Population Genetic Structure in *Lophelia pertusa*

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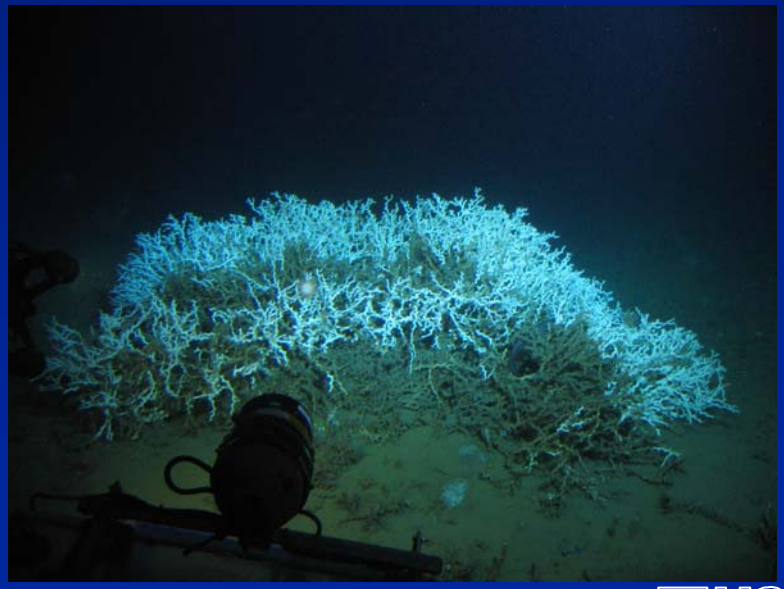

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Protection of Deep Reefs

- Spatial scale and pattern of connectivity
- Resilience – supply of new recruits
  - Local (self-seeded) = slow recovery
  - Far = higher resilience
- Need to protect larval sources
  - Very difficult to follow larvae directly!

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Genetic Markers

- Indirect, interpretive tool – estimate dispersal
- Marine species exhibit genetic structure at various spatial scales – even ‘good dispersers’
- Structure – ecological, physiological, and behavioral aspects of species biology
- Corals: larval stage important!

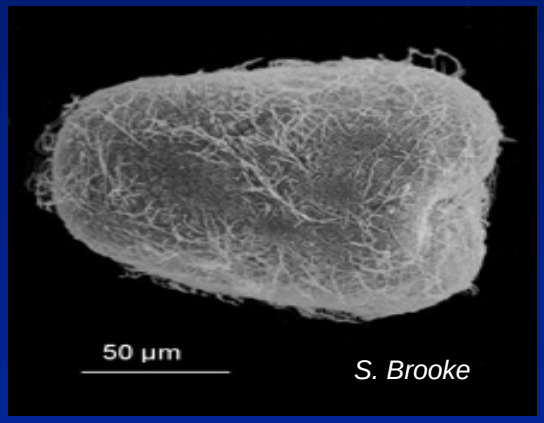
Dispersal Ability & Reproductive Biology of Coral

- Fertilization and larval types

Internal fertilization/
Brooded larvae

Pocillopora damicornis larva

External fertilization/
Gametes spawned



10-day-old *Oculina diffusa* larva

- Local hydrodynamics
- Recruitment success

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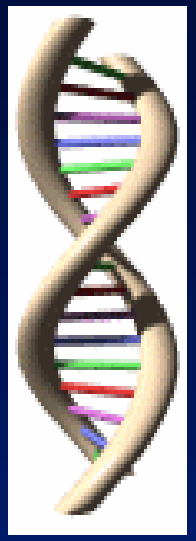
Genetic Structure in Corals



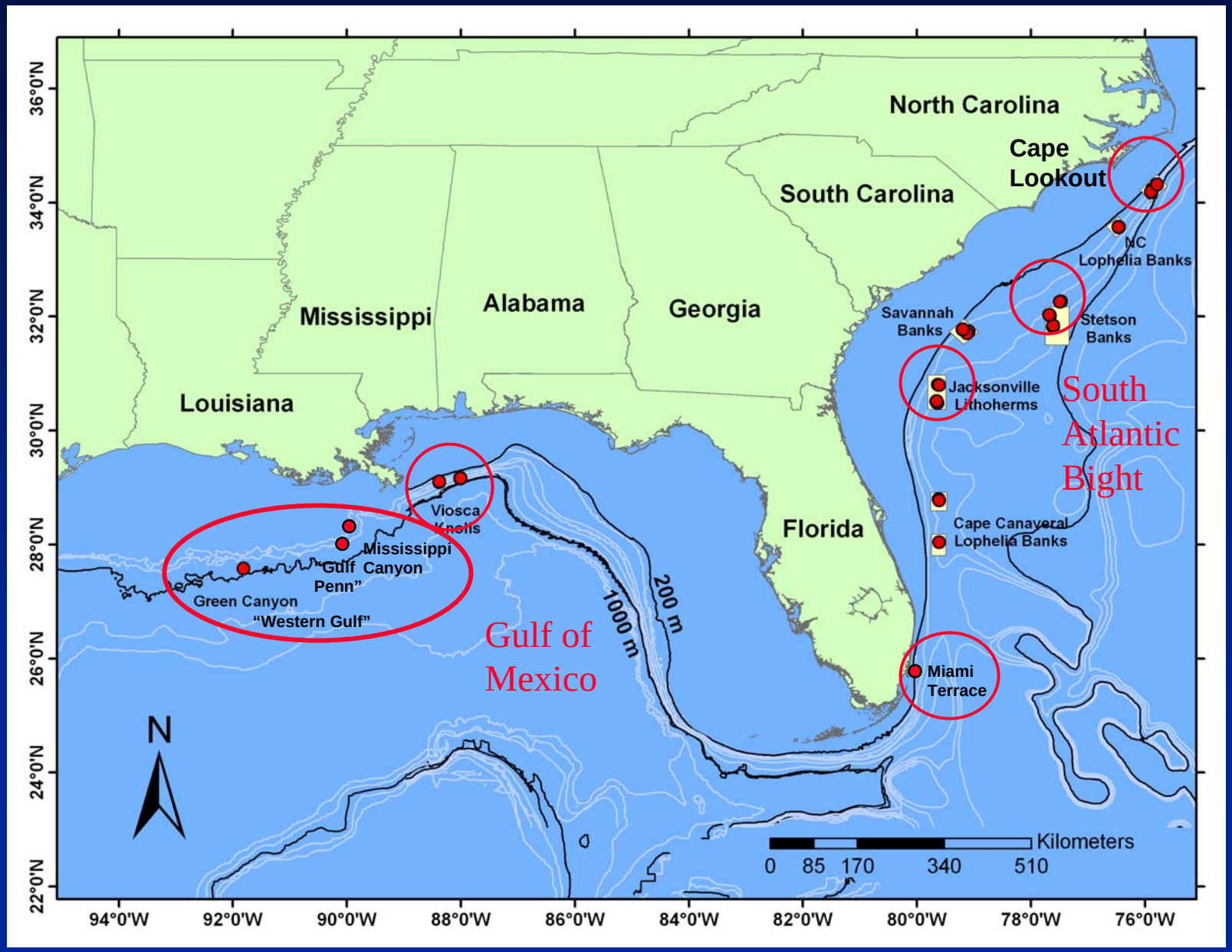
- Majority of studies = allozymes
- Six recent studies using microsatellites
- Coral species show range of connectivity
- Northeastern Atlantic *Lophelia* – LeGoff-Vitry et al. 2004

