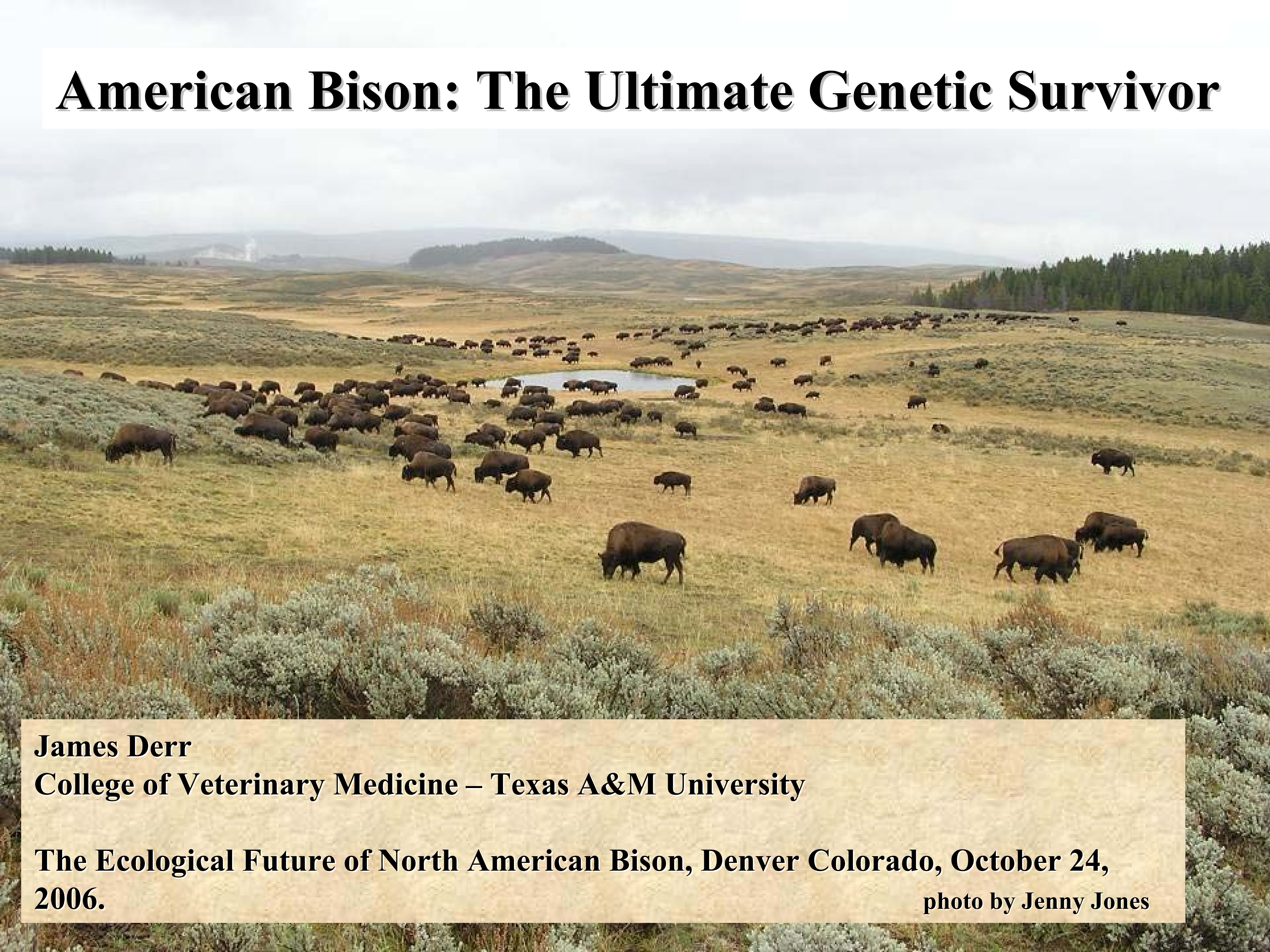
American Bison: The Ultimate Genetic Survivor



James Derr
College of Veterinary Medicine – Texas A&M University

The Ecological Future of North American Bison, Denver Colorado, October 24, 2006.

photo by Jenny Jones

Ph.D Students in the Bison Genetics Program at Texas A&M University

Todd J. Ward, Ph.D. 2000. “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. 2001. “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. 2003. “The Utilization of Genetic Markers to Resolve Modern Management Issues in Historic Bison Populations: Implications for Species Conservation.” She is currently employed as a postdoctoral research assistant in the Department of Large Animal Medicine and the Department of Veterinary Pathobiology at Texas A&M University.

