

Assessing Changes in Abundance of Smalltooth Sawfish (*Pristis pectinata*) using Genomics

Joint Meeting of Ichthyologists & Herpetologists 2026

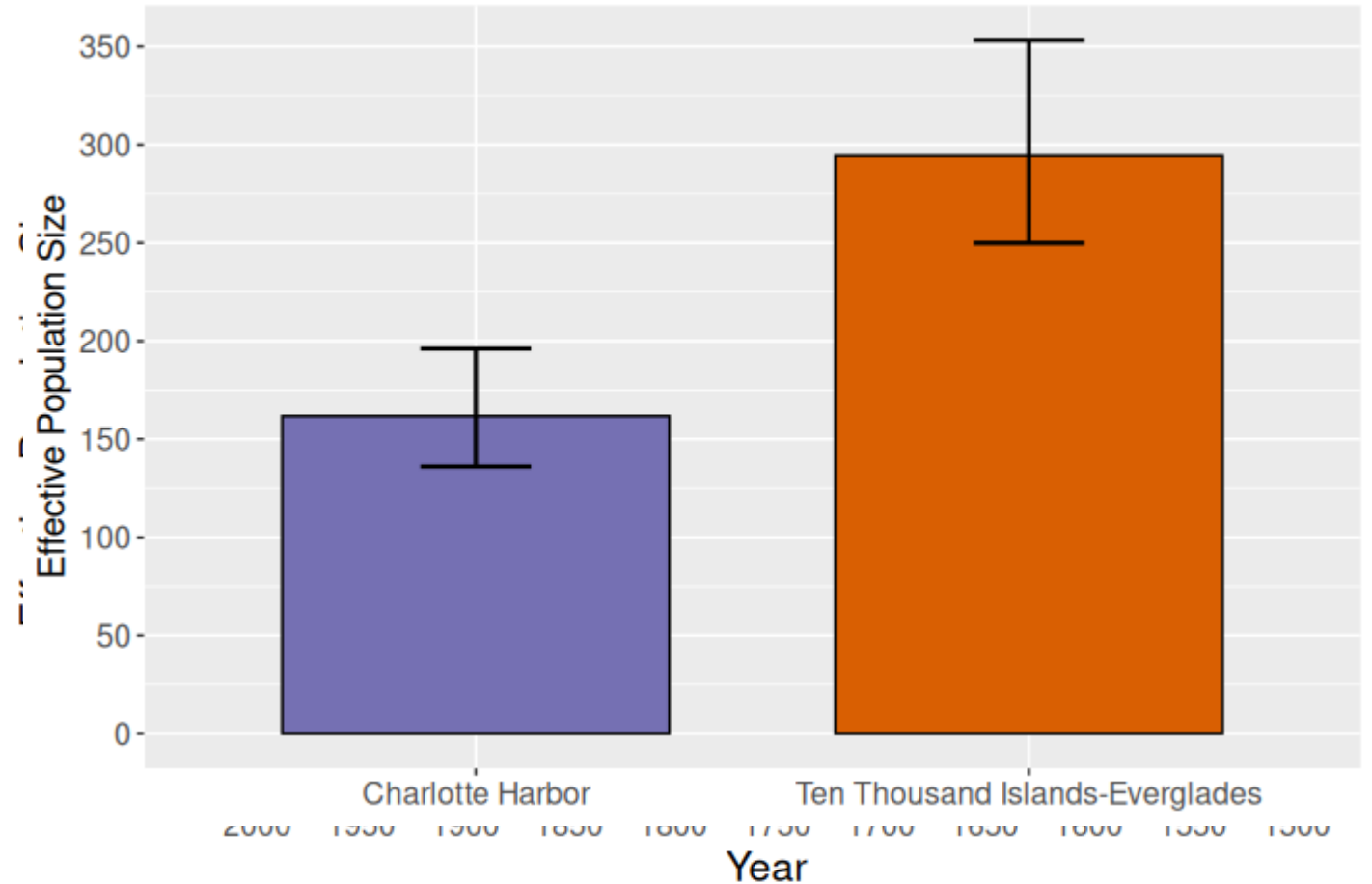
Learning from unusual sawfish mortality events: causes, effects, and conservation applications

D.G. Swift, E.C. Anderson, C.M. Hollenbeck, K.A. Feldheim, R.D. Grubbs,
G.R. Poulakis, J.K. Carlson, T.R. Wiley, A.B. Brame, S.V. Fordham, D.S. Portnoy



