



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).
- Male incubation (Stoddard 1931, Lehmann 1984)
 - 20–30% of nests
(Brennan et al. 2014).
- Re-nesting, within days
(Curtis et al. 1993).



Families, coveys, and the fall shuffle

- Summer: family unit.
- Nesting tapers off: groups of multiple families.
- Fall shuffle: (Sept.-Nov., Lehmann 1984).
- Winter covey: 6–16 birds.
- Personnel transfers.



Northern bobwhite genetics

- Range-wide population declines.
- Retain genetic variation.
- Fall shuffle: $\uparrow$ gene dynamics, $\downarrow$ inbreeding.
- Little information on covey genetics, promiscuity, and social groups $\rightarrow$ 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.

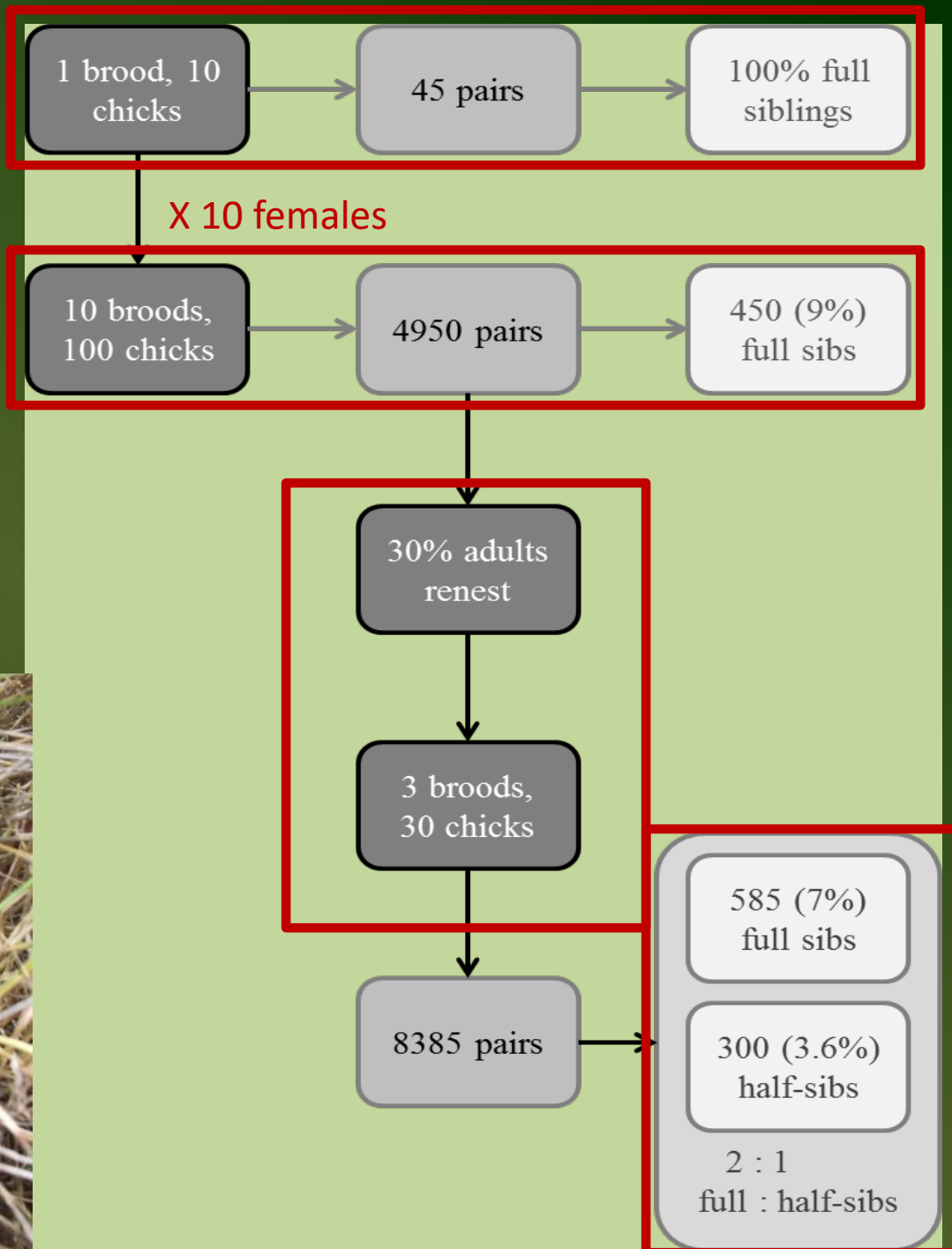
Hypothesis 2: Relatedness through the winter