Pink Egg packets of *Acropora sp.*

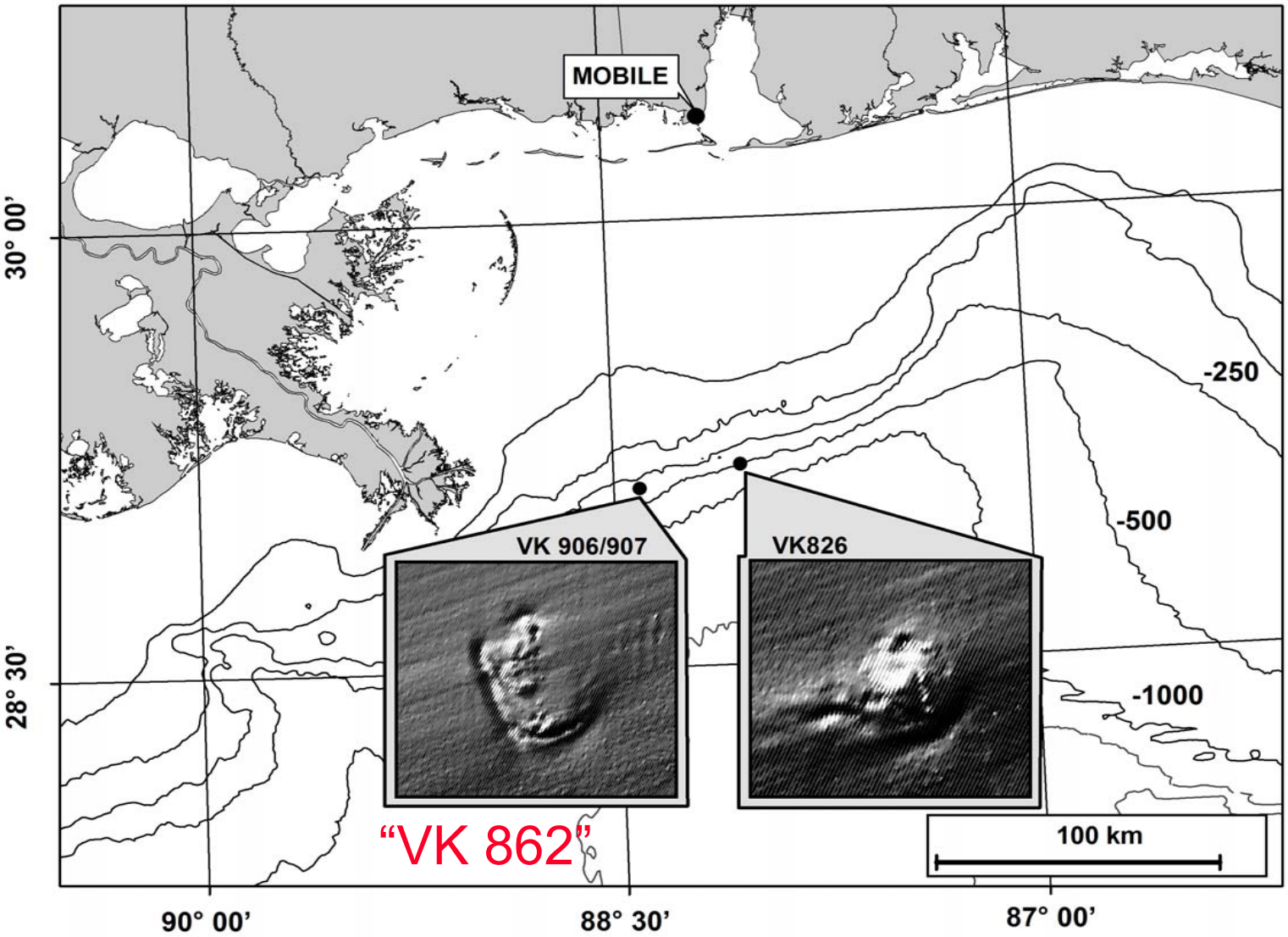
Objectives

- Develop suite of variable microsatellite markers for Gulf *Lophelia pertusa*
- Assess geographic patterns of genetic diversity in *Lophelia pertusa*
  - Quantify genetic diversity in *Lophelia*
  - Assess connectivity across several spatial scales:
    - Within Gulf of Mexico (<1–290 km)
    - Within South Atlantic Bight (18–990 km)
    - Between GoM and SAB (~1700–2300 km)
    - Between U.S. and European margin populations (~5400–7900 km)

