

Problem:

Mule deer (*Odocoileus hemionus*) and White-tail deer (*O. virginianus*) co-occur in Kansas and are known to hybridize, but gene flow dynamics are poorly understood and shared haplotypes across locus-sets may be either due to gene flow (ancient and/or ongoing) or incomplete lineage sorting. No studies to date have assessed broad-scale genomic variation within white-tail deer or between species.

Methods:

We scored 433 deer by species based on morphology, mtDNA Cytb gene tree, nuDNA PRNP gene tree (phased), and clustering of thousands of SNPs (ddRADseq), and assessed discordance among datasets in relation to geography. We also present preliminary genomic data on spatial structure and gene flow among both species.

Landscape genomics of free-ranging deer (*Odocoileus*) in Kansas

TJ Hafliger¹, Robert E. Wilson^{2,3}, Sarah A. Sonsthagen⁴, Andrew G. Hope¹

¹Kansas State University, Manhattan, KS, USA; ²University of Nebraska, Lincoln, NE, USA; ³Nebraska State Museum, Lincoln, NE, USA; ⁴U.S. Geological Survey-Nebraska Cooperative Fish and Wildlife Research Unit, School of Natural Resources, University of Nebraska-Lincoln Lincoln, NE, USA.



Results:

1. No evidence of early generation hybrids
2. Clear separation between species based on SNPs but high levels of discordance among datasets, which is geographically prevalent in samples from north and west.
3. No phylogenomic structure apparent in mule deer within Kansas
4. Two apparent genomic clusters within white-tail deer although with strong isolation by distance
5. Incidence of chronic wasting disease (CWD) and discordance among species assignment appear to be limited to regions of Kansas where both species occur.

Discussion:

Gene trees based on Cytb and PRNP loci each had two primary clades dominated by individuals of respective species but with discordance among specimens. Although there is no evidence of early generation hybrids, and despite four independent robust datasets, we still cannot rule out ongoing gene flow, particularly given discordance is clustered where species overlap. We suggest that white-tail in southeast Kansas reflect a unique genetic legacy from white-tail elsewhere, and are not yet strongly impacted by CWD.

Continuing Research:

Further genomic analyses should be insightful, including detailed clustering analyses within each species, additional admixture analyses, assessment of genomic diversity, landscape connectivity, and isolation of sex-linked loci. Comparing genomic signatures to PRNP alleles associated with susceptibility to CWD should inform continuing risks of disease.

Acknowledgements:

We thank Kaitlyn Headlee for help with sequencing and data processing. Funding was provided by USDA APHIS in collaboration with KDWP (Levi Jaster and Shane Hesting)

