Genetic Population structure of the Gulf Menhaden (*Brevoortia patronus*)

Presentation from SFFMC Menhaden Advisory Committee & GSMFC Spring Meeting

Joel Anderson
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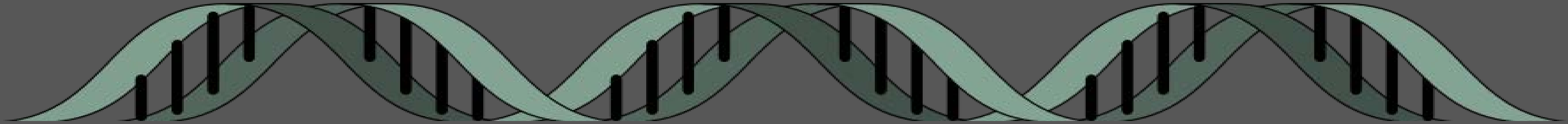
Joel Anderson, Texas Parks and Wildlife Department, Coastal Fisheries Division

SFFMC Menhaden advisory committee
Gulf States Marine Fisheries Commission spring meeting



- Bowen and Avise (1990) first documented genetic differences between Atlantic and Gulf menhadens

- Bowen and Avise (1990) also estimated the effective population size (N_{ef}) using mtDNA, estimates were > 250,000 in the Gulf and Atlantic

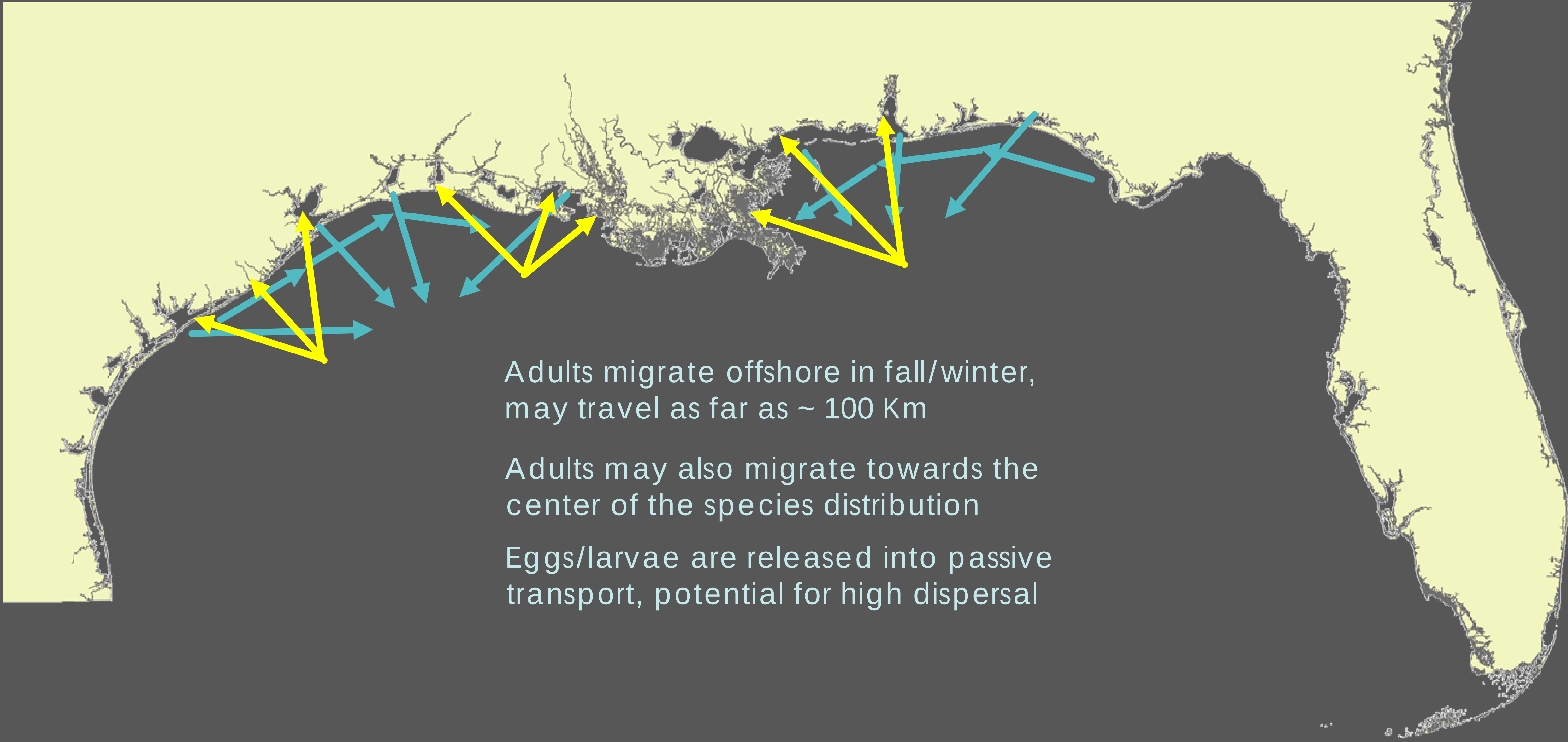
- Lynch et al. (2010) suggested that the genetic divergence observed between Atlantic and Gulf menhaden was consistent with populations of the same species