Background

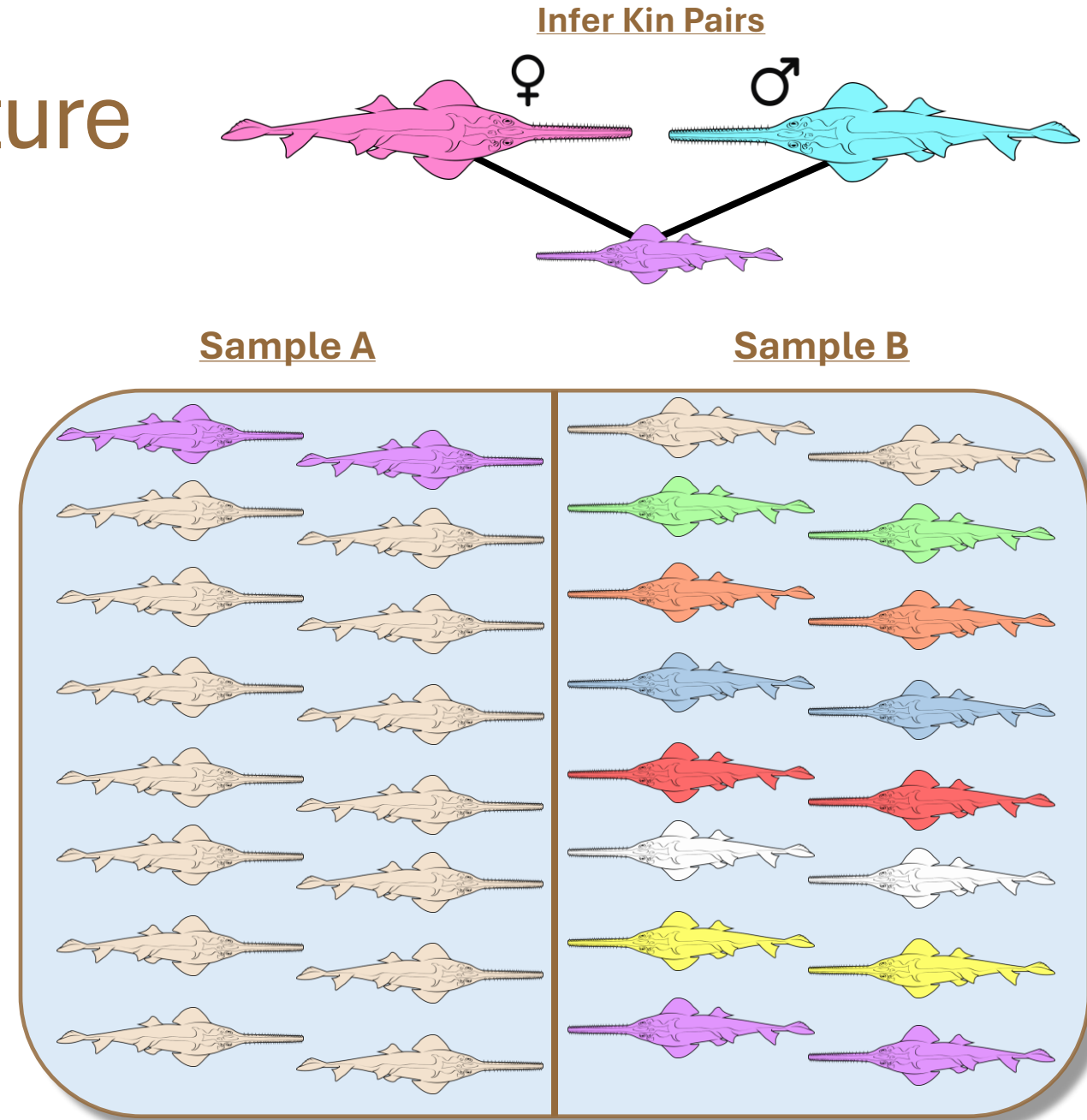
- Effective size ~500
- ~94% decline
- Asexual reproduction
 - Fields et al. 2015
- Lots of kin!



