

BISON GENETICS - THE NEW WAR AGAINST BISON

by Kathleen O'Neal Gear and W. Michael Gear

In a May 21, 2010 article in the New York Times, entitled, "Deal Puts Yellowstone Bison on Ted Turner's Range," author Kirk Johnson wrote, "Most ranch-raised bison, unlike their Yellowstone cousins, carry a few cattle genes... But Yellowstone bison, marooned in the park during the decades of widespread slaughter elsewhere, are considered genetically pure." He also writes, "The 'Yellowstone 87' are a kind of Noah's ark of their kind. Genetically, these bison still carry the shaggy swagger of their Ice Age forebears that lived alongside saber-toothed cats and woolly mammoths."

The bovine DNA dilemma has been simmering, little noticed by most of us out caring for our animals, for the past ten years, but it's about to grab us by the throat and sink its teeth into our jugulars.

Here's the issue: With the advent of DNA testing it has become clear that some bison, and maybe a lot, have cattle genes. This is probably an artifact of their salvation by cattle ranchers in the nineteenth and early twenties centuries. They lived with cattle. Some of them successfully bred with cattle. So...should bison with cattle genes be eliminated from the gene pool, as is being suggested by public parks across the country, and already being implemented at

some, like the Ordway Prairie herd managed by the Nature Conservancy, where "The bison with cattle mitochondrial DNA have been removed from the herd"? (See <http://www.mnn.com/local-reports/south-dakota/nature-conservancy/studying-bison-dna> and <http://www.hcn.org/issues/321/16267>). Be careful how you answer, because what's at stake is nothing less than the survival of the bison industry and even, perhaps, the genetic viability of the entire

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species.

First, let's look at the facts. If you go on-line to the Texas A&M web site you'll find Dr. James Derr's section on "Bison Conservation Genetics and Disease." While the entire section is interesting, the most important for us is: "An Analysis of Domestic Cattle introgression in some important U.S. bison populations...the cold hard facts..." Dr. Derr states that after having tested 5,246 bison from 12 US federal populations, that "all appear free of cattle mtDNA except for a small number of animals (14) at the National Bison Range." And after having tested 5,655 bison from over 100 private, State and NGO (non-government) populations, he says he found evidence of domestic cattle

mtDNA "in all of these herds except for a very few." When Dr. Derr refers to "mtDNA" he's talking about a strand of DNA found outside the nucleus of the cell in the mitochondria—the little powerhouse of the cell—which is donated only by the mother. It's called mitochondrial DNA (mtDNA), and refers to bison maternal lineages. Mitochondrial DNA is different from nuclear DNA, which refers to the DNA found in the nucleus of the cell.

In his 2007 article in the *Journal of Heredity*, "A Comprehensive Evaluation of Cattle Introgression into US Federal Bison Herds," Dr. Derr says that "nuclear introgression was found in 7 (63.6%) of the examined populations." For the layperson, that means Dr. Derr found cattle genes in around 64% of US federally-managed bison herds. Currently, around 27% of the 20,000 animals in public herds have been tested, so this is a reliable estimate.

Are Derr's estimates regarding private herds as accurate? The problem is that while about 95% of all buffalo are being cared for in private herds, only about *one percent* has been DNA tested. And there are two kinds of DNA tests, one for mitochondrial DNA, and the other for nuclear DNA. Why is that important? Because there are only twelve known bison mitochondrial haplotypes—maternal lineages. Anyone who has read the classic book, *The*

Seven Daughters of Eve, which discusses and traces the seven maternal lineages of human beings, will realize immediately that from the perspective of mtDNA, bison have a greater genetic diversity than we do. And this is critical, especially with reference to the “Yellowstone 87.” More on this later.

Before we continue, **let’s talk about where the “cattle genes” might come from. Is the only possibility modern ranching contamination?**

The evolutionary origins of bison date to around 9 million years ago in Spain with an animal called *Parabos*. *Parabos* survived until around 1.8 million years ago. During this time, *Parabos* gave rise to

the animal that is the direct ancestor of both *Bison* and *Bos*—*Proleptobos*. *Proleptobos* evolved in China approximately 4 million years ago.

The *bison-bos* family branched from *Proleptobos* around 2.2 million year ago, **and *Bos* and *Bison* split around 2 million years ago**. From an evolutionary perspective, this is the blink of an eye. ***Bison* and *Bos* are still virtually identical in their genomes. It’s the differences, the polymorphisms, that create questions.**

For example, what are “cattle genes?” How do we define them? Are they unquestionably *Bos taurus*, modern domesticated cattle genes? (If so, *Bos taurus* did not arrive in North America until after 1492 when Columbus brought them aboard his ships.) Is

it possible that these genes are older? How much older?

