Oyster Reefs as Critical Habitat: Assessing Short-and-Long-Term Effects of the Deepwater Horizon Spill and other Stressors

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[5] Harbor Branch Oceanographic Institution at Fl. Atlantic Univ.
[6] The Citadel

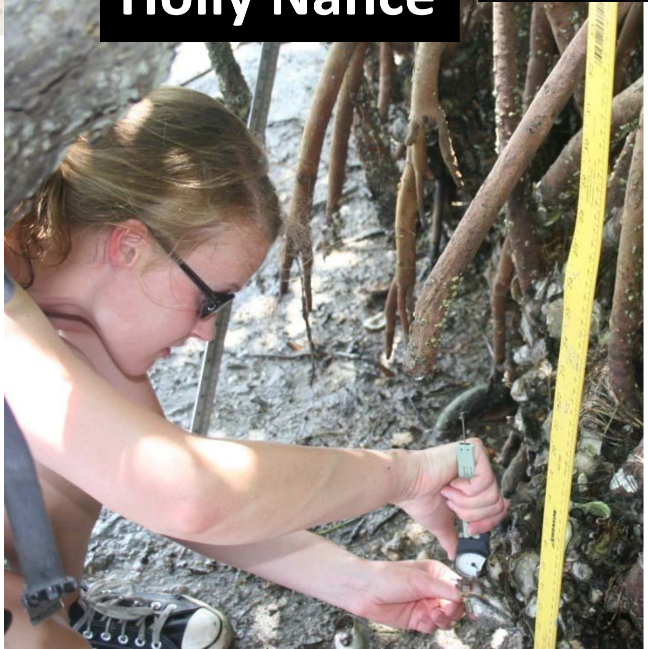
Photo: L. Coen

Team Oyster


Steve Geiger


Loren Coen

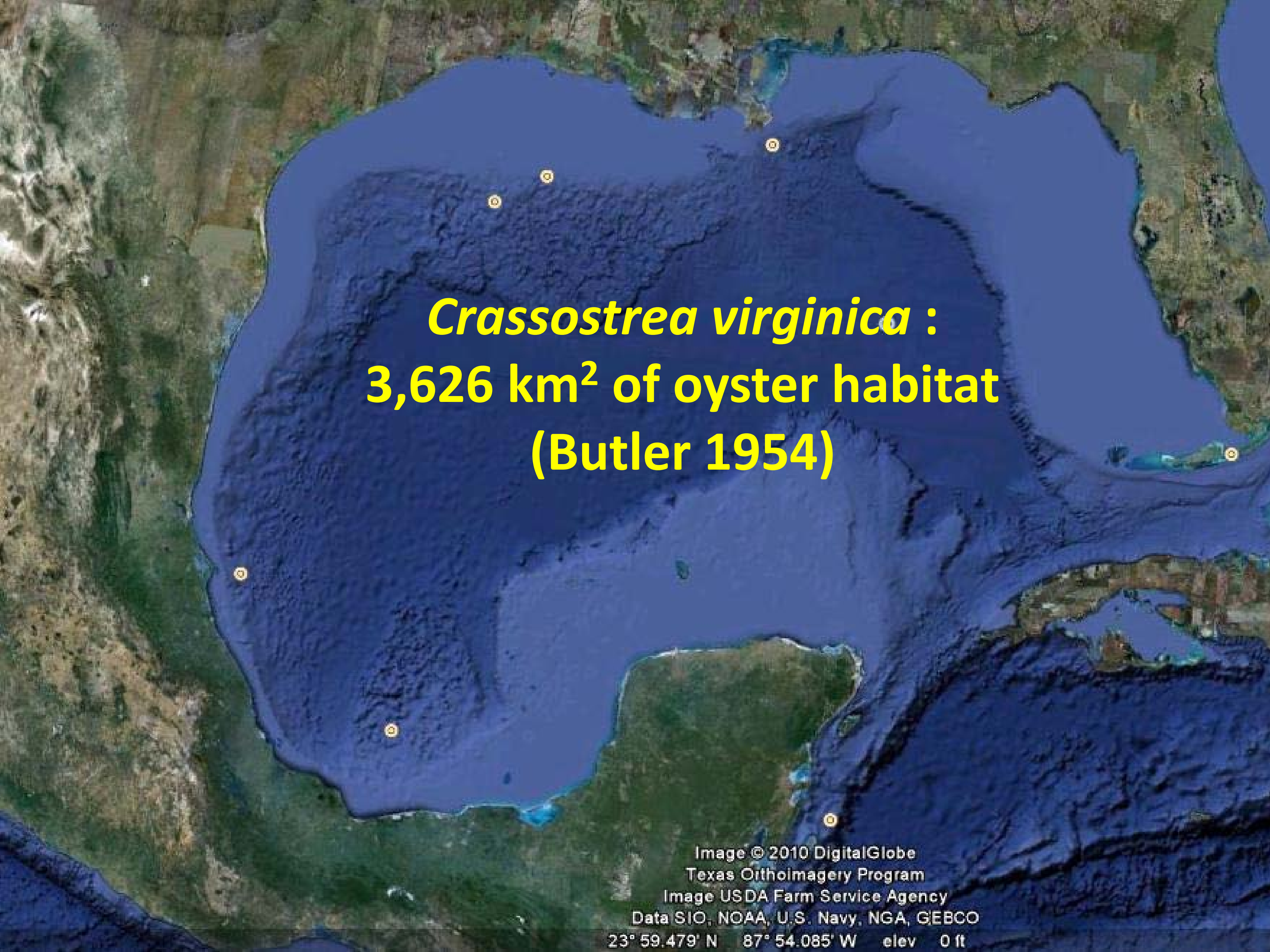

David Kimbro


Holly Nance


John Weinstein

Oysters are both ecological engineers and foundation species

Support >200 associated species (some fishery species)



Crassostrea virginica :
3,626 km^2 of oyster habitat
(Butler 1954)

Image © 2010 DigitalGlobe
Texas Orthoimagery Program
Image USDA Farm Service Agency
Data SIO, NOAA, U.S. Navy, NGA, GEBCO

In the Gulf of Mexico …

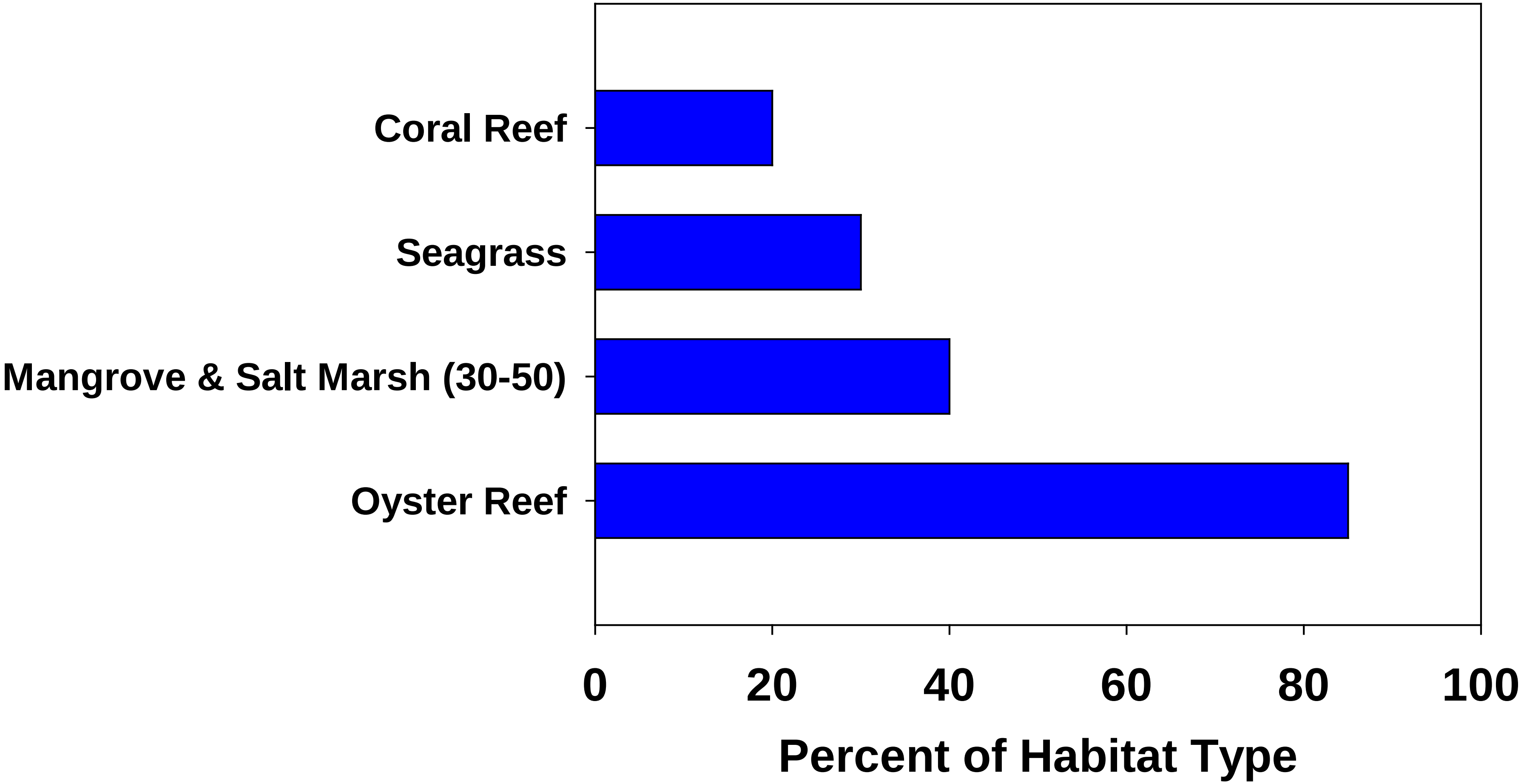
69 % of US Oyster landings are from the Gulf of Mexico (Turner 2006 Estuaries & Coasts)

- 4,019 oil & gas platforms
- 25,000 miles of active pipelines (on the seafloor!)
- 50% of the US oil & gas production

