

Summary of recent publications and monitoring of Yellowstone bison genetics



(Pringle 2011, Pérez-Figueroa et al. 2012, Halbert et al. 2012,) and NPS response
Wallen et al. draft manuscript

Widespread mitochondrial disease in North American bison.

By Thomas Pringle

Published on Nature Precedings website
07 February 2011



., "these bison are predicted significantly impaired in aerobic capacity, disrupting highly evolved cold tolerance, winter feeding behaviors, escape from predators and competition for breeding"



Douglas et al. (2010) noted an alarming number of mutational anomalies and the possibility of mitochondrial dysfunction in bison

deleterious mutations in both cytochrome b (V98A) and ATP6 (I60N) occur within a single common bison haplotype... haplotype 6



Thoughts...

Pringles reference to the double mutation in haplotype 6 bison is a fact to consider. Our work with UM shows that there are more bison in the central herd that exhibit the haplotype 6 genotype.

Pringle's conclusion that oxydative phosphorylation functions are impaired in haplotype 6 bison and thus they are less likely to survive hard winters and the effects of predation are not substantiated

Genetic mutation does not automatically equal genetic disease.

If the mutations were as deleterious as claimed, they would have been eliminated by natural selection

New work with TAMU



Collect blood and preserve live cells from the individual bison representing the two haplotypes and test whether there is any differences in bioenergetics by stressing the cells.

4 key parameters of mitochondrial function - basal respiration, ATP turnover, proton leak, and maximal respiration (Seahorse Bioscience XF Cell Mito Stress Technology)

Conserving genomic variability in large mammals: Effect of population fluctuations and variance in male reproductive success on variability in Yellowstone bison

Andrés Pérez-Figueroa, Rick L. Wallen, Tiago Antao, Jason A. Coombs,
Michael K. Schwartz, P.J. White, and Gordon Luikart

Biological Conservation 150 (2012) : 159-166



Loss of genetic variation through genetic drift can reduce population viability.

However, relatively little is known about loss of variation caused by the combination of fluctuating population size and variance in reproductive success in age structured populations.