- 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

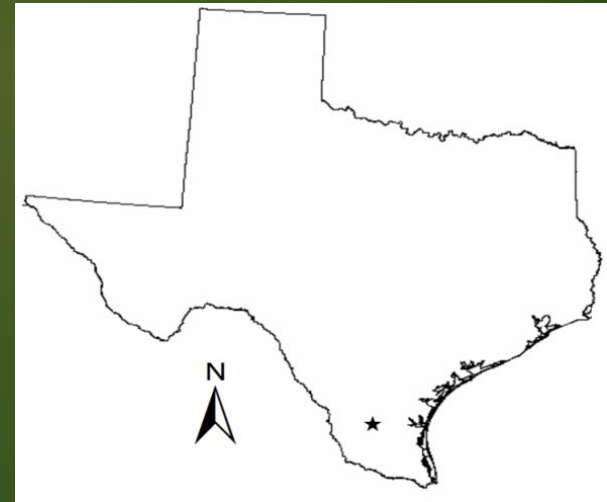
- Full: Half sib ratio
- Hypothetical situation:

Grahmann 2013



Study Area

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



Data Collection and DNA Amplification

- Hunter-harvested wings.
- Dec.-Feb. 2010–2011, 2011–2012.
- 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 (F_i)
 - SPAGeDi v. 1.4, Hardy and Vekemans 2002

Genetic relatedness

- 5 Pairwise coefficients of relatedness:

- Queller and
Goodnight's R



SPAGeDi v. 1.4,
Hardy and
Vekemans 2002

- Li et al. 1993



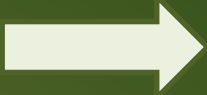
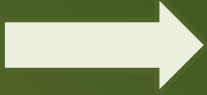
Coancestry v. 1.0,
Wang 2011