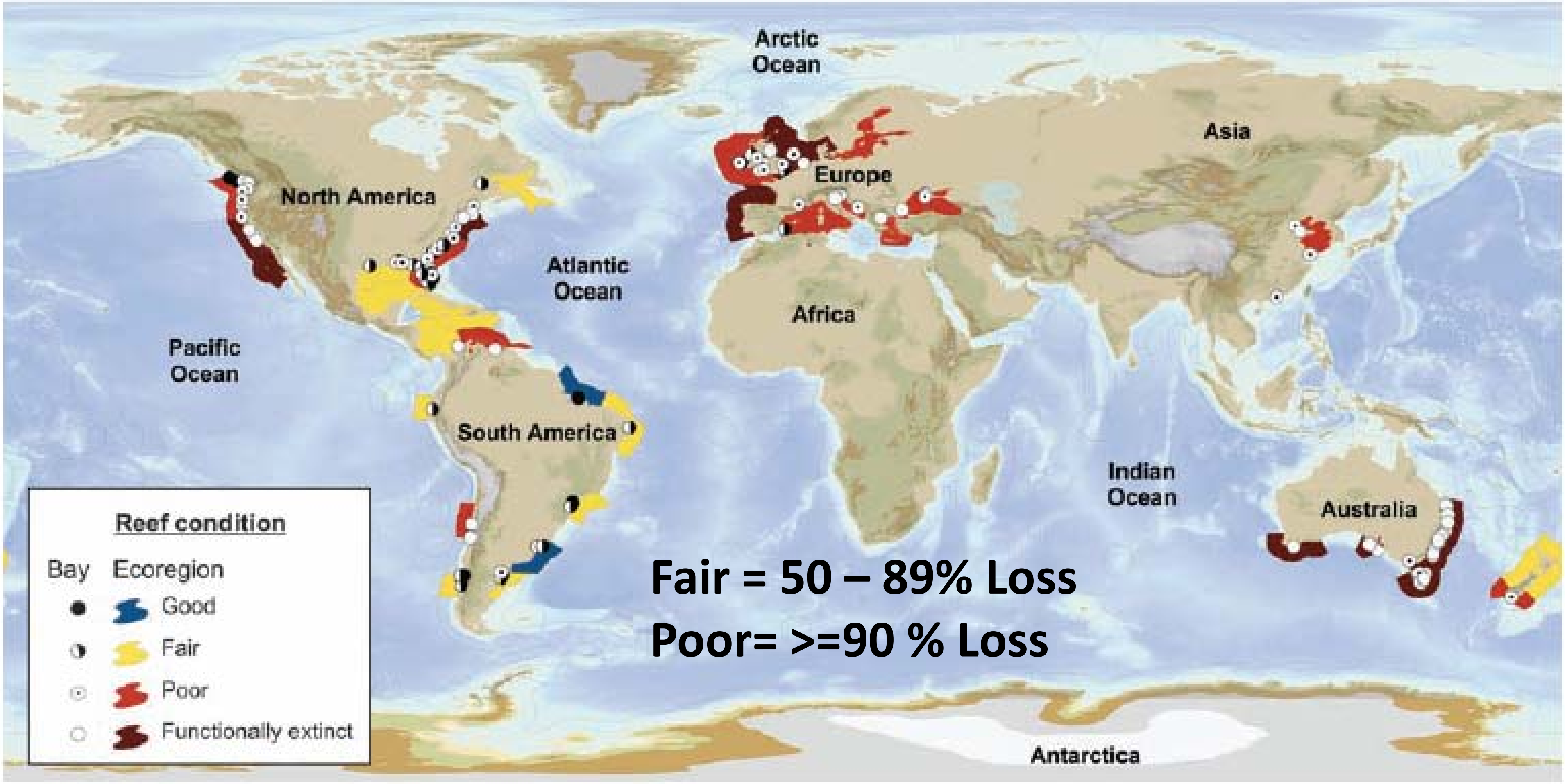
gulfofmexicoalliance.org/pdfs/gulf_glance_1008.pdf

Oyster Reefs in Trouble !

% Loss Worldwide (data from Beck et al. 2011 BioScience)



Impairment of Oyster Populations Worldwide

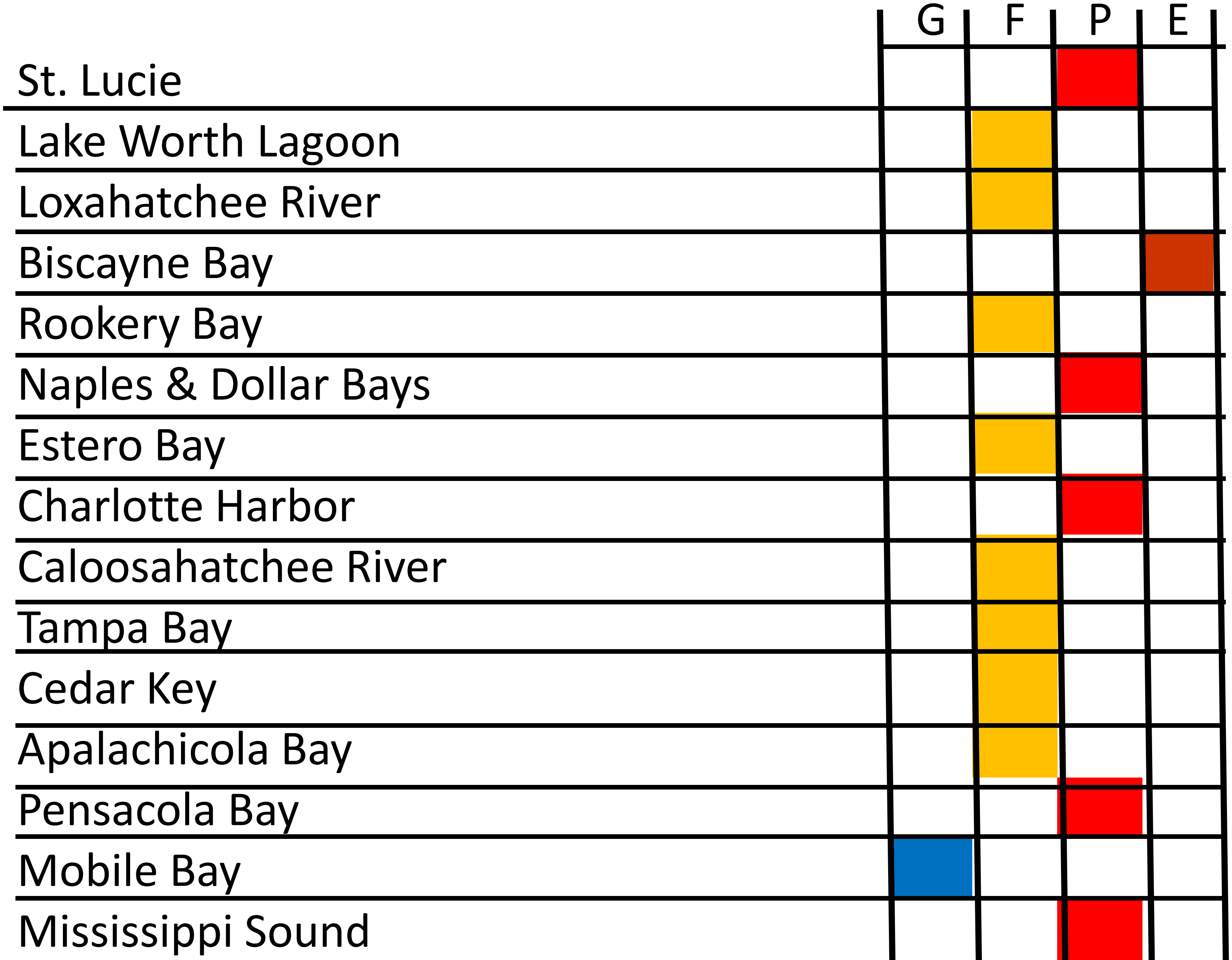


Fair = 50 – 89% Loss

Poor= >=90 % Loss

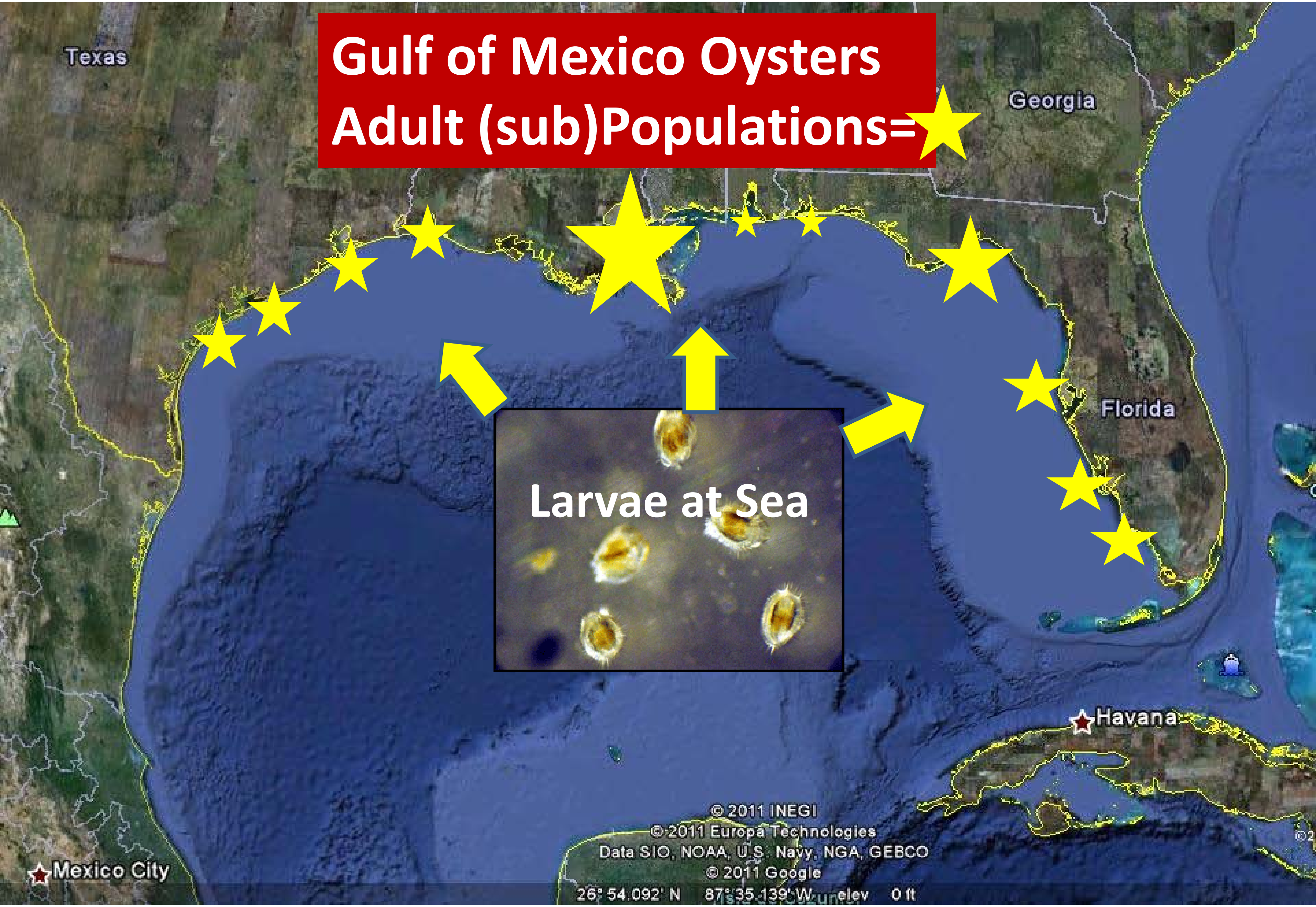
From Beck et al. (2011), and http://www.aibs.org/bioscience-press-releases/resources/Beck.pdf http://www.oyster-restoration.org/reports/Shellfish%20Reefs%20at%20Risk-single%20pages.pdf?PHPSESSID=651fa993ea180fac27fe78e83a2a674f