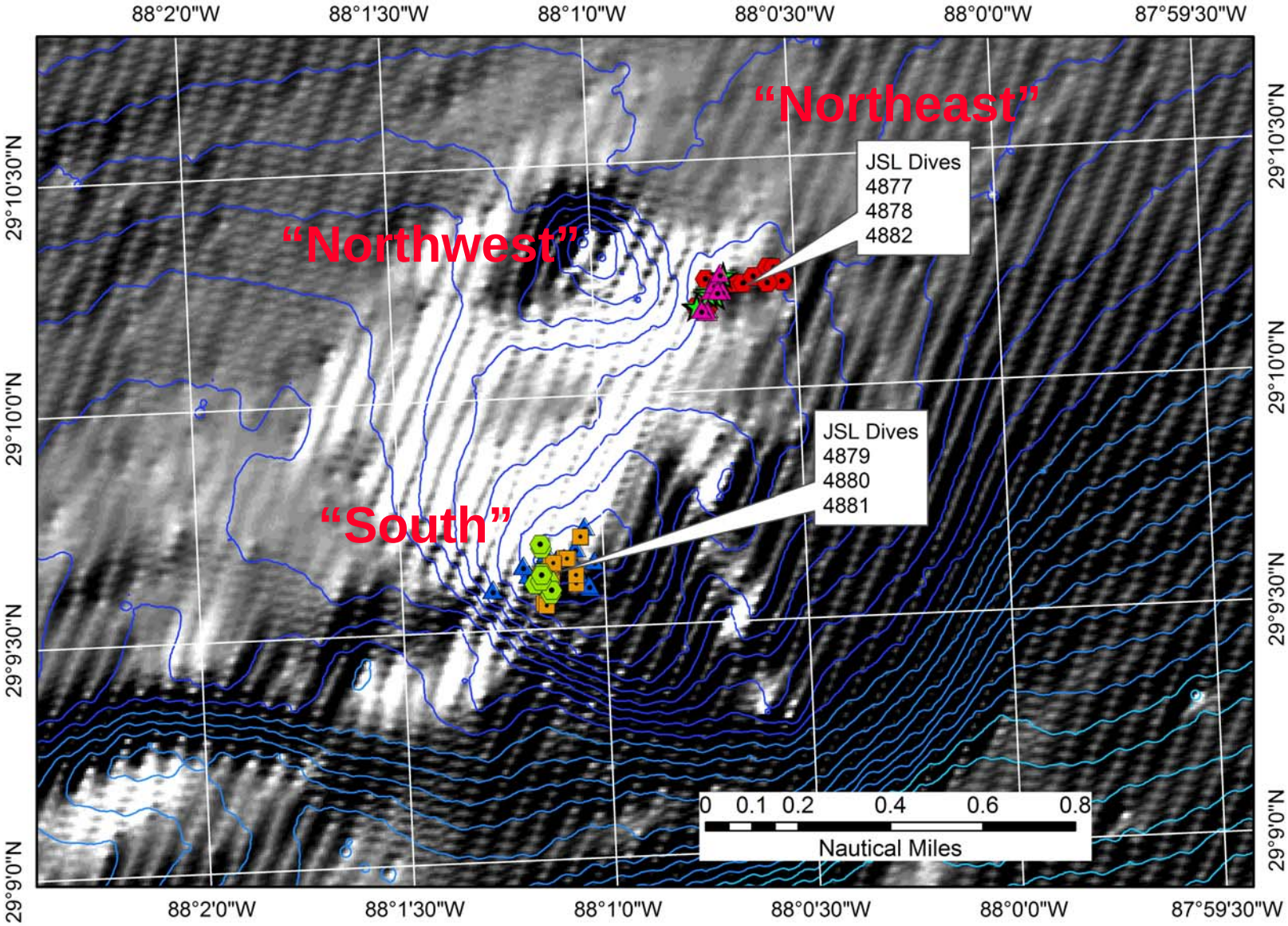
Lophelia Collection Sites



Locations of Viosca Knoll Sites

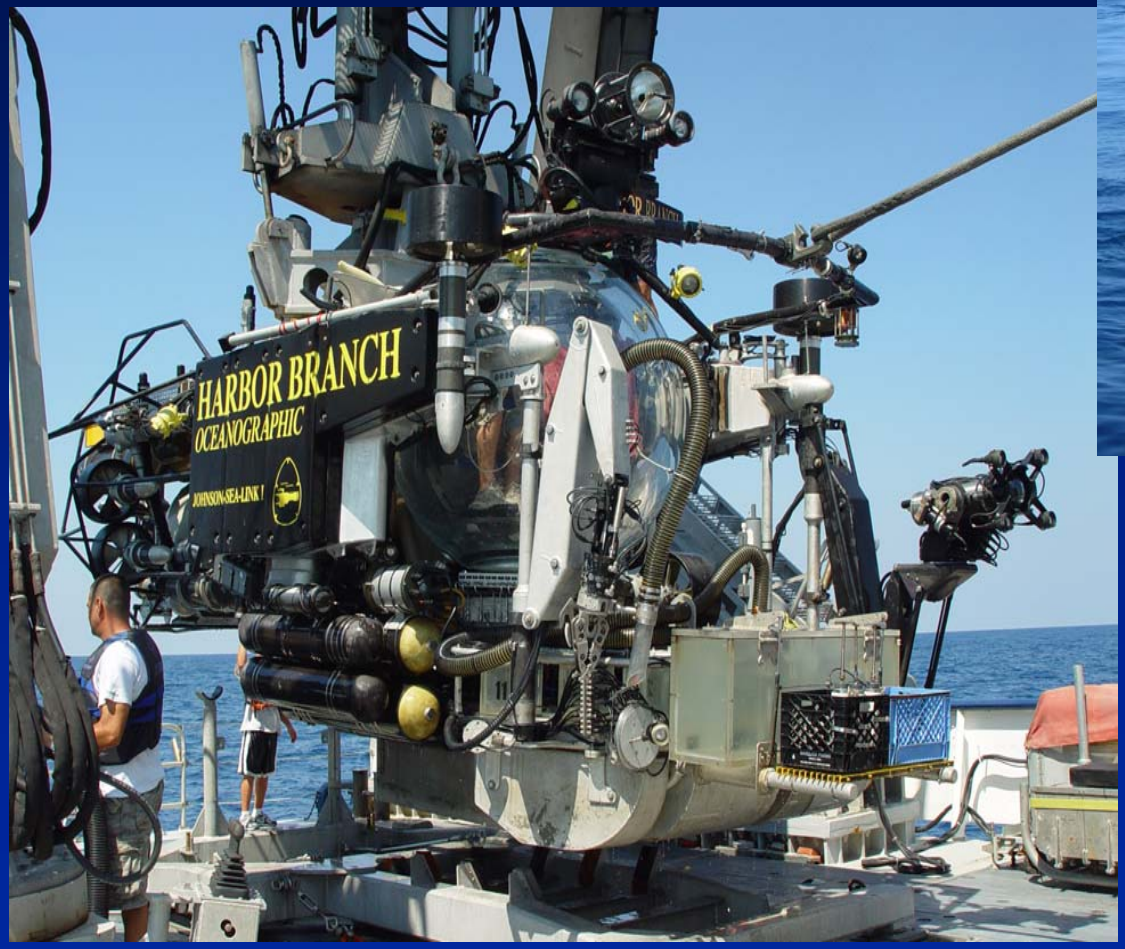


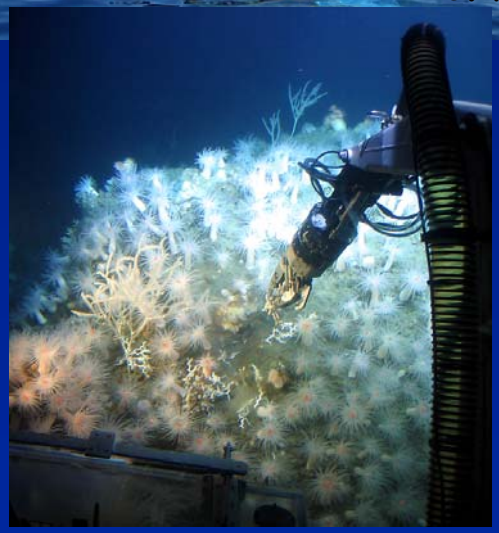
Sampled Areas of Viosca Knoll 826



Sample Collection

- Manned submersibles – Johnson Sea Link I & II





Coral Processing

- Georeferenced: Fixes taken for coral collections
- Photodocumented: Photos taken *in situ* and on deck
- Tissue preserved for DNA extraction:
  - DMSO buffer
  - 95% Ethanol
  - FTA cards
- Voucher specimens in ethanol

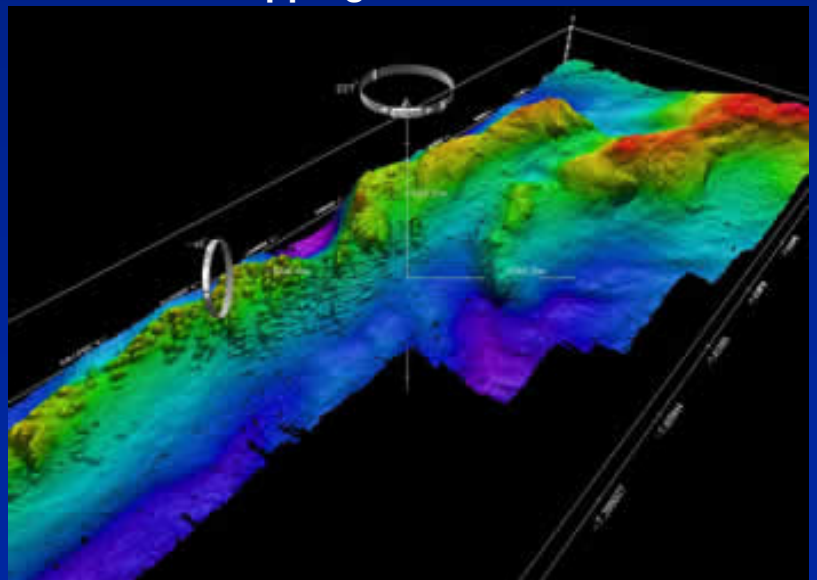
Northeast Atlantic Samples

- Rockall Banks off Scotland
- Mingulay Reef, Scotland – S. Hebrides

R/V Pelagia cruises
June–July 2006
S. Ross, A. Davies
Dredge and Boxcore

Dredge sample, Rockall Banks

3-D view of Mingulay ridge feature, multibeam mapping



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Microsatellite DNA Markers

Simple sequences, tandemly repeated

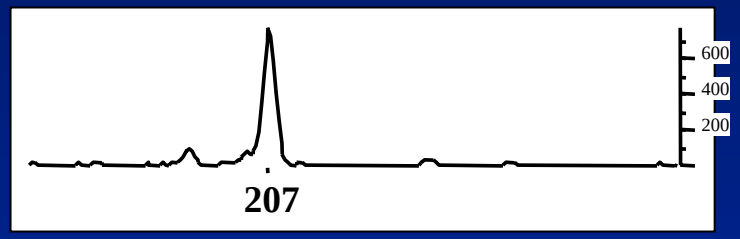
Examples: GA, ATT,ATC, GATC, GATA

Variation measured in base pairs (i.e., numbers of repeats)

