

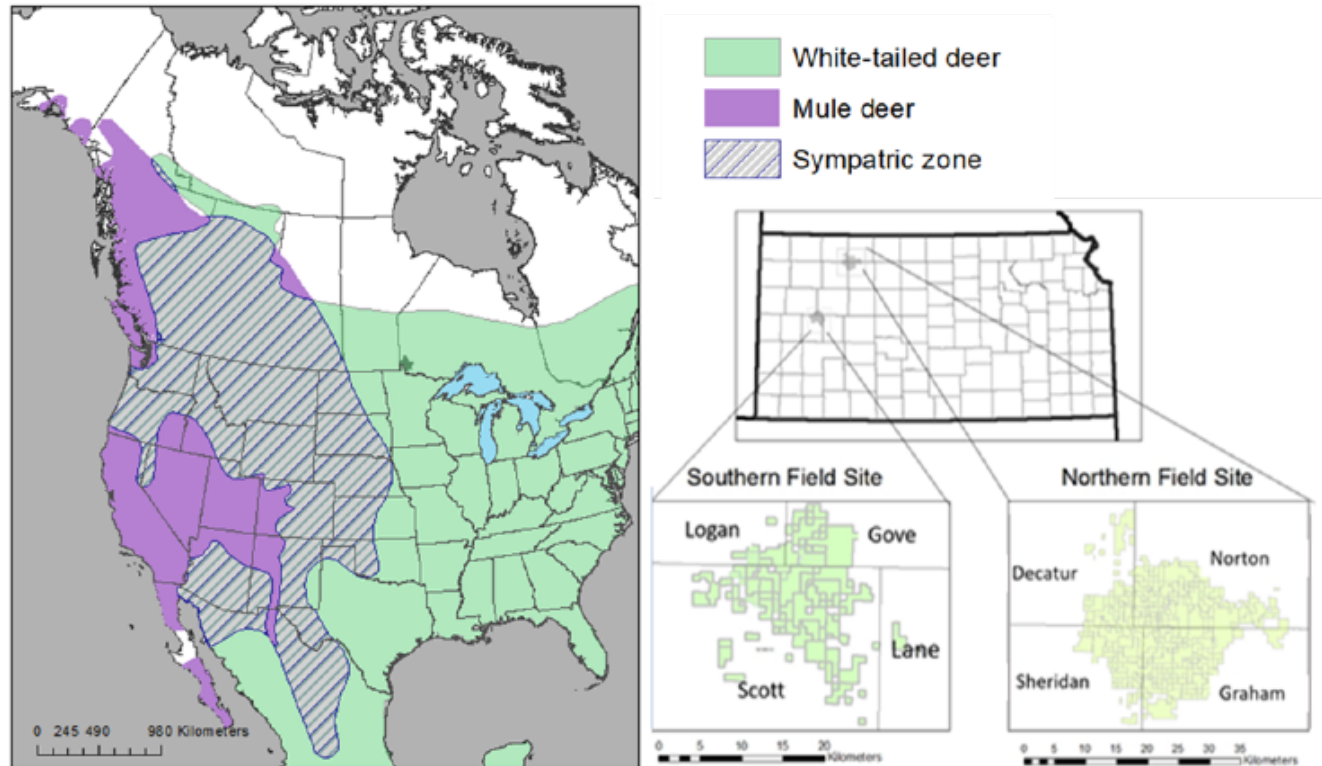
Population genomics of Great Plains white-tailed and mule deer reflects a long history of inter-specific hybridization