Christopher Seabury, Ph.D. 2004. “Genetic Evaluation Of The Ovine And Bovine Prion Protein Genes (*PRNP*)”. He is employed as a postdoctoral research assistant in the Department of Integrated Biosciences at Texas A&M University.

Bison as a Conservation Model for Genetic Survival

For many, the field of conservation biology is often considered a "crisis discipline" because many of the species that are of interest are critically threatened in some way.

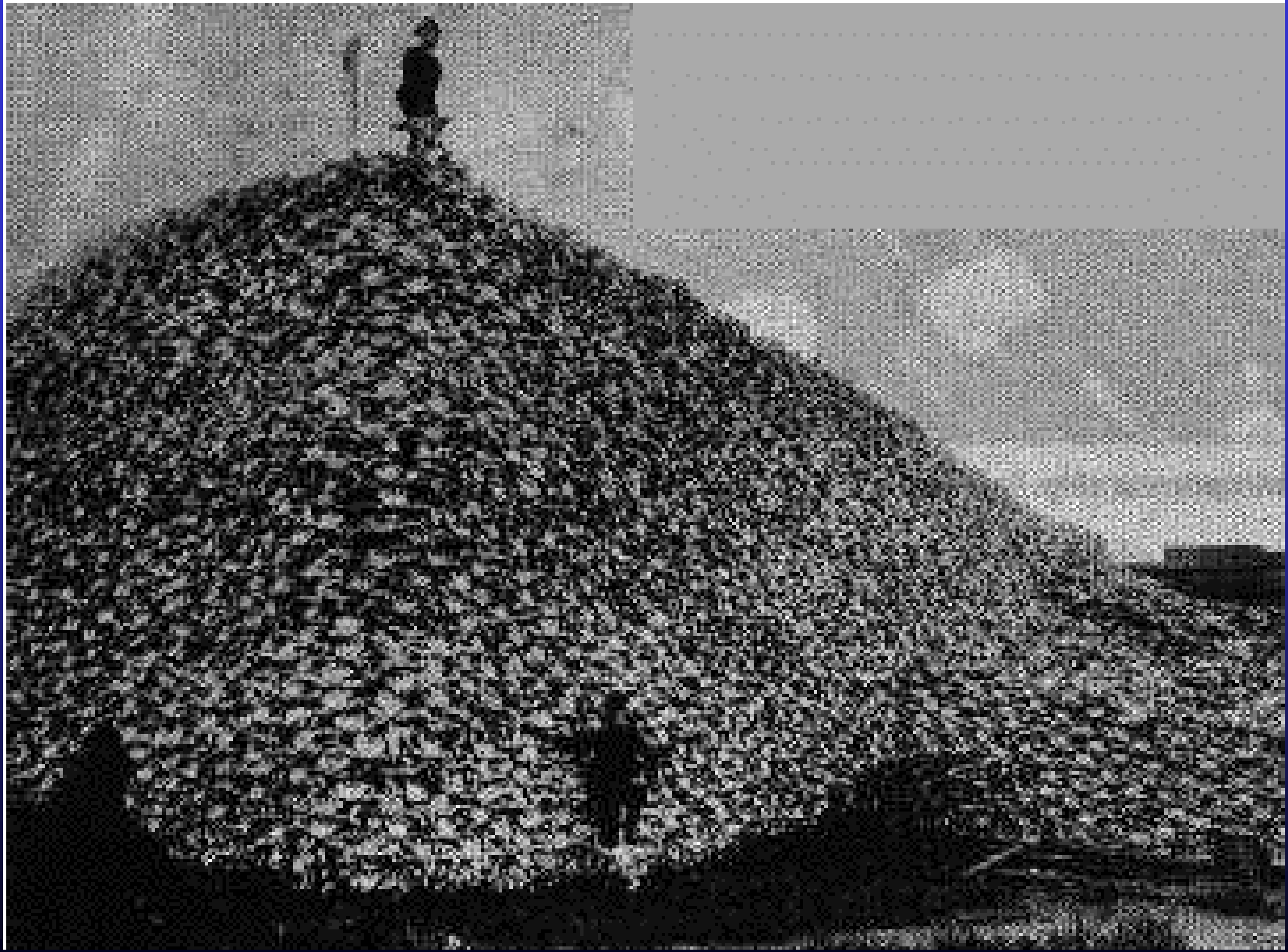
Clearly, as we heard from multiple speakers yesterday, the recovery of North American bison is one of the best documented success stories in conservation biology. About 10 years ago we started a series of comprehensive studies of bison conservation genetics that we hoped would allow us to incorporate what we learn into the long-term management of other species that are currently threatened or endangered.