➤ Estimate current and past abundance

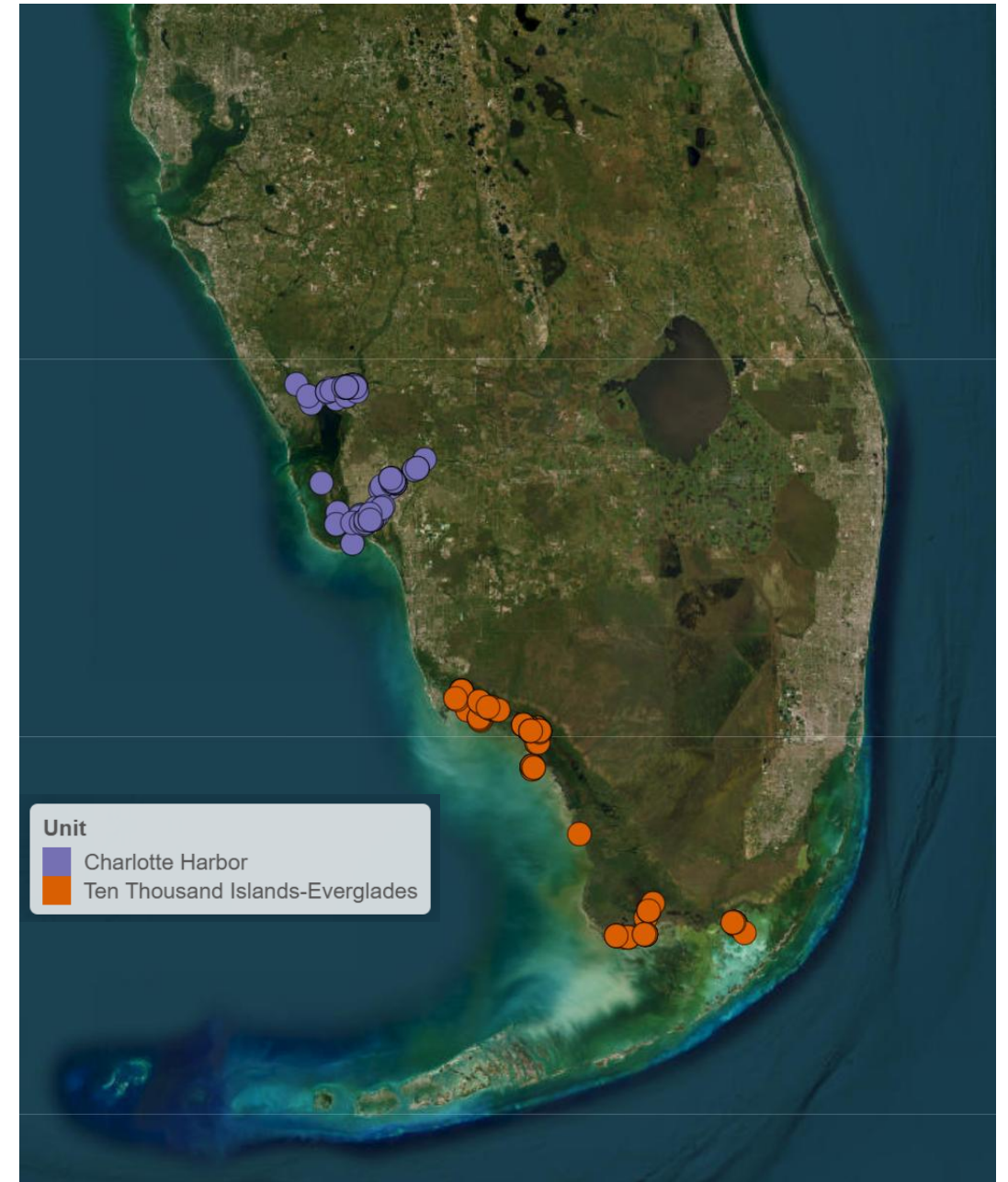
Close-kin mark-recapture

- Number of breeding adults
- Adult mortality
- Life history
 - Mating system
 - Fecundity
 - Reproductive periodicity
 - Habitat use



