Noninvasive Genetic Techniques and its Application in Wildlife Conservation

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Lecture Structure

- Introduction
- Sources and methods of collecting samples
- Applications
- Pitfalls
- How to avoid pitfalls

Introduction

- Historically, molecular techniques developed in the human genetics community
- Over time adopted by the wildlife community
Introduction

- Molecular studies in wildlife populations
  - Ecological
  - Evolutionary

- Assessing the genetics of wild populations 30 or 40 years
  - required large amounts of fresh tissue
  - animals were often killed
  - widely used for birds, rodents, insectivores
  - techniques fell under public scrutiny

Introduction

- First alternative was blood samples
  - used to study serum proteins
  - did not provide a lot of genetic information

- Recent advancement in molecular techniques offer promise for future research
  - microsatellites
  - Polymerase Chain Reaction (PCR)

Introduction

- Microsatellites
  - widely distributed in the genome making it easy to develop a suite of markers available for genetic studies
  - highly variable, which provides unique fingerprint
  - Can be amplified using PCR
Introduction

- PCR
- Tiny samples collected from hair, feathers, feces
- Uses a series of heating and cooling steps with a mixture of enzymes, base pairs, and template strands to replicate
- 20 million copies in 3 hours!

Sources and Collection Methods

Hair-Snare Design
Wire and Glue Hair Snares

Wire and Glue Snare

Collecting Hair – Ground Dwellers
Collecting Hair – Tree Dwellers

Feces
- Collected
  - On roads
  - In the woods
  - Edges
  - River banks

Feathers and Egg Shells
**Pods are located**

- Researchers wait for activities such as breaching and tail slapping
- Results in sloughed skin

**Saliva**
Regurgitates

- Found at roosting sites of owls

Urine

- Wolf and wolverine studies

Applications
Abundance Estimation

- Obtaining reliable results from mark-recapture methods based on live trapping is challenging
  - low capture probabilities
  - capture biases
- Unique genotypes can be used in traditional mark-recapture studies
- Advantages
  - increased capture probability
  - tag permanency
  - decreased intrusiveness
  - reduced bias

Abundance Estimation

- Romain-Bondi et al. (2004) studied endangered grizzly bear population in Washington
  - 6 bears (90% CI =1-27)
  - implications are natural recovery is very unlikely
  - recommend population augmentation

Genetic Diversity

- Important factor in long term population persistence
- Allows species to respond to environmental change
- Small, isolated populations may experience inbreeding depression
  - cheetah
  - Florida panther
Genetic Diversity

- Eastern Slopes Grizzly Bear Project
- Genetic variation in the Bow River Watershed
- Found little maternal diversity compared to the Northern Continental Divide population
- Overall genetic variation was good
- Suggests males travel far enough to provide variation

Gene Flow

- Gene flow - movements of individuals from one location to another and their subsequent integration into the gene pool of their new locality
- Increasingly isolated populations may experience reduced gene flow, thus decreased genetic variation
Demographic History

- Patterns of population expansion and decline
- Culver et al. 2008
  - Population size for Florida panther mid 20th century?
  - Genetic variation 1890s vs. 1990s
  - Found threefold decrease in genetic diversity
  - Used models to estimate effective population required to account for the decline

Population of Origin

- Assignment test - Uses allele frequencies to assign individuals to their most likely source population
- Blanchong et al. (2002)
  - Used genotypic data to confirm that Michigan deer infected with tuberculosis were harvested in area assumed to be free of the disease

Hybridization

- Hybridization can be a problem, especially when populations are small and are in close proximity to a similar species.
- If hybrids are fertile, continued hybridization could lead to genetic swamping
Hybridization

- 1973 red wolf received protection under the Endangered Species Act
- Red Wolf Recovery Program recognizes hybridization as the primary threat to recovery of the species

Hybridization

- Adams et al. (2003) – used fecal DNA to monitor hybridization between red wolves and coyotes
  - gave a better understanding of the amount of hybridization and the spatial distribution of wolves and hybrids
  - provided an important tool for curbing hybridization in the future

Others

- Phylogeography
- Identification of Sex
- Parentage
- Population Structure
- Landscape Genetics
- Dispersal and Immigration
- Migratory Movements
- Forensics
- Dietary Studies
- Documenting Rare Species
- Conservation Genetics
Pitfalls

- Amount of DNA collected from free ranging animals is often very low

- Allelic dropout is the amplification of only 1 of 2 alleles in a heterozygote pair
  - produces false homozygotes
  - may interpret as new captures
  - can significantly bias estimates

Pitfalls

- False alleles are a result of artifacts created during amplification
  - can be misinterpreted as true alleles
  - homozygous individual may be recorded as a heterozygote and identified as a new capture
  - McKelvey and Schwartz (2004) found allelic dropout caused a 5.5 fold increase in wolf abundance estimates

Pitfalls

- Shadow effect – when 2 or more individuals share the same genotype at the same loci
  - misclassification of unique individuals
  - negatively bias abundance estimates
  - occurs when too few loci are examined
  - when low heterozygosity loci are used
How to Avoid Pitfalls

- First thing first
  - differences exist among species
  - wolf feces provides much more DNA than bear feces
  - generalizations can be hazardous
  - thoroughly research literature
- Do trial test before diving into experiment
  - Determine what method provides the best results to reach your scientific goal

Questions?