From Website associated with the BioScience 2011 publication: G=good, F=Fair (ie, 50-89% loss!), P= Poor, E= Functionally Extinct



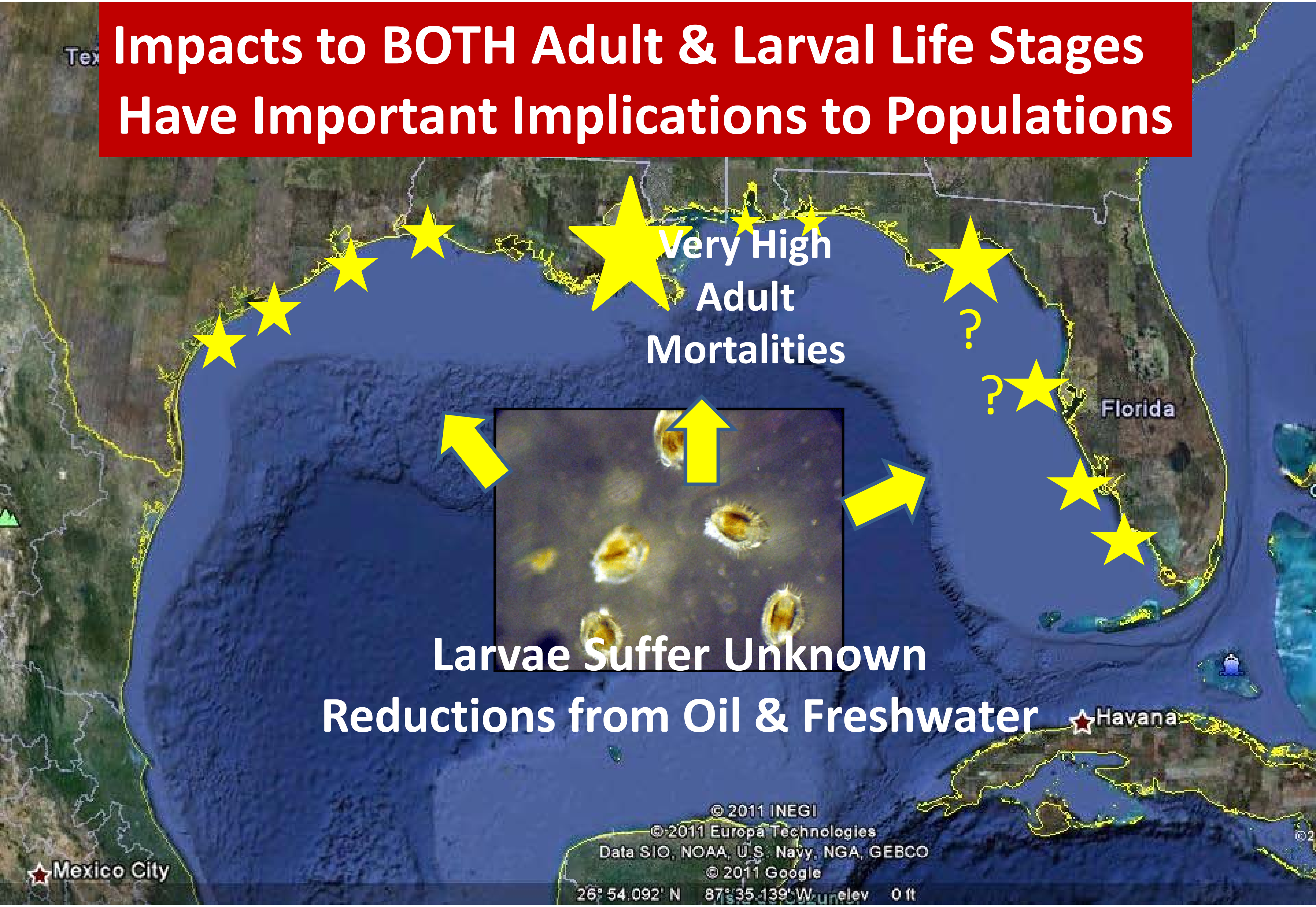
	G	F	P	E
St. Lucie			🟥	
Lake Worth Lagoon		🟨		
Loxahatchee River		🟨		
Biscayne Bay				🟫
→ Rookery Bay		🟨		
Naples & Dollar Bays			🟥	
Estero Bay		🟨		
→ Charlotte Harbor			🟥	
Caloosahatchee River		🟨		
→ Tampa Bay		🟨		
→ Cedar Key		🟨		
Apalachicola Bay		🟨		
Pensacola Bay			🟥	
Mobile Bay	🟦			
Mississippi Sound			🟥	

Gulf of Mexico Oysters Adult (sub)Populations=★



Larvae at Sea

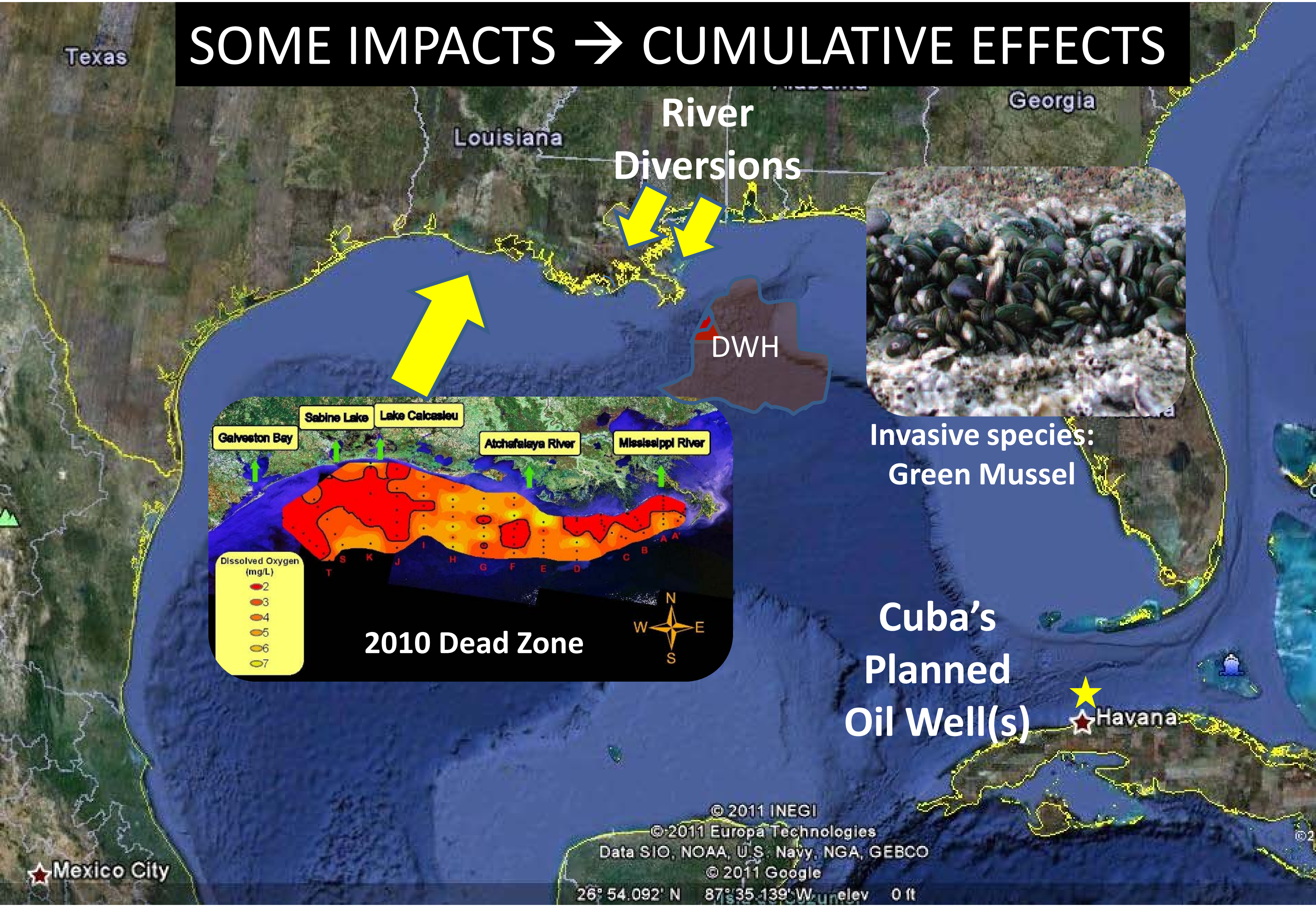
Impacts to BOTH Adult & Larval Life Stages Have Important Implications to Populations



