



Genetic Diversity in Bobcat (*Lynx rufus*) Populations in Northwest Nevada

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Overview

Bobcats (*Lynx rufus*) are found all over Nevada and are trapped for fur purposes, yet little is known about their genetics. Samples were taken from bobcats collected by fur trappers in Northwestern Nevada and used to determine basic population level analyses, including heterozygosity, allelic richness, and deviations from Hardy-Weinberg equilibrium. Based on the genetic data analyzed, the bobcat population is genetically diverse with high levels of heterozygosity and allelic richness. The population is not out of H-W equilibrium. It also has a slightly male-biased sex ratio of 1.3:1. To our knowledge, this is the first study of its kind for this population and provides baseline data to help monitor and manage this population.

Introduction

- Population genetic analyses can inform managers about the health of wildlife populations and can be used to determine genetic changes over time.
- Bobcats are found and trapped all over Nevada, yet genetic analyses have not been conducted on this population.
- DNA was obtained from bone fragments of trapped bobcats that were given to NDOW. Undergraduate researchers performed DNA extraction on these bone fragments.
- Data analysis from DNA was performed to lay a foundation of bobcat genetic data in northern Nevada and to determine basic population level genetic information.



Method

- DNA was extracted from 101 bobcat jaw fragments using Qiagen DNeasy Blood and Tissue extraction kits
- Seven polymorphic microsatellites (loci) were used: FCA026, FCA043, FCA045, FCA077, FCA090, FCA096, FCA132 (Table 1)
- Samples collected from hunting regions 012,0124,011,013,015,022,195,192,196 and 194 (Figure 1)
- PCR and genotyping analysis was performed by USDA, APHIS Wildlife Services National Wildlife Research Center
- GenePop and CERVUS 3.0.7 were used analyze the genetic data to determine heterozygosity, allelic richness, and H-W equilibrium deviations
- The population sex ratio was calculated from data obtained from microsatellite marker: ZNsex



Results

- All loci were polymorphic, ranging from 6 to 14 alleles (Table 1)
- Average 8.714 alleles per locus, shows high allelic richness
- Observed heterozygosity ranged from 0.596 to 0.900 (Table 1)
- Not out of Hardy-Weinberg equilibrium
- Male/female sex ratio was 1.3:1
- Large degrees of heterozygosity within each locus and overall in the population



Figure 1. NDOW Hunting Map: Data collected from highlighted regions

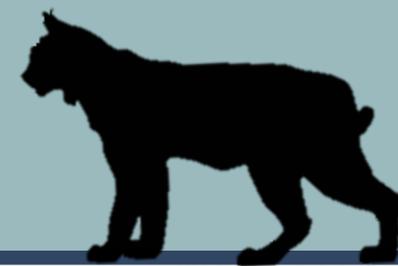
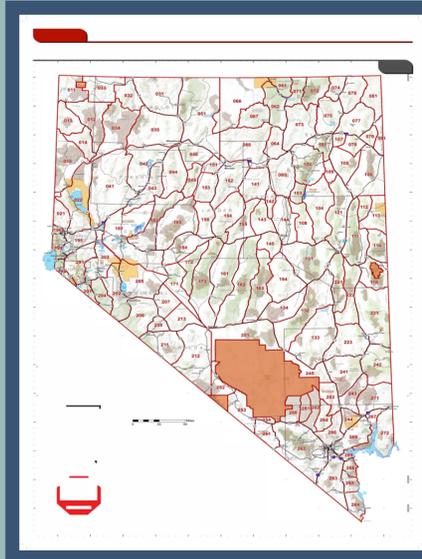


Table 1

| Allele Frequency Analysis | | | | |
|---------------------------|------------------------------|-----------------------|-------------------------|-------------------------|
| Locus | Allele variation within Gene | Number of individuals | Observed Heterozygosity | Expected Heterozygosity |
| FCA026 | 14 | 100 | 0.9 | 0.882 |
| FCA043 | 6 | 100 | 0.7 | 0.735 |
| FCA045 | 7 | 99 | 0.596 | 0.837 |
| FCA077 | 9 | 100 | 0.73 | 0.715 |
| FCA090 | 8 | 101 | 0.693 | 0.78 |
| FCA096 | 9 | 97 | 0.722 | 0.758 |
| FCA132 | 8 | 99 | 0.828 | 0.851 |

Conclusion

- The northwest Nevada populations are more genetically diverse than expected and not deviating from H-W equilibrium.
- Even with trapping pressures and urbanization, the population appears to be doing well with overall large genetic diversity.
- It appears to be more common to trap more males based on the male bias sex ratio. These sex ratio results are consistent with other studies.
- This bias could result from male bobcats having larger home ranges, roaming more than females, and being more risk prone.
- These results are the beginning of a long-term monitoring project. They are being shared with NDOW and will be used to compare with future genetic samples so that we can continue to determine genetic diversity and possible evolutionary changes.