Just to quickly review North American bison history

- Bison suffered a well documented population decline that between 1840 to 1905.
- Population numbers were reduced from millions to a few hundred animals distributed across North America.
- Although most of the blame for this tragedy falls on hunters , a number of other explanations are available. (Even, as we heard last night, preservation of our national masculinity..)
- An analysis of the fossil record also suggest that bison may have gone through a number of historical bottlenecks.

However, modern bison appear to be relatively free of the inbreeding depression and other fitness related problems usually associated with severe population bottlenecks. Why?

The Bone(s) of Contention……



So, why have bison recovered, with no or few apparent genetic consequences from this major population crash, when most other species, faced with this degree of insult, seem to suffer through long-term problems and/or became extinct?

There are multiple explanations:

- Previous (historic) population declines and near extinction events have purged bison genomes of many deleterious alleles.
- Following the bottleneck on the late 1800s, surviving bison were found in isolated populations that encompassed a high frequency of the overall (pre-bottleneck) genetic variation.
- Bison that survived the bottleneck retained genetic adaptability at important genes that influence fitness (the luck hypothesis).
- Surviving bison population encountered an influx of new genetic variation at the apex of this bottleneck (hybridization with domestic cattle).

The First Great Recovery
Foundation Plains Bison Herds
(1888 - 1905)

