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Using microsatellite DNA analysis to identify sources of recruitment among spiny lobster (*Panulirus argus*) stocks

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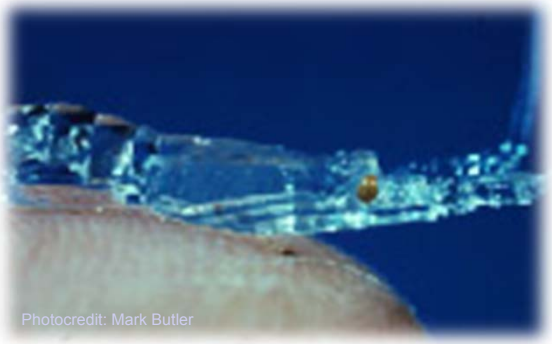
Identification of the Problem



- Info on stock structure/recruitment dynamics critical to assessment and management
  - Role of life-cycle in dispersal and transport
    - Phyllosome larvae (~8 months)
    - Pueruli post-larvae free-swimming, migrate inshore and settle
    - Benthic juveniles occupy mangrove and vegetated habitats
    - Sub-adults migrate to near shore habitats
  - Self-recruitment vs. regional connectivity
  - Potential for PaV1 transmission/translocation

Project Goal and Objectives

Goals: Identify recruitment patterns and temporal/spatial genetic structure among populations of spiny lobster

Specific objectives: Use microsatellite DNA analyses to:

- Determine the number of genetic stocks contributing to post-larval recruits in FL
- Evaluate whether the genetic source(s) vary temporally by examining monthly cohorts of FL post-larvae
- If possible, identify recruitment source(s) of Florida post-larvae by examining adults collected from throughout the range

Stock Concepts

Marine fishery managers – migratory ranges/migration rates; spatial scale of spawner-recruit connectivity; degree of local self-recruitment

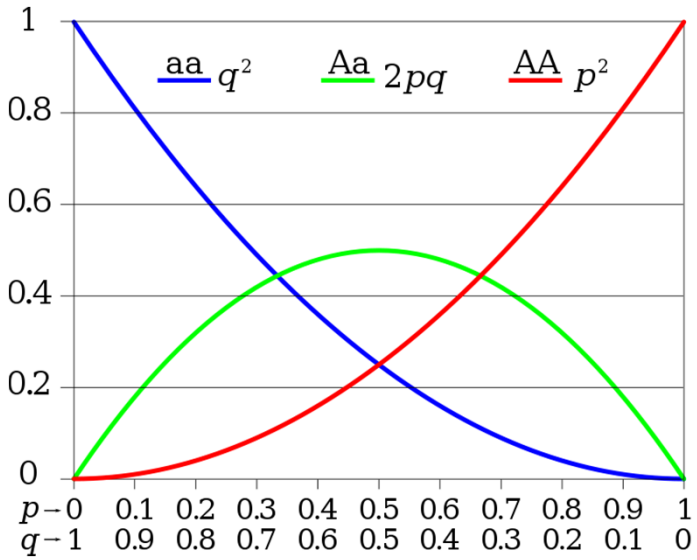
Pointy-headed geneticists – organisms should be partitioned by virtue of genetic commonality and shared evolutionary trajectory

- Ihssen et al. (1981) – intra-specific group of randomly mating individuals with temporal or spatial integrity in allele frequencies

- Booke (1981) – constancy in allele frequency, conformance to Hardy-Weinberg equilibrium (HWE) expectations, and phenotypically similar.

Hardy Weinberg Equilibrium

In the simplest case of a single locus with two alleles, A and a:



Expected genotype frequencies occur within a population when there is:

- no selection on traits
- no mutation
- ~~infinitely~~ (sufficiently) large population size
- **random mating**
- **no migration**

Linkage (Genotypic) Disequilibrium

Linkage disequilibrium (D) – non-random association of alleles at two or more loci

- Describes a situation in which some multilocus combinations of alleles occur more or less frequently in a population than would be expected from allele frequencies.