- Anderson (2006) demonstrated a lack of genetic structure in Gulf-wide sampling, suggesting a single randomly mating population of Gulf menhaden

    - The sample sizes in this study were not adequate to conclusively answer the question of stock structure

- All of the previous studies were lacking in their ability to definitively answer the question of whether there are distinctive populations of Gulf menhaden that exist on local scales

The life history and reproductive strategies of Gulf menhaden tend to suggest a lack of localized genetic divergence



Adults migrate offshore in fall/winter, may travel as far as ~ 100 Km

Adults may also migrate towards the center of the species distribution

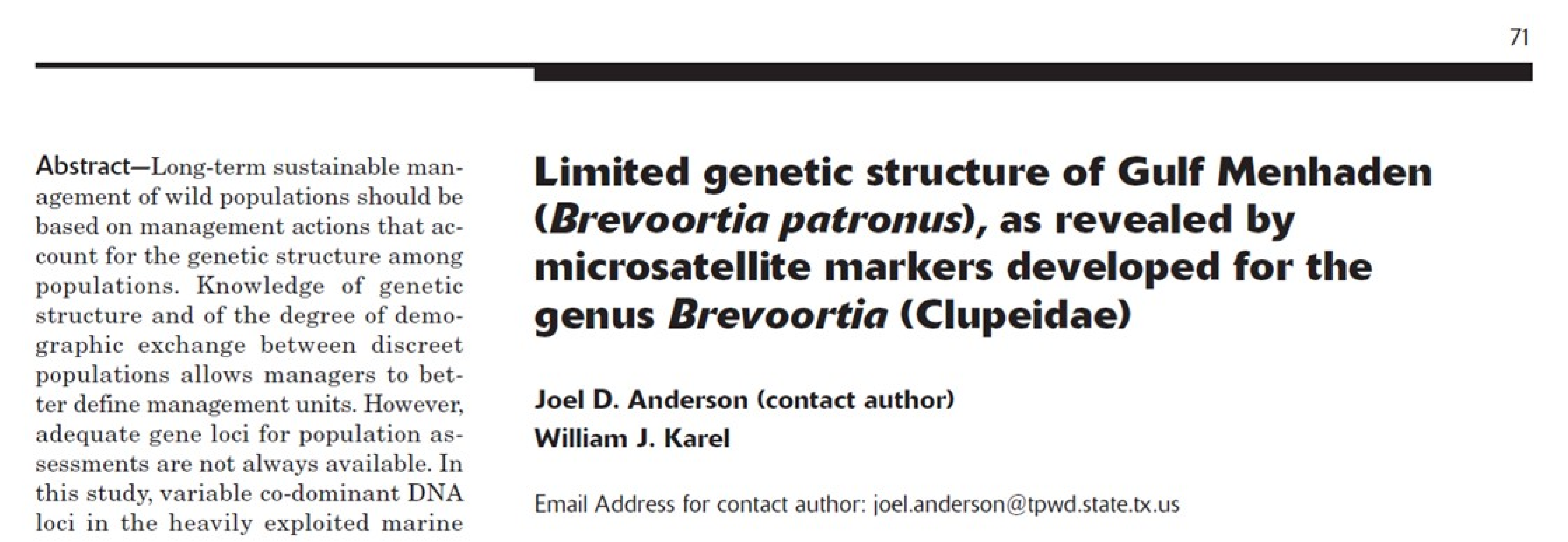
Eggs/larvae are released into passive transport, potential for high dispersal

- Previous genetic studies seem to indicate a single stock of Gulf menhaden

- The biology of the species suggests a mechanism for demographic connectivity of local groups of menhadens, which would preclude localized divergence

- The question of stock structure could be definitively addressed with a large suite of genetic markers

    - H_o : lack of genetically divergent populations in the Gulf
    - H_a : genetic divergence occurring on a local scale, resulting in exploitation of multiple genetic stocks



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Limited genetic structure of Gulf Menhaden (*Brevoortia patronus*), as revealed by microsatellite markers developed for the genus *Brevoortia* (Clupeidae)