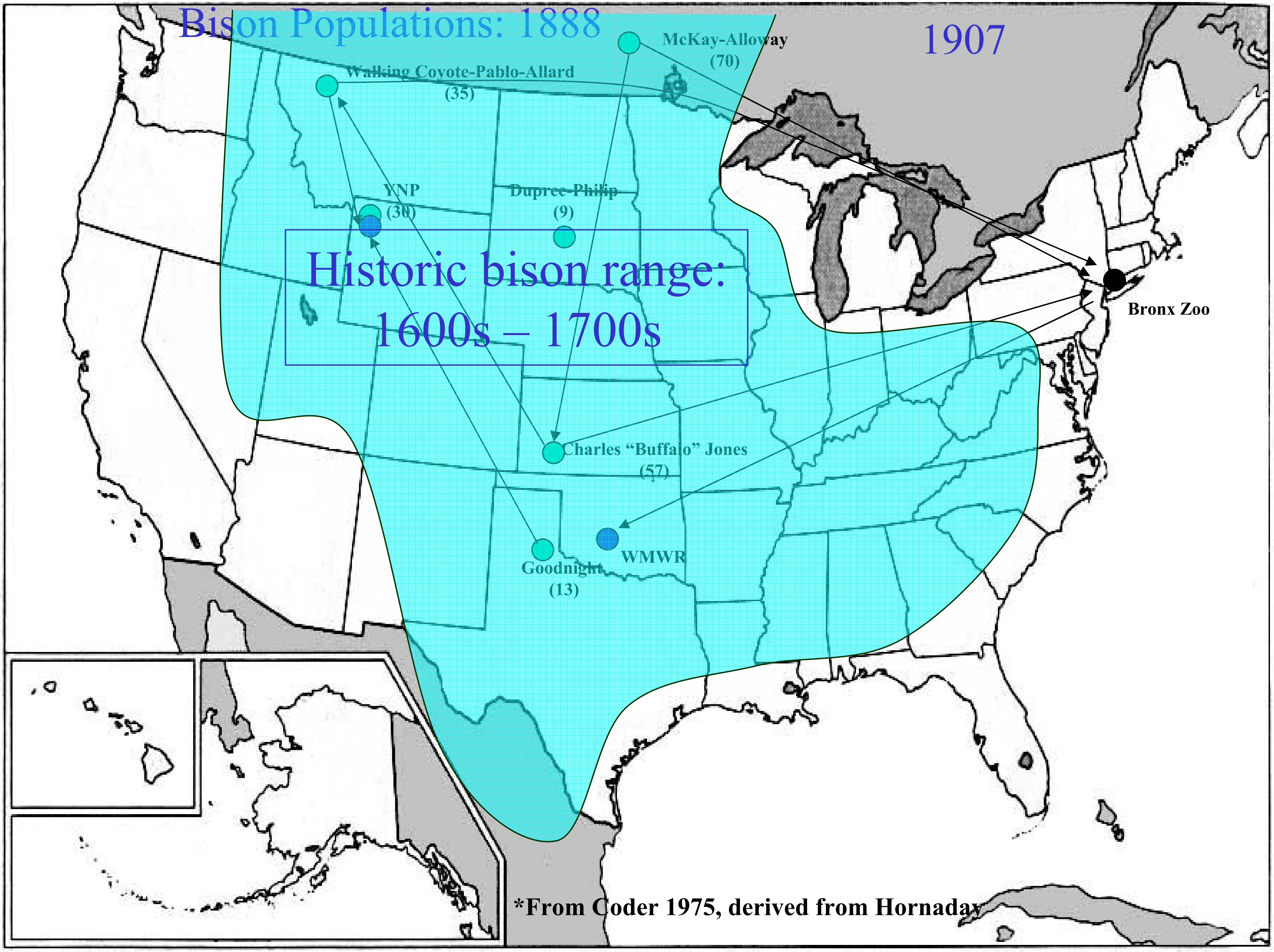
James McKay / William Alloway Herd - Canada
Walking Coyote (Pablo / Allard Herd) - Montana
Frederick Dupree - South Dakota
Charles (Buffalo) Jones - Kansas
Charles Goodnight - Texas

(Some of these herds were used to produce a few hybrids between bison and beef cattle to "improve" disease resistance and possible energy conversion in beef cattle.)

(The hybridization experiments worked…. improving beef cattle ideas did not.)

In addition, a few "wild" animals (22 - 25) remained in Yellowstone National Park.

Bison Populations: 1888



Historic bison range:
1600s – 1700s

*From Coder 1975, derived from Hornaday

Success of the "The Great Bison Recovery"

- Plains bison numbered over 5000 by the middle 1930s and they were considered by the American Bison Society as "out of danger of extinction"
- Current NA bison census: ~500,000 animals
- Most bison are in private herds
  - In some cases they are artificially selected for size, growth rate, behavior, less hump, more rump, etc
  - Most screened private herd have cattle introgression
- <20,000 bison maintained by US & Canadian governments
  - Different goals than private herds
  - Most likely an important source of non-hybridized bison that can be maintained for future generations

Our Studies Using Bison Recovery as a Model For Understanding Population Restoration

- Determine extent and distribution of genetic diversity in modern bison herds in order to:

  - Compare levels of genetic diversity among populations
  - Establish genetic relationships between populations
  - Use as platform to investigate management strategies
  - Test for mitochondrial and nuclear bison-domestic cattle introgression bison herds.