Flanking region **Flanking region**

CTAGCTAG GATAGATAGATA TTGTCA

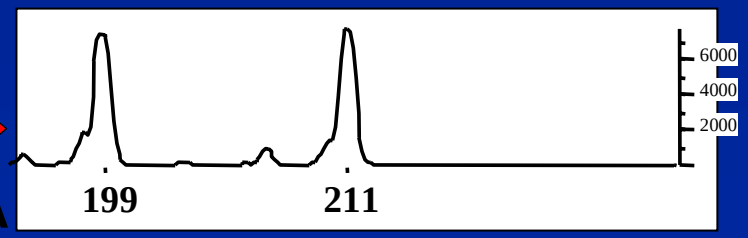
CTAGCTAG GATAGATAGATA TTGTCA



Homozygote

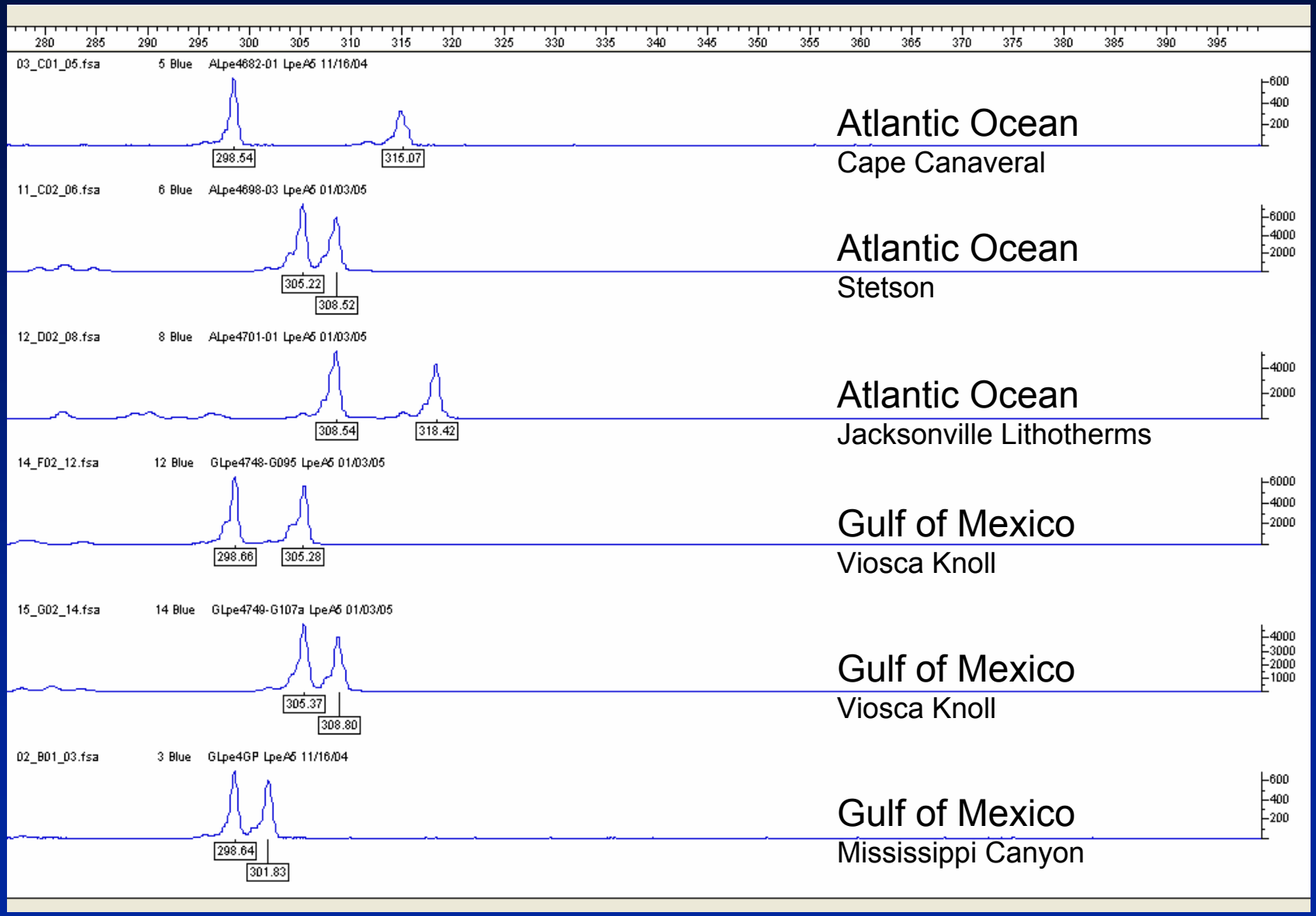
CTAGCTAG GATA TTGTCA

CTAGCTAG GATAGATAGATAGATA TTGTCA

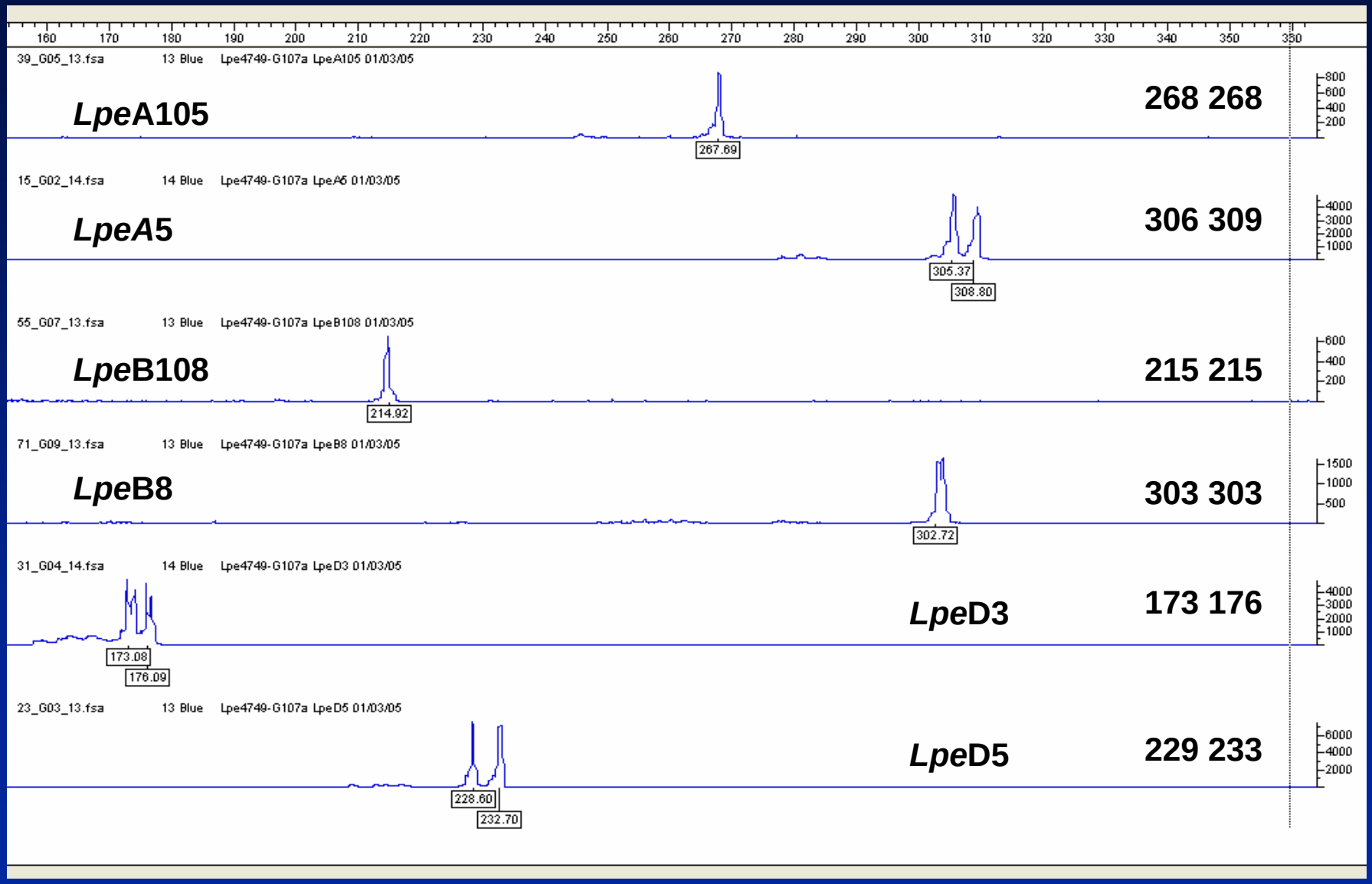


Heterozygote

Lophelia Genotypes at Marker *Lpe*A5



Multi-locus Genotype for One *Lophelia* Individual



Characteristics of *Lophelia* Markers

Name	Repeat	No. Alleles
LpeA5	AAC	11
LpeC44	TAGA	39
LpeC52	TAGA	23
LpeC61	TAGA	41
LpeC120	GATA	30
LpeC131	GATA	12
LpeC142	GATA	25
LpeC151	GATA	13
LpeD3	TGAC	53
Total		247
Avg. alleles/locus		27.4

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Genetic Characteristics of *Lophelia*

Population	N	Unique genotypes	# Clones
VK826 S	25	25	0
VK826 NE	16	12	4
VK826 NW	8	8	0
VK862	23	19	4
W Gulf	13	10	3
CLO N	15	11	4
CLO S	15	14	1
STS N	15	15	0
STS S	16	16	0
JAX	24	22	2
MTR	8	8	0
RB	6	6	0
MNG	6	6	0
		P_{ID}=2.5 X 10^{-5}	18