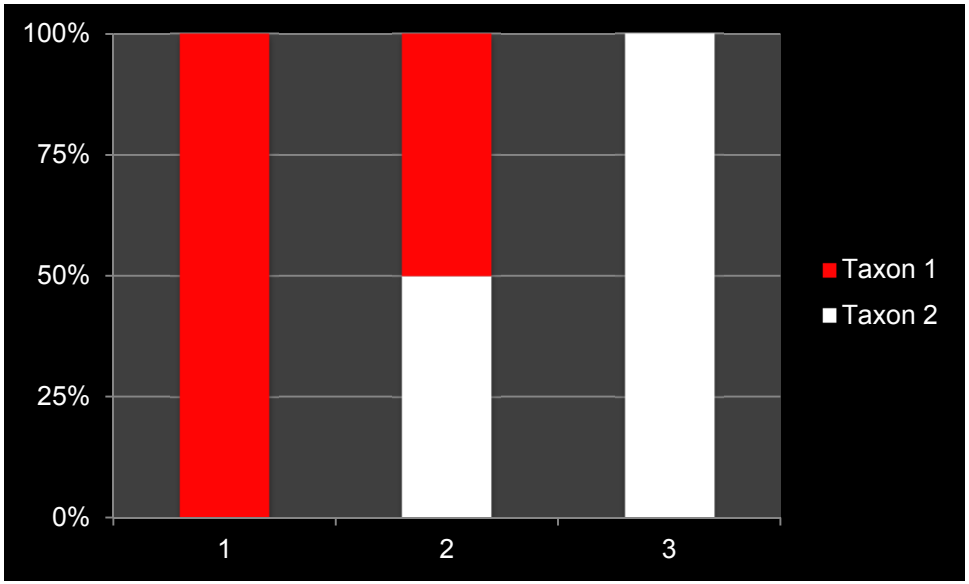
- Causes include: physical linkage, selection, **population subdivision**

	A_1	A_2	Total
B_1	$x_{11} = p_1q_1 + D$	$x_{21} = p_2q_1 - D$	q_1
B_2	$x_{12} = p_1q_2 - D$	$x_{22} = p_2q_2 + D$	q_2
Total	p_1	p_2	1

Bayesian Clustering – Population Assignment

STRUCTURE v2.3 – (Pritchard et al. 2000) Bayesian clustering of multilocus genotypes

- Model-based; departures from HWE and linkage disequilibrium = population structure
- Identify number of distinct genetic clusters in a data set
- Probabilistically assign specimens of unknown origin to distinct, known stocks or genetic clusters