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

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, archived over 15,000 bison DNA samples

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Just give me the results.


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Sampling Strategy (Halbert 2003)

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

Population	Census	Total	Males	Females
BNP	875	312	119	193
FN	379	167	83	84
GT	600	39*	10	29
NBR	350	152*	83	69
NS	63	49	20	29
SUH	40	33	NA	NA
TRN	312	270	115	155
TRS	371	324	120	204
TSBH	40	40	19	21
WC	350	293	117	176
WM	600	35*	0	35
YNP	3000	488*	214	274
Sum	**6980**	**2202**	**900**	**1269**

Approximately 30% sampling overall

[*] Sex determined by microsatellite analysis in some cases

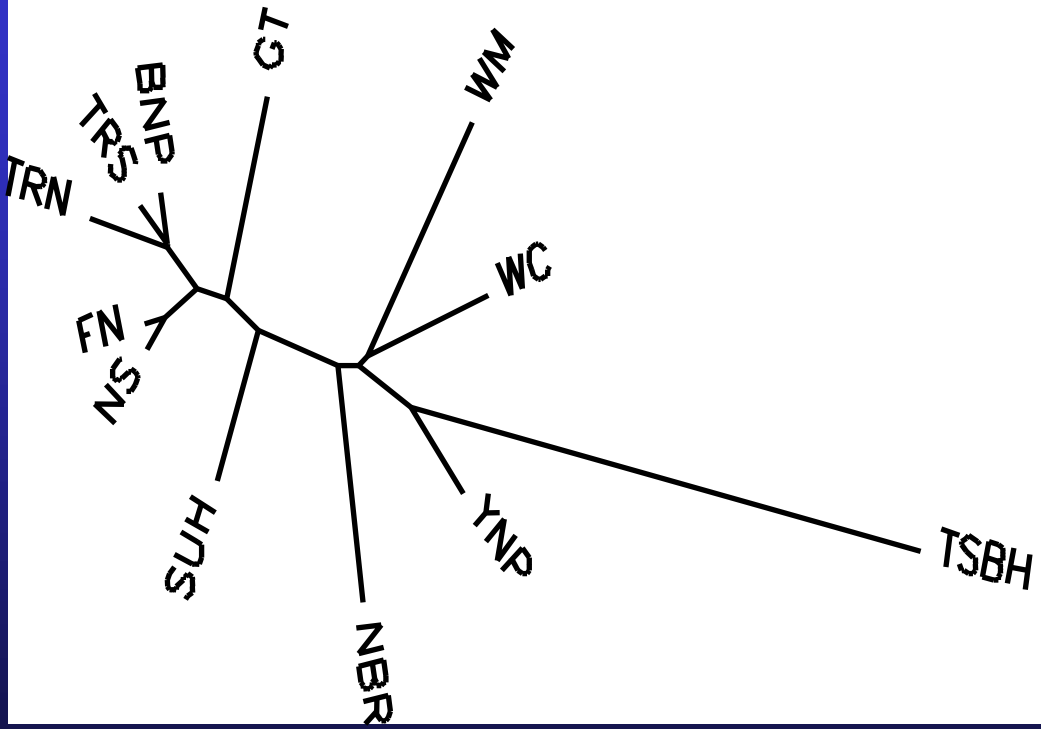
Summary Statistics

Results from 54 Microsatellite Loci

(Halbert 2003)

	BNP	**FN**	**GT**	**NBR**	**NS**	**TRN**	**TRS**	**TSBH**	**WC**	**WM**	**YNP**
% total alleles	69.4	67.4	62.6	**76.9**	73.7	54.3	65.4	**39.1**	74.0	64.3	74.6
A_R	4.11	4.06	3.96	**4.60**	**4.60**	3.26	3.99	**2.52**	4.49	4.21	4.44
H_E	0.574	0.590	0.560	0.647	0.631	0.513	0.574	**0.373**	**0.653**	0.599	0.627
Private Alleles	3	1	0	9	0	0	1	4	**10**	4	4
Fixed Loci	0	0	1	0	0	2	0	**7**	0	0	0

$(\delta\mu)^2$ Neighbor-Joining Distance Tree



The Survivors..
Population Level Conclusions

- Despite historic bottleneck, bison populations in general, have relative high 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.