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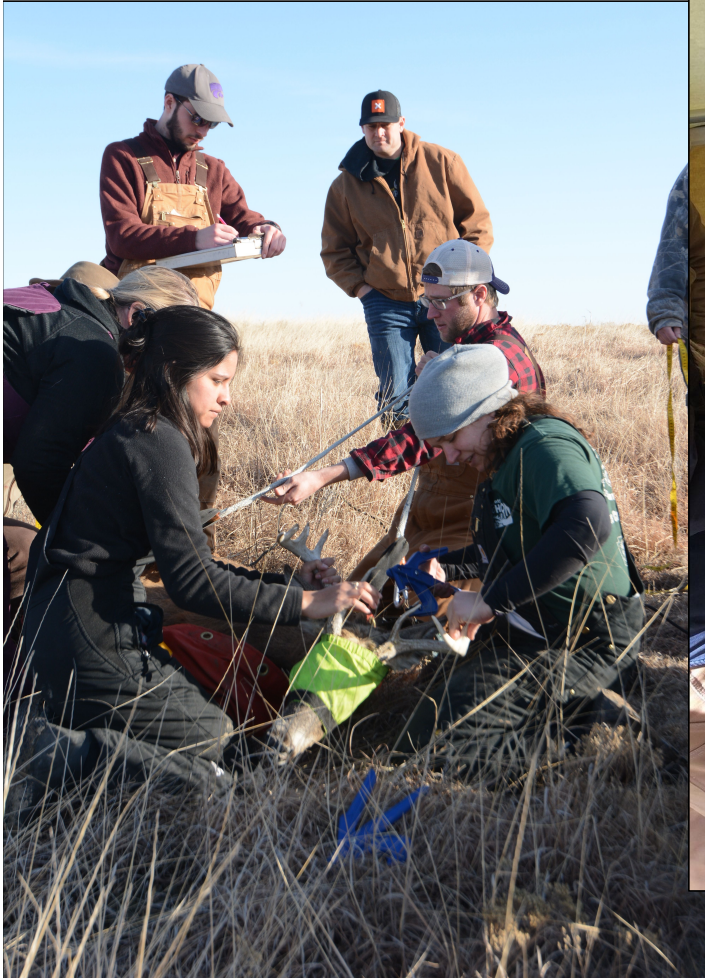


Background

- KS State-funded deer research
 - Occupancy
 - Movement
 - Interaction
 - Survival
- Sampling 2018-2020
 - 90 samples total
 - Mule: n=48
 - White-tail: n=42
 - Blood for genetics



Field Sampling



Evolutionary Approach

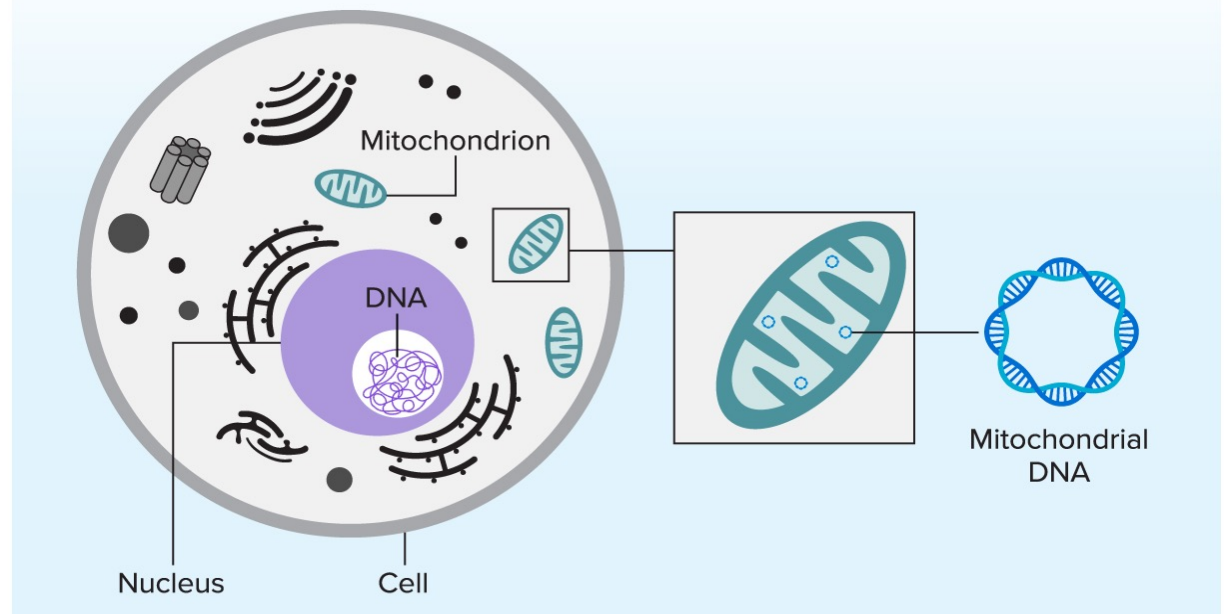
- Additional perspectives on:
 - Population identity
 - Regional differentiation
 - Movement
 - Mixing of regional gene pools
 - Interaction
 - Hybridization
 - Survival
 - Genetic demographic trends