The family *Bos* arrived in North America far earlier than *Bison*. *Euceratherium*, the Shrub Oxen, appeared at the beginning of the Pleistocene Ice Age, **1.8 million years ago, and was here waiting when *Bison priscus* entered Alaska** during the Mindel-Riss epoch, a global warming period that lasted from 380,000 to 200,000 years ago. In addition, we know that **ancient bison also lived alongside** the yak (*Bos grunniens*), the Woodland Ox (*Symbos*), and **several other ancient species of *Bos***. Both the Shrub Oxen, and the Woodland Ox went extinct approximately 10,000 years ago. The climate

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was rapidly changing, moving into the warming period that we live in today, the Holocene, and as the vegetation began to change there was a catastrophic decline of species. North America also lost mammoths, mastodons, camels, giant sloths, giant short-faced bears, dire wolves, and many other species. *Bison*, who were obviously extraordinarily adaptable, survived.

Did *bison* interbreed with any of the prehistoric species of *Bos*? Is it possible that such ancient crosses might be the source of the “cattle” genes we see today in *bison*? The simple truth is, no one knows. No one has done the research to answer the

question. Is it possible? Yes, it is. **The only way to answer the question is to sequence the entire modern bison genome, as well as several prehistoric bison genomes, and compare them.** Did these same genes exist 5,000 years ago in *bison*? If so, they are not “cattle” genes. **They’re ancient bison genes that either originate from the shared ancestry of *bos-bison*, or they result from the crossing of species some time between 10,000 to 380,000 years ago, perhaps even earlier.**

In answer to our question, “As controls for determining that they are indeed genes from *Bos taurus*, do you utilize studies of prehistoric bison DNA from North America, or prehistoric *bos*

DNA from North America?” Dr. Derr answered on August 25, 2010, “...we have examined genetic variation in some historical bison samples but the paper we published did not

include historical samples. I have however proposed sequencing multiple bison genomes including one genome from a pre-1850 era bison.”

A pre-1850 sample will be interesting, but it won’t help answer the question. By that time, *bison* had been living beside domestic cattle for over three hundred years. Certainly some of them interbred. **Why is getting an answer so critical?**

An October 21, 2009, Rapid City Journal article puts the potential problems of this genetic debate into perfect perspective when it says, **“The scarcity of bison without cattle ancestry leads some to argue that wild,**

apparently pureblood bison could qualify as an endangered species.”

We hope you just dropped your cup. The Endangered Species Act clarifies that “trafficking” in endangered species is punishable by a \$50,000 fine and not less than one year in prison—per charge.

If pure bison are declared endangered, and the push is already on, there’s a chance that you will no longer be able to sell such animals, or sell their offspring—if private ownership is allowed at all.

Lest you think we’re being alarmist, see <http://boldventure.info/dilemma.html>,

where author Jon Nichols suggests that **bison with cattle genes may lose their legal status as bison and fall under the classification of domestic cattle.**

Nichols also suggests reclassifying American bison.

“Pure” bison would be “Bison Bison Bison,” (as all are categorized today), and bison with remnant bovine DNA could be renamed, “Bison Bison Americus.”

Creating such a division will be the first step toward establishing a legal framework for declaring “pure” bison as endangered.

Or read the High Country News article, May, 1, 2006, where Frances Backhouse writes, “The West it turns out, has almost no wild, genetically pure bison left...according to Derr’s research, there are only about

6,000 pure bison in North America.”

Or take a look at http://scienceblogs.com/grrlscientist/2007/01/preventing_genomic_extinction.php, where the author says, “To prevent ‘genomic extinction’ of bison through hybridization, biologists are focusing on the protection and perpetuation of the herds with pure or nearly pure genetics.”

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interesting endeavors involves the work of an outstanding graduate student, Flo Gardipee, who has been testing Yellowstone bison feces for mitochondrial DNA. She’s discovered that **Yellowstone has only two of the twelve known bison mitochondrial DNA haplotypes:** haplotypes 6 and 8. In fact, the 2,000 bison in the Hayden Valley--roughly half of the Park’s herd--have only *one*—haplotype 6.

(<http://www.sciencedaily.com/releases/2007/01/070128104947.htm>).

