

Bison Conservation Genetics Study at Wind River Ranch, New Mexico

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SUMMARY

Bison face a variety of threats to their long-term survival as a species, including the spread of new diseases, low genetic diversity, and the introgression of domestic cattle genes. At Wind River Ranch (WRR), NM, we are studying the genetic diversity and cattle hybrid status of the resident wild bison herd to ensure its conservation significance. Three WRR bison were identified cattle hybrids using a mitochondrial marker. WRR has two distinct bison mitochondrial lineages, one unique to WRR, and one shared by bison at Yellowstone, the National Bison Range, the Texas State Bison Herd, and the Fort Niobrara NWR.

OBJECTIVES

- Identify individual bison with cattle genetic introgression.
- Identify unique evolutionary lineages in the bison population.
- Provide enriching research experiences for undergraduate students at New Mexico Highlands University (NMHU).



METHODS

- We sampled hairs from 53 bison at Wind River Ranch during a yearly inspection of the herd.
- DNA was isolated from bison hairs using a standard protocol with extended protein digestion (after Shapiro et al., 2004).
- We amplified and sequenced the D-loop region of the mitochondrial genome using primers BISC-R-16348F and BISC-R-16990R (Shapiro et al., 2004). PCR and cycle sequencing reactions were performed at NMHU. Sequences were visualized using an ABI 3100 at UNM.
- Bison gene sequences were compared to published bison and cattle sequences (Douglas et al., 2011).



Students collecting bison hair for genetic analysis.



Wacey Cochise, Salese Nealy, and Lisa McBride analyzing bison samples in the lab.

RESULTS

- We analyzed 37 bison D-loop sequences (sequence length of 439 bases).
- Three hybrid bison shared 100% sequence identity with *Bos taurus* sequences (Fig 1).
- The D-loop sequence analysis identified two lineages of bison at WRR. The lineage WRR_1 is common (83% sampled), sharing 100% identity with bison from Fort Niobrara NWR, Montana's National Bison Range, Yellowstone NP, and a private herd in Montana (Fig 2).
- Lineage WRR_2 is rare (8% sampled), and is not shared with any published sequence.
- Concerning the overall diversity in bison mitochondrial lineages, the WRR herd lineages are from both major clades of bison: the exclusively plains bison "clade I" (from Fort Niobrara, Yellowstone, National Bison Range, and private herds) and the mixed plains and wood bison clade II (from Texas State herd, private herds, and Elk Island Canada; Douglas et al. 2011).

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|----------------|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| WRR Bison BL4 | T | C | A | C | C | C | C | - | - | - | - | - | - | - | - | - | C | A | A | A | A | T | T | G | C | A | T | T | A | C | C | A | |
| WRR Bison BL2 | T | C | A | C | C | C | C | - | - | - | - | - | - | - | - | - | - | C | A | A | A | A | T | T | G | C | A | T | T | A | C | C | A |
| WRR Bison G35* | A | C | G | C | C | C | A | T | A | C | A | C | A | G | A | C | C | A | G | A | A | T | T | G | A | A | T | T | A | C | C | T | A |
| WRR Bison Z3W* | A | C | G | C | C | C | A | T | A | C | A | C | A | G | A | C | C | A | G | A | A | T | T | G | A | A | T | T | A | C | C | T | A |
| Bos taurus | A | C | G | C | C | C | A | T | A | C | A | C | A | G | A | C | C | A | G | A | A | T | T | G | A | A | T | T | A | C | C | T | A |

Figure 1. Section of D-loop sequences highlighting DNA base differences between *Bos taurus*, hybrids, and bison. *Hybrid bison from WRR.

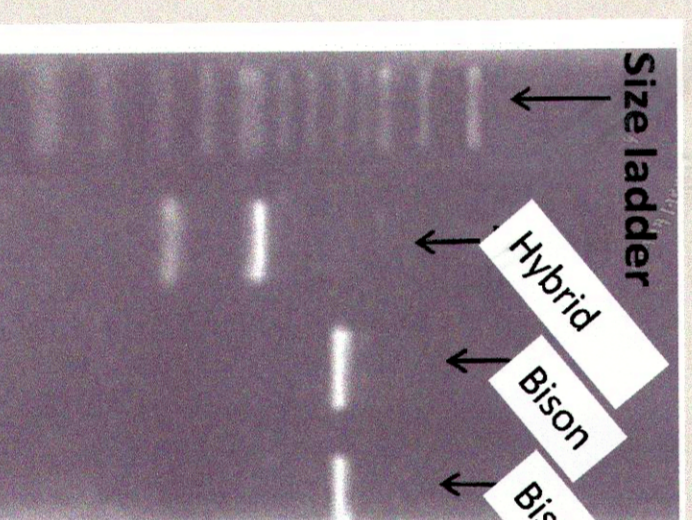
EDUCATION & OUTREACH

We have great success using the bison-cattle hybrid study as a springboard for inspiring and motivating students to try research in a more applied scenario close to campus. **We use this study as 1) a research experience for undergraduates and 2) as a teaching module for new biology students.**

- The teaching module is conducted over four days:
- Students collect bison fecal material at WRR and perform DNA isolation and PCR in the lab.
- They amplify the mitochondrial Cytochrome b gene, and do a restriction enzyme digest of the gene product.
- Students use gel electrophoresis to view the gene products.
- Bison/cattle hybrid genes appear in two pieces, bison appear as one product (band).