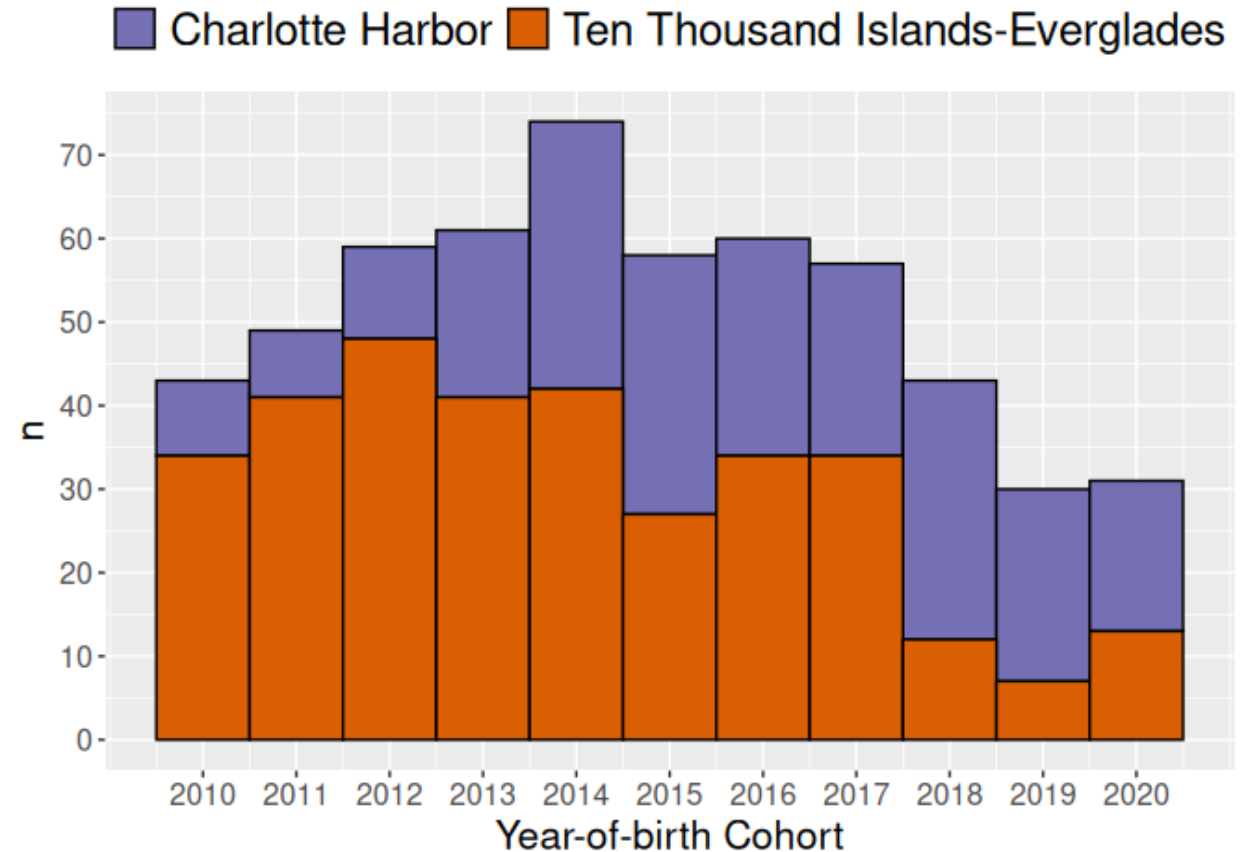
Genomic dataset

- 565 individuals (<3 years old)
 - Charlotte Harbor (40%)
 - Ten Thousand Islands-Everglades (60%)