Evolutionary “Basics”

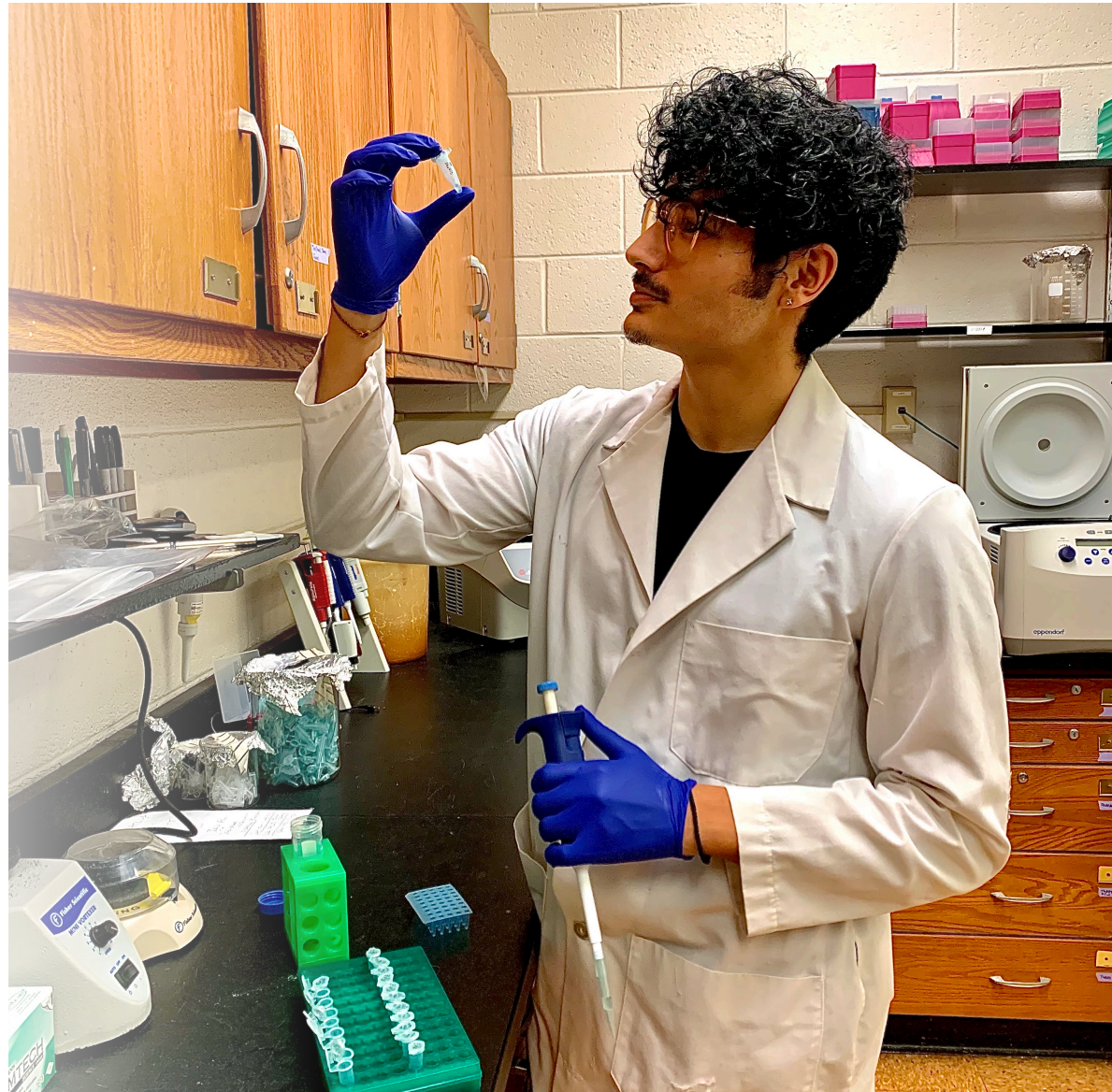
- DNA sources
 - Mitochondrial DNA is maternal only
 - Simple
 - Small
 - Easy to work with
 - Nuclear DNA is from both parents
 - Complex
 - Lots of it
 - Modern genomics