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

The cold, hard facts….

DianeHargreaves.com

Some bison just look different?

Photo supplied by Elaine Leslie

Some Bison Look Very “Funny”

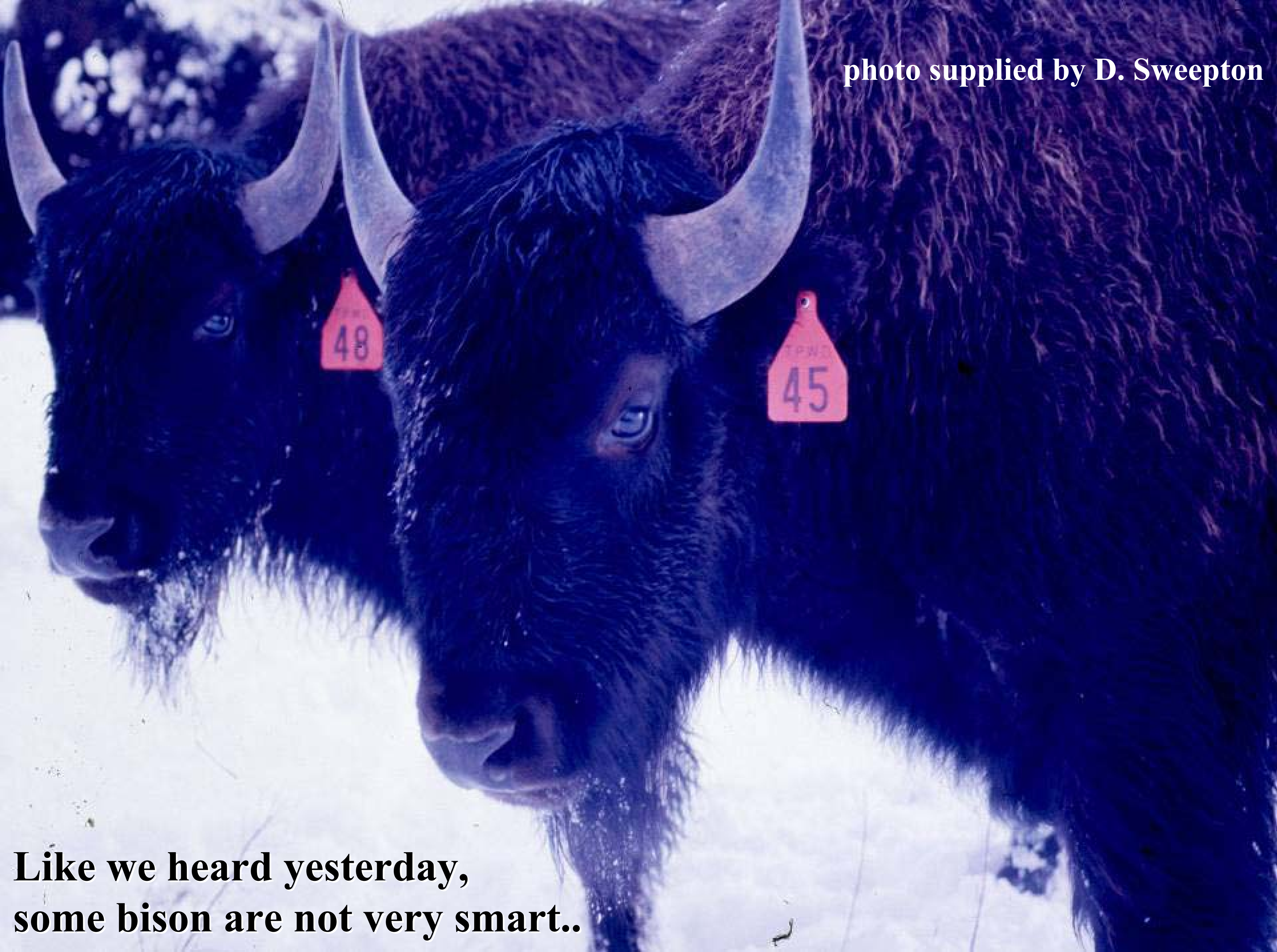


photo supplied by D. Sweepton

**Like we heard yesterday,
some bison are not very smart..**

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. (reported in this presentation)