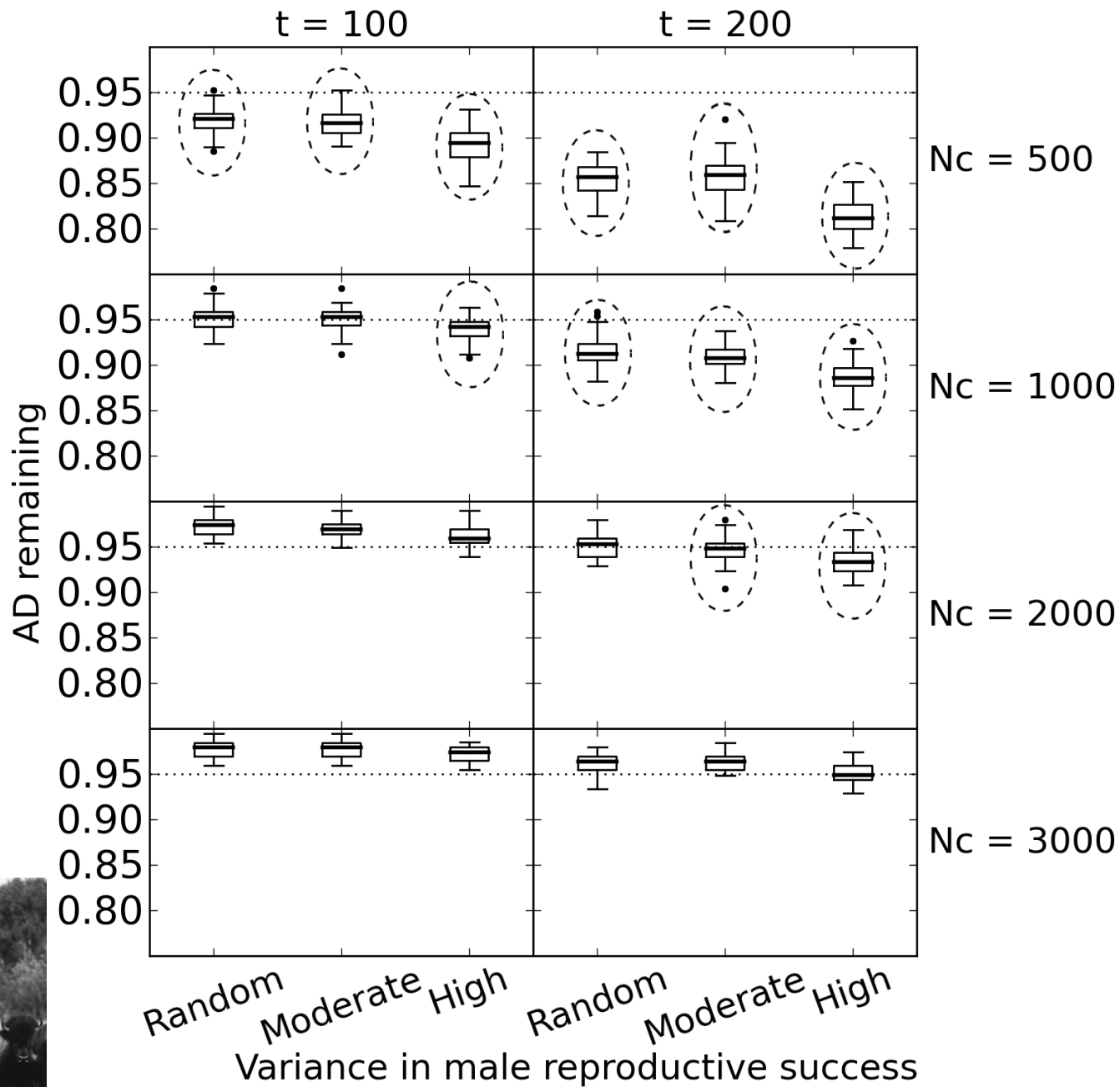


Genetic Variation and Long - term Persistence

Influence of male
reproductive success

Allelic Diversity (AD) and
Effective Population Size
(N_e)





Average AD remaining after 200 years

Stable Population size		% Allelic Diversity						
250		75.4						
500		85.3						
1,000		91.1						
2,000		94.7						
3,000		96.3						
		High Fluctuation (2,000 - 4,500)				Low Fluctuation (3,000-3,500)		
		RND	Juv	Adult		RND	Juv	Adult
		95.4	96.1	94.7		95.3	95.7	94.9



With sufficient migration, a fragmented population will behave just like a single large population of the same total size.

Frankham et al. 2002 Conservation Genetics

Conclusions: Fluctuations in population size are unlikely to greatly accelerate the loss of genetic variation, at least for the relatively large populations with positive population growth rates



Recommendation = 3000 -3500

Focus harvest on young age classes or randomly

Genetic Population Substructure in Bison at Yellowstone National Park

Natalie D. Halbert,
peter J. P. Gogan, Philip
W. Hedrick, Jacquelyn
M. Wahl, and James N.
Derr

Journal of Heredity
103(3):360-370



Description of Subpopulation Structure

Breeding Range	Heterozygosity	Allelic Diversity	Sample size
Northern	0.596	4.56	152
Central	0.621	4.63	453



$$F_{ST} = 0.0321$$

2 migrants per generation (8 years)

These 2 subpopulations have differentiated in a relatively short period of approximately 8 generations.

Male migration alone describes the differentiation between the two breeding groups

2 genetically distinct subpopulations

Hypothesis: level of divergence is expected to continue to increase in the future

Conclusion: The identification of genetic subpopulations in this study raises serious concerns for the management and long-term conservation of Yellowstone bison.