Mitochondria have their own DNA



Evolutionary Methods

- Tissue samples
 - Extract DNA
 - Mitochondrial
 - Nuclear
- Sequence DNA
 - mtDNA gene
 - Single Nucleotide Polymorphisms (SNPs)
- Analyze DNA
 - Within and between populations

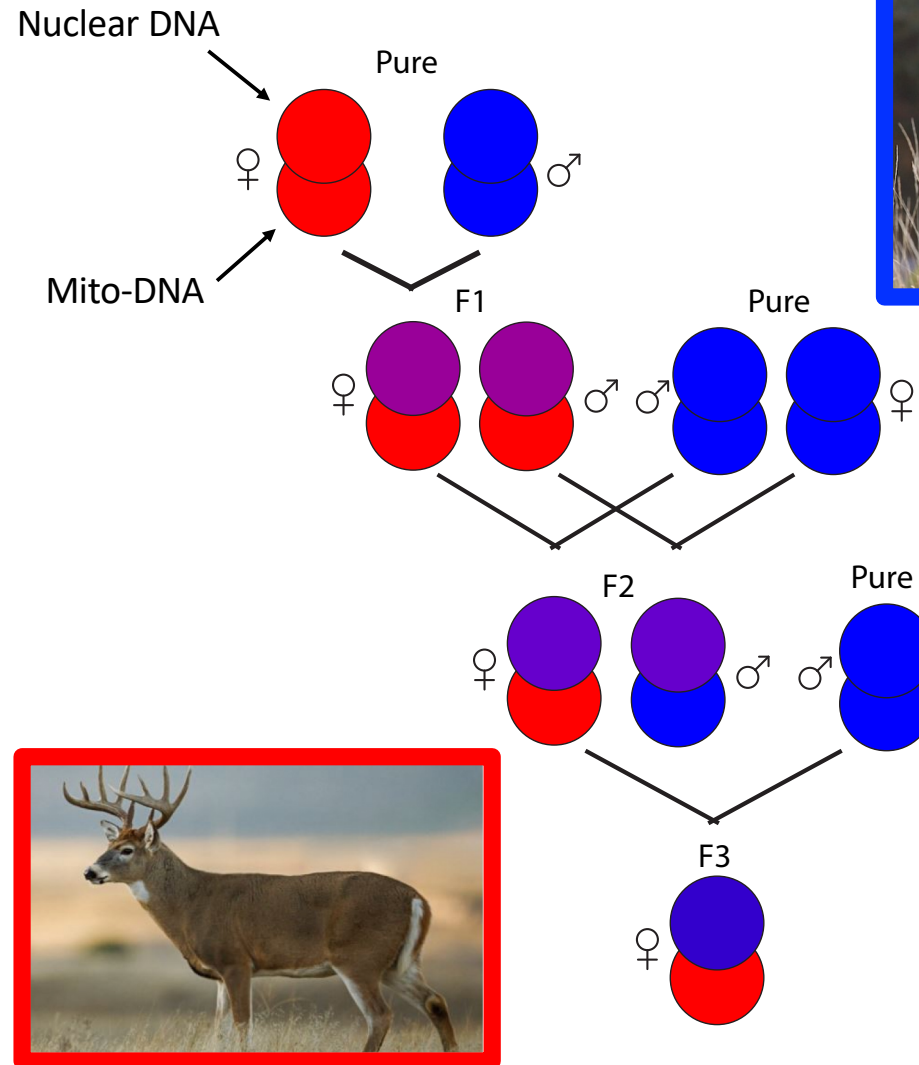


Different sources of DNA

Focus	Mitochondrial DNA	Nuclear DNA (SNPs)
Cost	Cheap	Still Expensive
Difficulty	Easy	Still Difficult
Sample quality	Fresh to degraded	Still often need fresh
Genetic Diversity	Good	Very good
Population identity	Traditionally good; But may be wrong	Very fine detail
Movement between populations	Poor	Fine detail
Hybridization	Limited information without nuclear, but long lasting	Good for a few generations
Demographic trends	Coarse-scale	More reliable

