Genetic diversity and relatedness of northern bobwhite coveys in South Texas

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Northern bobwhite (*Colinus virginianus*) mating behaviors

- High polyandry (71%; Burger et al. 1995).
- Re-nesting, within days (Curtis et al. 1993).
Families, coveys, and the fall shuffle

- Summer: family unit.
- Nesting tapers off: groups of multiple families.
- Winter covey: 6–16 birds.
- Personnel transfers.
Northern bobwhite genetics

• Range-wide population declines.
• Retain genetic variation.
• Fall shuffle: ↑ gene dynamics, ↓ inbreeding.

• Little information on covey genetics, promiscuity, and social groups → genetic diversity and gene flow.
Objectives

• Genetic diversity
• Population structure
• Relatedness

Within and among northern bobwhite coveys.
Hypothesis 1: Fall Shuffle and “Mixing”

“Mixing”: sibling distribution within / among coveys.

• Families intact through shuffle and into winter: Coveys = full sibs & parents.

• Families separated during shuffle: Full and half sibs distributed among coveys.
Hypothesis 2: Relatedness through the winter

- On average, coveys sampled at beginning of winter have more related individuals than those sampled at the end of winter.
- Family members intact during shuffle.
- Coveys are not static over the winter:
  - hunting
  - predation
Hypothesis 3: Promiscuity

- Full: Half sib ratio
- Hypothetical situation:

Grahmann 2013
Study Area

- 3,558 ha of private ranch
- Jim Hogg County, Texas.
- Sandy mesquite (*Prospis glandulosa*) savanna
- Sandy mesquite woodland
- Deep sand grassland (Elliot 2011, TPWD and Missouri Resource Assessment Partnership).
Data Collection and DNA Amplification

- Hunter-harvested wings.
- Age, sex, covey for each bird.
- Coveys: ≥3 birds harvested, sampled all birds.
- 11 microsatellite DNA loci:
  - Schable et al. 2004
  - Faircloth et al. 2009
Genetic diversity and structure

• Genetic diversity:
  \( A_R \) (HP-Rare v. 1.1, Kalinowski 2005).
  \( H_O \) (ARLEQUIN 3.5, Excoffier and Lischer 2010).

• Genetic structure:
  AMOVA (Weir and Cockerham 1984).
  \( F_{ST} \) (ARLEQUIN 3.5, Excoffier and Lischer 2010).

• Inbreeding coefficient (\( Fi \))
  SPAGeDi v. 1.4, Hardy and Vekemans 2002
Genetic relatedness

- Queller and Goodnight’s $R$
- Li et al. 1993
- Ritland 1996
- Lynch & Ritland 1999
- Wang 2002

SPAGeDi v. 1.4, Hardy and Vekemans 2002
Coancestry v. 1.0, Wang 2011
Genetic relatedness

- 3 Full pedigree maximum-likelihood algorithms:
  - Wang 2004
  - Milligan 2003
  - Wang 2007

- Full sib, half sib, parent–offspring pairs

- Relatedness compared with Pearson’s correlations in Coancestry v. 1.0 (Wang 2011).
Results

- 96 birds, 29 coveys
- Dec–Feb 2010–2011
- 77 birds, 23 coveys
- 70 juveniles, 7 adults
- Summer 2011 drought
- Dec-Feb 2011-2012
- 19 birds, 6 coveys
- All adult

<table>
<thead>
<tr>
<th></th>
<th>N</th>
<th>$A_R$</th>
<th>$H_O$</th>
<th>$H_E$</th>
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<td>Pooled (n = 96 birds)</td>
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<td>Average</td>
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<td>2.2</td>
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<td>0.03</td>
<td>0.02</td>
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</table>
Genetic diversity and structure

Pooled over winters

F_{IS} = 0.183, P < 0.01
F_{ST} = 0.073, P < 0.01
F_{IT} = 0.115, P < 0.01
2010-2011 matrix of relatedness
5 Colony runs, P ≥ 0.99

Not related: 95%
Parent-offspring: 0.03%
Full sibs: 0.4%
Half sibs: 4.0%
Full:half sib: 1:32 – 1:137

n = 2887 pairs

• 13 coveys (56.5%)
• No change in # coveys with related birds over time.
2011-2012 matrix of relatedness

Not related: 94%
Parent-offspring: 0%
Full sibs: 1.8%
Half sibs: 6.2%
Full:half sib: 1:5 – 1:7
n = 161 pairs

• 2 coveys (33.3%)
Relatedness among winters

Green: Half sib               Purple: Full sib / parent-offspring

Not related: 98%
P-O / Full sibs: 0.3%
Half sibs: 3.8%

Full:half sib: 1:22 – 1:57

n = 1463 pairs
Coancestry

\[ \alpha = 0.05, \ df = 4559 \]

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<th>Colony</th>
<th>TrioML</th>
<th>Wang</th>
<th>LynchLI</th>
<th>LynchRD</th>
<th>Rit</th>
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- Colony: weak correlation to other relatedness estimators.
- Generally, results robust to a variety of estimators of relatedness.
Discussion

• Allelic richness low, heterozygosity moderate.
• Population structure moderate.
• Influence of sample size: hunter methods.
• Full covey: better estimates.
Fall shuffle, “mixing” of coveys

• H1: “Mixing”: sibling distribution within / among coveys.
• Pattern of relatedness within and among coveys.
• Mixing can start as early as late summer.
• Brood amalgamation.
• Fall shuffle → distributing families well.
Fall shuffle, “mixing” of coveys

- H2: Distribution of relatives throughout season.
- 12 birds, losses, gains (Lehmann 1984).
- 1 bird/ 3 days (Yoho and Dimmick 1972)
- Hunting

Lehmann 1984, Appendix E
Promiscuity

- H3: 2:1 full to half sibs
- In contrast, high ratio of half:full sibs (32-137:1).
- Promiscuity more frequent than assumed.
Conclusions

• Fall shuffle, promiscuity: genetic diversity.
• Gene flow among pastures, nearby ranches.
• Very important to isolated populations.
• Snapshot: defined area, short time period.
• Further studies: parentage analyses, movements, and covey dynamics.
Acknowledgements

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Questions?


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