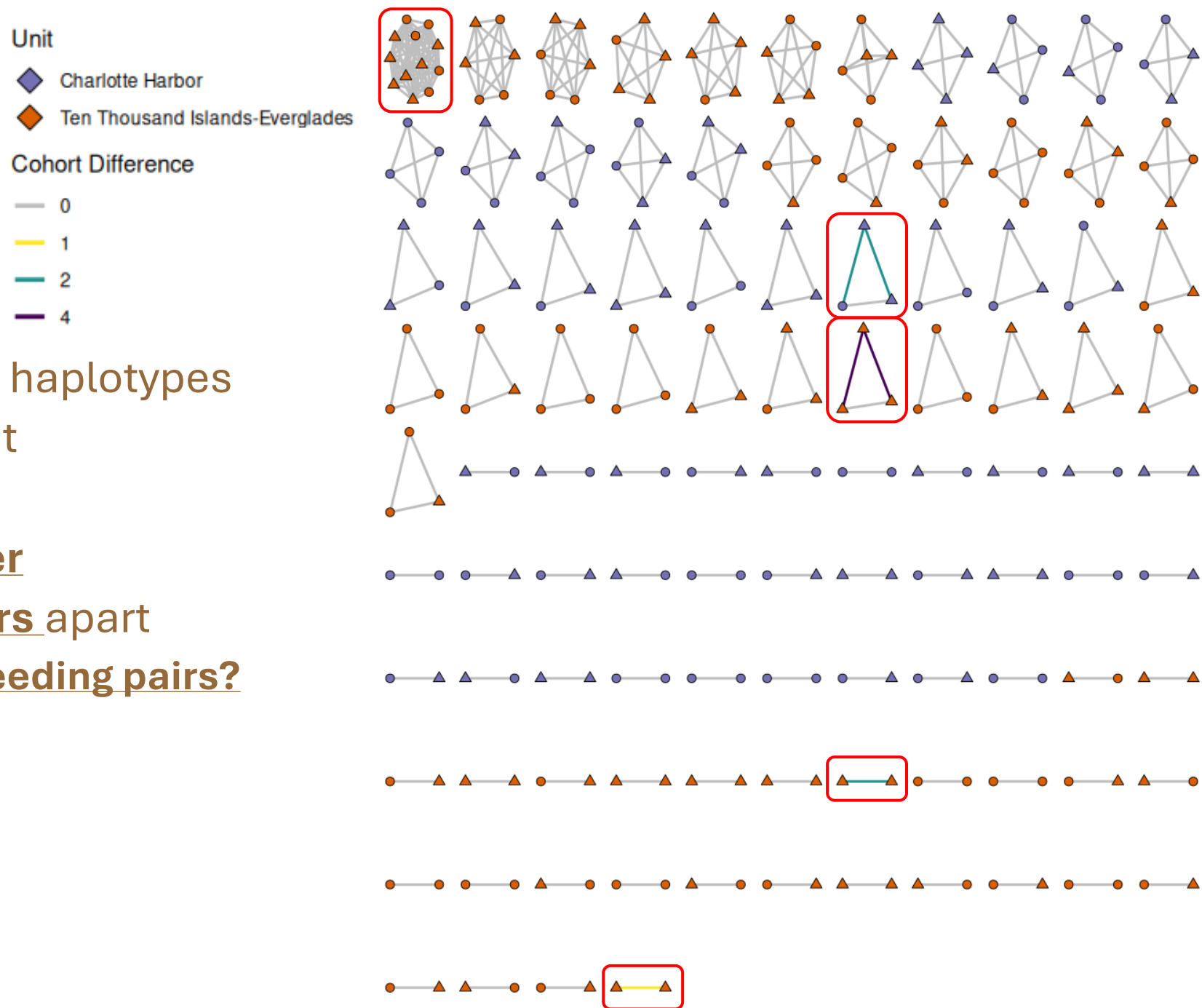
Genomic dataset

- 565 individuals (<3 years old)
 - Charlotte Harbor (40%)
 - Ten Thousand Islands-Everglades (60%)
 - Born 2010-2020
- ~2,000 SNP-containing nuclear loci
- Mitochondrial genome haplotypes



Full siblings

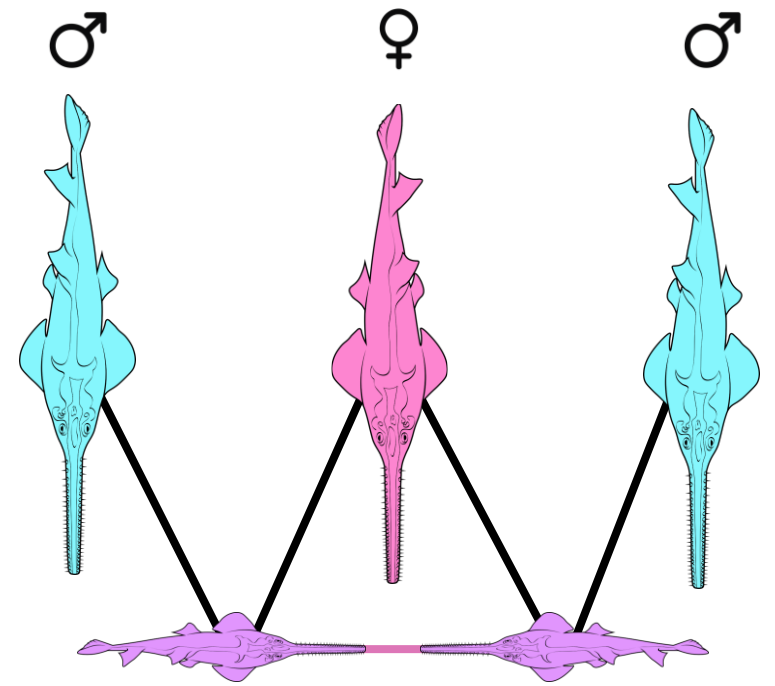
- 353 pairs
 - Same mitochondrial haplotypes
 - 100% from same unit
 - 98% from same litter
 - 6 pairs born 1-4 years apart
 - Limited viable breeding pairs?