Avg. = 9%

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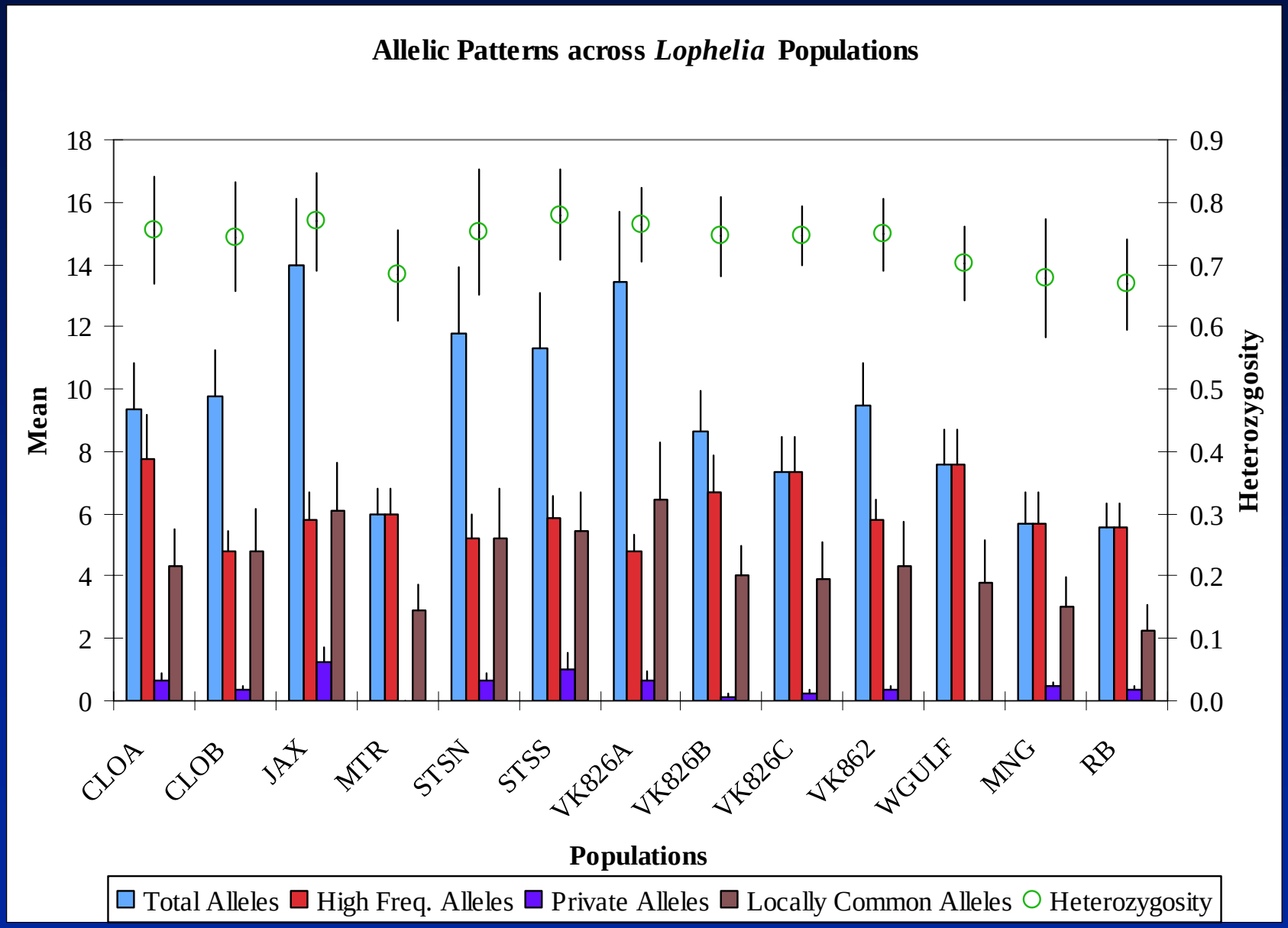
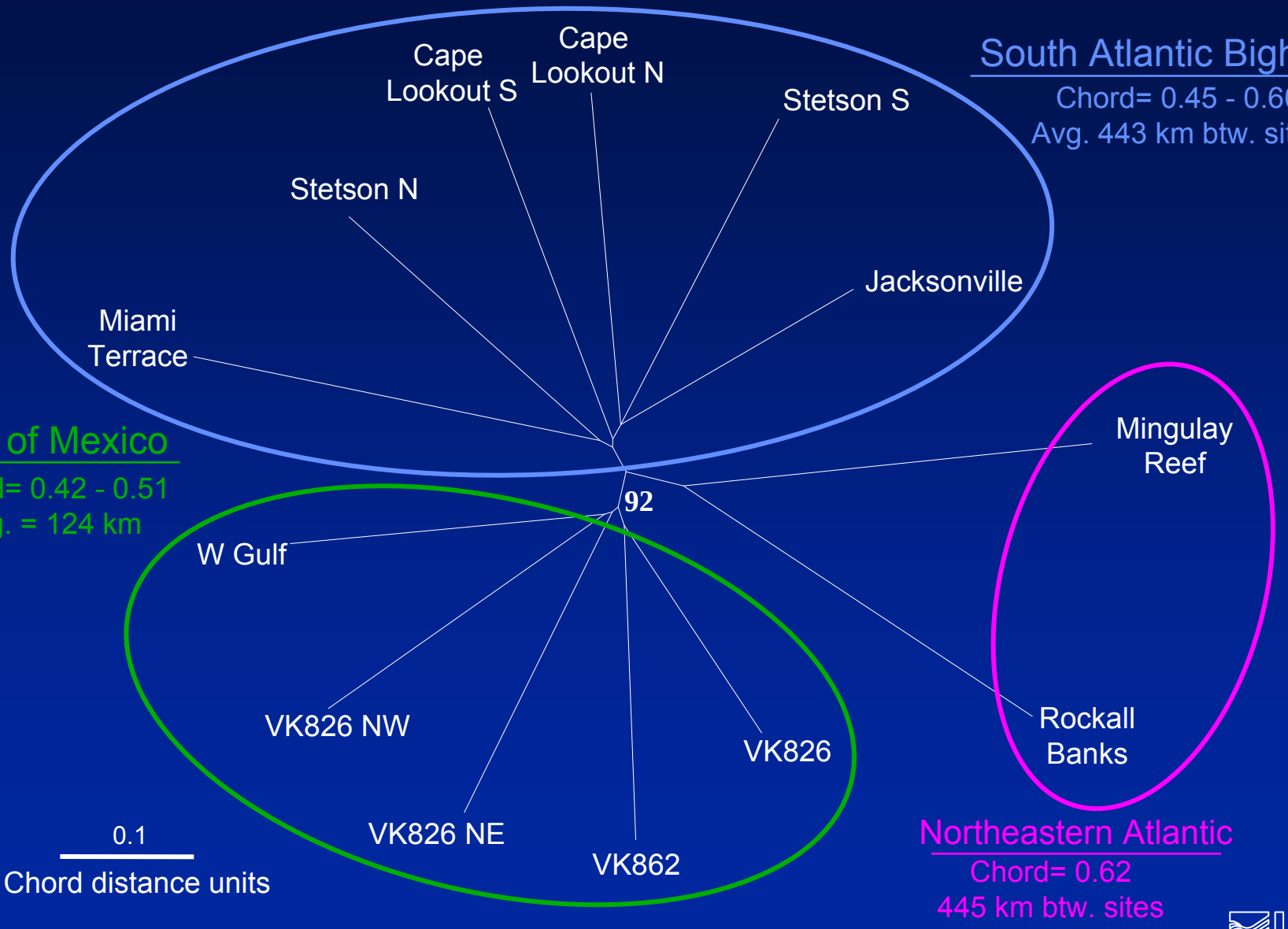
Genetic Characteristics of *Lophelia*