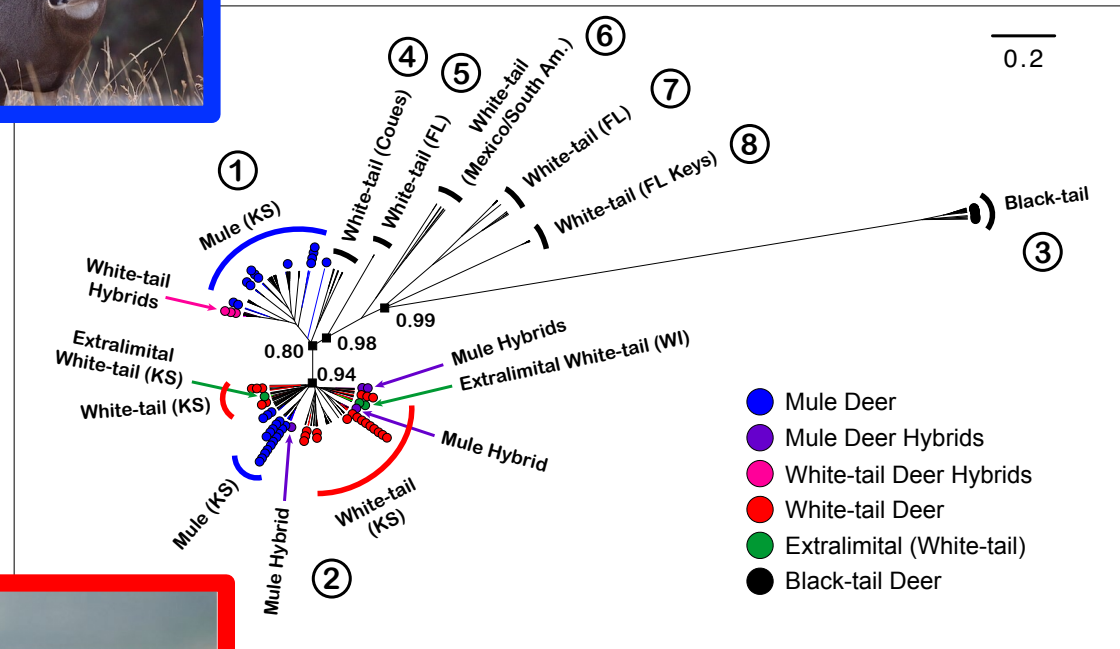
Hybridization

- May occur in one direction or both
- Unknown fitness consequences
- mtDNA and nuclear signals often don't match
- Potential loss of signal after a few generations