High School students showing collection of bison patties: from the Science Agricultural Summer Experience (SASE) project directed by Dr. Edward Martinez.



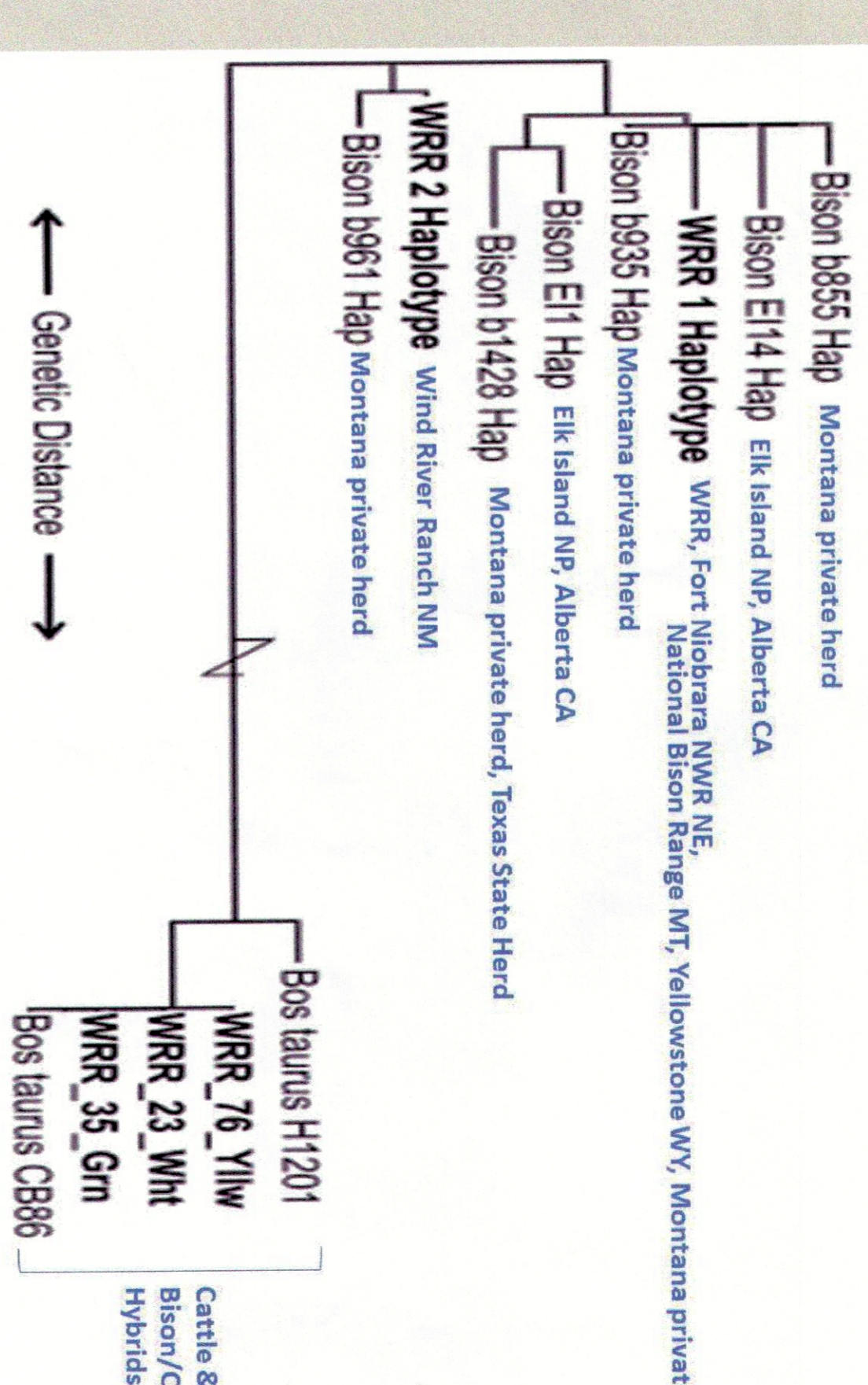
Size ladder
Hybrid
Bison
Bison



High school students conducting gel electrophoresis (SASE program).

CONCLUSIONS

Figure 2: Evolutionary tree showing relationships among bison and cattle samples from this study and reference individuals from Douglas et al (2011).



- WRR bison are an important resource adding to national efforts to conserve the genetic integrity and future genetic diversity of the species.
- The majority of bison at Wind River Ranch are free from cattle introgression (92%). However, further sampling of the herd and analysis of the nuclear genome will be conducted to further test this claim.
- The presence of a lineage from conservation herds including Yellowstone is significant because WRR bison are brucellosis-free and may therefore be an asset in our national bison genetic 'portfolio.'
- The unique lineage of bison at WRR discovered in this study is a further indication that the herd is a conservation genetics resource. Additional sampling may reveal additional lineages.

FUTURE WORK

We plan to collect hair samples from all animals in the herd. We will expand our study to include microsatellite markers, a reliable tool for assessing cattle gene introgression in the nuclear genome. Microsatellites are also very useful for estimating overall levels of genetic diversity in the herd, and degree of relatedness.

Acknowledgments
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References

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