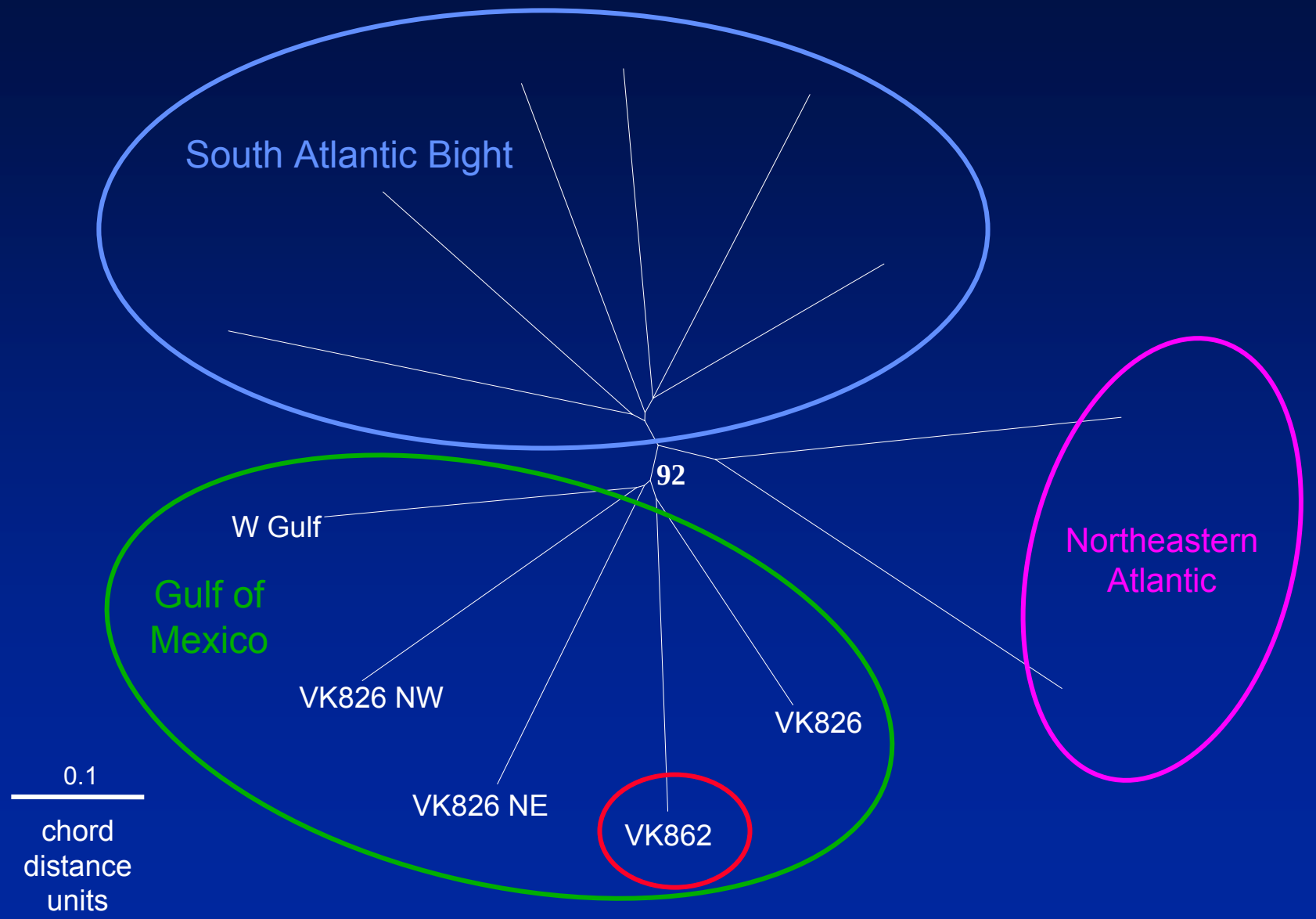
Measures of Population Structure

- ‘Private’ alleles = unique to population
- Differences in allele frequencies
- Genetic distance (chord) – degree of shared heredity between pairs of populations
- F_{ST}, AMOVA: Allocation of genetic variation among vs. within populations

Evolutionary Relationships among *Lophelia* Populations

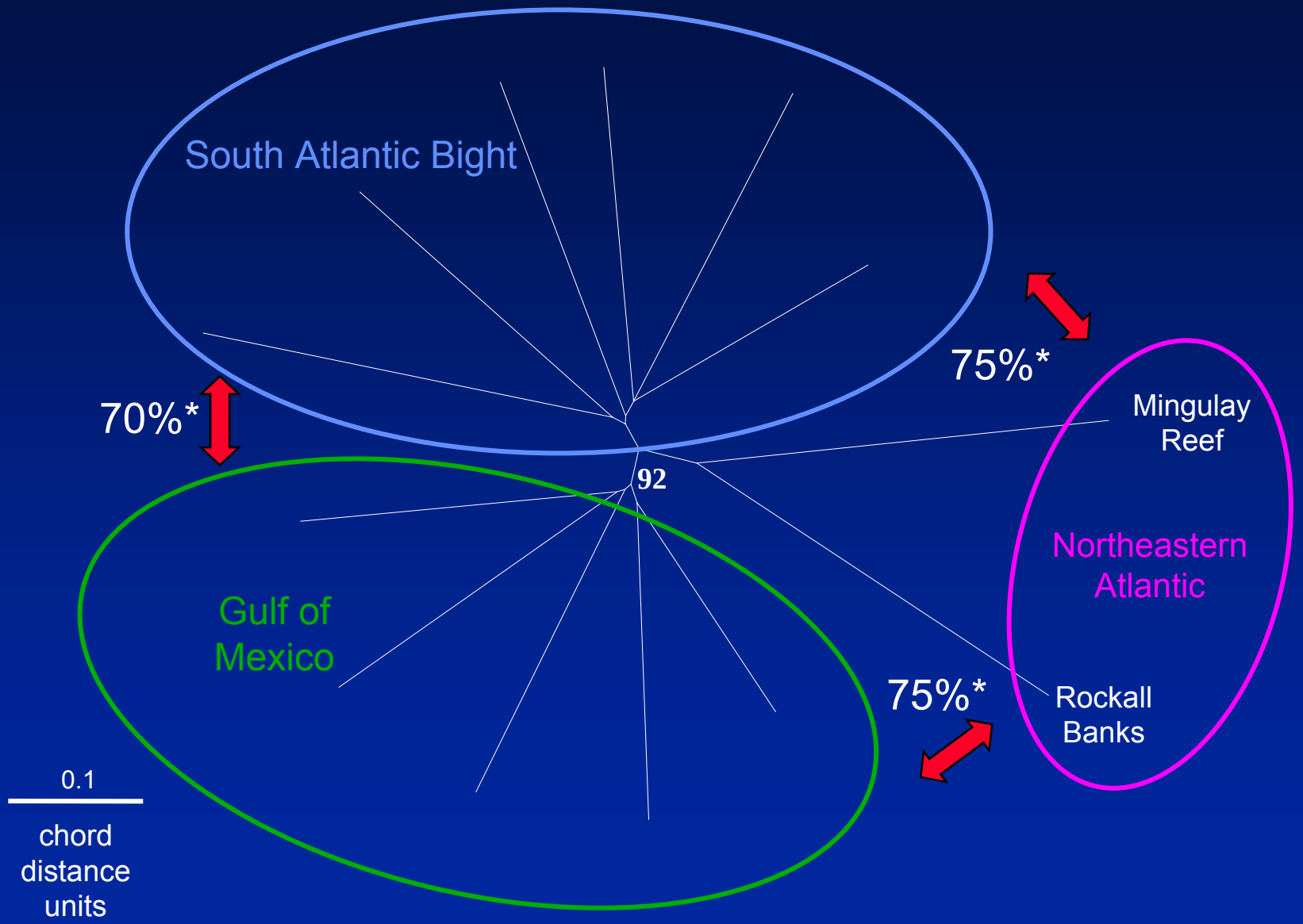


Allele Freq. Differences among *Lophelia* Populations



Allele Freq. Differences among *Lophelia* Populations

Allele Freq. Differences among *Lophelia* Populations



Gulf *Lophelia* F_{ST} and R_{ST} Estimates

F_{ST}

R_{ST} Site	VK826 S	VK826 NE	VK826 NW	VK862	W Gulf
VK826 S		0.029*	0.011	0.036*	0.009
VK826 NE	0.072		0.046*	0.048*	0.033*
VK826 NW	0.0	0.077		0.033*	0.0
VK862	0.011	0.094	0.065		0.056*
W Gulf	0.048	0.078	0.049	0.139	

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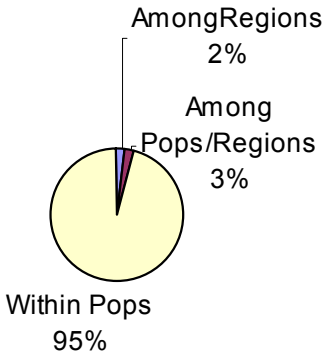
AMOVA Results