- Ritland 1996

- Lynch & Ritland 1999

- Wang 2002

Genetic relatedness

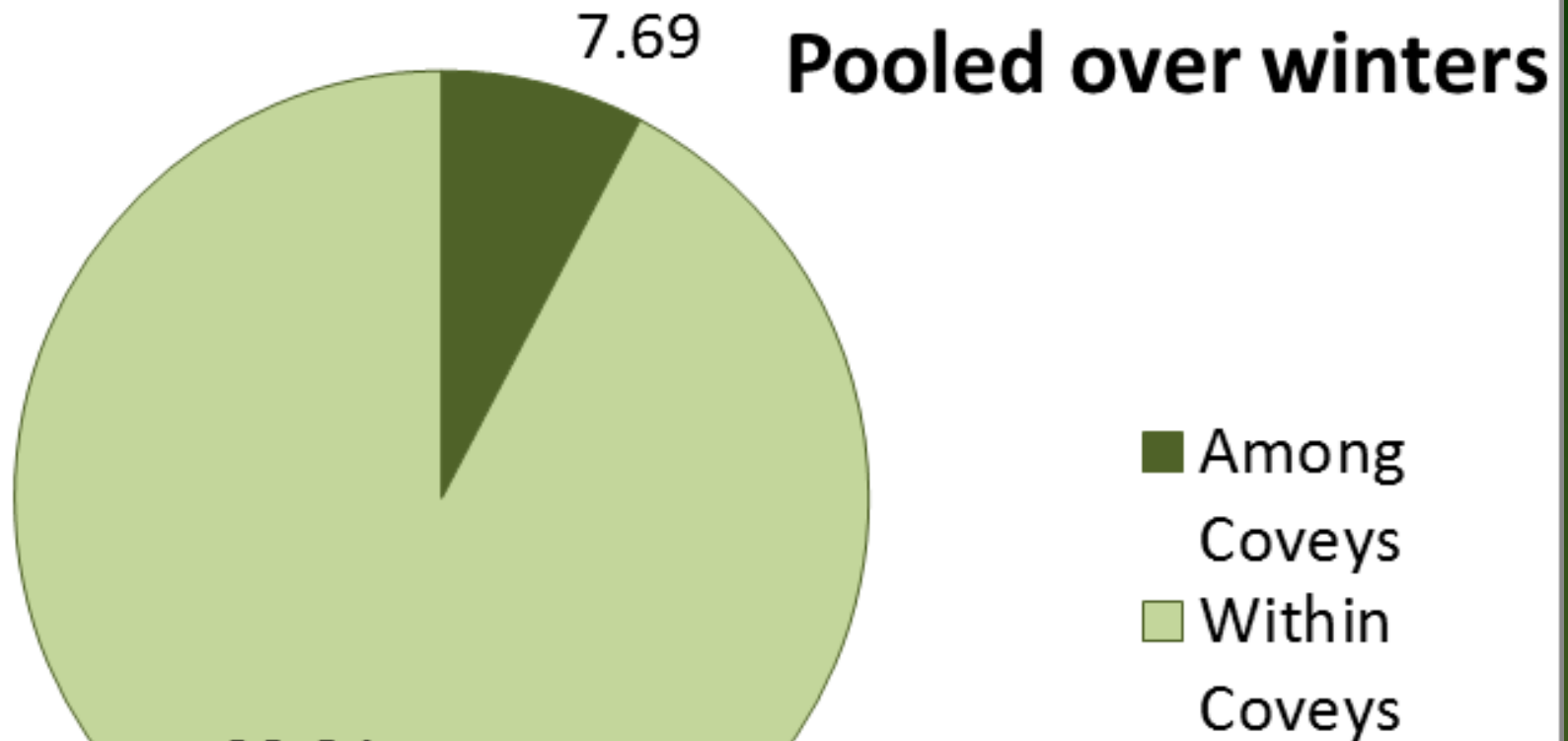
- 3 Full pedigree maximum-likelihood algorithms:
 - Wang 2004  Colony v. 2.0.4.5,
 - Milligan 2003  Coancestry v. 1.0,
 - Wang 2007 Wang 2011
- Full sib, half sib, parent–offspring pairs
- Relatedness compared with Pearson's correlations in Coancestry v. 1.0 (Wang 2011).

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

	N	A_R	H_O	H_E	F_i
Pooled ($n = 96$ birds)					
Average	3.29	2.2	0.67	0.72	0.08
SE	0.08	0.03	0.02	0.01	0.03