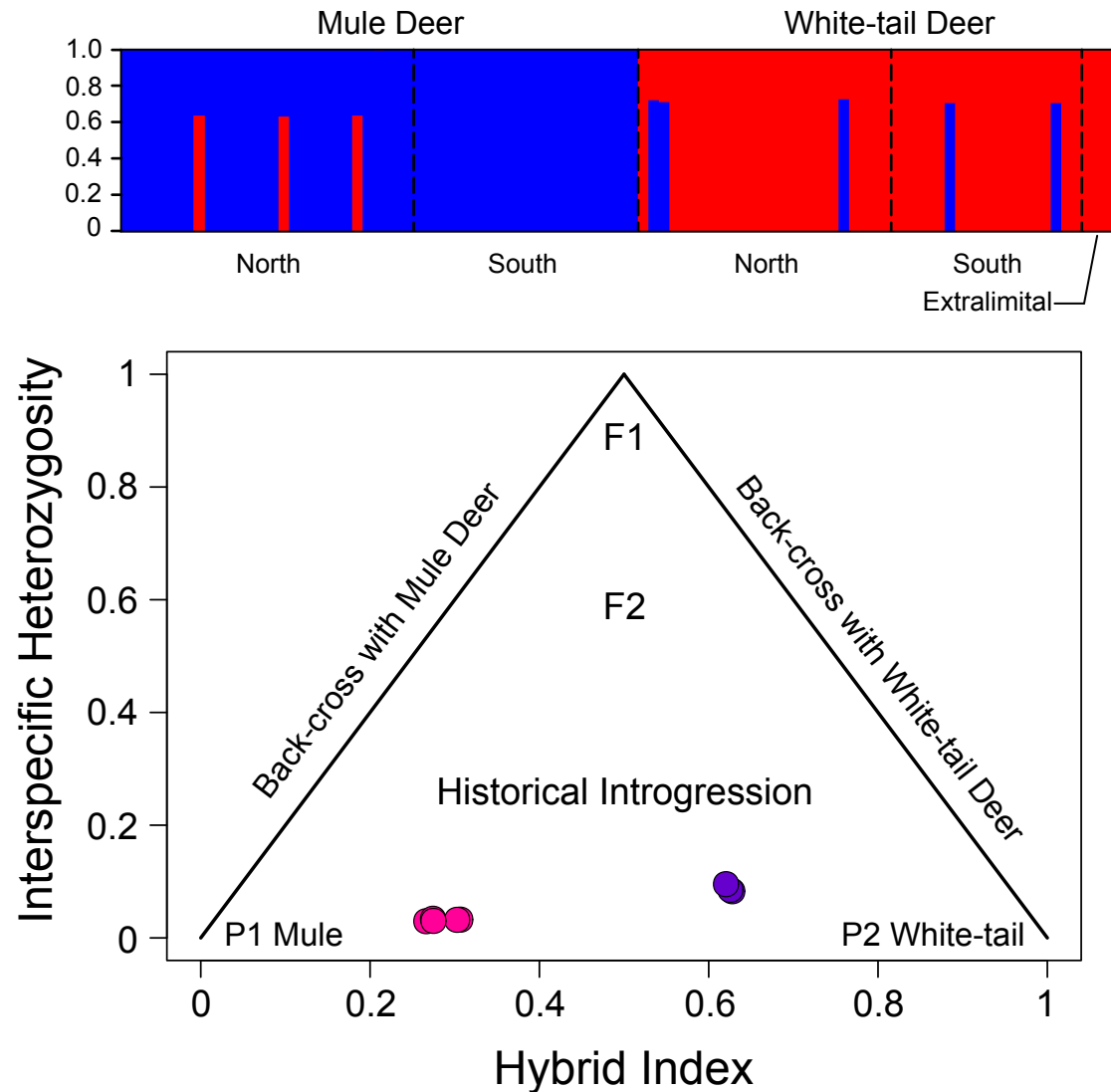
Hybridization - mtDNA

- Only maternal signal
- Ancient hybridization: Mule Males x White-tail Females
- Modern hybridization: Mostly Mule Males x White-tail Females??
- Both directions likely