Very High
Adult
Mortalities

Larvae Suffer Unknown
Reductions from Oil & Freshwater

SOME IMPACTS → CUMULATIVE EFFECTS



River Diversions

DWH

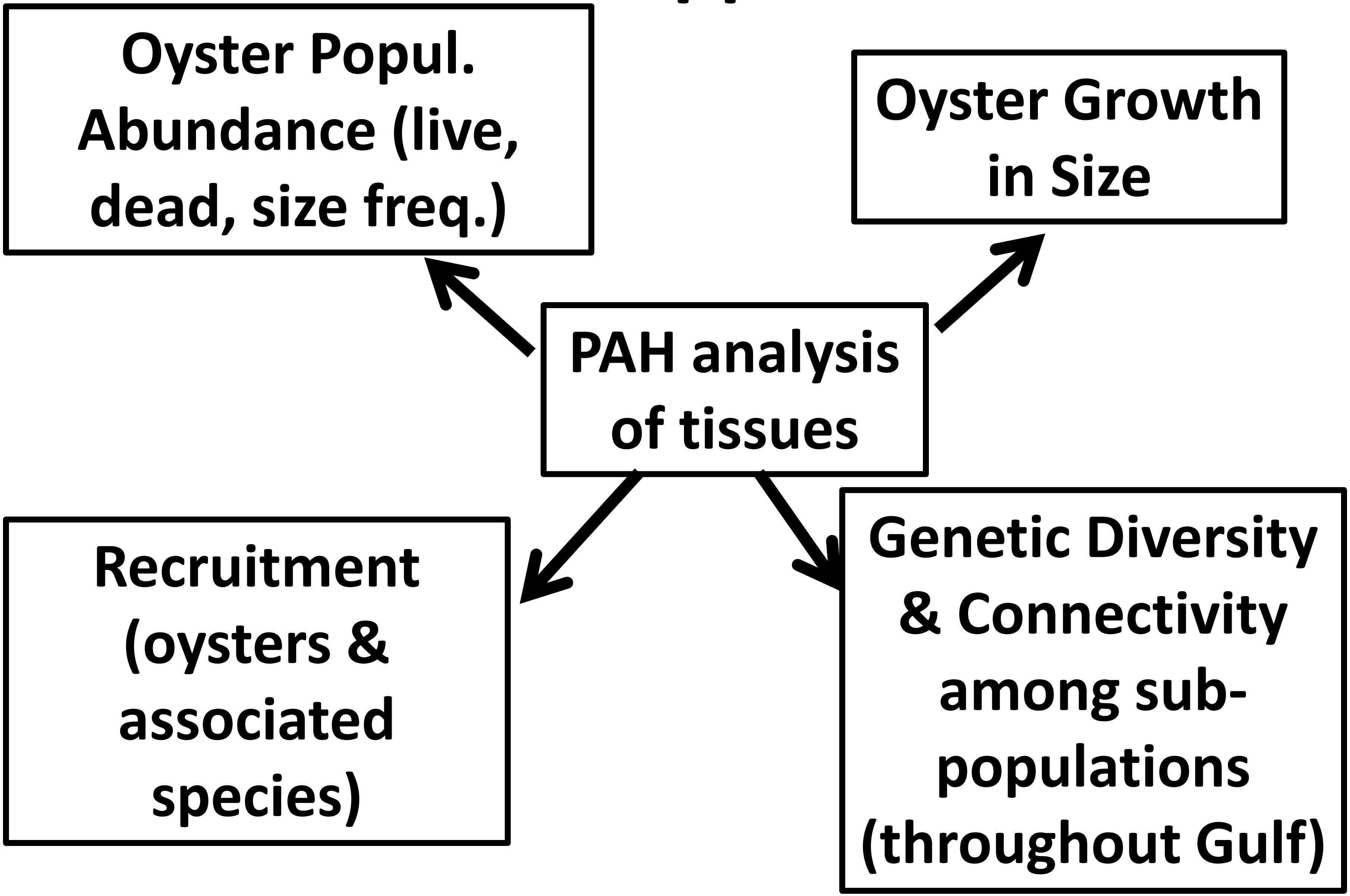
Invasive species: Green Mussel

2010 Dead Zone

Cuba's Planned Oil Well(s)

© 2011 INEGI
© 2011 Europa Technologies
Data SIO, NOAA, U.S. Navy, NGA, GEBCO
© 2011 Google
26° 54.092' N 87° 35.139' W elev 0 ft

Our Approach



Oyster Popul. Abundance (live, dead, size freq.)

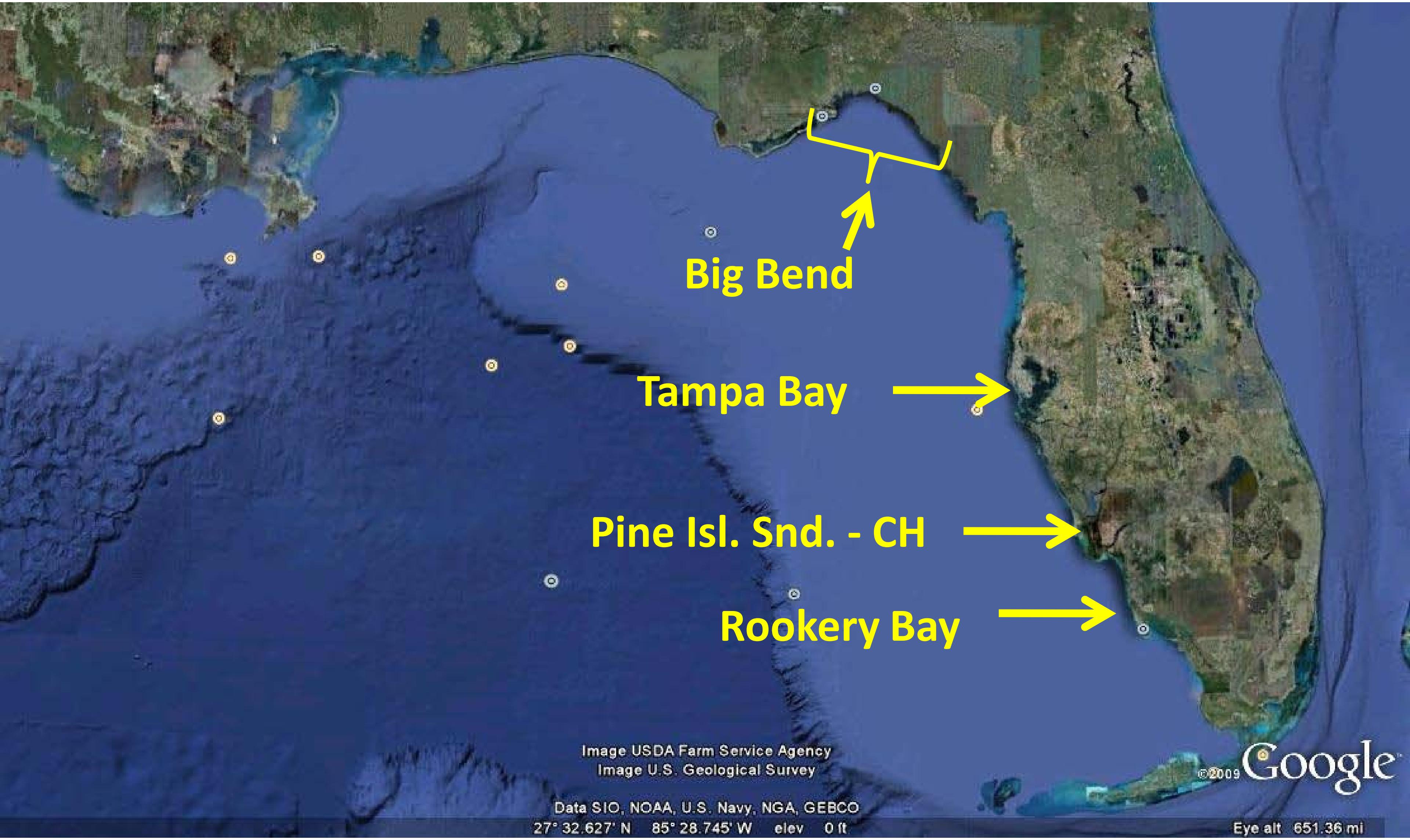
Oyster Growth in Size

PAH analysis of tissues

Recruitment (oysters & associated species)

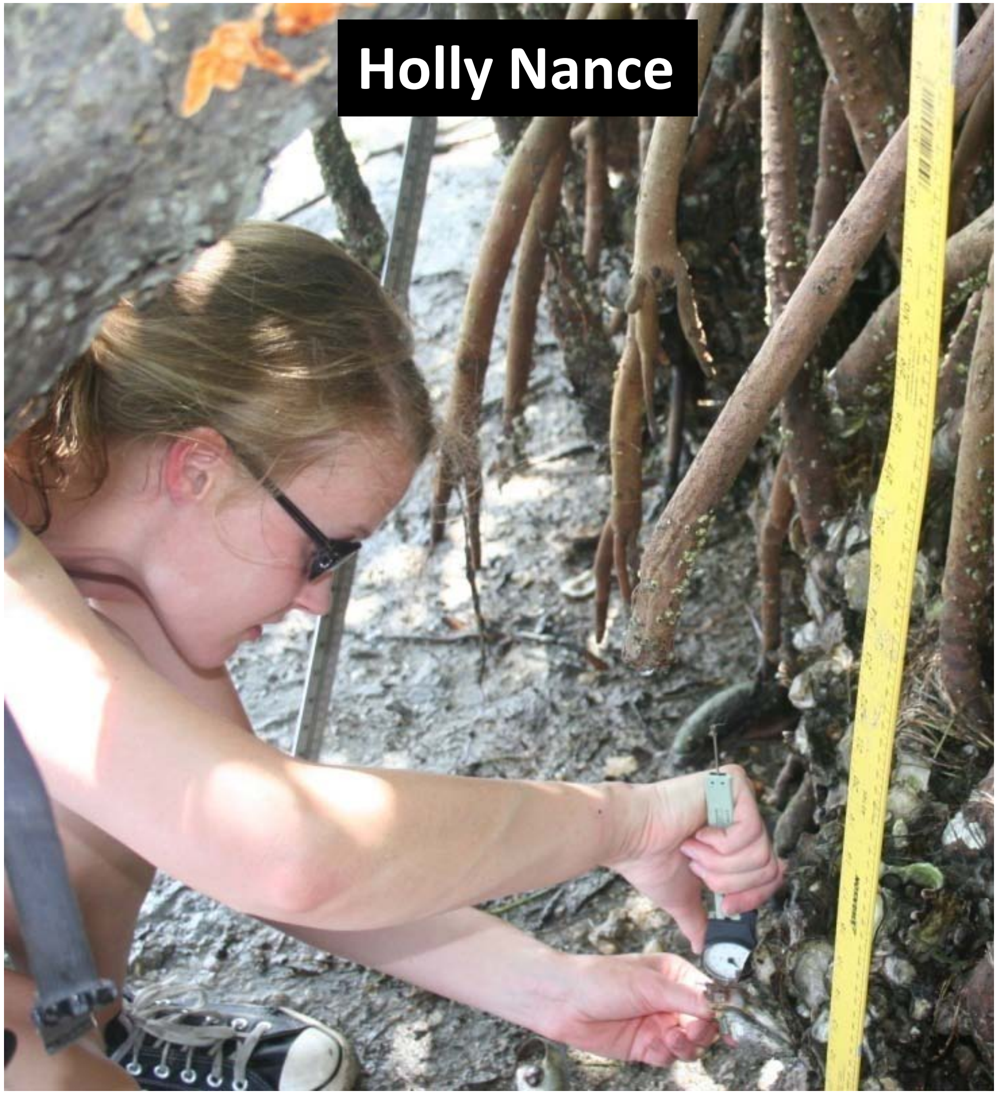
Genetic Diversity & Connectivity among sub-populations (throughout Gulf)

