

# Conservation Genetics In A Bison-Cattle Hybrid Herd At Rio Mora National Wildlife Refuge

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## Introduction

- American Bison (*Bison bison*) are a keystone species in prairie grassland ecosystems.
- Bison experienced a severe genetic bottleneck in the late 1800s and their numbers declined drastically.
- The species recovered from the bottleneck and now there are more than 500,000 bison today.
- Hybridization with cattle has threatened bison fitness and genetic adaptations necessary for survival in North American grassland habitats.
- Bison are found in both Federal and private herds around North America.

## Objectives

- Identify bison individuals located at Rio Mora NWR that have genetic evidence of cattle introgression in mitochondrial DNA.
- Identify lineages in the bison herd at the Rio Mora NWR.

## Methods

- Hair and scat samples were collected and DNA was isolated from 53 bison.
- The mitochondrial D-loop region was amplified and sequenced (Fig. 1) using primers from Shapiro et al. (2004).
- Rio Mora NWR D-loop sequences were then compared to published bison and cattle (Douglas et al. 2011).
- Bioedit and MEGA were used for the genetic analysis of the sequences.
- A neighbor-joining phylogenetic analysis was run with the sequences in order to determine relationships among haplotypes.



## Results

- A total of 8 samples were recently analyzed.
- Overall, 45 samples have been sequenced and analyzed.
- Two bison hybrids were discovered (Fig. 1)
- Three haplotypes were found at Rio Mora NWR (Fig. 2)
  - 2 were common
  - RMNWR\_2 is rare

RMNWR Mixed 1	A	A	A	T	A	T	A	C	A	T	A	A	C	A	T	T	A	A	T	G	T	A	A	T	A	A	A	A	A	A	C	A	C	A	T	A	T	T	A	T	
RMNWR 2	-	A	A	T	A	T	A	C	A	T	A	A	C	A	T	T	A	A	T	G	T	A	A	T	A	A	A	A	A	A	A	C	A	C	A	T	A	T	T	A	T
RMNWR Mixed 3	-	A	A	T	A	T	A	C	A	T	A	A	C	A	T	T	A	A	T	G	T	A	A	T	A	A	A	A	A	A	A	C	A	C	A	T	A	T	T	A	T
EI 14	-	A	A	T	A	T	A	C	A	T	A	A	C	A	T	T	A	A	T	G	T	A	A	T	A	A	A	A	A	A	A	C	A	C	A	T	A	T	T	A	T
B961	-	A	A	T	A	T	A	C	A	T	A	A	C	A	T	T	A	A	T	G	T	A	A	T	A	A	A	A	A	A	A	C	A	C	A	T	A	T	T	A	T
B1428	A	A	A	T	G	T	A	C	A	T	A	A	T	A	T	T	A	A	T	G	T	A	A	T	A	A	A	A	A	A	A	C	A	C	A	T	A	T	T	A	T
EI 1	A	A	-	T	A	T	A	C	A	T	A	A	T	A	T	T	A	A	T	G	T	A	A	T	A	A	A	A	A	A	A	C	A	C	A	T	A	T	T	A	T
B855	-	A	A	T	A	T	A	C	A	T	A	A	C	A	T	T	A	A	T	G	T	A	A	T	A	A	A	A	A	A	A	C	A	C	A	T	A	T	T	A	T
Bos taurus	T	A	A	T	G	T	A	C	A	T	A	A	C	A	T	T	A	A	T	G	T	A	A	-	A	A	A	G	A	C	A	T	A	A	T	A	T	T	A	T	
RMNWR Hybrid	T	A	A	T	G	T	A	C	A	T	A	A	C	A	T	T	A	A	T	G	T	A	A	T	A	A	A	G	A	C	A	T	A	A	T	A	T	T	A	T	

Figure 1: Section of D-Loop sequences highlighting DNA base differences between *Bos taurus*, hybrids, and bison.