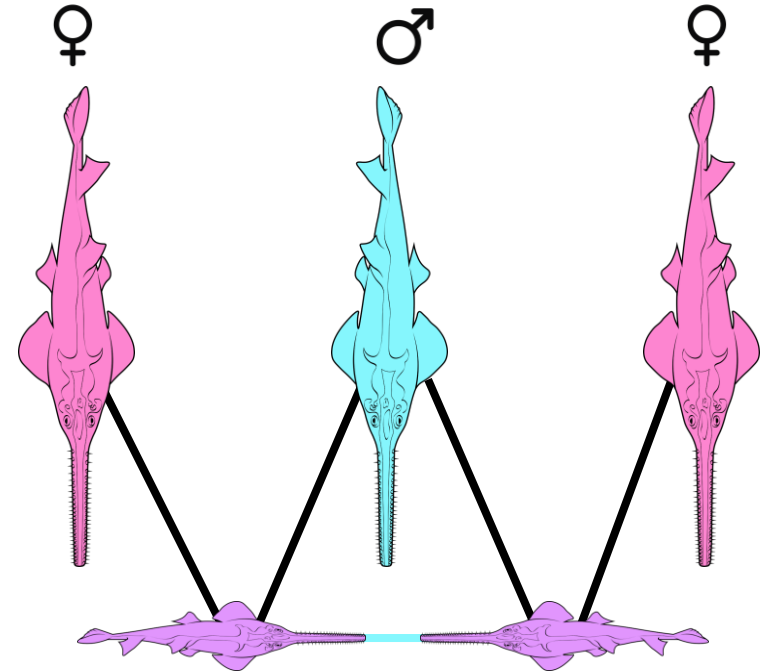
Half siblings

- Less closely related
 - Less power -> more conservative
- 184 pairs
 - 135 share a mother (**73%**)
 - Same mitochondrial haplotype
 - 49 share a father (**27%**)
 - Different mitochondrial haplotype

