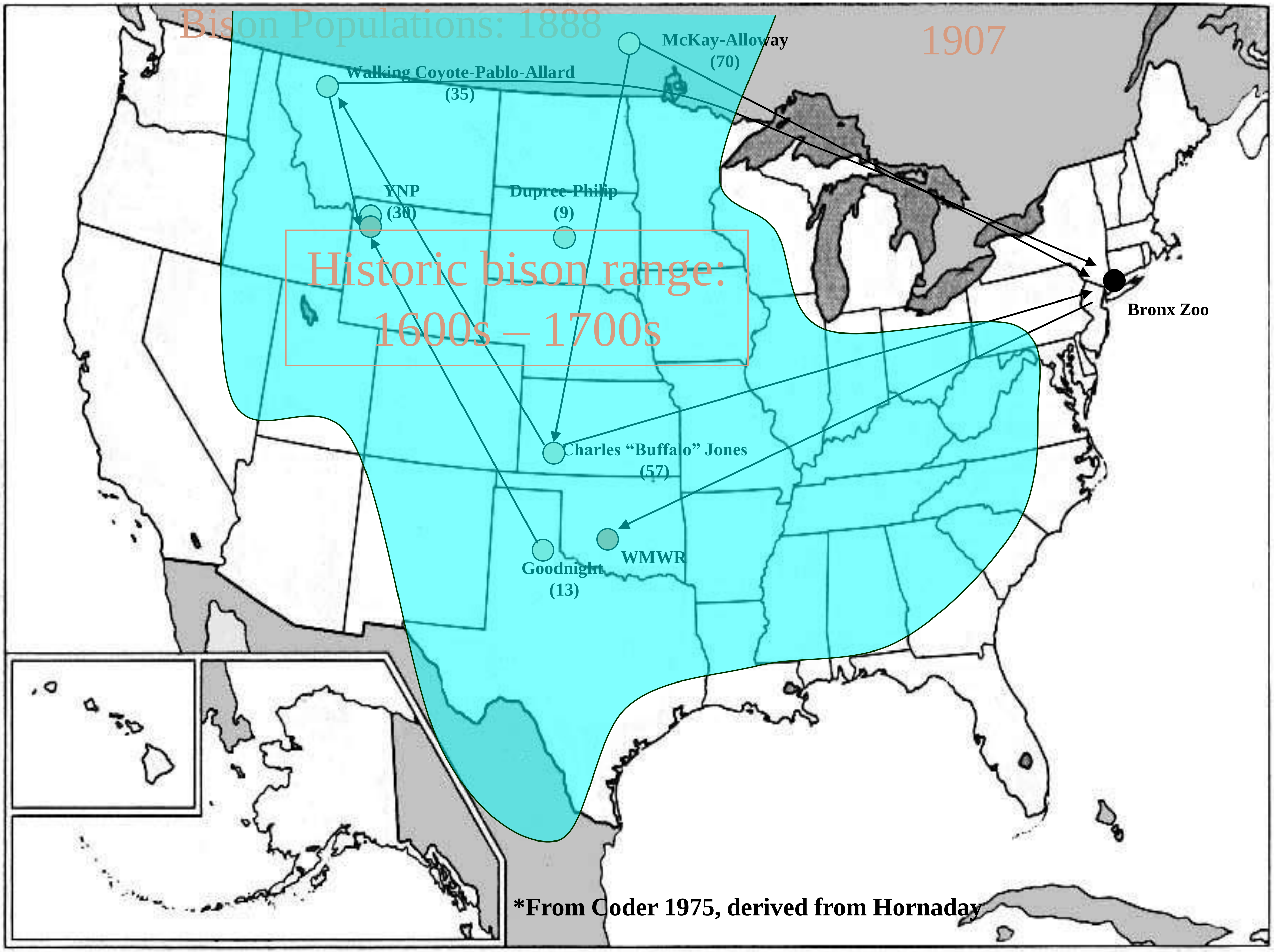
American Bison Conservation Genomics

***Conservation genomics is the use of biotechnology for the conservation, preservation and restoration of biodiversity*.**