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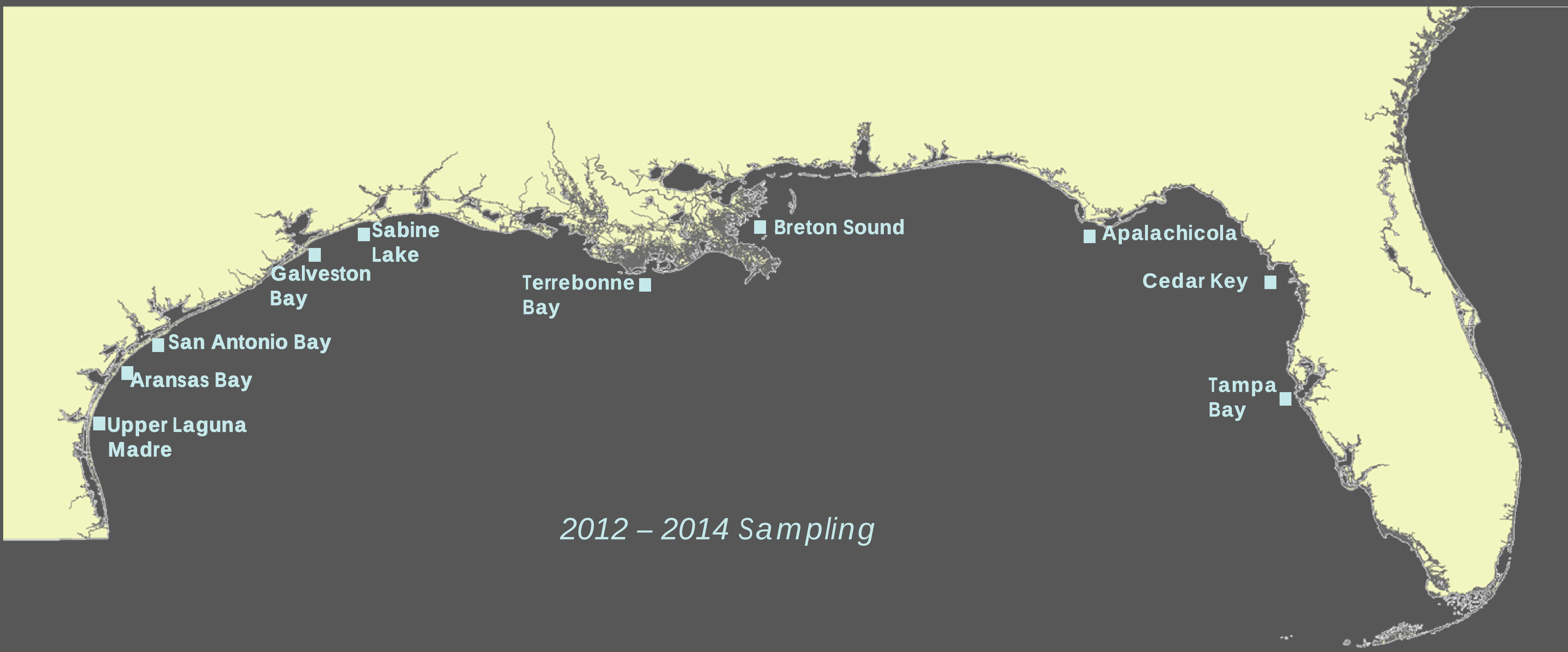
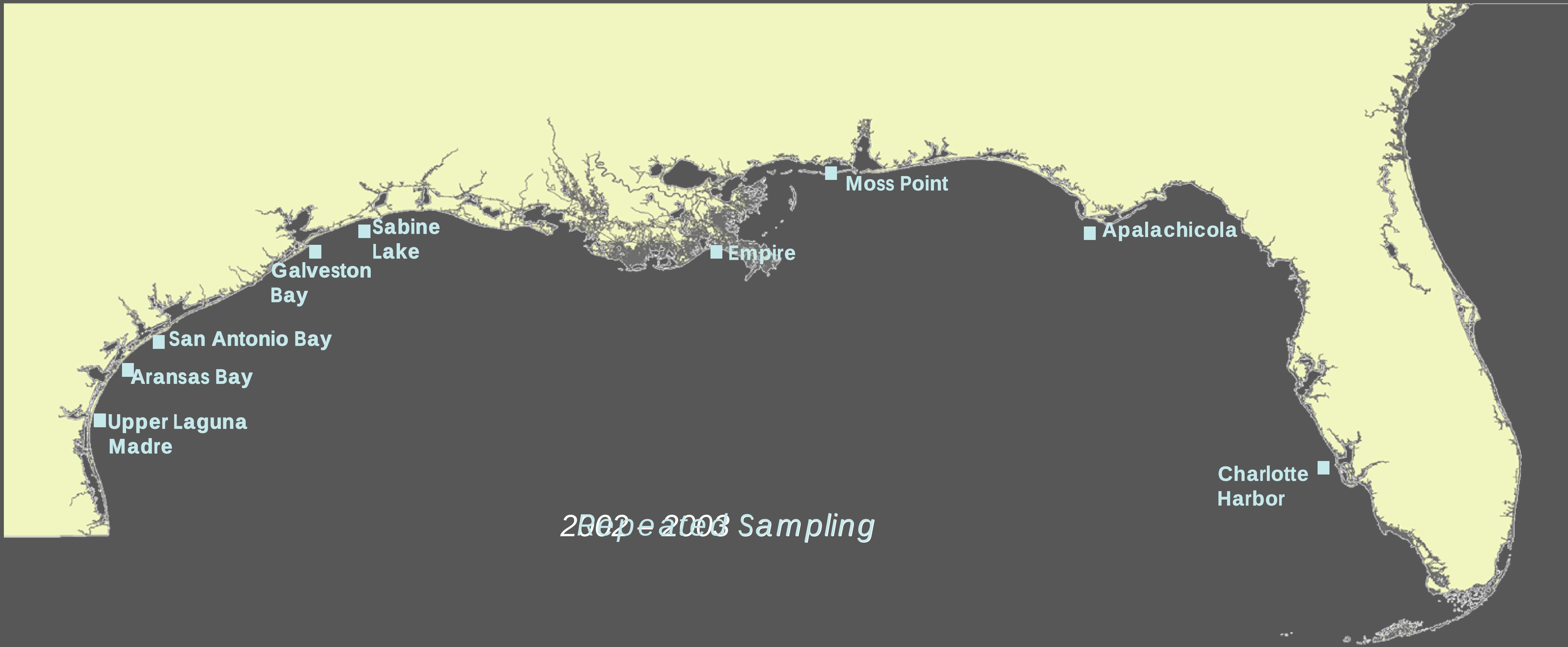
Abstract—Long-term sustainable management of wild populations should be based on management actions that account for the genetic structure among populations. Knowledge of genetic structure and of the degree of demographic exchange between discreet populations allows managers to better define management units. However, adequate gene loci for population assessments are not always available. In this study, variable co-dominant DNA loci in the heavily exploited marine