Maternal
Half Sibling

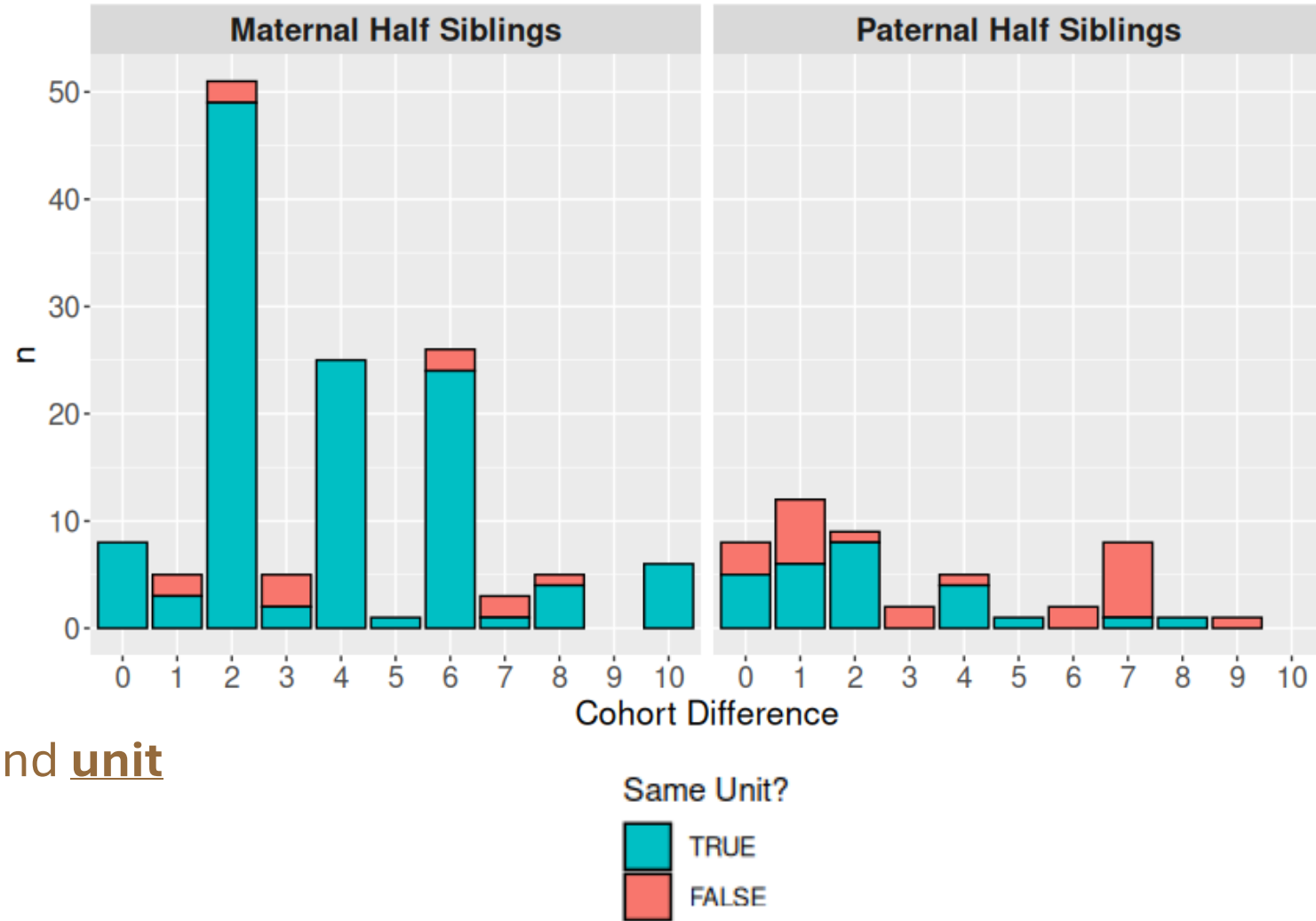


Paternal
Half Sibling



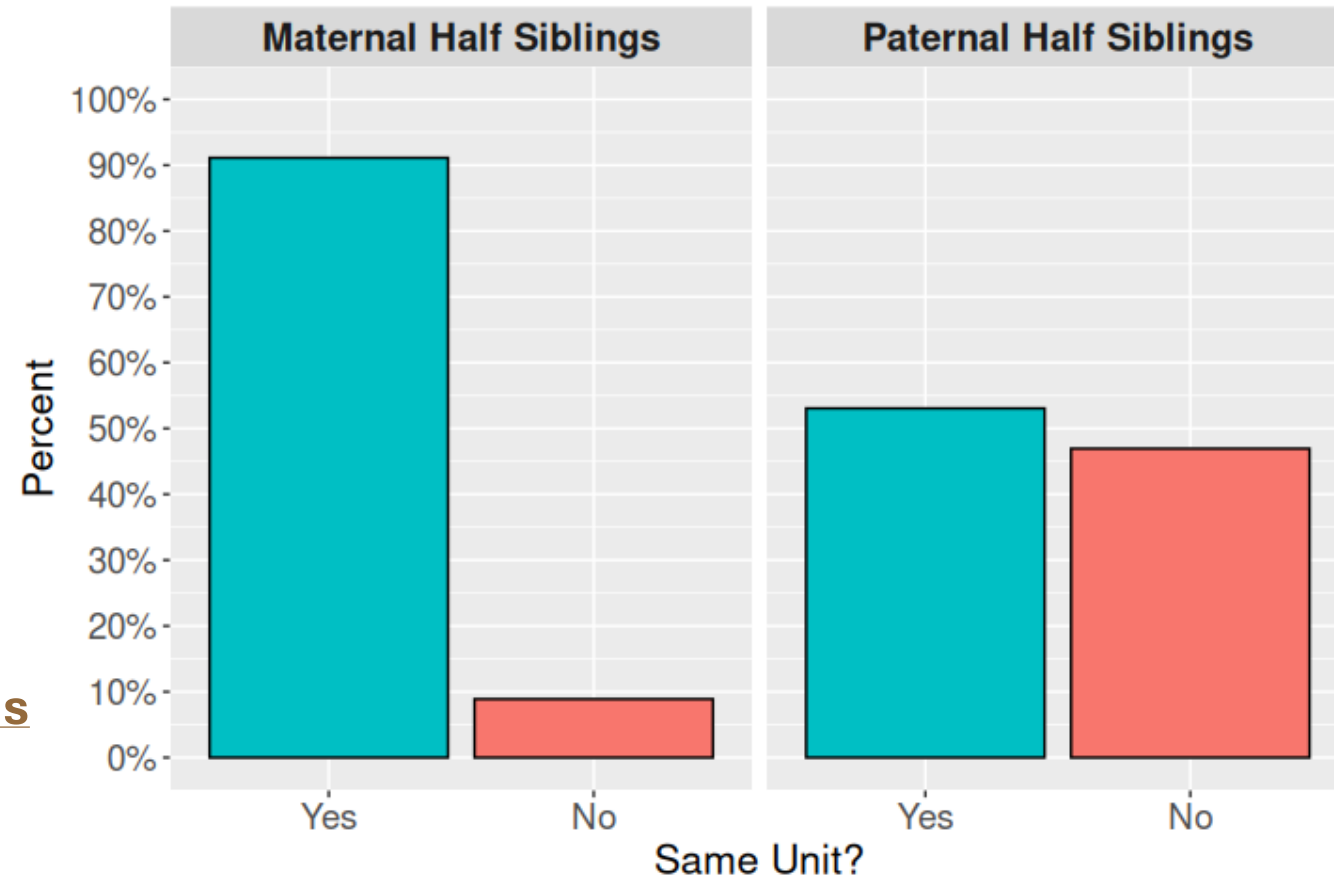
Half siblings, by cohort

- Maternal half siblings (135)
 - 6% born in same cohort
 - Polyandry
 - 90% born 2 cohorts apart
 - Biennial breeding cycle
- Paternal half siblings (49)
 - 16% from same cohort
 - Polygyny
 - Less structured by cohort and unit