Such frighteningly low genetic diversity would terrify most of us. We’d be on the phone calling everyone we know to find animals with other haplotypes to bring into our herds to assure our animals’ health and well-being.

It seems to have a different affect on people who consider themselves “bison conservationists.” Rather than understanding that this fact may doom the Park’s herd, it makes them think Yellowstone DNA is rare beyond belief and worthy of special legal protections.

Before we continue, let us clarify that many

of you have at least a few animals in your herd with haplotype 6 or 8, or both. There were simply so few bison alive at the turn of the twentieth century that all twelve of the haplotypes eventually became widely distributed across the continent. So, if you’re only

running a mtDNA test, those animals will come out as “pure.” Does it mean they are? Not necessarily. Animals with pure mtDNA, donated by the mother, may have cattle genes donated by the sire, but they will only show up in a nuclear DNA test.

Lastly, let’s talk about the fundamental problems associated with testing bison DNA. So far we’ve assumed that the tests are accurate. Are they?

Maybe not. Before you read what follows, we need to clarify that the term “Polymorphic SNP” refers to a Single Nucleotide Polymorphism, an allelic version of a gene. Alleles whose sequence contains only a single changed nucleotide are called SNPs. The Bovine SNP50 BeadChip test is a useful tool because it cross-references bison DNA with 52,978 Single Nucleotide Polymorphisms (SNPs) from cattle.

In an article by Cino Pertoldi, et. al., published in the 2010 issue of Conservation Genetics (11:627-634), and entitled, “Genome Variability in European and American Bison detected using the BovineSNP50 BeadChip,” the authors write, “**No comparison of SNP variation between bison and cattle breeds has been conducted here.** This is because an ascertainment bias is introduced when comparing the genetic variability in cattle and bison as the markers on the chip were selected based on polymorphisms in cattle. Hence, the comparison between bison and cattle should be interpreted with caution.”

James Derr recognizes this problem. In his August 25, 2010 email, he wrote, “I have used the cattle derived SNP50 BeadChip with bison. I think it does provide some resolution for resolving introgression between cattle and bison and some people appear to be using the chip with success. However, **this tool was developed from cattle breeds and using it in bison presents some important limitations.**”

Earlier in the Pertoldi, et. al., article, they say, “Inspection of the polymorphic SNPs in the bison reveals long chromosomal regions fixed for one allele and leaves little doubt that the European and American bison have extremely depauperate genomes. There are several possible reasons for the presence of such haplotype blocks such as genetic hitchhiking, variable mutation rates, and recombination, gene-flow, drift and inbreeding.

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between the different possible reasons.” Finally, they say, “However, it is likely that many of the shared blocks and of highly polymorphic regions are ancestral as the small Ne (number sampled) of the bison, the relatively low mutation rate of SNPs and the fact that North American bison is a relatively recent evolutionary product, coming into existence about 4,000-5,000 Y.B.P. (Wilson and Strobeck, 1999) *make it unlikely that the observed polymorphisms are due to mutations that occurred in bison recently.*”(emphasis added.)

The authors, using the best test available, say it’s impossible to determine the origins of such polymorphisms because “the markers on the chip were selected based on polymorphisms in cattle.” That’s what they mean

when they speak about an “ascertainment bias.” The test itself is based upon and biased toward cattle genes. Why don’t we have a better test? Because there is no baseline on the bison genome—it’s never been completely sequenced--so they have to use the well-established genome of domestic cattle as the baseline. That’s why the test is biased. Until the bison genome is sequenced, there is no way of knowing what are unquestionably “bison” genes, and what are domestic cattle genes.

Yet we have public parks around the country in a flurry to get rid of animals with “cattle DNA.”

Any thinking person who cares about wildlife conservation and the fate of the American buffalo should be terrified by the “purity” concept. If these are ancient bison genes and wildlife managers follow this current trend, we could be losing the very genes that have allowed bison to survive to present day.

The potential holocaust of rare bison genetics is staggering.

Until there is an intensive sequencing of the bison genome that allows us to answer evolutionary questions about this issue...*no one* should be selecting animals based upon their “purity.”

*In addition to the articles referenced above, other useful references are: McDonald, Jerry, North American Bison. Their Classification and Evolution; Martin, Paul S., et. al., Quaternary Extinctions. A Prehistoric Revolution; Shapiro, Beth, et. al., “Rise and Fall of the Beringian Steppe Bison,” published in the journal, *SCIENCE*, vol. 306, November 26, 200*