

Genetic structure and gene flow of black bears in the southern Appalachians



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Background

- American black bear (*Ursus americanus*)
- Severe population decline
 - ❖ Fragmentation and habitat loss
 - ❖ Overharvest
- Great Smoky Mountain National Park (GSMNP)
 - ❖ Population increases
 - ❖ Possible decline in late 1960s
- Southern Appalachian Black Bear Study Group (SABBSG) founded

Background

“Efficacy of DNA sampling to monitor population abundance of black bears in the southern Appalachians”

- Summer of 2003
- Hair snares
- 129 individuals identified in National Park Study Area (NPSA)
- 60 individuals identified in the National Forest Study Area (NFSA)

Settlage 2005, Settlage et al. 2007

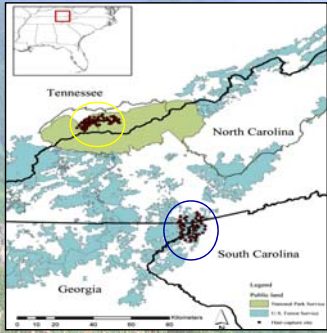
Justification

- Last genetic study completed in 1985 (*Wathen et al. 1985*)
- Increasing fragmentation and encroachment
- Regional management plan

Objectives

- 1) Estimate within-population genetic variation
- 2) Estimate among subpopulation genetic differentiation
- 3) Estimate gene flow between subpopulations

Study Area

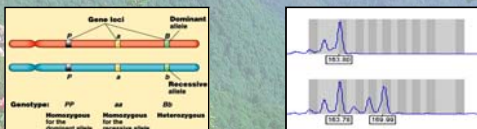


- NPNSA
 - ❖ GSMNP
- NFSA
 - ❖ Chattahoochee NF
 - ❖ Sumter NF
 - ❖ Nantahala NF

Settlage et al. 2007

Genetic Analysis

- **DNA extraction** (USGS- Leetown Science Center)
- **9 Microsatellite loci** (Paetkau and Strobeck 1994, Paetkau et al. 1995)
 - ❖ Group of molecular markers found in nuclear DNA
 - ❖ Heterozygous or homozygous



Assumptions

- **Hardy-Weinberg equilibrium**
 - ❖ Markov Chain Monte Carlo (MCMC)/Fisher's exact test
 - ❖ Program ARLEQUIN (Excoffier et al. 2005)
- **Linkage disequilibrium**
 - ❖ Non-random mating, genetic drift, recent admixture or sample size
 - ❖ Sequential Bonferroni adjustments
 - ❖ Program ARLEQUIN

Genetic Structure

- **Population heterozygosity**
 - ❖ Low levels
 - ❖ High levels
- **Analysis of molecular variance (AMOVA)**
 - ❖ Based on differences among all pairs of genotypic alleles
 - ❖ Within population (F_{IS})
 - ❖ Among populations (F_{ST})

Clustering

- Program STRUCTURE 2.2 (Pritchard et al. 2000)
 - ❖ Individual's probability of belonging to a sampled population
 - ❖ Population clusters (k) 1-5
 - ❖ Admixture model with correlated allele frequencies
 - ❖ Burn-in and likelihood estimation run- MCMC 100,000 iterations
 - ❖ Highest value of the log probability
 - ❖ Δk – rate of change in likelihood distribution (Evanno et al. 2005)

Gene Flow

- Slatkin's linearized F_{st} (Slatkin 1995)
- Program STRUCTURE 2.2
- Program GeneClass2 (Piry et al. 2004)
 - ❖ Estimate likelihood that a genotype originated from within the population where the individual was sampled
 - ❖ Re-sampling to generate critical values for rejecting the possibility that an individual was born in a population where it was sampled