Field Ecology & PAH Sampling



Work to Date

Population Genetics



Holly Nance

Genetic analyses

- Currently have over 700 oysters from 17 sites from South FL to TX
- Sample sizes are roughly 40-50 oysters per site
- Have genotyped over 400 oysters to date, from 9 of 17 sites, at 10 microsatellite loci
- Currently optimizing 3-4 more msat loci, for a total of 13-14 loci

Objectives

- Characterize habitat, recruitment, growth, and survival in *C. virginica* along the Gulf coast of Florida
- Characterize genetic structure, diversity, connectivity, and demographic history before and after DWH

Background of *C. virginica* genetics

- Previous work in GOM has found significant structure at both mtDNA and nDNA (Hoover and Gaffney 2005; Galindo-Sanchez 2008; Varney et al 2009)
- Fine-scale and temporal sampling have not been done
- Demographic history and processes behind patterns of structure are unknown

Questions

- Is there genetic differentiation within and/or between estuaries?
- Are these patterns temporally stable?
- What processes are causing these patterns?
- Has DWH affected connectivity, diversity, and N_e?

Preliminary Data

- Based on 7 msat loci (Brown et al 2000; Reece et al 2004), genotyped across 763 individuals from 17 reefs
- Most loci are not in HWE in every sample
- Excess of homozygotes at most loci in most populations suggests null alleles or inbreeding are prevalent

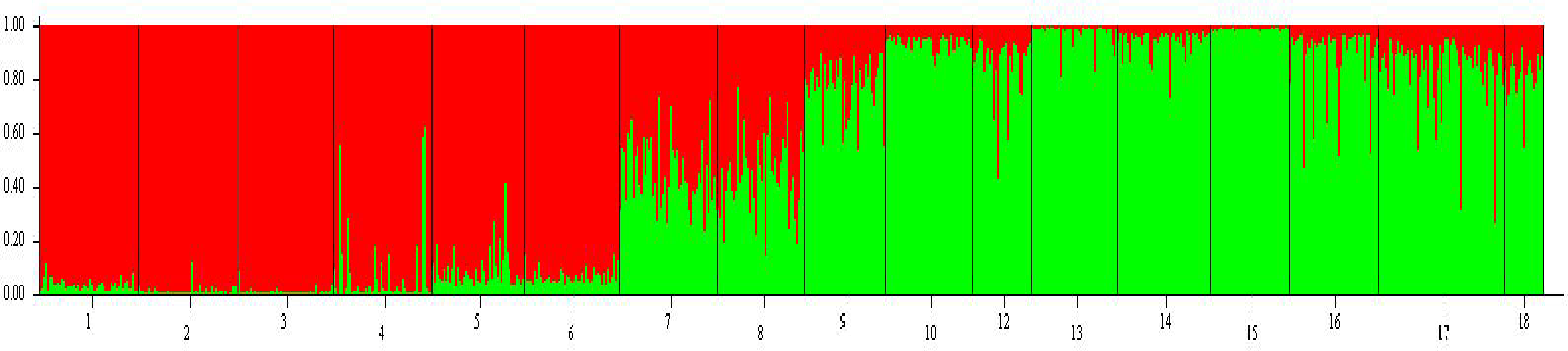
Rookery Bay, FL

Spatial Structure

- Overall $F_{ST} = 0.013$, $p = 0.000$
- $F_{CT} = 0.008$, $p = 0.001$; $F_{SC} = 0.002$, $p = 0.002$
- Weak but significant differentiation between and within regions

STRUCTURE

- Population assignment method that groups individuals such that HW and Linkage Equilibrium are maximized (Hubisz et al 2009)
- Preliminary analyses suggest there are 2 genetic clusters across the Gulf of Mexico



Pairwise genetic differences

	FL								AL		LA				TX		
	RBD	CCT	TAB	SCB	TB1	TB3	SMA	ALH	PP	SBW	BS	GT	GBD	CL	HMR	CWS	LPR
RBD	*																
CCT	**0.01**	*															
TAB	0.00	**0.01**	*														
SCB	0.00	**0.01**	0.01	*													
TB1	0.00	0.00	0.00	0.00	*												
TB3	0.00	**0.01**	**0.01**	0.00	0.00	*											
SMA	0.00	**0.01**	**0.01**	0.01	0.00	0.00	*										
ALH	0.01	**0.01**	**0.01**	**0.01**	0.00	**0.01**	0.00	*									
PP	**0.02**	**0.02**	**0.02**	**0.01**	**0.01**	0.01	**0.01**	**0.02**	*								
SBW	**0.02**	**0.03**	**0.03**	**0.02**	**0.01**	**0.02**	0.01	**0.01**	0.01	*							
BS	**0.01**	**0.02**	**0.02**	**0.01**	**0.01**	**0.01**	**0.01**	**0.01**	0.01	-0.01	*						
GT	**0.03**	**0.05**	**0.04**	**0.02**	**0.03**	**0.02**	**0.03**	**0.04**	**0.01**	**0.02**	**0.02**	*					
GBD	**0.02**	**0.03**	**0.03**	**0.03**	**0.02**	**0.02**	**0.01**	**0.03**	0.00	0.01	0.00	0.01	*				
CL	**0.02**	**0.04**	**0.03**	**0.02**	**0.02**	**0.02**	**0.02**	**0.03**	**0.01**	0.01	**0.01**	0.00	0.01	*			
HMR	**0.02**	**0.03**	**0.02**	**0.02**	**0.02**	**0.02**	**0.01**	**0.02**	0.01	0.00	0.00	**0.02**	0.00	0.01	*		
CWS	**0.01**	**0.01**	**0.02**	**0.01**	**0.01**	0.01	0.00	**0.01**	0.00	0.00	0.00	**0.02**	0.01	**0.01**	0.00	*	
LPR	**0.01**	**0.02**	**0.02**	0.01	0.01	0.00	0.01	**0.01**	0.01	0.01	0.01	**0.02**	0.01	**0.02**	**0.02**	0.01	*

…but no Isolation by Distance. What processes are responsible for these patterns of genetic structure?

Summary

- Populations weakly differentiated
- No significant isolation by distance
- STRUCTURE results found 2 genetic groups
- Genetic drift is likely not a dominant force acting on *C. virginica* pops
- How do either null alleles, life history and reproductive mode, and recent history of *C. virginica* affect spatial structure?

Work to Date

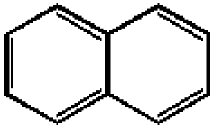
Adult Oyster Tissue PAH Analysis (Weinstein, The Citadel)

To date, processed >81 oysters 2010 samples for 14 of 16 priority pollutants

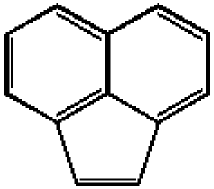
from:

Big Bend
Tampa Bay
Rookery Bay

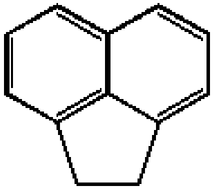
PAH analyses: 16 Priority pollutants



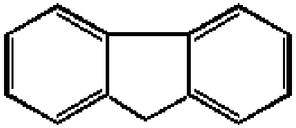
Naphthalene



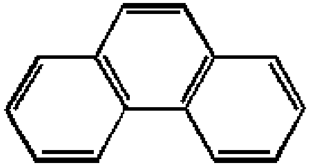
Acenaphthylene



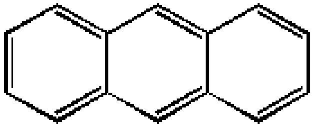
Acenaphthene



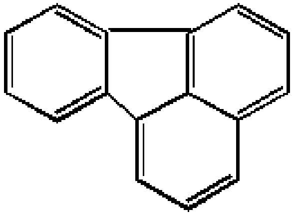
Fluorene



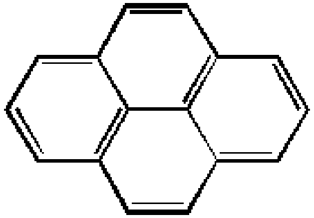
Phenanthrene



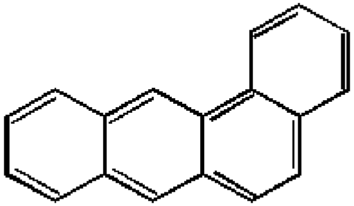
Anthracene



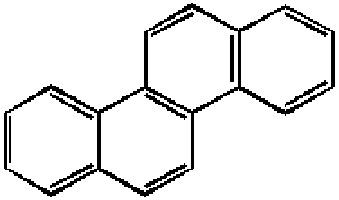
Fluoranthene



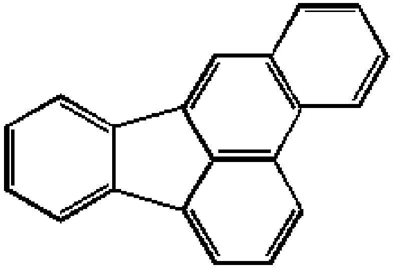
Pyrene



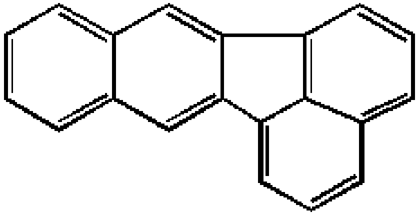
Benzo(a)anthracene



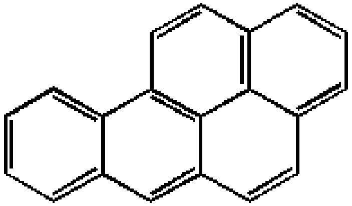
Chrysene



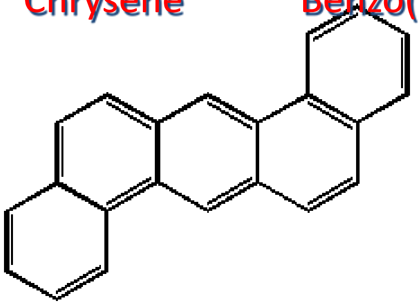
Benzo(b)fluoranthene



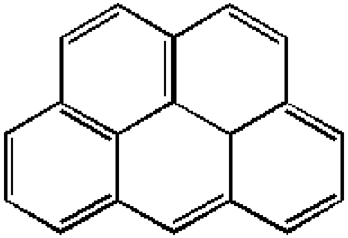
Benzo(k)fluoranthene



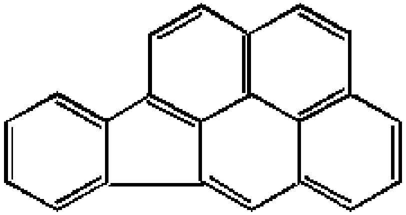
Benzo(a)pyrene



Dibenz(a,h)anthracene



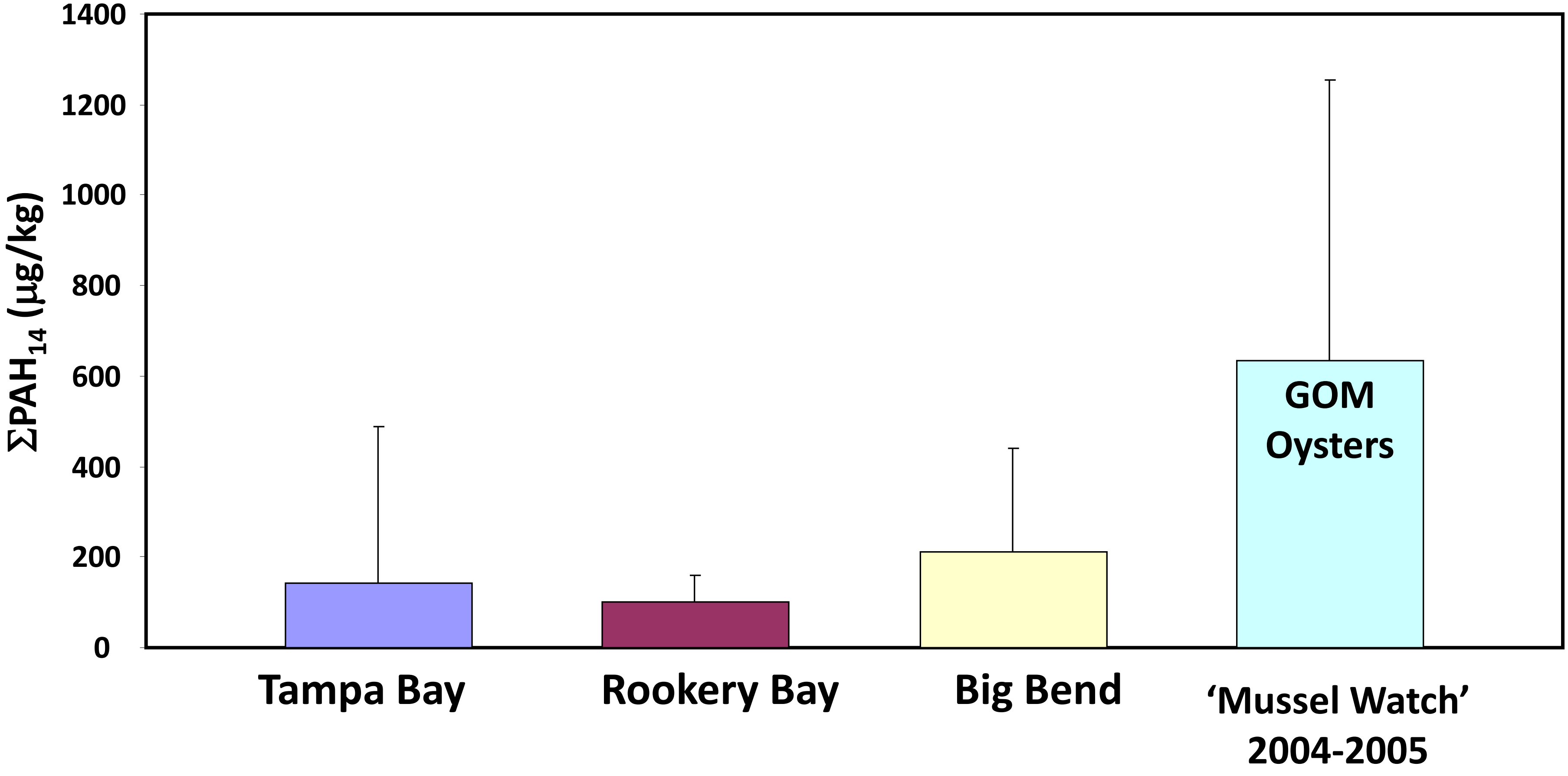
Benzo(g,h,i)perylene



Indeno(1,2,3-cd)pyrene

Oyster PAH Data by Site

Dec. 2010 – Feb. 2011



Work to Date

Field Ecology

Steve Geiger
(Tampa Bay)

Loren Coen
(Pine Isl CH)

David Kimbro
(Big Bend)

Ed Proffitt
(Rookery &
Johnson Bays)

Trays of fresh cultch to assess recruitment by oysters and associated species

FAU MS student,
Dana Smith

Bags containing live juvenile oysters (collected locally) marked & deployed for growth analyses

Preliminary Results:
Growth not different among regions in Florida…..
BUT
Growth is still barely more than measurement error at this early stage (2-3 months)

Quadrat samples from natural oyster reefs collected for abundance & size-frequency analyses

Collected 0.135 m^2 quadrats

Counted and measured all live & dead oysters; & collected and preserved all associated inverts

Nested Sampling Design

FIXED

Region
(Big Bend,
Tampa Bay,
Pine Isl.-CH
Rookery -
Johnson)

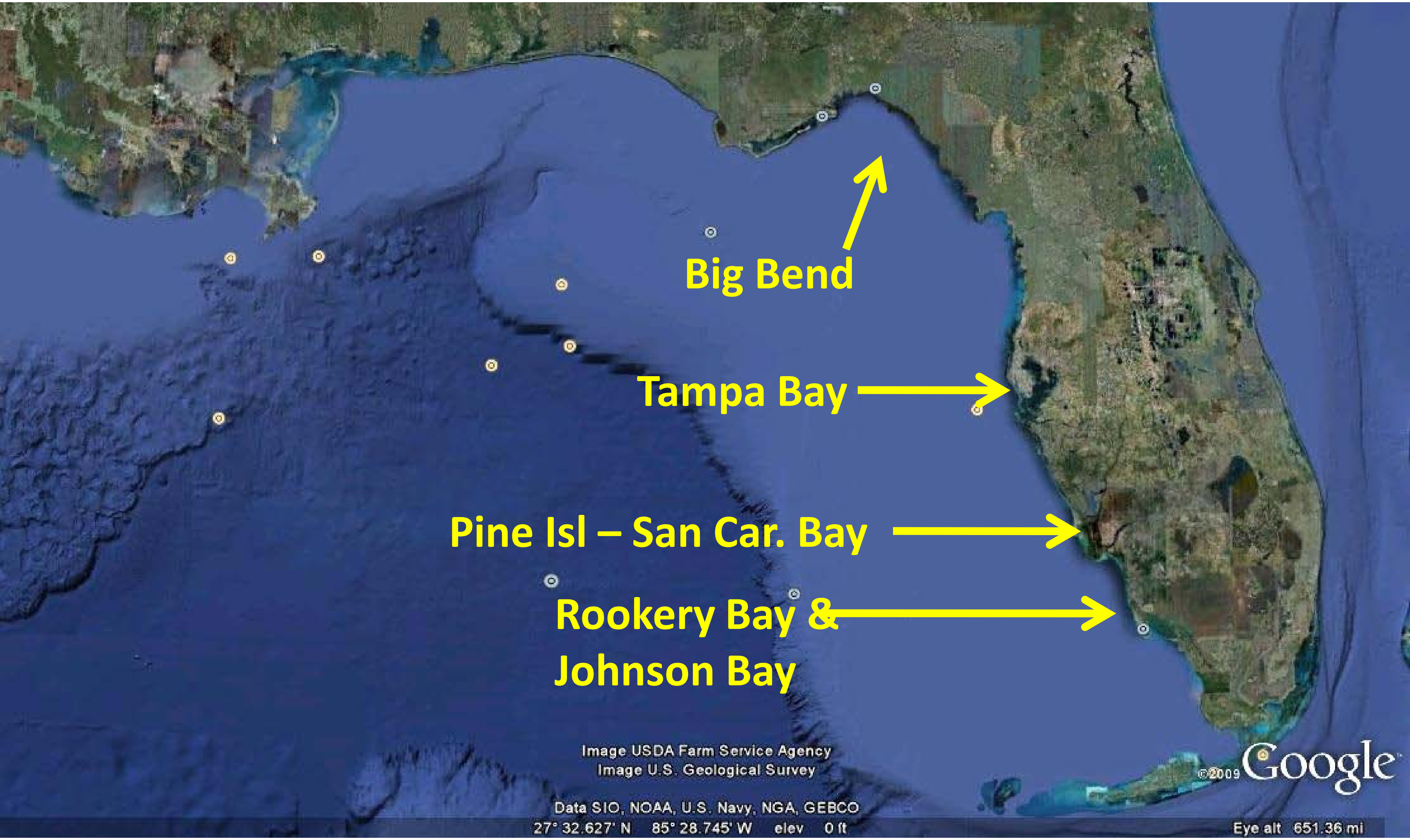
RANDOM

Sites within Region
(3 selected)