- Genetic diversity is directly proportional to a species ability to adapt, survive and thrive and the loss of genetic diversity is detrimental to overall population health and long-term survival.
- To date, one of the most detailed conservation genomics studies of any wildlife species focused on American bison.
- This species experienced severe and well documented population declines between 1800 and 1900 that reduced the census size of this species by over 99%.
- The spectacular recovery to over 700,000 animals present today is a testament to their genetic constitution and represents one of the most significant accomplishments in modern conservation biology.

Bison Populations: 1888

1907



Historic bison range:
1600s – 1700s

*From Coder 1975, derived from Hornaday

Public Bison Populations Sampled for Genetic Studies

State & Private Herds

Antelope Island State Park, UT
Henry Mountains, UT
Custer State Park, SD
Finney Game Refuge, KS
Maxwell Game Refuge, KS
Texas State Bison Herd, TX
Santa Catalina Island, CA

NGO and Native American Herds

The Nature Conservancy herds in AB, CO, KS, NE, OK, SK.

Native American Herds in SD, ND, NM.

More than 100 private bison herds

Federal Herds

Wichita Mtns. NWR
Ft. Niobrara NWR
National Bison Range NWR
Neal Smith NWR
Sully's Hill National Preserve
Badlands NP
Theodore Roosevelt NP
Wind Cave NP
Grand Teton NP
Yellowstone NP
Wood Buffalo NP (Can.)
Elk island NP (Can.)
Mackenzie Sanctuary (Can.)

To date, over 18,000 bison DNA samples analyzed

Sampling Strategy

Attempted to collect at least 20% of the census size of each herd

Herd name[a] (Abbreviation)	**Location**	**Census**	**Total sampled**
Badlands NP (BNP)	South Dakota	875	328
Fort Niobrara NWR (FN)	Nebraska	380	178
Grand Teton NP (GT)	Wyoming	600	39[d]
National Bison Range (NBR)	Montana	350	179[d]
Neal Smith NWR (NS)	Iowa	63	62
Sully's Hill NGP (SUH)	North Dakota[b]	35	29[d]
Theodore Roosevelt NP – North Unit (TRN)	North Dakota	312	309
Theodore Roosevelt NP – South Unit (TRS)	North Dakota	371	368[d]
Wichita Mountains NWR (WM)	Oklahoma	600	37[d]
Wind Cave NP (WC)	South Dakota	350	345
Yellowstone NP (YNP)	Wyoming[c]	3000	505[d]
	Total	**6936**	**2379**

[a] NP, National Park (National Park Service herd); NWR, National Wildlife Refuge (Fish and Wildlife Service herd); NGP, National Game Preserve (Fish and Wildlife Service herd)

[b] in 2006, the entire SUH herd was moved into an isolated enclosure within the Fort Niobrara National Wildlife Refuge

[c] Parts of Yellowstone NP lie within the states of Idaho and Montana

[d] Sex determined by microsatellite typing in some cases

Just give me the results.

Summary Statistics

Based on 54 Microsatellite Loci

	BNP	**FN**	**GT**	**NBR**	**NS**	**SUH**	**TRN**	**TRS**	**WC**	**WM**	**YNP**	**TSBH**
% total alleles[a]	69.9%	67.5%	62.6%	76.7%	76.1%	55.5%	54.6%	66.0%	74.5%	63.8%	74.2%	39.0%
N_A[b]	4.6	4.4	4.1	5.0	5.0	3.6	3.6	4.3	4.9	4.2	4.8	2.5
H_E[c]	57.8	59.5	56.1	64.6	63.9	56.6	52.2	58.2	65.2	59.1	62.5	37.7
Private Alleles	2	1	0	6	0	0	0	1	10	2	4	4
Fixed Loci	0	0	1	0	0	0	2	0	0	0	0	7