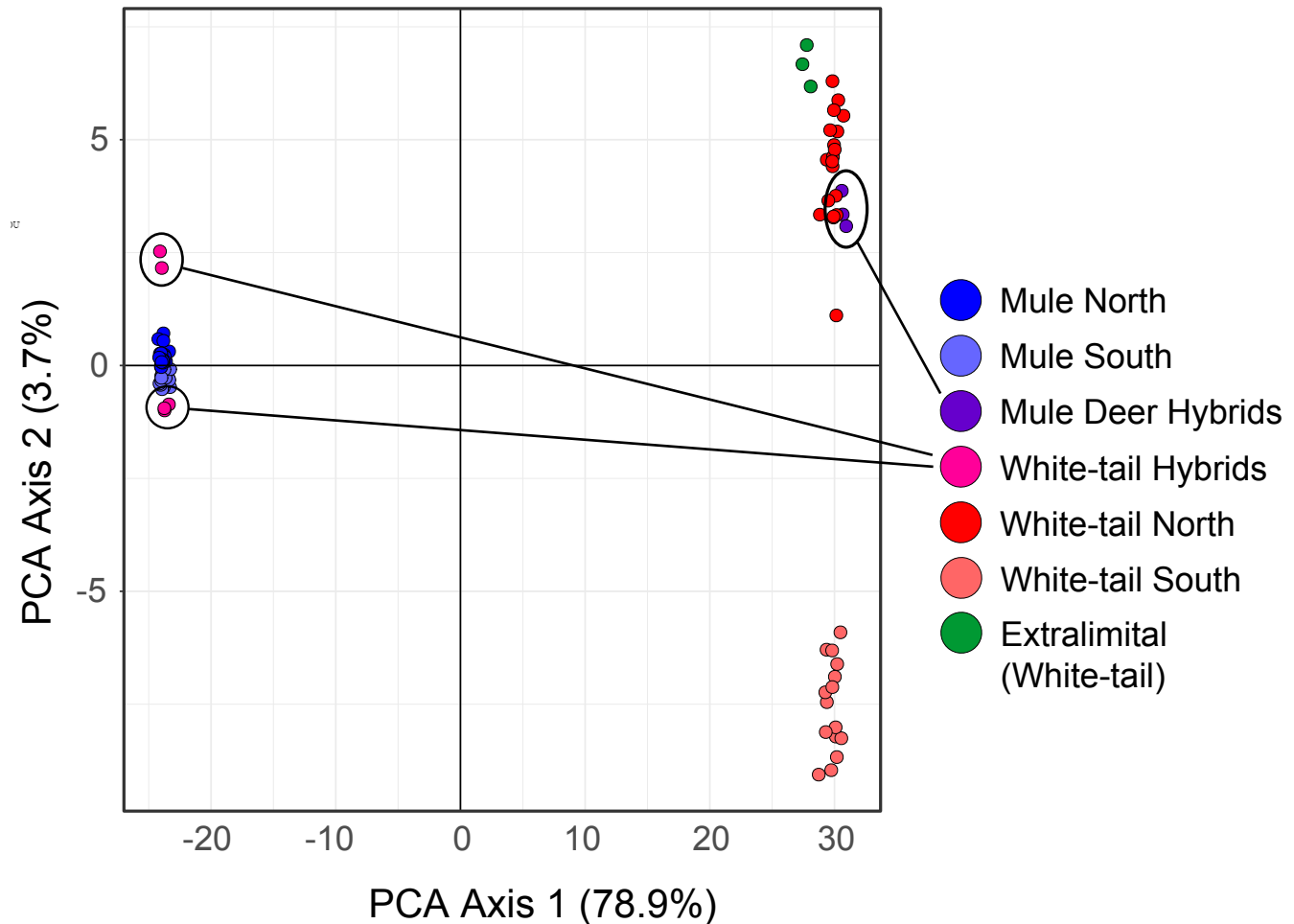
Hybridization – Nuclear DNA

- Hybrids detected in 3 populations
- ~9% individuals are of hybrid origin
- All hybrids are multi-generational with back-crossing in both directions