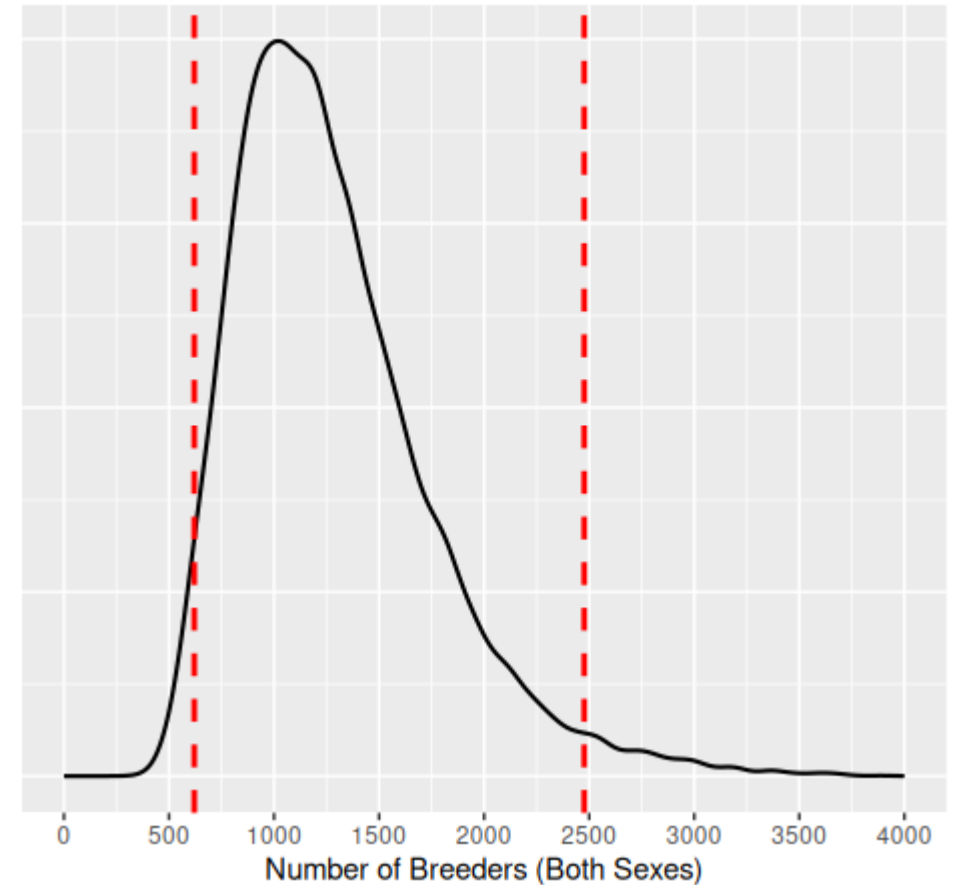
Half siblings, by unit

- Maternal half siblings (135)
 - **91% born in same unit**
 - **Female nursery site fidelity**
- Paternal half siblings (49)
 - **53% born in same unit**
 - **Males mix between nursery sites**



Breeder abundance

- Using paternal half siblings
 - 2 methods
 - Pseudolikelihood
 - Approximate Bayesian computation
- Point estimate: ~1,000 (both sexes)
- 95% confidence interval: 400-2,000



Caveats

- Abundance is influenced by mortality
 - 93% (85-100%)
 - Carlson & Simpfendorfer (2015)
 - ~77% from **cross-cohort** paternal half sibs
- **Sources of mortality?**
- Limited paternal half sibs
- Limited spatial sampling
- Models are still in development



Conclusions

- Current abundance: ~1,000 breeders
 - Past abundance: ~16,000 breeders
- Inform population viability analysis



Next steps

- Impacts of mortality events
 - Estimate abundance and survival before and after
- Database of genomic tags
 - Recaptures -> mortality rate

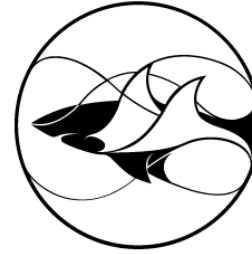


Acknowledgements

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and

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