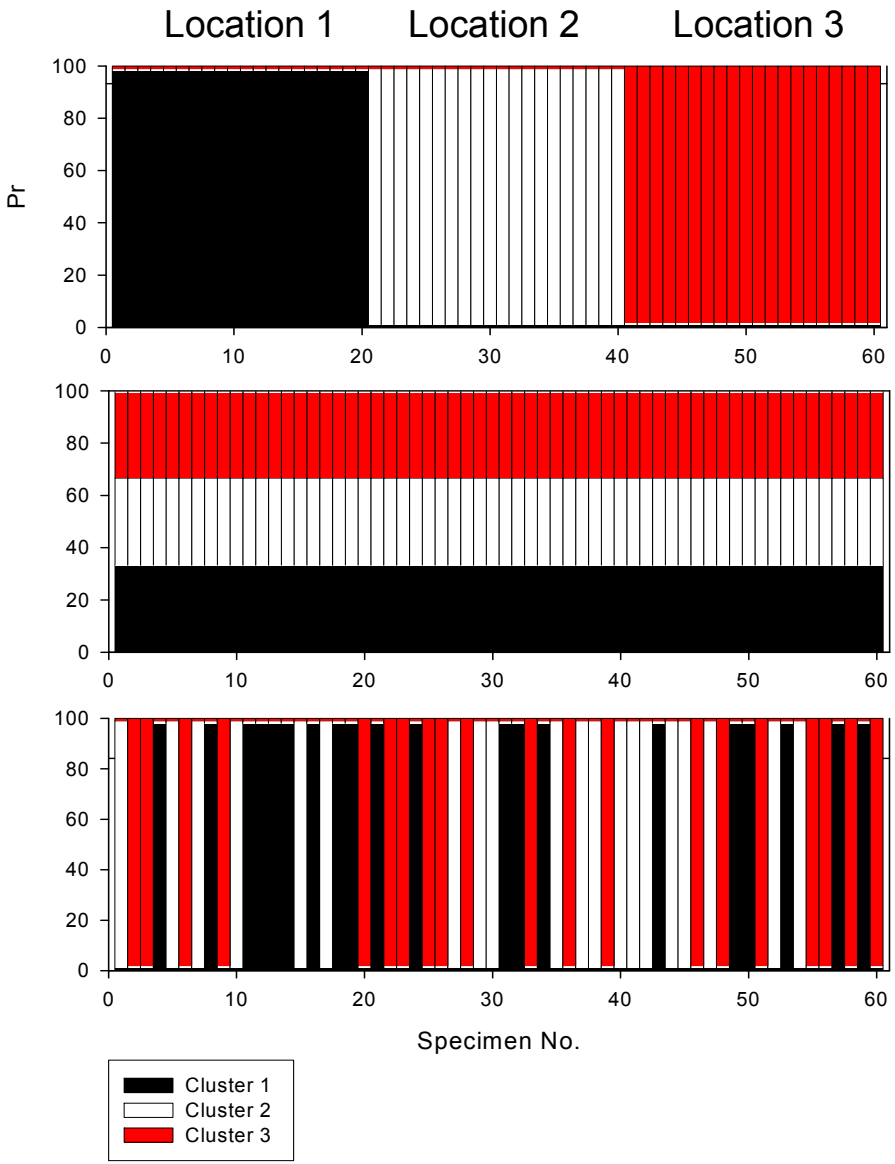
Data = *X*

Number of pops = *K*

Pr (*X* | *K*)

For *K* = 1 thru n

Possible Patterns when testing K = 3

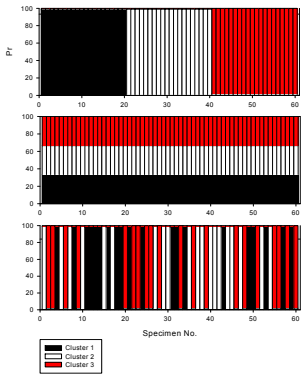


Highly Structured Genetic Stocks (HSS)

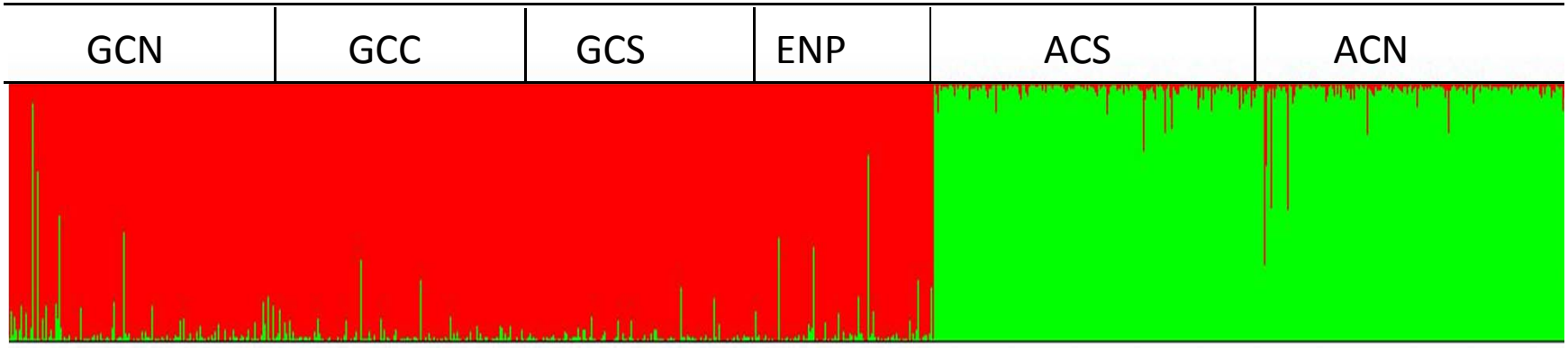
Single Randomly Mating Population (RMP)

Admixture from Multiple Genetic Stocks (AMS)

Example: Common Snook

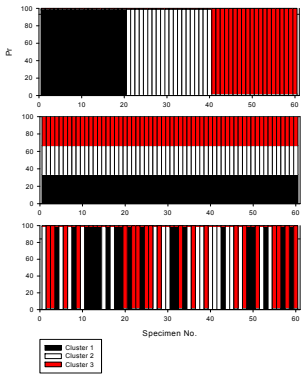


- From Florida Gulf and Atlantic (n ≈ 1,000):
  - Highest Pr ($X \mid K$) at $K = 2$
  - Individuals assigned faithfully to Gulf or Atlantic stock with high probability