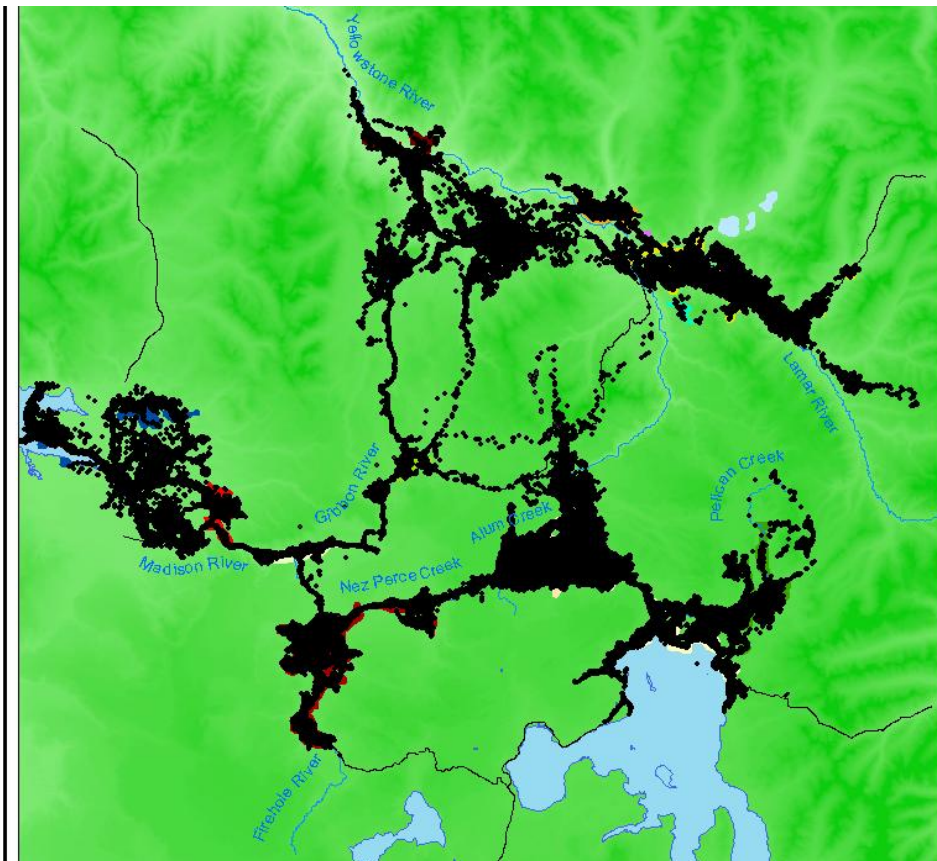
The continued practice of culling bison without regard to possible subpopulation structure has the potentially negative long-term consequences of reducing genetic diversity and permanently changing the genetic constitution within subpopulations and across the Yellowstone metapopulation.

Yellowstone Bison—Should We Preserve Artificial Population Substructure or Rely on Ecological Processes?

P. J. White and Rick L. Wallen



Journal of Heredity Advance Access
published August 23, 2012



Halbert et al. raised concerns about the management and long-term conservation of Yellowstone bison because of disproportionate culling of the 2 subpopulations in some winters.