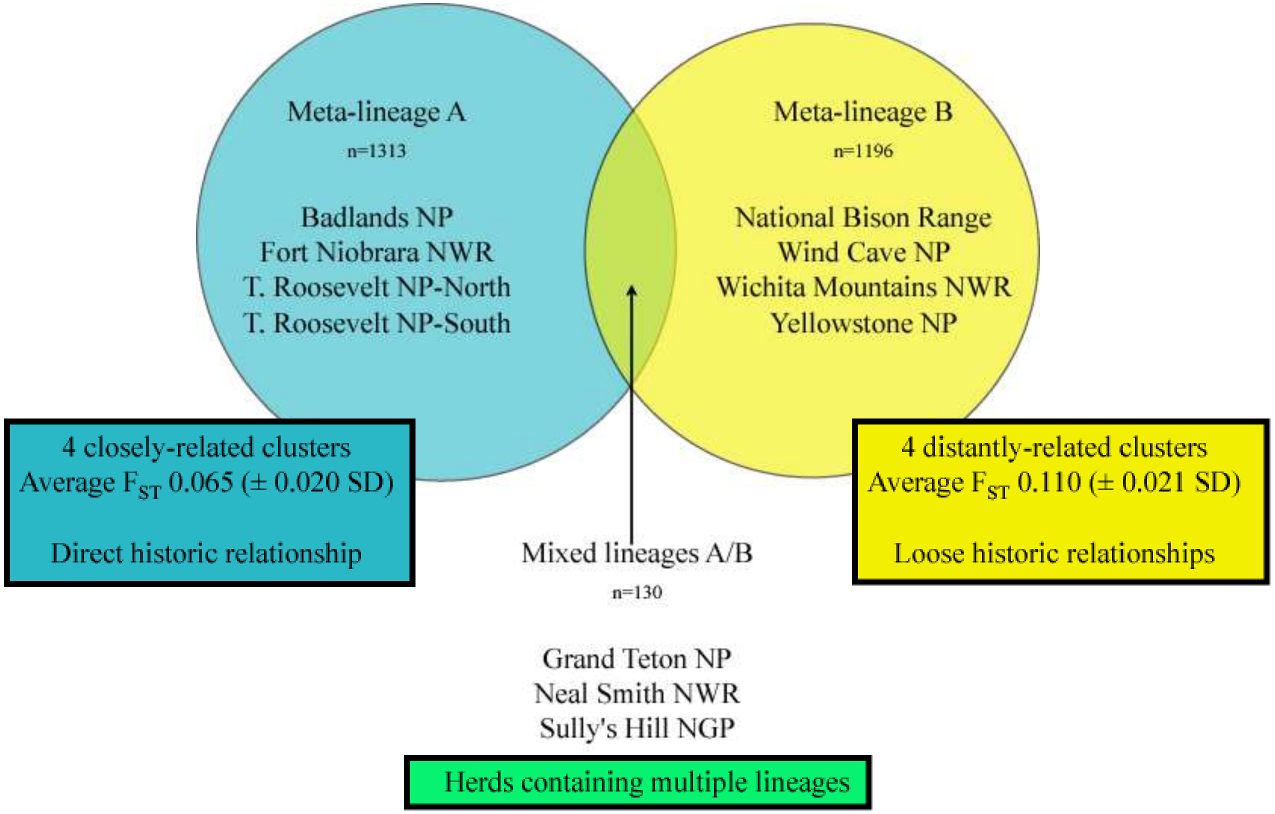
[a] % of alleles present in each population based on 326 total alleles identified in this study

[b] N_A, average number of alleles per locus

[c] H_E, average expected heterozygosity

Genetic relationships among US federal herds

based on STRUCTURE analysis



Meta-lineage A
n=1313

Badlands NP
Fort Niobrara NWR
T. Roosevelt NP-North
T. Roosevelt NP-South

Meta-lineage B
n=1196

National Bison Range
Wind Cave NP
Wichita Mountains NWR
Yellowstone NP

4 closely-related clusters
Average F_{ST} 0.065 (± 0.020 SD)