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

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

Developing technology. (ongoing research and discovery)

- Bovine SNP microchips with the potential to genotype over 20,000 different genetic markers rapidly, cheaply and simply.

Mitochondrial DNA

- Inherited only through the female lineage.
- Is a haploid genome, no recombination.
- The genome is relatively small (about 16,500bp).
- Required for energy production in the cell.
- High rate of nucleotide substitution.
- DNA sequence is very well characterized.

Results of mtDNA screen for federal, state and private bison herds

- 3,378 bison sampled from all 12 US federal populations.
- Most of the federal herds appear free of cattle mtDNA except for a small number of animals (11) at the National Bison Range. The origin of introgression was confirmed through DNA sequencing.

(There are two 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).

Results of mtDNA screen for federal, state and private bison herds (cont.)

- All of the private herds tested (except just a few) contain animals with domestic cattle mtDNA.
- All of the state owned bison herds tested (except for possibly one) contain animals with domestic 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…

Photo by Jenny Jones

Nuclear Genome: Microsatellite Markers

- **Determine the frequency of cattle chromosome regions in bison genomes using a set of 15 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.**

ALSO microsatellite markers allow us to (the so called population genetic markers):

- **develop a powerful set of molecular markers to use for parentage testing and population genetic determinations (i.e., inbreeding, effects of various culling strategies, effect of chronic small population size, etc) .**

- **produce reverse pedigrees in bison herds for breeding management strategies (i.e., the awesome ongoing study at Wind Cave NP).**

Bison hybridization in the *Poll* region (bison chromosome 1)

0.0 AGLA17
162M1

0.8 Private 1

1.6 BM6438
POLL

2.0 Private 2

2.9 INRA212

3.7 SOD1M2

4.4 TGLA49
ARO24

5.5 ARO9

7.8 BMS1928

8.7 INRA117

All bison alleles

All cattle alleles

All bison alleles

Statistics and Error Rates…

- Diagnosed hybrid populations… no problem.

- Introgression “free” populations however…
  - Highly dependent on number of bison sampled and the real frequency of cattle alleles in the population.

Effect of sample size on power of detecting domestic cattle introgression using 15 independent nuclear markers*

	Sample Size									
	GT						**WC**	**YNP**		
Introgression	**39**	**50**	**100**	**150**	**200**	**300**	**375**	**532**	**700**	**800**
5%	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
1%	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
0.10%	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
0.01%	0.61	0.70	0.91	0.97	0.99	1.00	1.00	1.00	1.00	1.00
0.001%	0.09	0.11	0.21	0.30	0.38	0.51	0.59	0.72	0.81	0.85
0.0001%	0.01	0.01	0.02	0.04	0.05	0.07	0.09	0.12	0.15	0.17
0.00001%	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.01	0.02	0.02

*Calculation from Davis *et al.* 1988

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).

- There are not enough samples from Grand Teton NP and not enough total animals in the Sullys 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.

The Second Recovery of North American Bison….

- **Important considerations**:
  - A bison population with domestic cattle introgression requires that they be handled differently in long-term conservation and ecological efforts. However, this does not dismiss important contributions such as unique genetic attributes and diversity in these herds.
  - The second bison recovery, over the next decade, will primarily involve establishment of new populations from populations with high genetic diversity and a relatively small chance of being highly contamination with domestic cattle genetics.
  - So, just like your mama told you, your history and lineage is important (i.e., were your ancestors born in a barn or what?…….. the prairie?)

Bison are the 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.

Given all of this, for bison or any other species, for long-term conservation, one 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.