3 Regions

Percentages of Molecular Variance



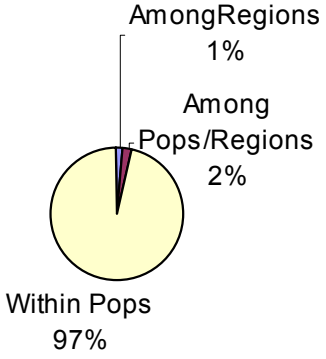
F_{ST} = 0.047

R_{ST} = 0.080

P=0.0001

Gulf vs. SAB

Percentages of Molecular Variance

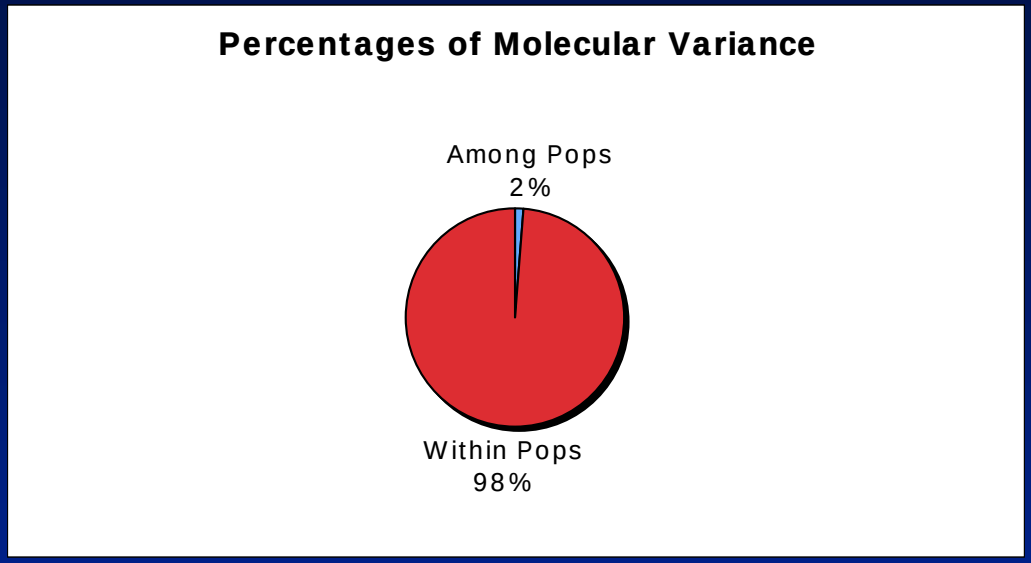


F_{ST} = 0.038

R_{ST} = 0.067

P=0.0001

AMOVA Results



Gulf

F_{ST} = 0.015
R_{ST} = 0.013
P=0.001

SAB

F_{ST} = 0.016
R_{ST} = 0.034
P=0.001

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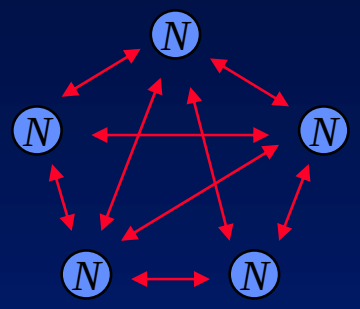
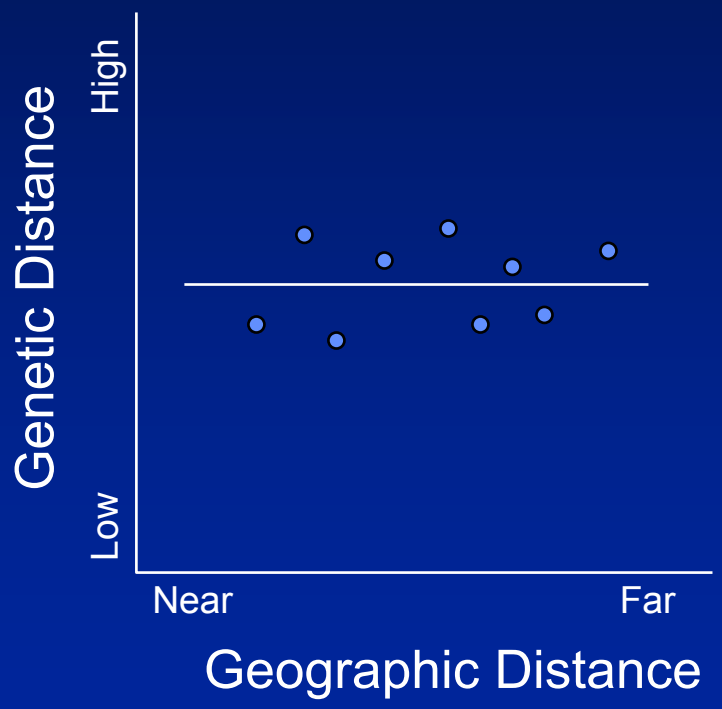
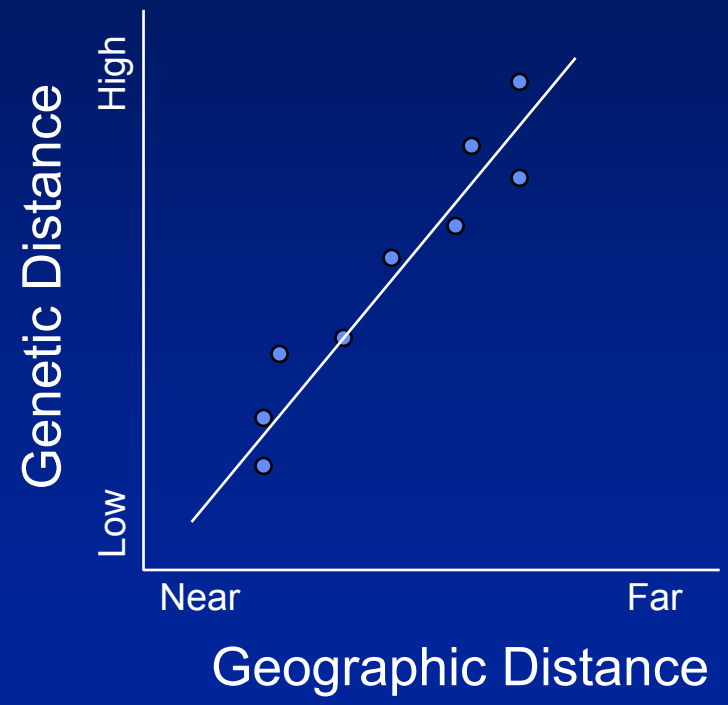
Mechanisms Underlying Patterns?

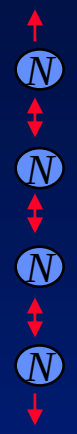


Island Model
(Wright 1969)



Stepping Stone Model
(Slatkin 1987)





"Isolation By Distance"