Direct historic relationship

Mixed lineages A/B
n=130

Grand Teton NP
Neal Smith NWR
Sully's Hill NGP

4 distantly-related clusters
Average F_{ST} 0.110 (± 0.021 SD)

Loose historic relationships

Herds containing multiple lineages

The US Federal Herds:
Population Level Conclusions

- Despite historic bottleneck, bison populations in general, have reasonable and apparently healthy levels of genetic variation compared with other large mammals.
- Clear differences in genetic variation and diversity exist among populations based on their histories, population size and management.
- Genetic relationships are generally consistent with known population histories.
- More on this later.

An analysis of domestic cattle introgression in some important U.S. bison populations ….

The cold, hard facts….

Some bison just look different?

Photo supplied by Elaine Leslie

Don’t forget, hybrids happen

But most bison (hybrid or not) look just fine..

photo supplied by D. Sweepton

Nevertheless.. Hybrids do Happen.

- The hybridization experiments conducted by some of the owners of the five foundation herds of the late 1800s, have left a legacy of a small amount of cattle genetics in many of our existing bison herds.

The Technology

Currently technology.

-Mitochondrial DNA sequencing and genotyping to identify and define domestic cattle maternal lineages.

(T. Ward and N. Halbert (and others) worked to develop these procedures).

-Nuclear microsatellites markers developed from bovine positional cloning and gene mapping projects to uncover evidence of hybridization and to estimate relative levels of cattle introgression.

(T. Ward, R. Schnabel and N. Halbert (among others) conspired to develop these procedures)

mtDNA results - federal, state and private bison herds

- 5,246 bison sampled from all 12 US federal populations. All appear free of cattle mtDNA except for a small number of animals (14) at the National Bison Range*. The origin of introgression was confirmed through DNA sequencing.

  14 / 5,246 animals = 0.2668%

- 5,655 bison sampled from over 100 private, State and NGO populations. Evidence of domestic cattle mtDNA was found in all of these herds except for a very few.

  387/5,655 animals = 6.84%.

So what if a bison herd has cattle mtDNA?

Clearly, the ability to identify bison populations with hybrid ancestry provides information to make responsible conservation decisions regarding the introduction of animals into bison populations that have no evidence of past hybridization.

In addition, ongoing studies appear to support the observation that there is a “biological” disadvantage in bison with cattle mtDNA…

Nuclear Genome: *Microsatellite Markers For Hybrid Detection*

Determine the frequency of cattle chromosome regions in bison genomes using a set of 14 unlinked microsatellite markers with a statistical framework to determine the power of hybrid detection based on the frequency of cattle alleles and the number of animals examined.

Diagnosed hybrid populations:

- Linked markers
- Allele sequencing (repeat-flanking region)