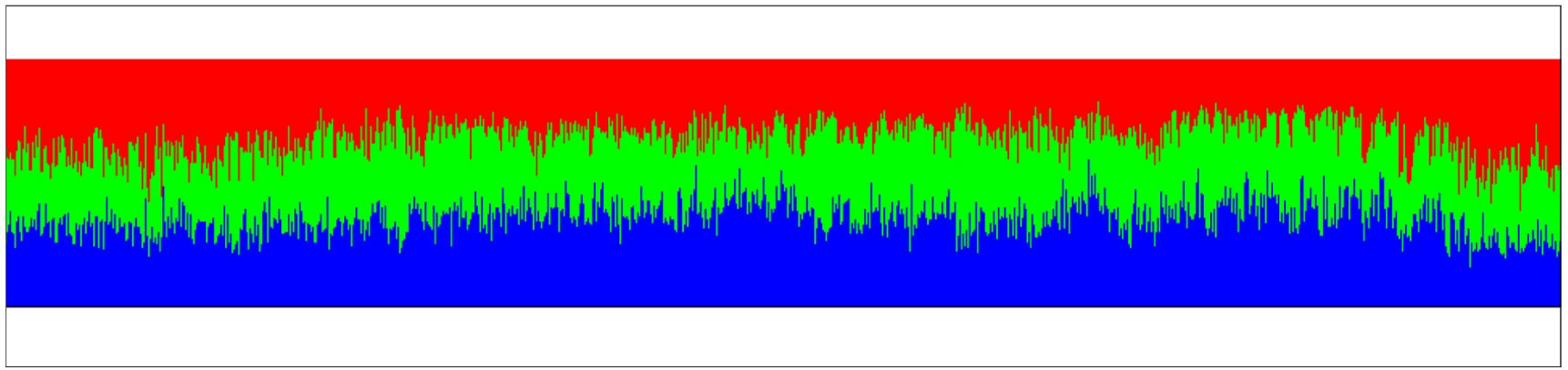


TWO HSS; very low connectivity between coasts

E.g., Atlantic Tarpon

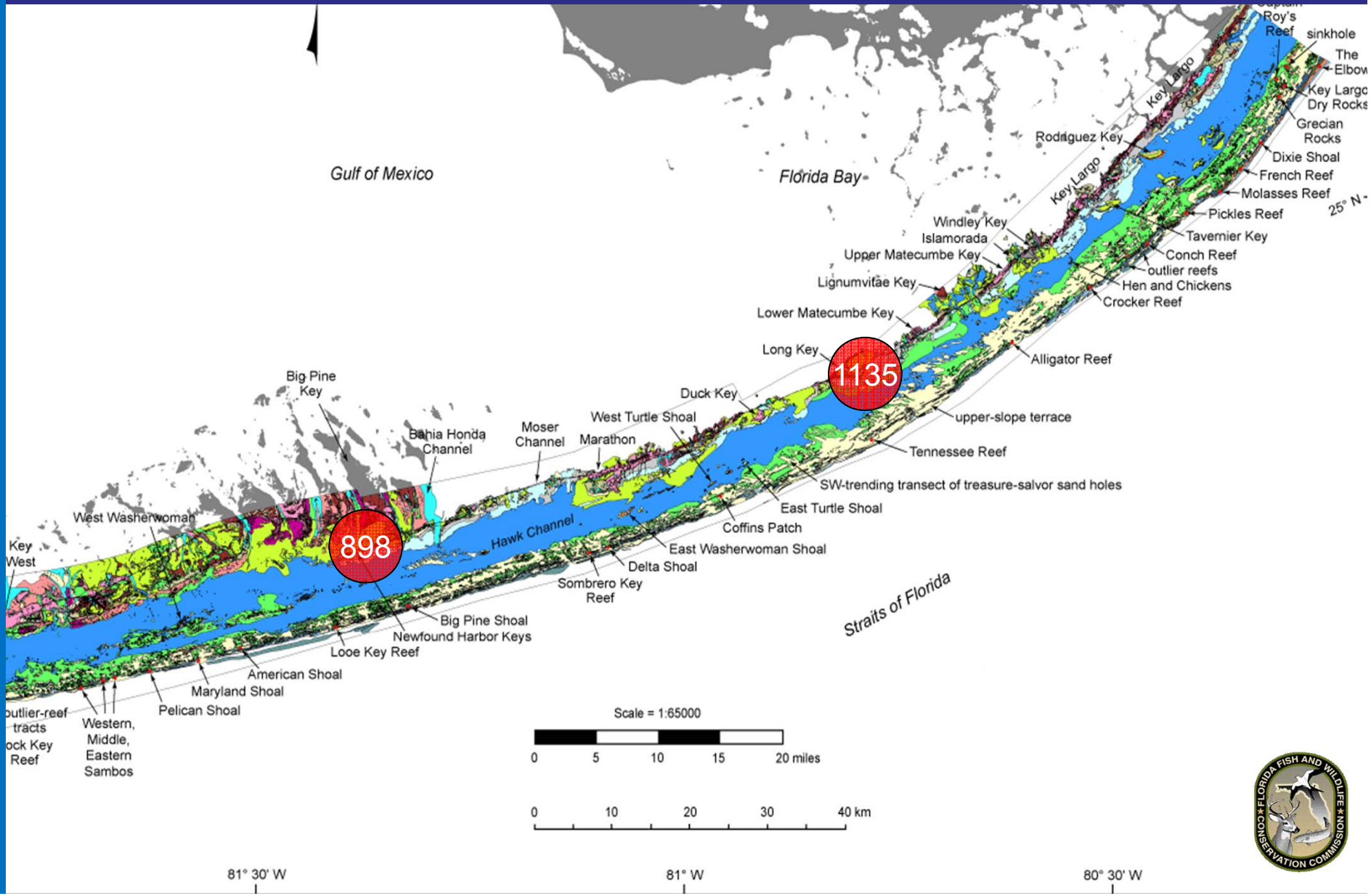


- From Florida Gulf and Atlantic (n = 1,000):
  - Highest Pr ($X \mid K$) at $K = 1$
  - when $K = 3$ assumed, individuals assigned to each population with ~equal probability