In cooperation with interstate partners, menhaden were sampled from across their range in the northern Gulf of Mexico from Texas to Florida



TEXAS PARKS & WILDLIFE

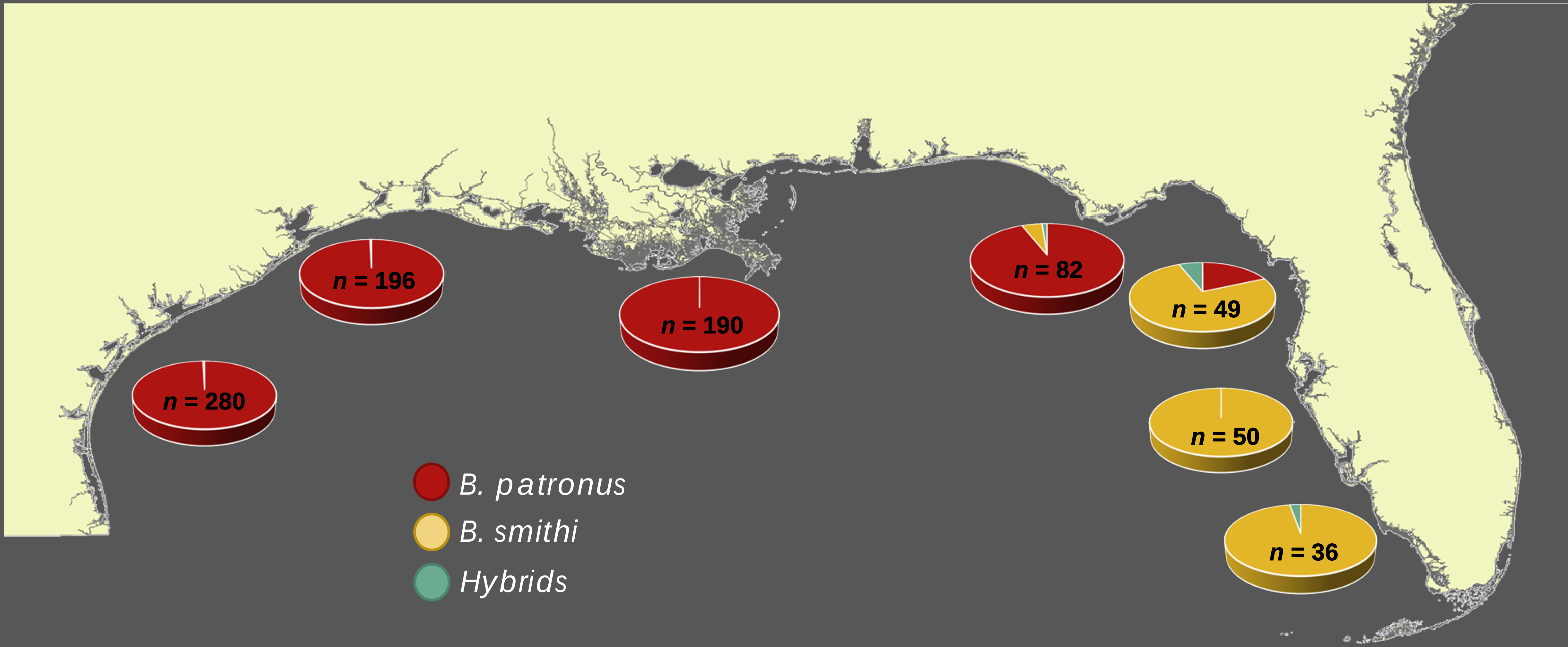
In cooperation with interstate partners, menhaden were sampled from across their range in the northern Gulf of Mexico from Texas to Florida