Genetic diversity and structure



$$F_{IS} = 0.183, P < 0.01$$

$$F_{ST} = \mathbf{0.073}, P < \mathbf{0.01}$$

$$F_{IT} = 0.115, P < 0.01$$

2010-2011 matrix of relatedness

5 Colony runs, $P \geq 0.99$

Not related: 95%

Parent-offspring: 0.03%

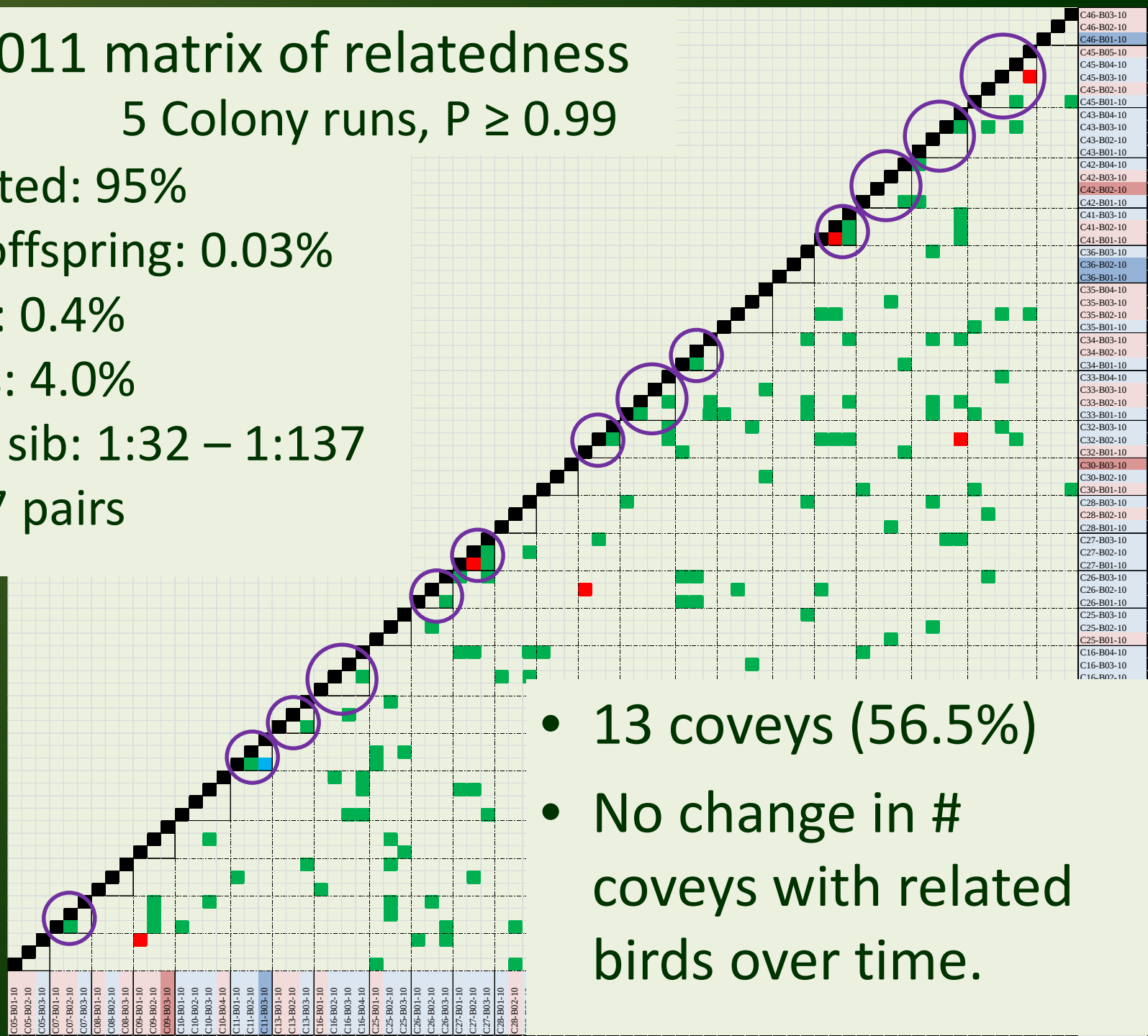
Full sibs: 0.4%

Half sibs: 4.0%

Full:half sib: 1:32 – 1:137

$n = 2887$ pairs

Green:
Half sib
Red:
Full sib
Blue:
parent -
offspring



- 13 coveys (56.5%)
- No change in # coveys with related birds over time.