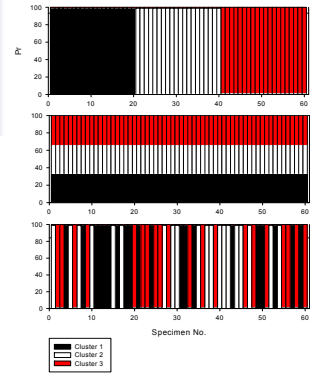


SINGLE RMP; NO GENETIC STRUCTURE

Post-larvae Collections in Florida

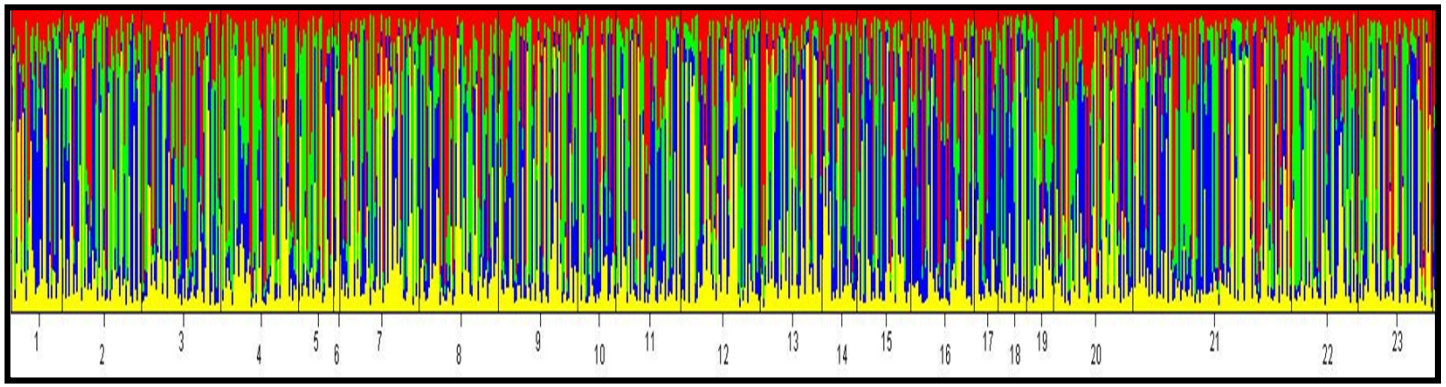


Individual Assignment of Post-larvae