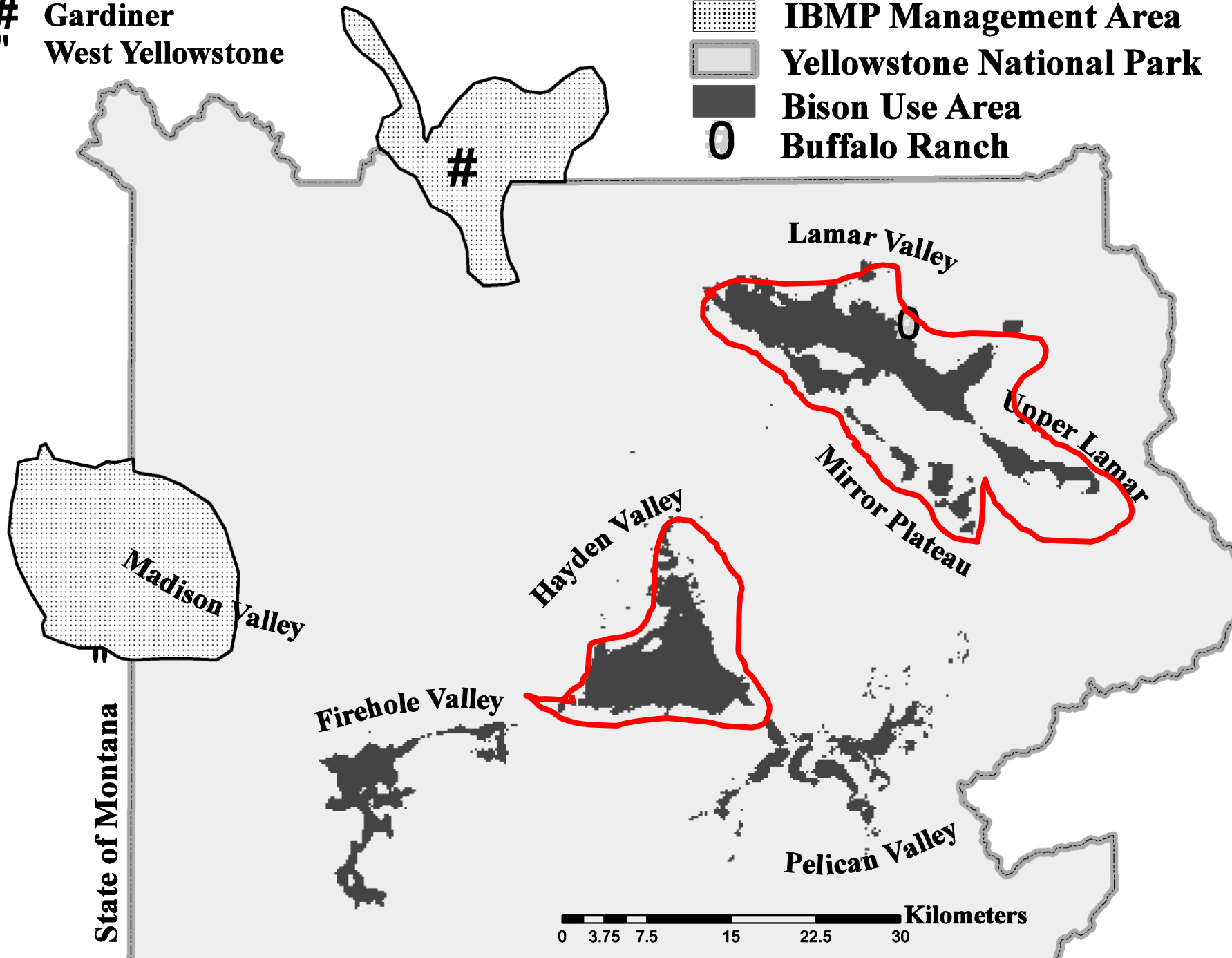
Natural population substructure?

... Ignore that humans contributed to the observed population and genetic substructure



Gardiner
" West Yellowstone

 IBMP Management Area
 Yellowstone National Park
 Bison Use Area
0 Buffalo Ranch



State of Montana

0 3.75 7.5 15 22.5 30 Kilometers

Allow ecological processes to influence substructure characteristics



Diversity indices may in fact decrease over time if migratory patterns we have observed continue...

Draft manuscript near submission

Population substructure in Yellowstone bison

By R. Wallen, F. Gardipee, G. Luikart, P. J. White



Large differences in genetic variation between breeding groups comparing mtDNA ($F_{ST} = 0.4$)

Small differences between breeding groups using nuclear DNA ($F_{ST} 0.01 - 0.02$)

10 to 20 migrants per generation

Observations of radio marked females show 15 bison dispersed to a new breeding range and 13 of those produced calves on the new range.

We expect F_{ST} values to fluctuate as the population responds to the bison density in the two breeding herds, management actions (e.g., culling), and natural selection.

Conclusion... Yellowstone bison can be characterized as a single population with genetically similar, yet distinguishable, breeding groups on the northern and central ranges.

Effective emigration among the two breeding groups is occurring

Recommendations

- Preserve a near equal sex ratio
- Manage for breeding groups of about 1500 bison on the northern and central ranges
- Monitor diversity indices every one to two generations

We are still looking in to the details of bison genetics





Questions?