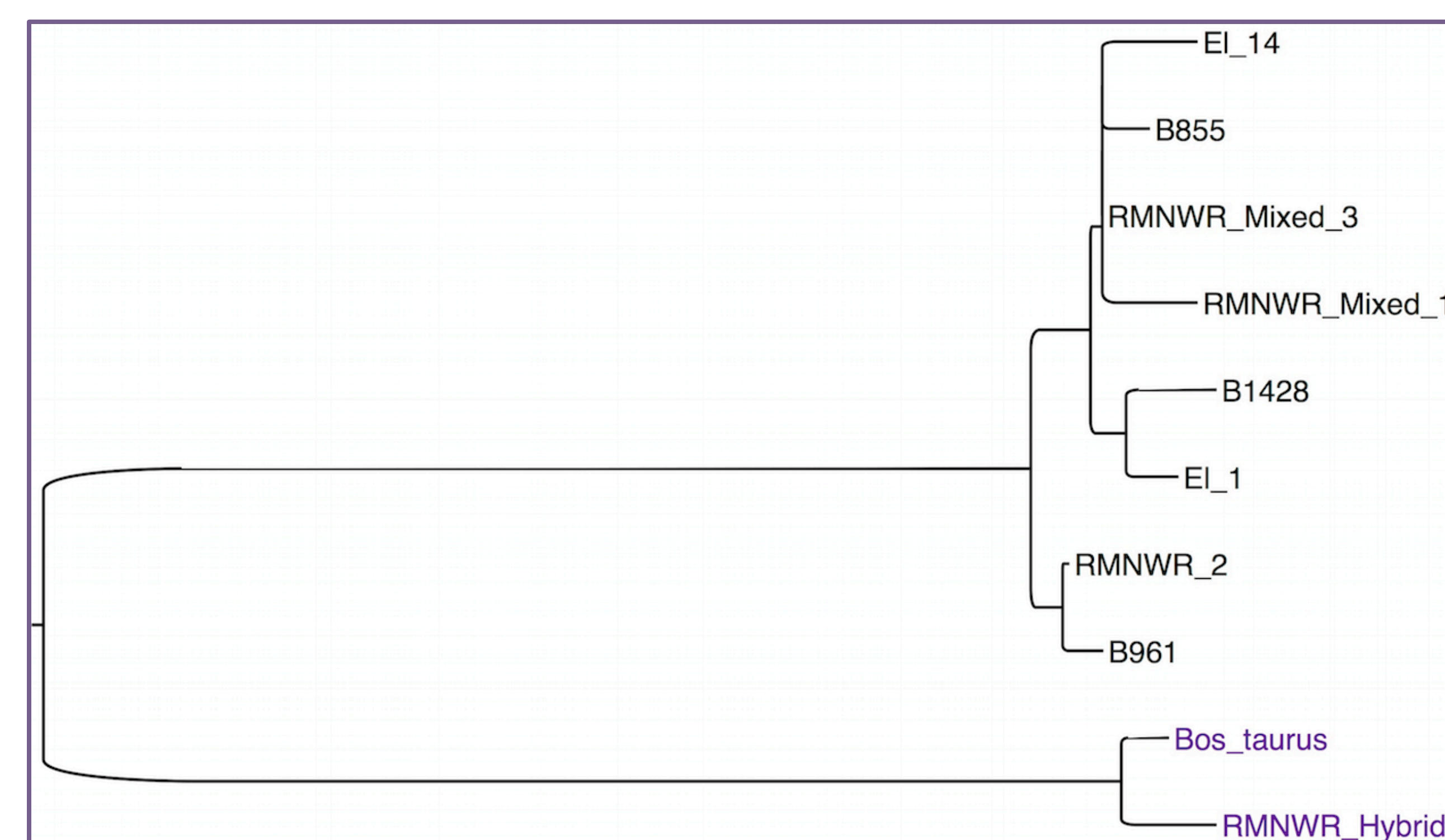


Figure 2: Evolutionary tree showing relationships among bison and cattle samples from this study and reference individuals from Douglas et al (2011).



## Conclusion

- 75% of the bison sequences analyzed were *Bison bison*.
- 25% were bison-cattle hybrids
- A unique and unpublished lineage was found at Rio Mora NWR and may be a conservation genetic resource for the future.

## Significance

- Understanding the genetic make-up of the Rio Mora NWR herd is important when it comes to herd management.
- Knowing which individuals are hybrids also helps with the management of the bison herd at Rio Mora NWR.

## Future Work

- Complete DNA sampling of the herd as more calves have been born over the past two years
- Expand our study to include microsatellite markers to discover whether cattle gene introgression has occurred in the nuclear genome.
- Assess diversity in an immune gene (MHC class II) in the herd

## References

- Douglas, K. C., Halbert, N. D., Kolenda, C., Childers, C., Hunter, D. L., Derr, J. N. 2011. Complete mitochondrial DNA sequence analysis of *Bison bison* and bison-cattle hybrids: function and phylogeny. *Mitochondrion*, 11, 166-175.
- Shapiro, B., Drummond, A. J., and Rambaut, A. 2004. Rise and fall of the Beringian Steppe Bison. *Science*, 306, 1561-1565.

## Acknowledgments