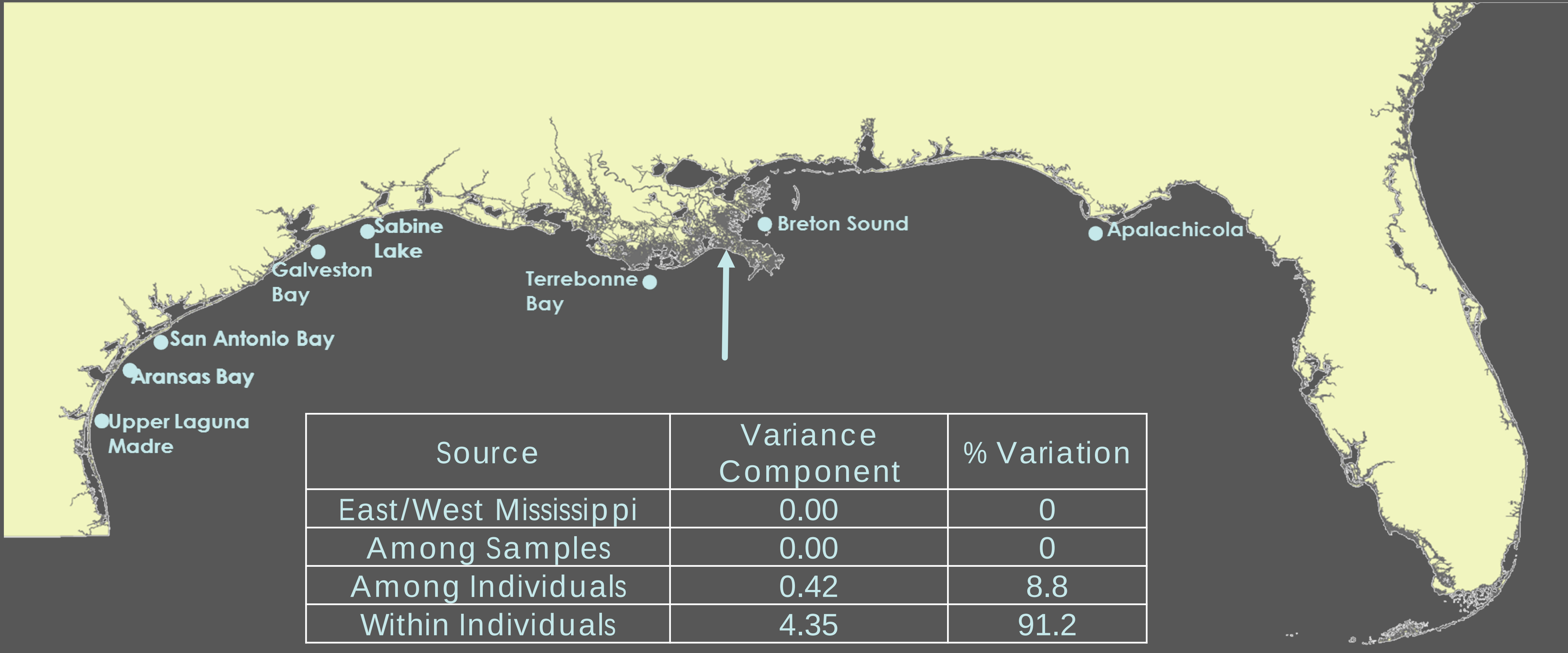
2002 – 2003

Expanded Sampling

Distribution of menhaden species in Gulf-wide sampling (new samples):