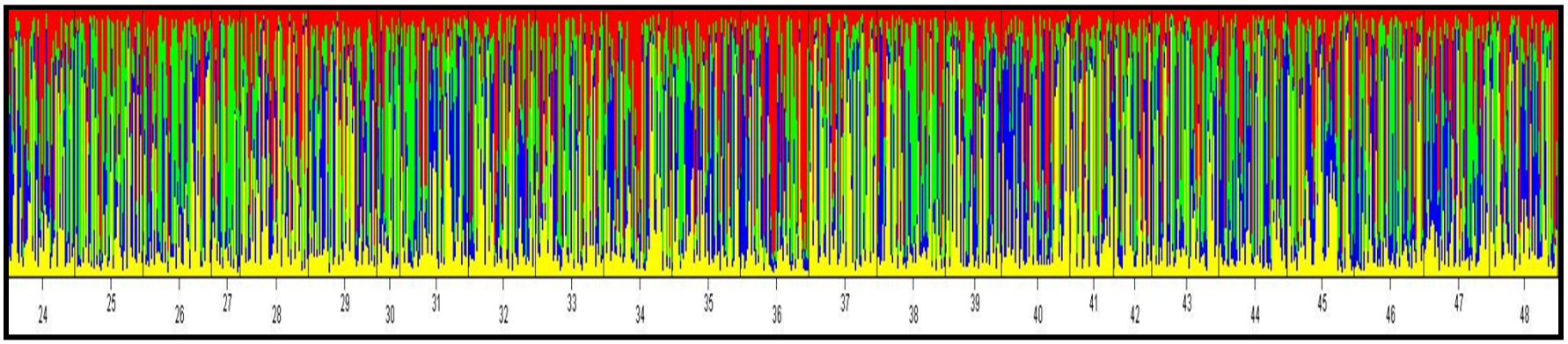


$\Pr(X \mid K) = 4$

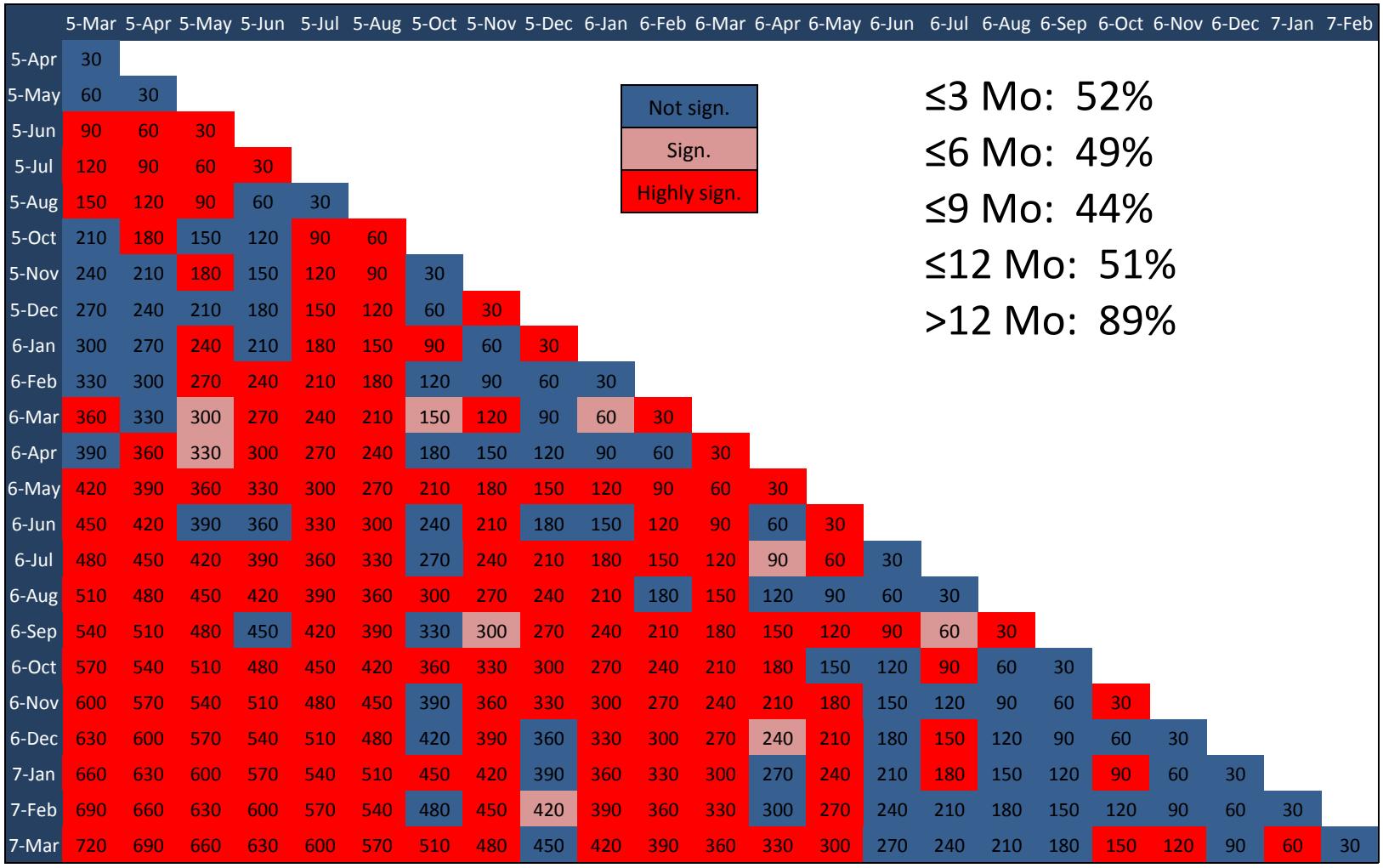
Big Munson, FL



Long Key, FL



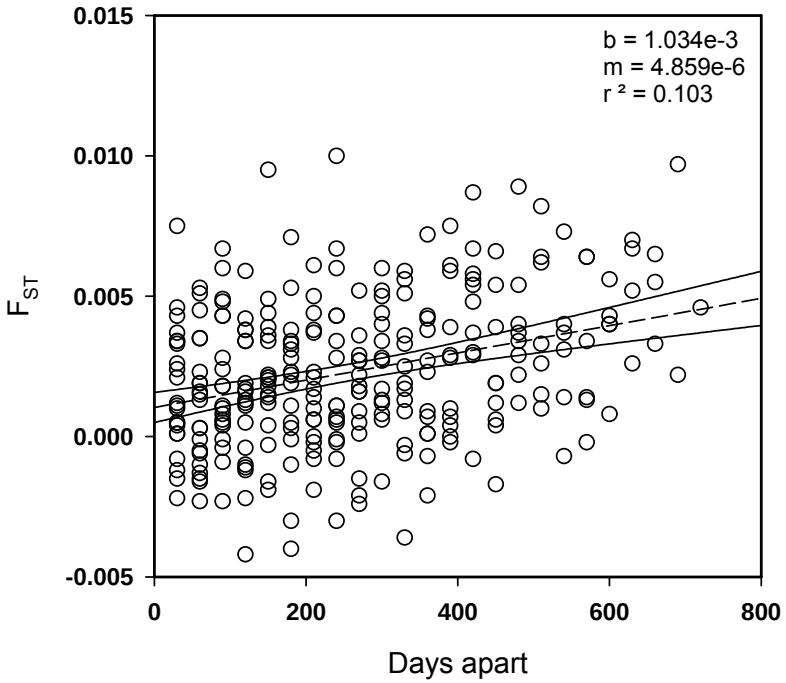
Temporal Differences in PL Allele Frequencies