2011-2012 matrix of relatedness

Not related: 94%

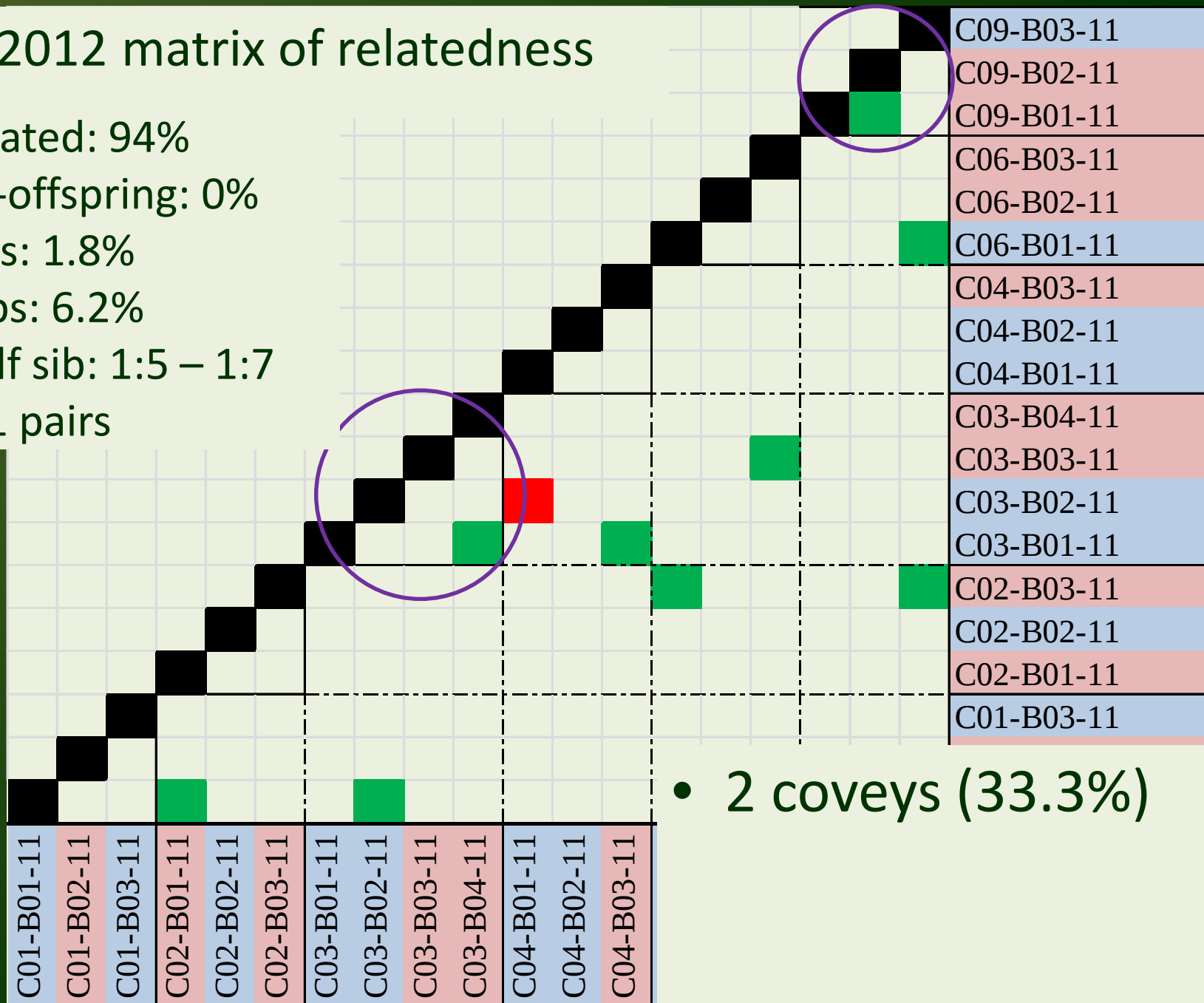
Parent-offspring: 0%

Full sibs: 1.8%

Half sibs: 6.2%

Full:half sib: 1:5 – 1:7

$n = 161$ pairs



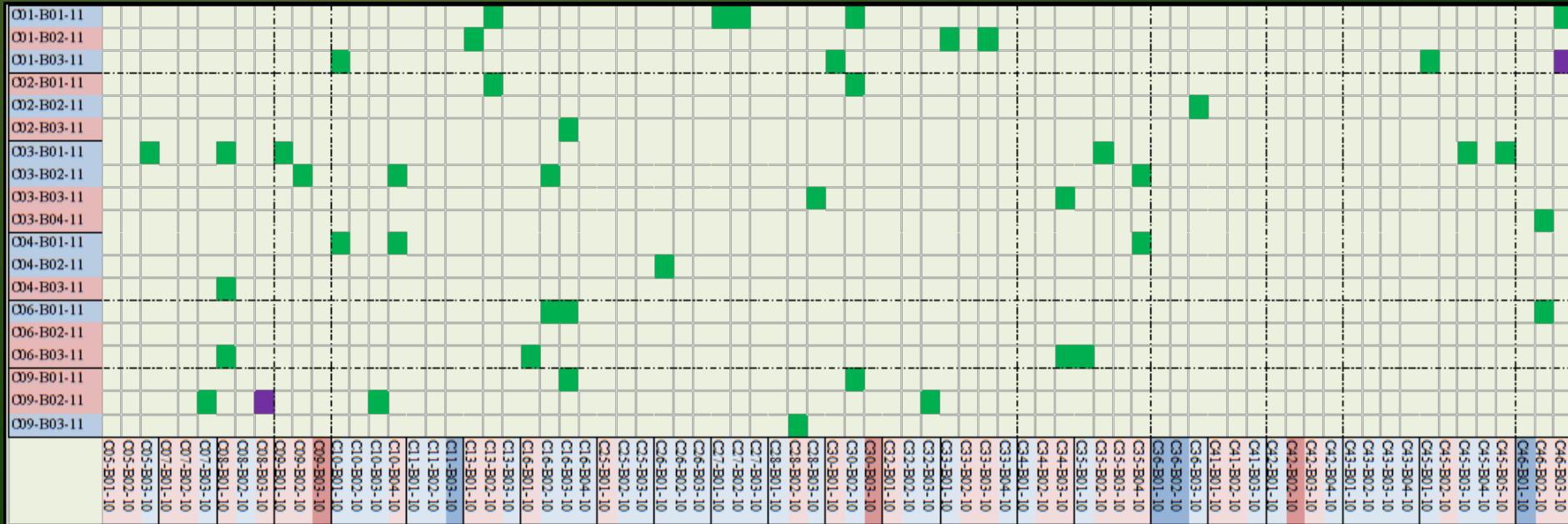
• 2 coveys (33.3%)

Relatedness among winters

Green: Half sib

Purple: Full sib / parent-offspring

2011-2012



2010-2011

Not related: 98%

P-O / Full sibs: 0.3%

Half sibs: 3.8%

Full:half sib: 1:22 – 1:57

$n = 1463$ pairs

Coancestry

$\alpha = 0.05, df = 4559$

	QG	Colony	TrioML	Wang	LynchLI	LynchRD	Rit	QG	DyadML
QG		0.284	0.723	0.833	0.904	0.725	0.717	0.999	0.739
Colony	+		0.384	0.274	0.263	0.378	0.362	0.287	0.383
TrioML	+	+		0.672	0.658	0.744	0.707	0.722	0.979
Wang	+	+	+		0.926	0.686	0.641	0.836	0.697
LynchLI	+	+	+	+		0.658	0.662	0.908	0.682
LynchRD	+	+	+	+	+		0.905	0.723	0.768
Rit	+	+	+	+	+	+		0.716	0.731
QG	+	+	+	+	+	+	+		0.738
DyadML	+	+	+	+	+	+	+	+	

- Colony: weak correlation to other relatedness estimators.
- Generally, results robust to a variety of estimators of relatedness.