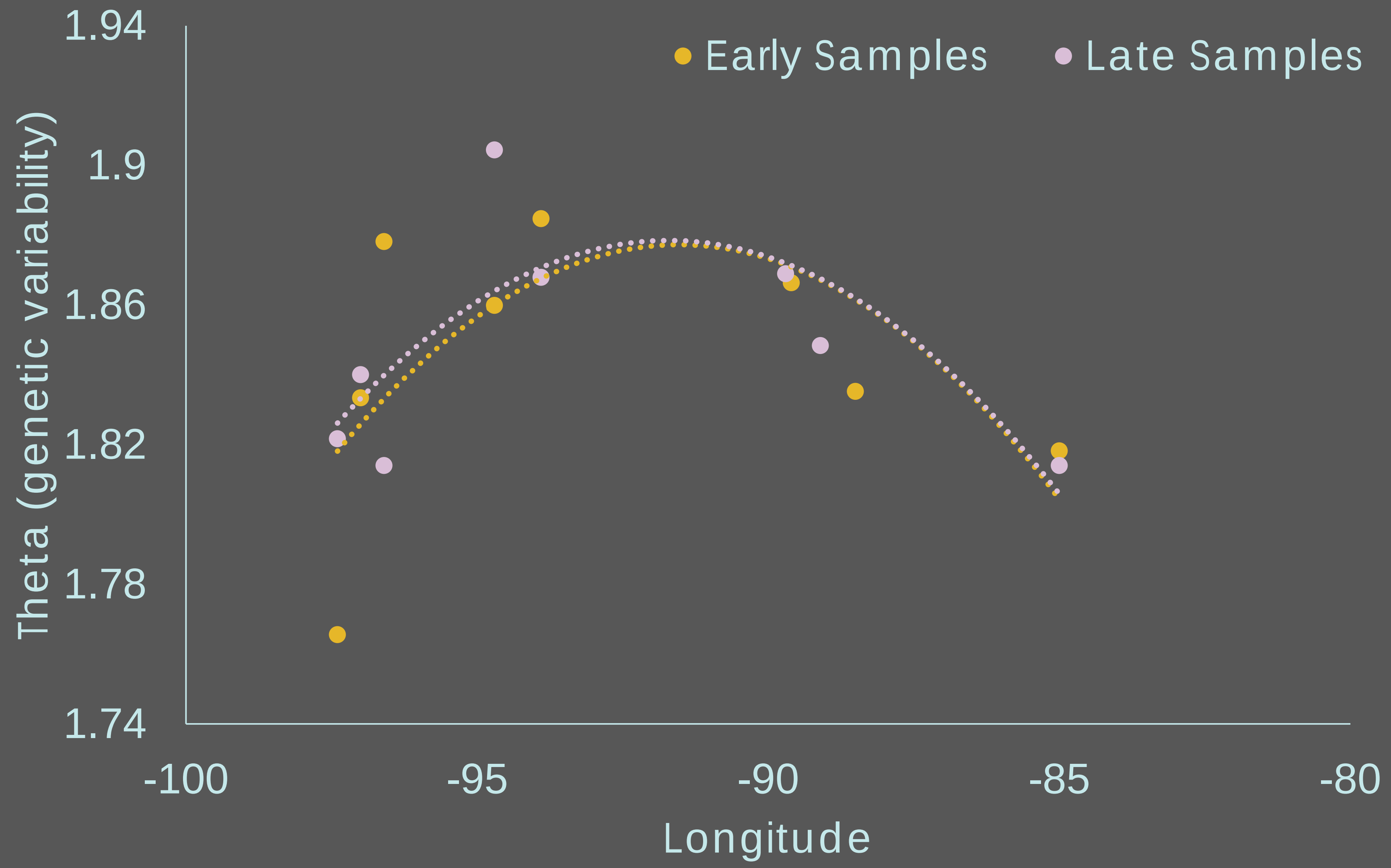
Gulf menhaden – ***A***nalysis of ***MO***lecular ***VA***riance (AMOVA)



Source	Variance Component	% Variation
East/West Mississippi	0.00	0
Among Samples	0.00	0
Among Individuals	0.42	8.8
Within Individuals	4.35	91.2