RANDOM

Reefs within Sites
(5 selected)

Field Ecology: Regions Reminder

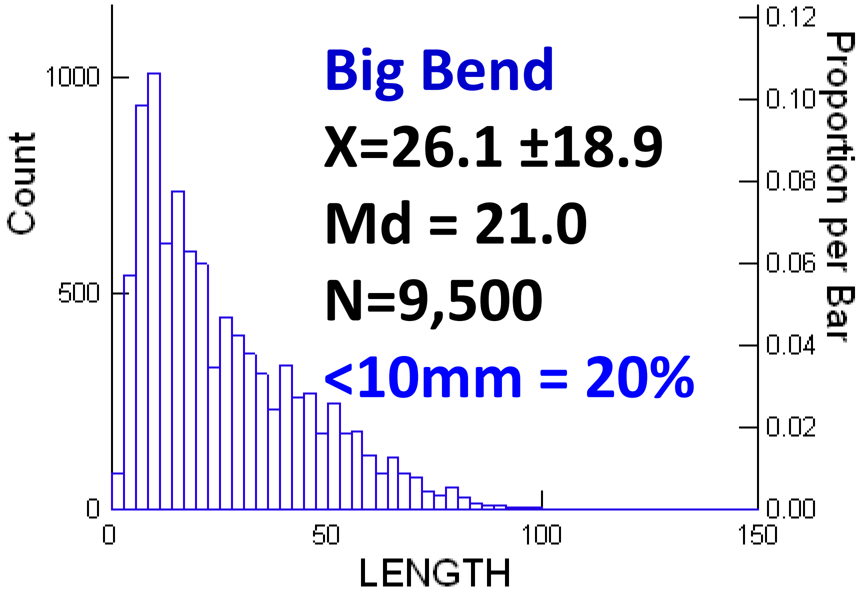


Big Bend

Tampa Bay

Pine Isl – San Car. Bay

Rookery Bay &
Johnson Bay



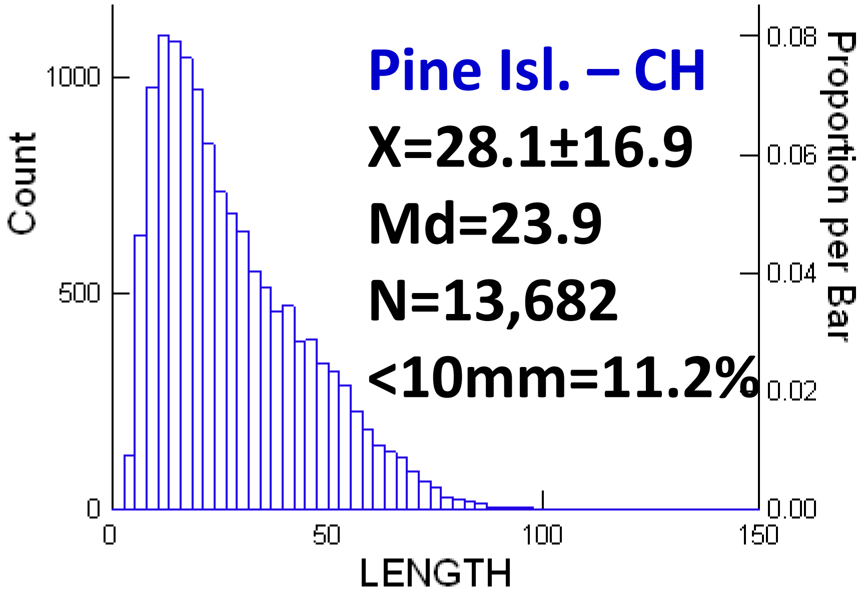
Big Bend

X=26.1 ±18.9

Md = 21.0

N=9,500

<10mm = 20%



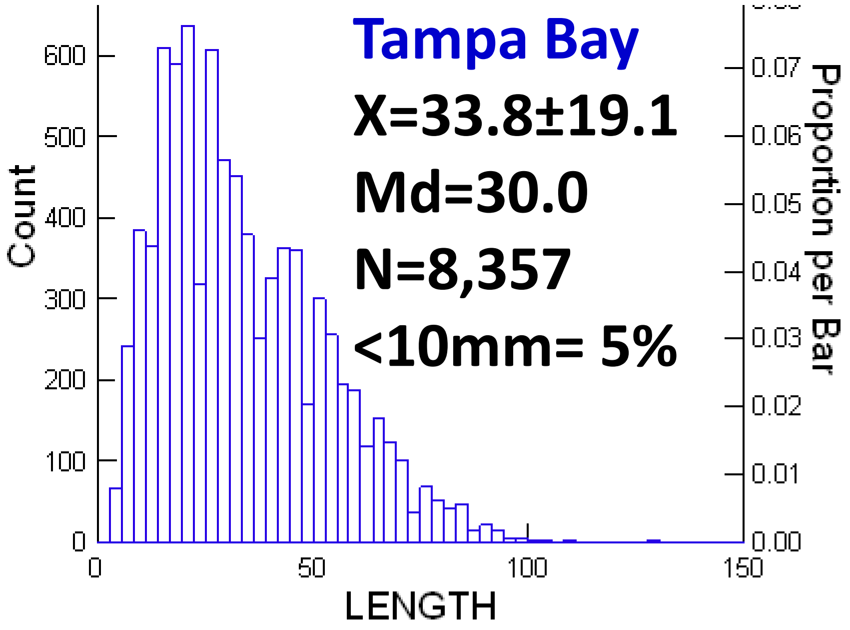
Pine Isl. – CH

X=28.1±16.9

Md=23.9

N=13,682

<10mm=11.2%



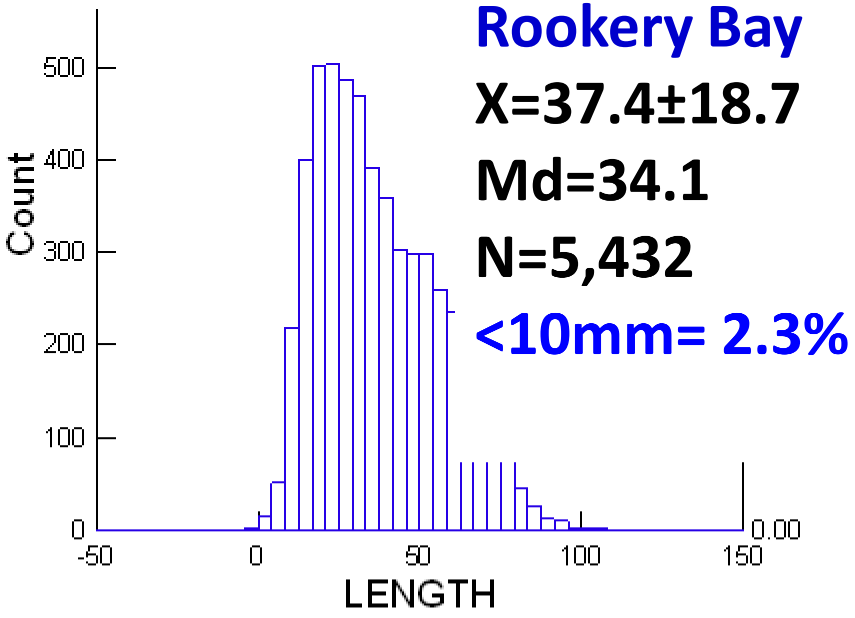
Tampa Bay

X=33.8±19.1

Md=30.0

N=8,357

<10mm= 5%



Rookery Bay

X=37.4±18.7

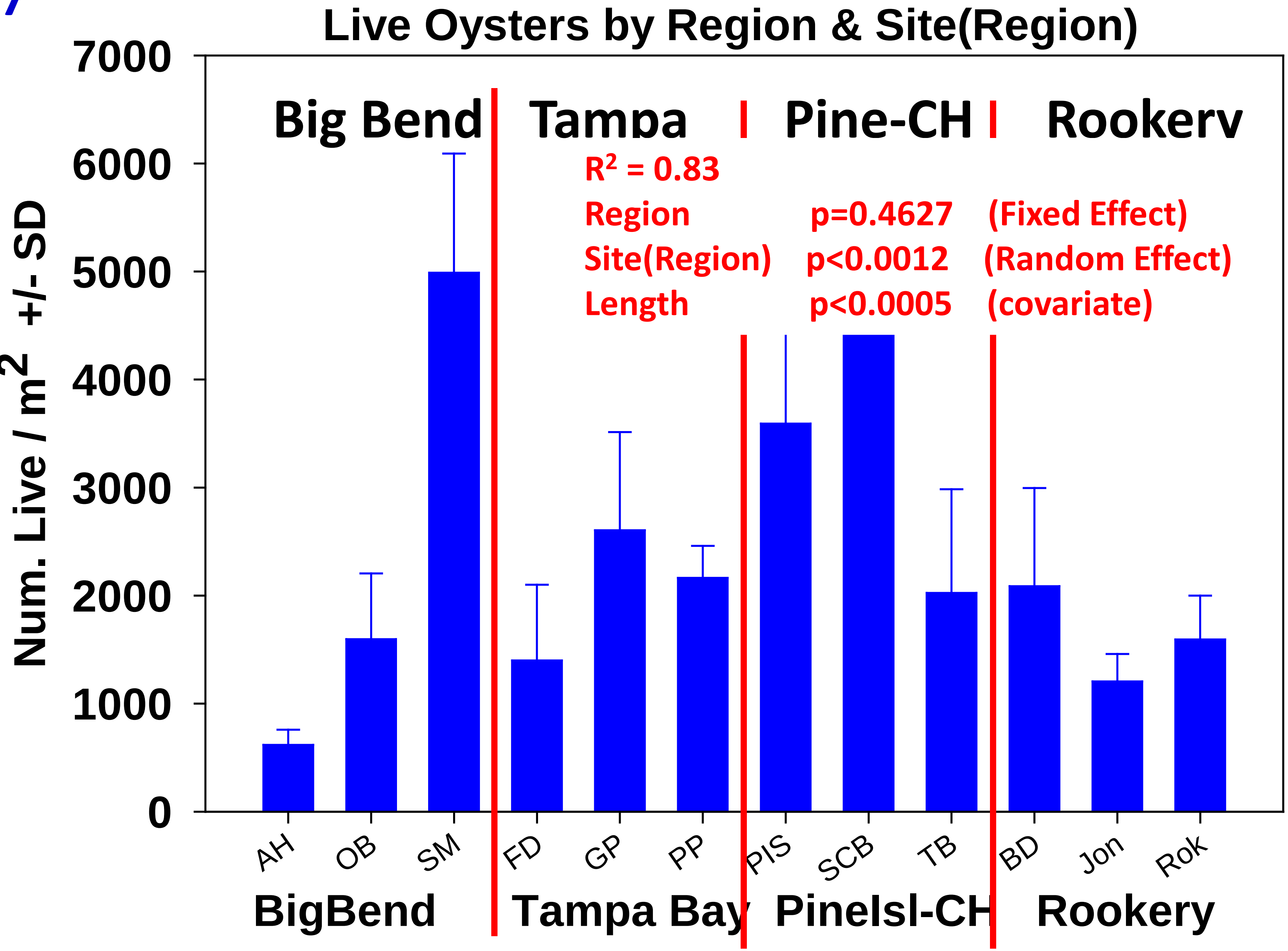
Md=34.1

N=5,432

<10mm= 2.3%

36,971 oysters measured

Florida Gulf Coast Mean: 2,427.4 ± 1,490.9 Live Oysters / m2 (1 SD), n=57

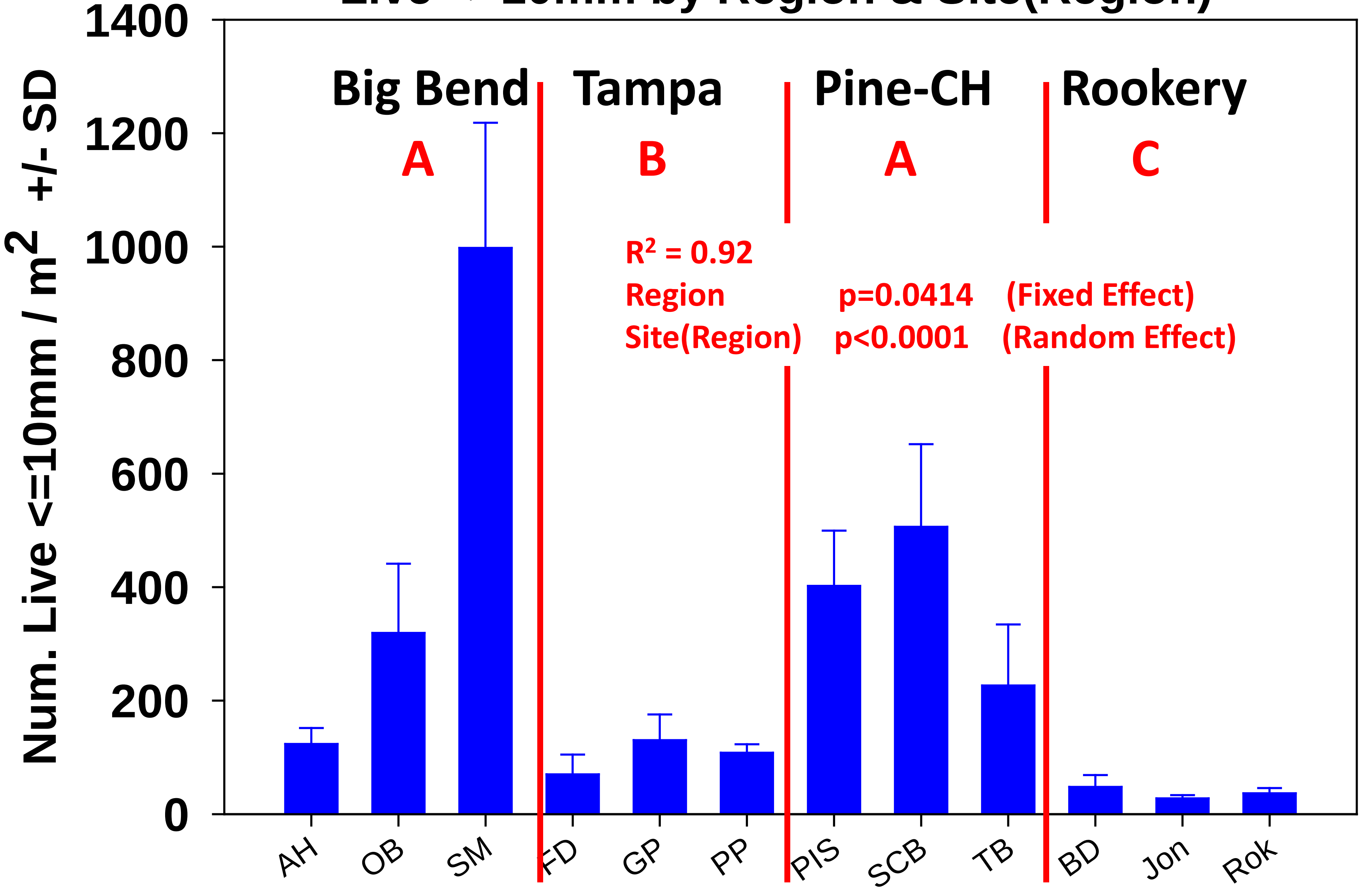


Live Oysters by Region & Site(Region)

$R^2 = 0.83$

Region	$p=0.4627$	(Fixed Effect)
Site(Region)	$p<0.0012$	(Random Effect)
Length	$p<0.0005$	(covariate)

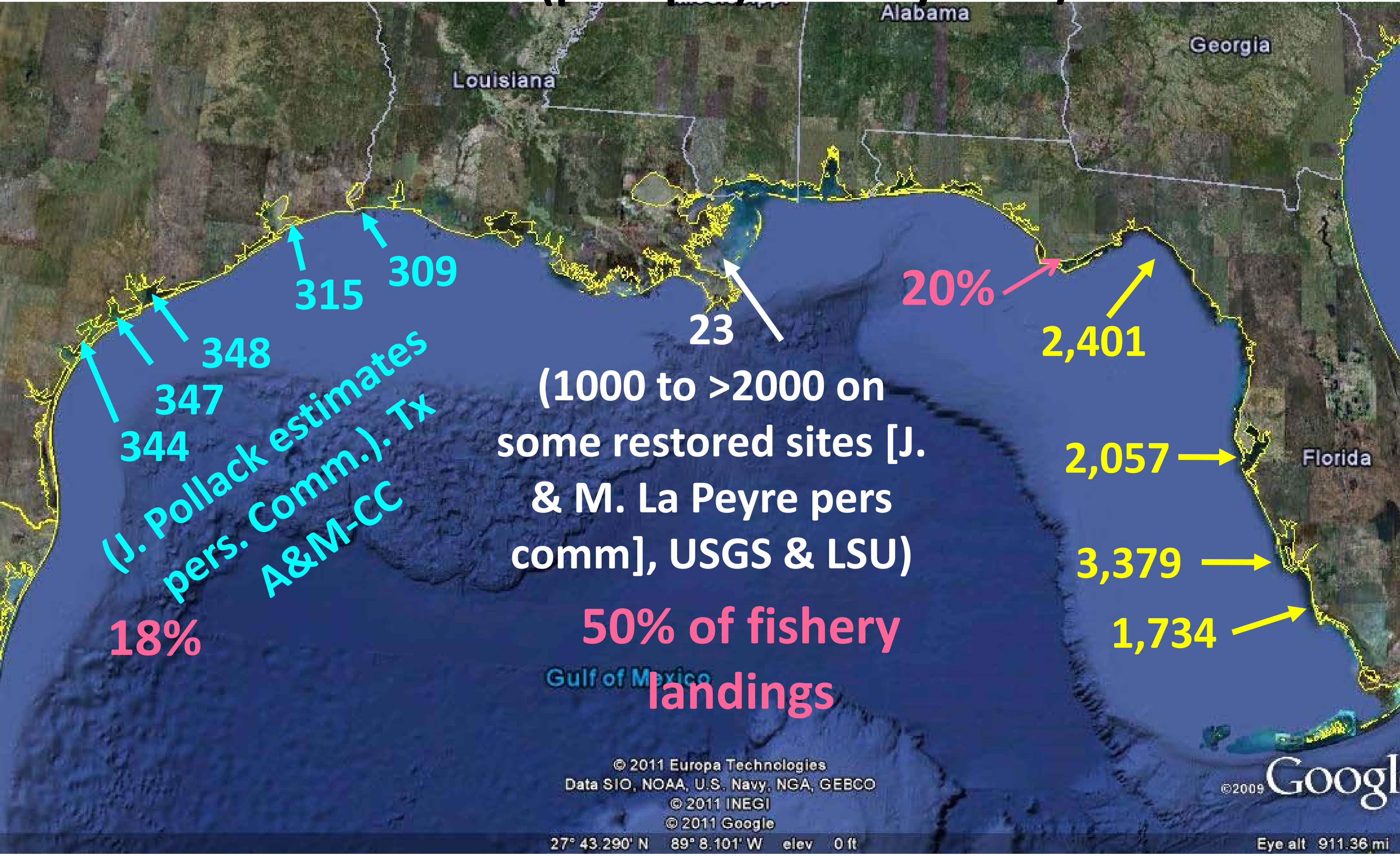
Juvenile Oysters
Live <=10mm by Region & Site(Region)



$R^2 = 0.92$

Region	p=0.0414	(Fixed Effect)
Site(Region)	p<0.0001	(Random Effect)

Oyster (post-spill) Densities in Florida Compared to Other GOM states (pre spill): live oysters / m^2



309

315

348

347

344

(J. Pollack estimates pers. Comm.). Tx A&M-CC

18%

23

(1000 to >2000 on some restored sites [J. & M. La Peyre pers comm], USGS & LSU)

50% of fishery landings

20%

2,401

2,057

3,379

1,734

Summary

1. No evidence of PAH in oyster tissues
2. Abundance differences *among* and *within* regions
   a) Many small oysters in Big Bend in winter 2010 probably from Summer / Fall recruitment event
   b) 10x Less recruitment at southernmost region
3. Population genetics samples
   a) Florida populations are distinct from others
   b) Data suggest most recruitment is from local larvae
   c) Some populations appear to have gone thru a recent bottleneck
4. ALL data provide a 2010 Baseline Condition for Gulf coast Florida! (population densities, size-frequency, genetic diversity & connectivity, PAH, associated species abundances)

Pedro Lara, FAU graduate student, oysters on reefs & mangrove prop roots

Questions?