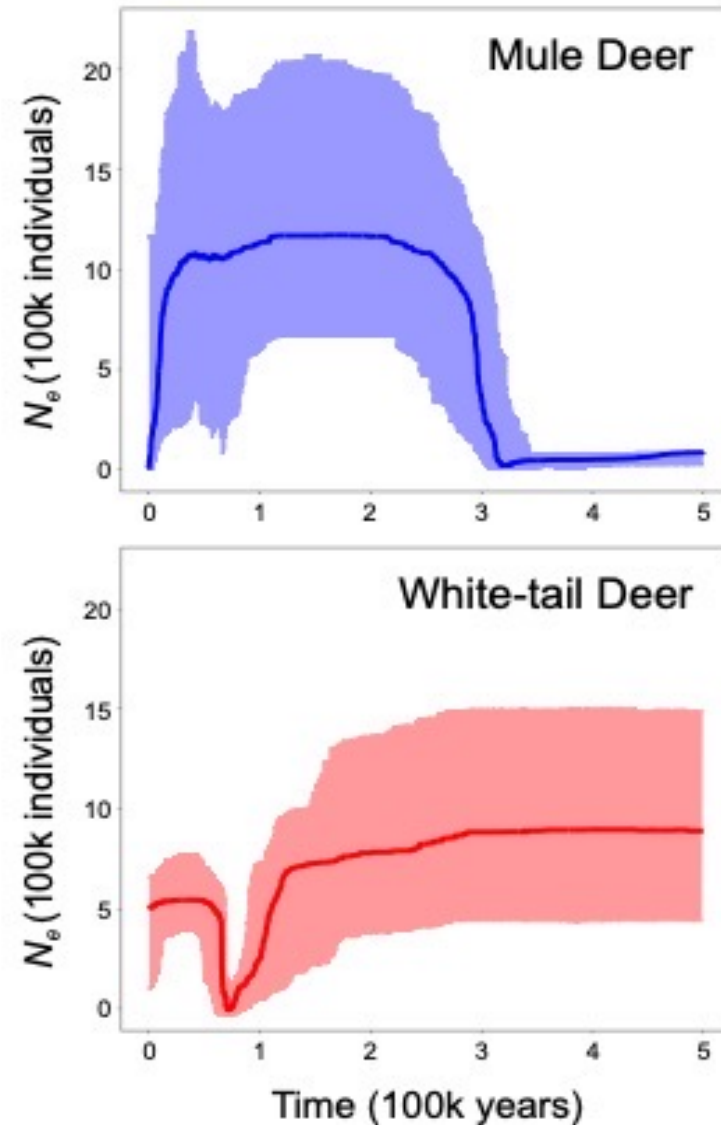
Hybridization – Nuclear DNA

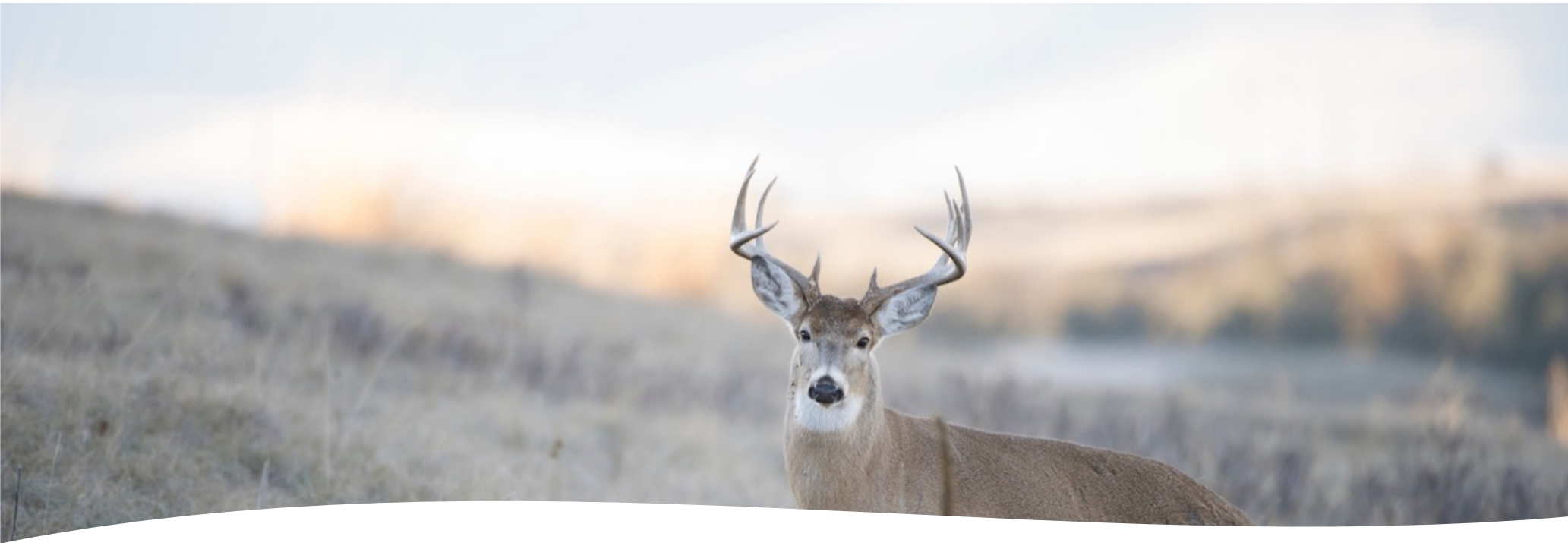
- White-tailed deer are genetically distinct by population
- Mule deer are all genetically similar
- Hybrids show a mismatch between morphological and genetic species assignment



Genetic demography

- Mule deer exhibit a recent decline in effective population size
- White-tail deer exhibit a bottleneck followed by rebound
- Genetic diversity of mule deer is very low
- Genetic diversity of white-tailed deer is high





Take-homes

- Hybridization has been occurring throughout history of deer
- Only certain genomic combinations "work"
- No recent hybrids detected
- Mule deer exhibit high genetic connectivity
- Genetic diversity matches census population trends
- Many unknowns for future research

Ongoing directions

- APHIS funding for genomics of CWD susceptibility
 - Statewide sampling through 2022
 - Thanks to Shane Hesting and regional KDWP managers for sampling!!
 - Targeting prion susceptibility gene
 - Diagnose susceptibility to CWD across multiple populations
 - Compare with CWD test results
 - Compare with genomic diversity
 - More samples needed, including diagnostic voucher specimens!





Thanks to...

- KDWP, especially Levi Jaster
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- KSU, Division of Biology