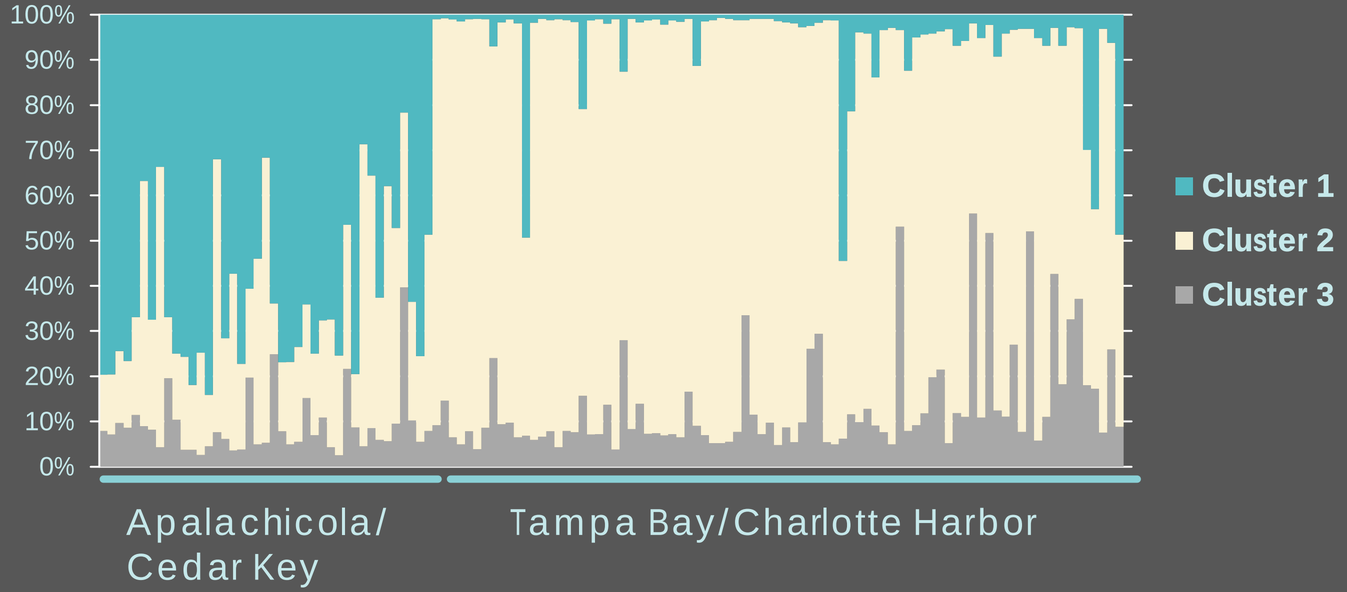
Gulf menhaden – Locus-by-locus estimate of among-sample divergence