Discussion

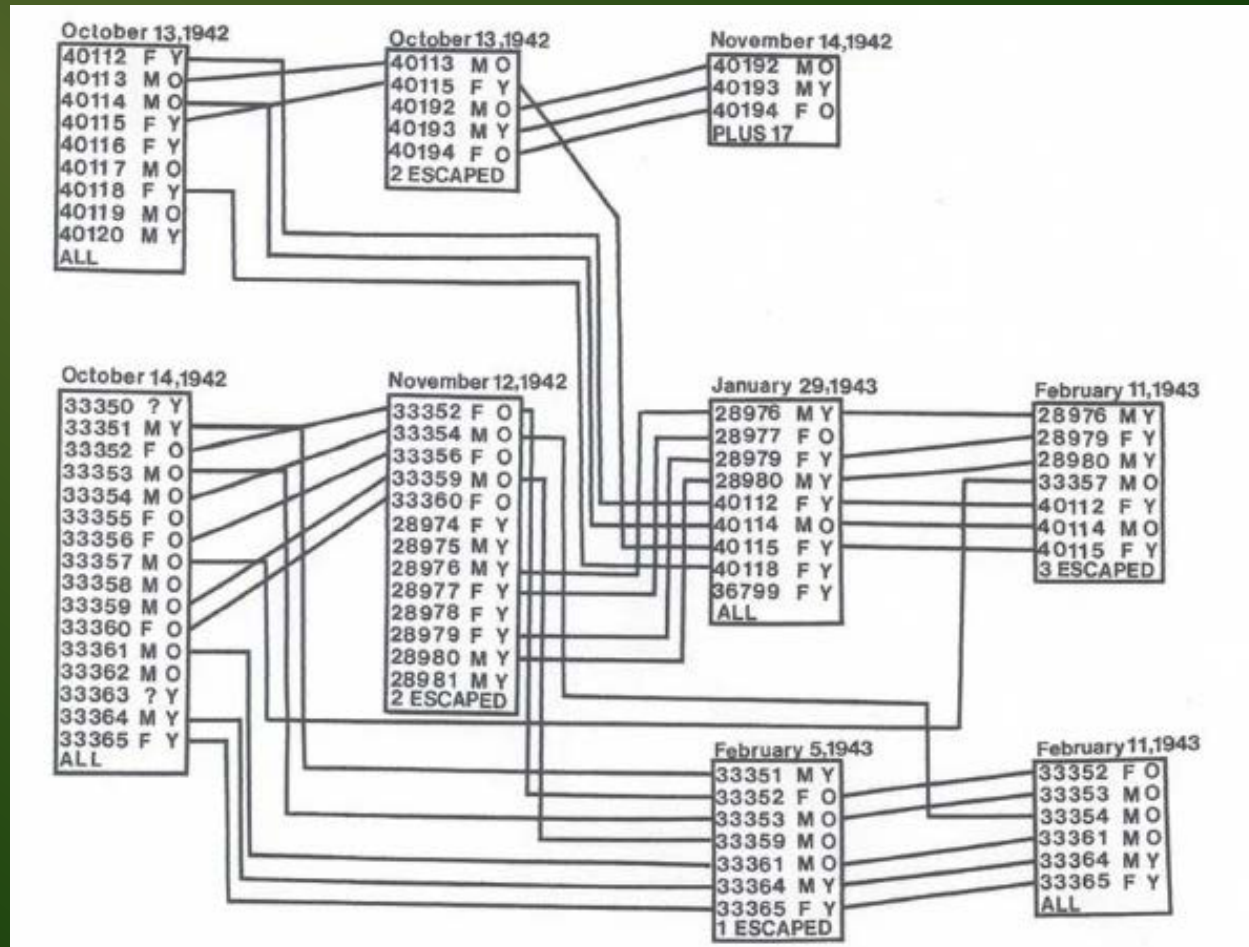
- Allelic richness low, heterozygosity moderate.
- Population structure moderate.
- Influence of sample size: hunter methods.
- Full covey: better estimates.

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



Promiscuity

- H3: 2:1 full to half sibs
- In contrast, high ratio of half:full sibs (32-137:1).
- Promiscuity: behavioral studies (Burger et al. 2005, Brennan et al. 2014).
- Promiscuity more frequent than assumed.



Conclusions

Grahmann 2011

- 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.



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Questions?



C. Lange

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