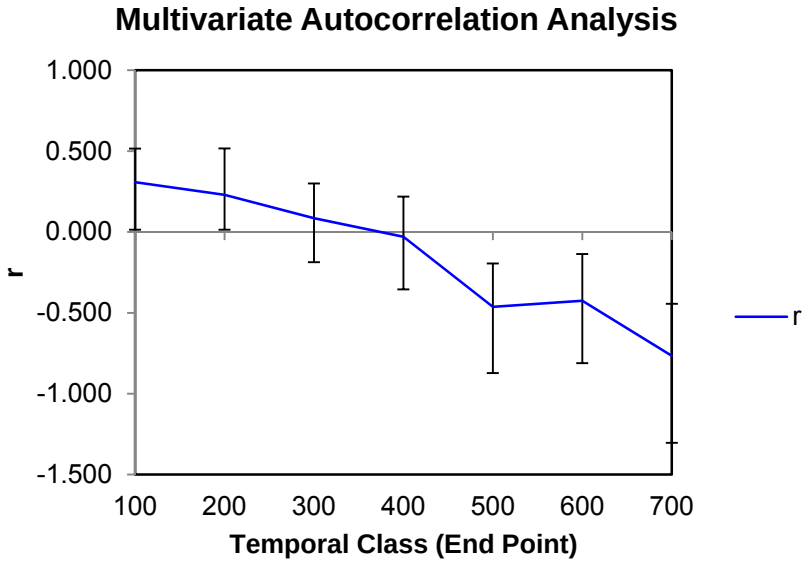


	5-Mar	5-Apr	5-May	5-Jun	5-Jul	5-Aug	5-Oct	5-Nov	5-Dec	6-Jan	6-Feb	6-Mar	6-Apr	6-May	6-Jun	6-Jul	6-Aug	6-Sep	6-Oct	6-Nov	6-Dec	7-Jan	7-Feb
5-Apr	30																						
5-May	60	30																					
5-Jun	90	60	30																				
5-Jul	120	90	60	30																			
5-Aug	150	120	90	60	30																		
5-Oct	210	180	150	120	90	60																	
5-Nov	240	210	180	150	120	90	30																
5-Dec	270	240	210	180	150	120	60	30															
6-Jan	300	270	240	210	180	150	90	60	30														
6-Feb	330	300	270	240	210	180	120	90	60	30													
6-Mar	360	330	300	270	240	210	150	120	90	60	30												
6-Apr	390	360	330	300	270	240	180	150	120	90	60	30											
6-May	420	390	360	330	300	270	210	180	150	120	90	60	30										
6-Jun	450	420	390	360	330	300	240	210	180	150	120	90	60	30									
6-Jul	480	450	420	390	360	330	270	240	210	180	150	120	90	60	30								
6-Aug	510	480	450	420	390	360	300	270	240	210	180	150	120	90	60	30							
6-Sep	540	510	480	450	420	390	330	300	270	240	210	180	150	120	90	60	30						
6-Oct	570	540	510	480	450	420	360	330	300	270	240	210	180	150	120	90	60	30					
6-Nov	600	570	540	510	480	450	390	360	330	300	270	240	210	180	150	120	90	60	30				
6-Dec	630	600	570	540	510	480	420	390	360	330	300	270	240	210	180	150	120	90	60	30			
7-Jan	660	630	600	570	540	510	450	420	390	360	330	300	270	240	210	180	150	120	90	60	30		
7-Feb	690	660	630	600	570	540	480	450	420	390	360	330	300	270	240	210	180	150	120	90	60	30	
7-Mar	720	690	660	630	600	570	510	480	450	420	390	360	330	300	270	240	210	180	150	120	90	60	30

Long Key, FL

Temporal Differences in Gene Correlation





Omega Value and Probability for the Correlogram

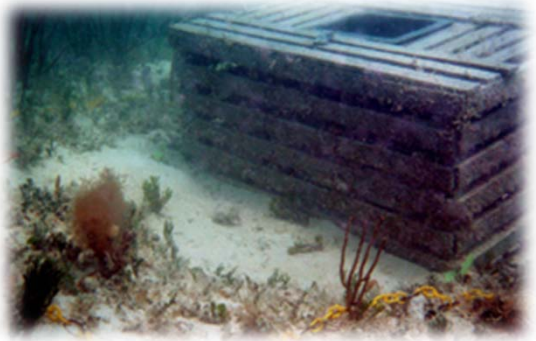
	Value	P(rand >= data)
Omega	**43.263**	**0.010**

Correlogram is Significant!

Summary Findings and Conclusions

- Post-larvae – FL Keys
  - Temporal variance in allele frequencies and genetic distances among annual collections in FL Keys
  - Bayesian clustering indicates cohorts are admixtures of migrants from ≥4 (different) genetic sources

- Adult lobster – range-wide
  - Analysis in progress



Collections and Continuation