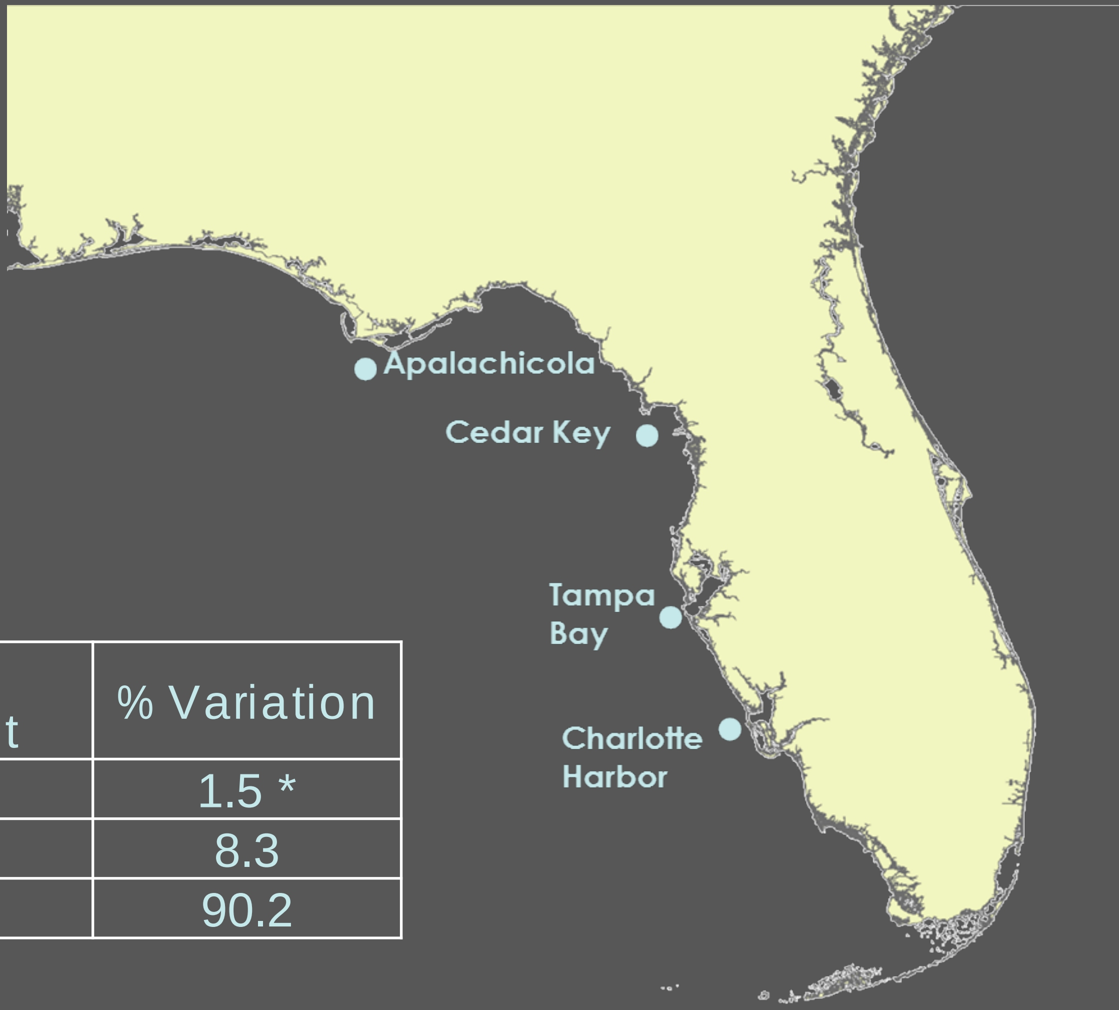
Locus	Divergence among samples (F_{ct})	P-value	Heterozygosity
1	-0.0009	0.947	0.906
2	0.0008	0.161	0.900
3	-0.0001	0.435	0.902
4	-0.0002	0.412	0.695
5	0.0013	0.161	0.848
6	0.0041	0.110	0.123
7	-0.0003	0.593	0.895
8	0.0010	0.120	0.639
9	-0.0004	0.577	0.672
10	-0.0003	0.408	0.158
11	-0.0005	0.632	0.838
12	-0.0002	0.487	0.824
13	-0.0011	0.695	0.590
14	-0.0007	0.605	0.527
		Overall:	**0.680**



Early Samples
Late Samples
Theta (genetic variability)
1.94
1.9
1.86
1.82
1.78
1.74
-100
-95
-90
-85
-80
Longitude

*Yellowfin menhaden – **A**nalysis of **MO**lecular **VA**riance (AMOVA)*





Source	Variance Component	% Variation
Among Samples	0.04	1.5 *
Among Individuals	0.19	8.3
Within Individuals	2.09	90.2

Gulf menhaden – estimates of effective population size

- What is effective population size (*N_e*)?

  Definition: The effective population size is the number of individuals that an idealized population would need to have in order to harbor genetic properties similar to the population of interest.

  Can be thought of as proportional to the number of successful spawners in each generation

- Methods for estimating *N_e*:

  Linkage disequilibrium among alleles at various genetic markers

  Temporal shifts in allele frequencies at multiple genetic markers

  Point estimates based on genetic divergence (require knowledge of mutation rates of genetic markers)

- There is a lot of statistical error associated with all of these methods

Gulf menhaden – estimates of effective population size

Method	Lower	Upper	Point
LD (historical samples)	611	∞	1,437
LD (new samples)	1,139	∞	∞
Temporal method	819	1655	1,201
Divergence (θ_H)	462	46,125	4,612

- Estimates of N_e generated from Texas samples range from 1,201 – 4,612
- Confidence intervals overlapping ∞ suggest that N_e may be very large, and poorly estimated by our study-wide sample size
- All point estimates of N_e are similar to or higher than those reported for other marine fishes, and within the range considered necessary for preservation of genetic diversity

General conclusions: population genetics of B. patronus and B. smithi in the Gulf of Mexico

- Multiple studies have now suggested that there is a lack of evidence for multiple genetic populations of Gulf menhaden in the Gulf of Mexico
- The finding of a “single genetic stock” was supported here by two temporally spaced data sets collected independently of one another
- The distribution of genetic diversity in Gulf menhaden suggests that diversity is highest in the central portion of the species range
- In contrast to Gulf menhaden, yellowfin menhaden *B. smithi* have repeatedly been shown to harbor distinctive populations, distributed around the Florida peninsula
- Estimates of N_e in Gulf menhaden are generally unstable, but suggest a relatively large effective population size

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