Bison Hybridization Summary

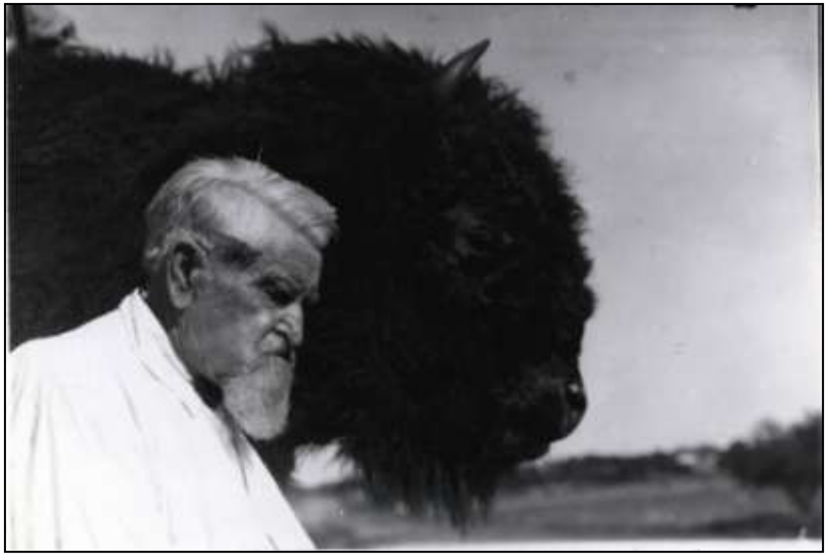
- Based on mitochondrial and microsatellite investigations, domestic cattle introgression is present in most US federal bison herds except possibly Yellowstone NP and Wind Cave NP (please note I'm not using the word "PURE" to describe these herds).
- Our study did not include enough samples from Grand Teton NP and not enough total animals in the Sully's Hill National Game Preserve herd have a reasonable chance of finding cattle markers. Nevertheless, the lineage histories of both of these herds includes animals from hybrid herds.
- Estimated levels in federal herds identified to have cattle genetics were all very low compared with the total bison genes in the herd.

Bison Hybridization Summary (cont.)

- All private and State bison herds investigated (over 100) have evidence of nuclear and/or mitochondrial introgression from domestic cattle with the exception of the private Castle Rock herd on the Vermejo Park Ranch in New Mexico.
- Additionally, the Henry Mountains bison herd in Utah may be free of cattle introgression based on it’s reported unbranched lineage to Yellowstone NP and a limited number of DNA samples tested (> 50 animals). This should be confirmed.
- There are a few possible Alaskan herds (Delta Junction Herd and/or the Farewell herd) that were established from NBR and may pre-date this introduction event of cattle genetics. If this is true, then these herds are the only surviving intact genomes from the NBR lineage.
- There are a few recent satellite herds that consist of animals from the Yellowstone NP lineage without evidence of domestic cattle introgression (American Prairie Foundation, The Nature Conservancy, the USDA quarantined herd and some private herds.

Why do we all care about this genetics stuff?

For bison, or any other species, for their long-term conservation and healthy production, a major consideration must be the preservation of their germplasm.



If this germplasm is lost through extinction, genetic drift or diluted and contaminated through extensive hybridization it can never be fully recovered.

The Role of Yellowstone NP in the Conservation of Bison

- Only historic bison herd in the US that retained animals continuously through the bottleneck.
- The largest US federal bison herd based on census size and landscape resulting in the only herd with distinct population substructure.
- Comparatively high and healthy levels of genetic diversity.
- No evidence of domestic cattle genetic contamination and all US bison herds without evidence of cattle genes are related to the YNP herd.
- Yellowstone NP bison herd is the “Spoke in The Wheel” for US bison conservation with many important genetic and historical indices for American bison emanating for this population.

Should there be more effort to investigate genetic resistance / susceptibility genes in bison brucellosis research?

Diane Hargreaves.com

Genetic resistance genes for brucellosis research in bison..

- I think Yes, with caution.
- Disease resistance in livestock has made significant advances since the completion of the genome sequencing projects.
- USDA and NIH are currently funding genetic resistance studies.
- The only published association of a gene variant and brucellosis was reported from the PRNP gene (Seabury et.al. 2005).
- Many addition genes have now been characterized should be investigated in bison.
- However, any breeding plan that includes single gene selection for or against genetic traits must be very well planned and monitored.

With an eye toward the future of bison conservation and preservation…

Greater Yellowstone region bison have historically and still are one of the most important herds in the long term conservation of this species.

However, disease limits and complicates the role of this herd species conservation.

Therefore, as satellite herds are developed (by various methods) that are free of disease, free of cattle genetics and that have high levels of diversity, the significance of this herd for species conservation will diminish.

The good news is that Yellowstone bison genetic diversity is being removed and preserved in satellite herds to insure responsible stewardship and long term conservation in spite of this disease.