Results and Discussion

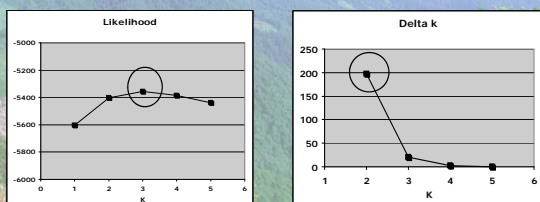
- Hardy-Weinberg equilibrium
 - ❖ MU23 ($p = 0.040$) for the NPSA
 - ❖ G10B and MU23 ($p = 0.043$ and $p = 0.044$) for the NFSA
 - ❖ No significance after adjustments
- Linkage disequilibrium
 - ❖ Association among 3 of 36 pairs of loci for the NPSA
 - ❖ Association among 3 of 36 pairs of loci for the NFSA

Results and Discussion

- Population heterozygosity
 - ❖ 0.76 for the NPSA
 - ❖ 0.74 for the NFSA
- Analysis of molecular variance (AMOVA)
 - ❖ $F_{st} = 0.042$
 - ❖ $F_{ls} = 0.037$ and $F_{is} = 0.010$ for the NPSA and NFSA, respectively

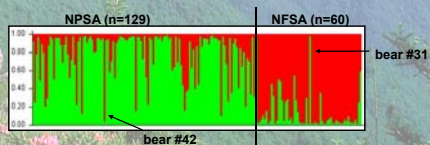
Results and Discussion

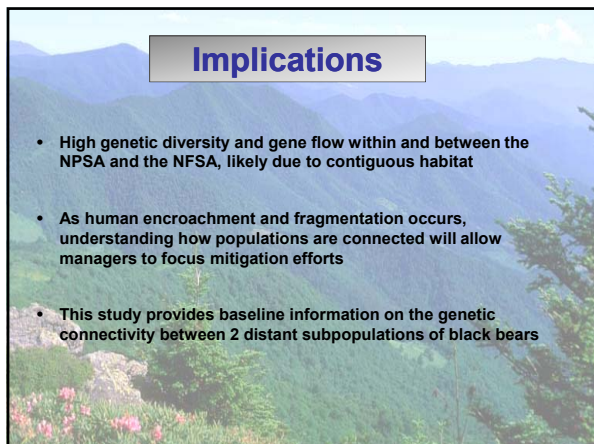
- Population Clustering
 - ❖ Log probability of likelihood
 - ❖ Δk – rate of change in likelihood distribution



Results and Discussion

- Gene Flow
 - ❖ Bear #42 (NPSA, male) and bear #31 (NFSA, sex unknown) were 1st generation migrants
 - ❖ Six bears exchanged between study areas every generation
 - ❖ 3 additional bears within each study area found to be 1st generation migrants (1 male, 5 unknown)





Implications

- High genetic diversity and gene flow within and between the NPSA and the NFSA, likely due to contiguous habitat
- As human encroachment and fragmentation occurs, understanding how populations are connected will allow managers to focus mitigation efforts
- This study provides baseline information on the genetic connectivity between 2 distant subpopulations of black bears



Acknowledgments

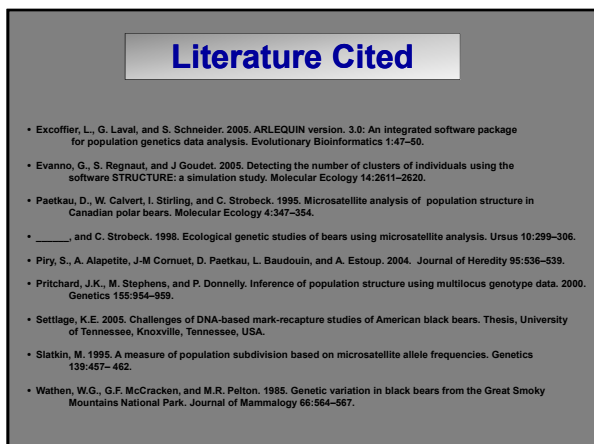
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Questions