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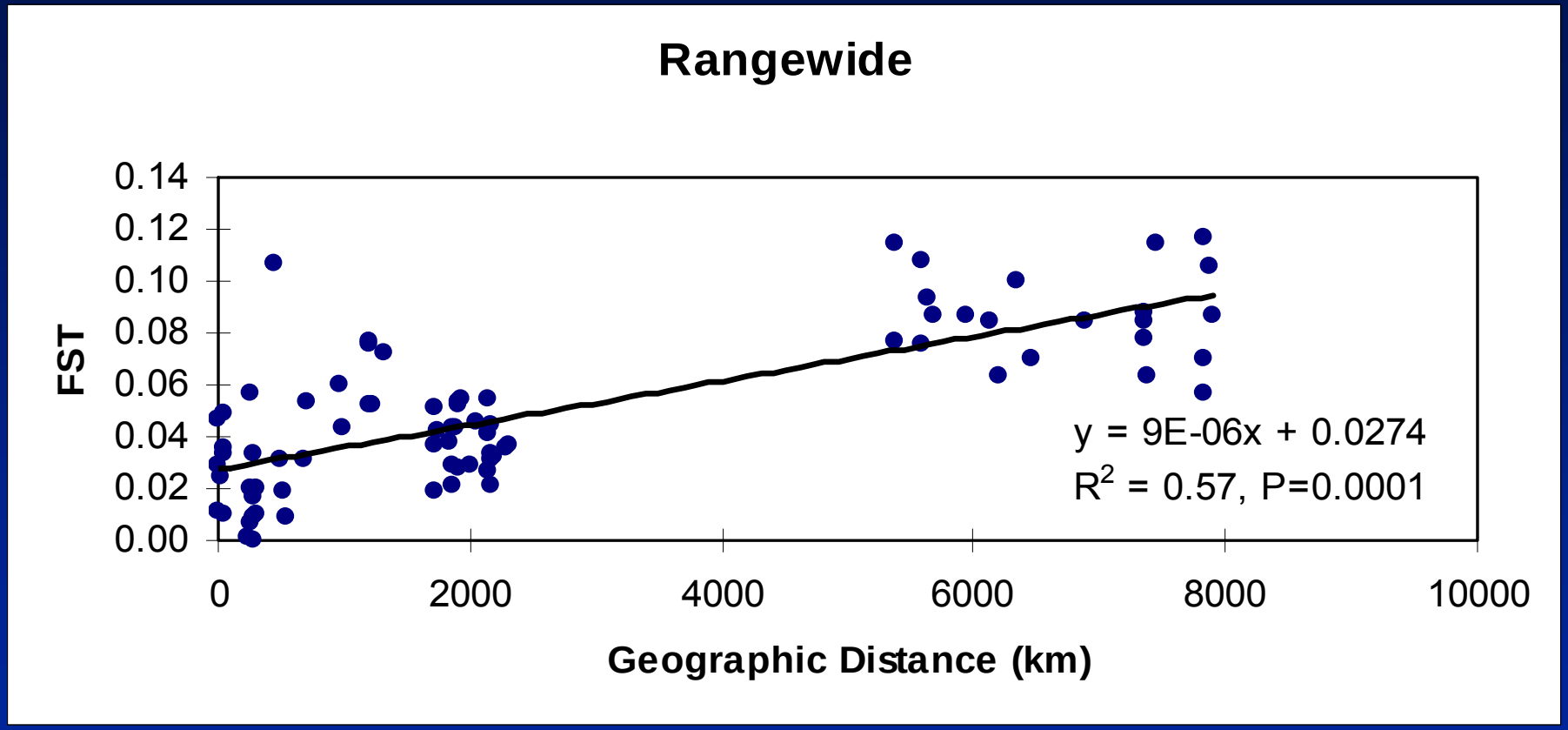
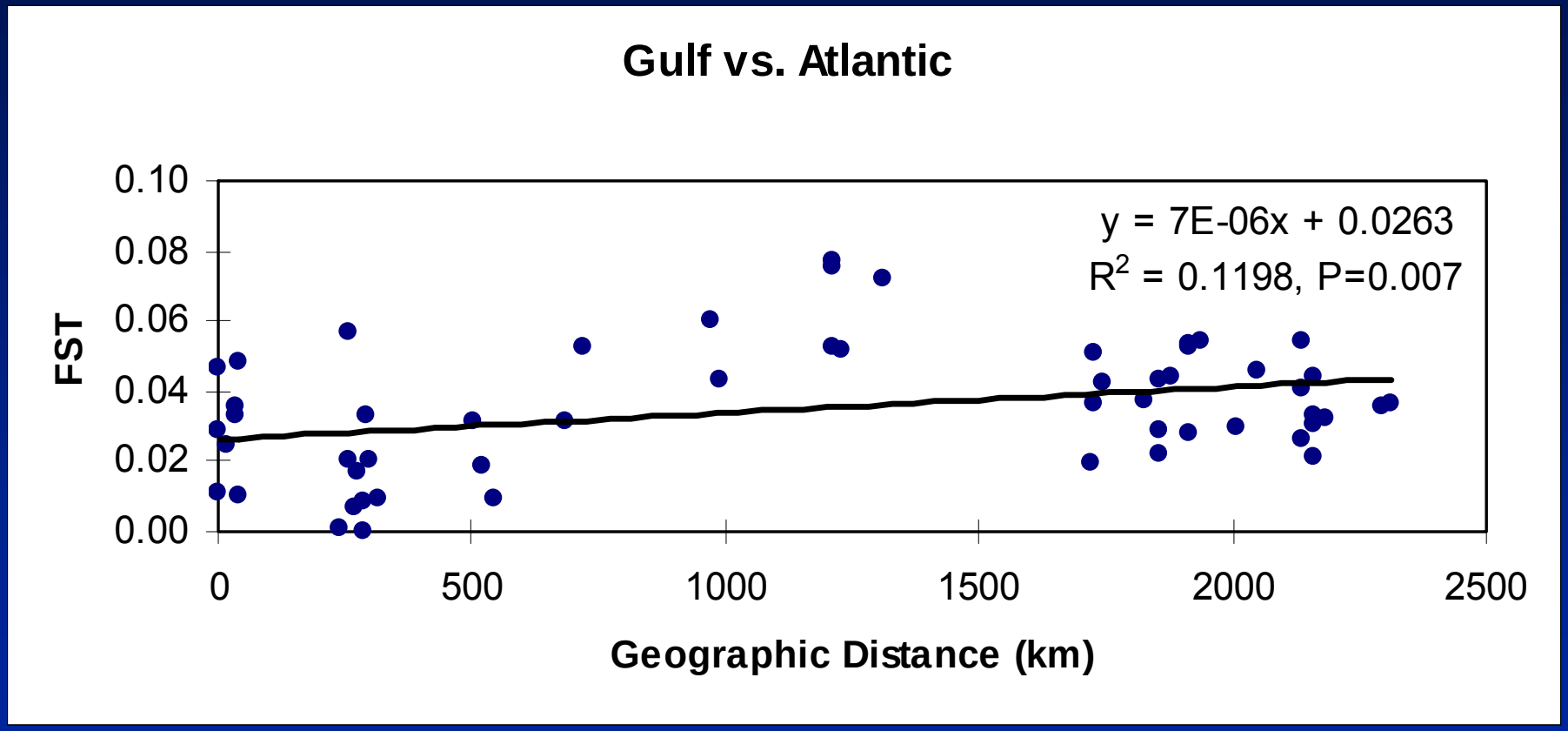
Isolation by Distance – Rangewide



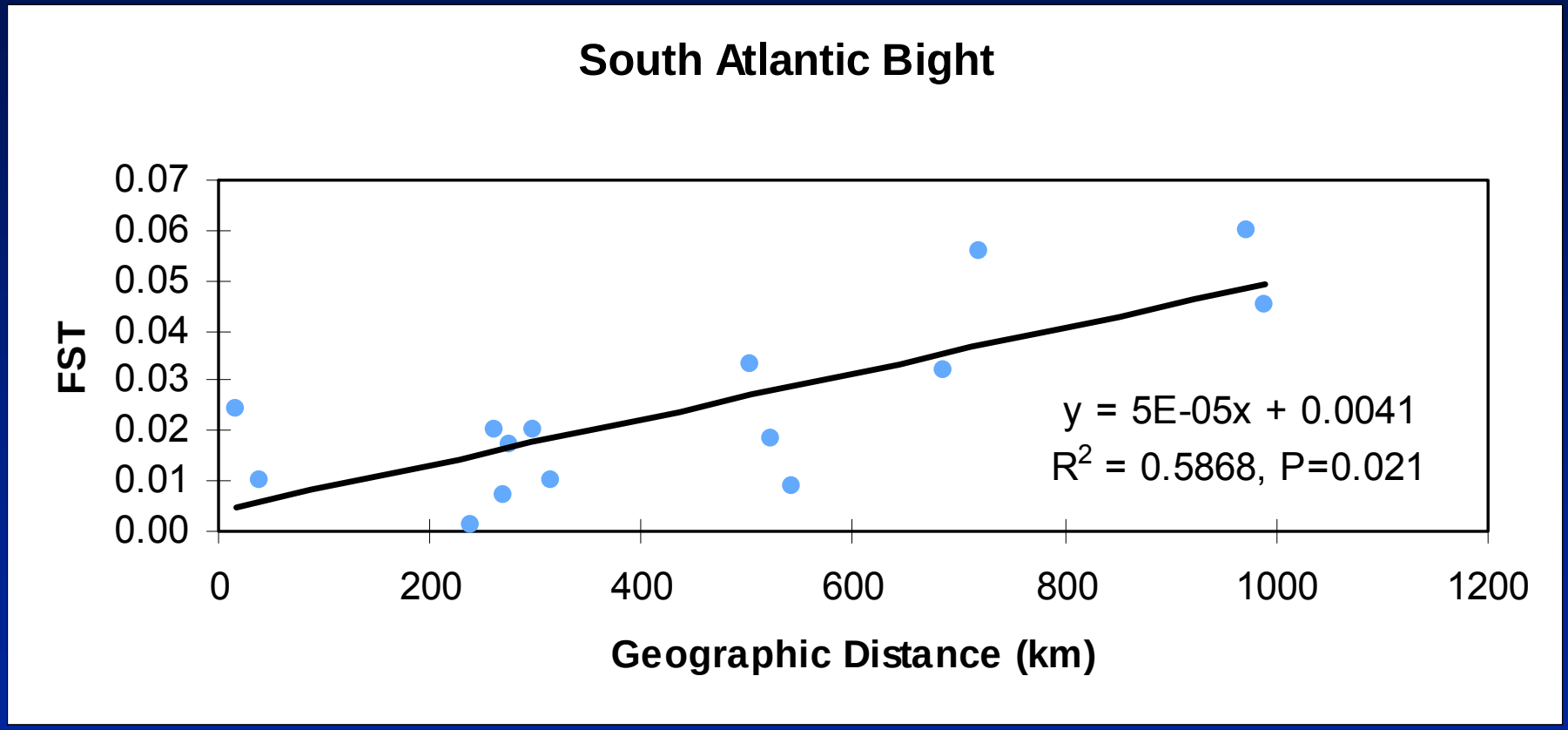
Note: Significant when genetic distance=chord

Isolation by Distance – Gulf vs. SAB



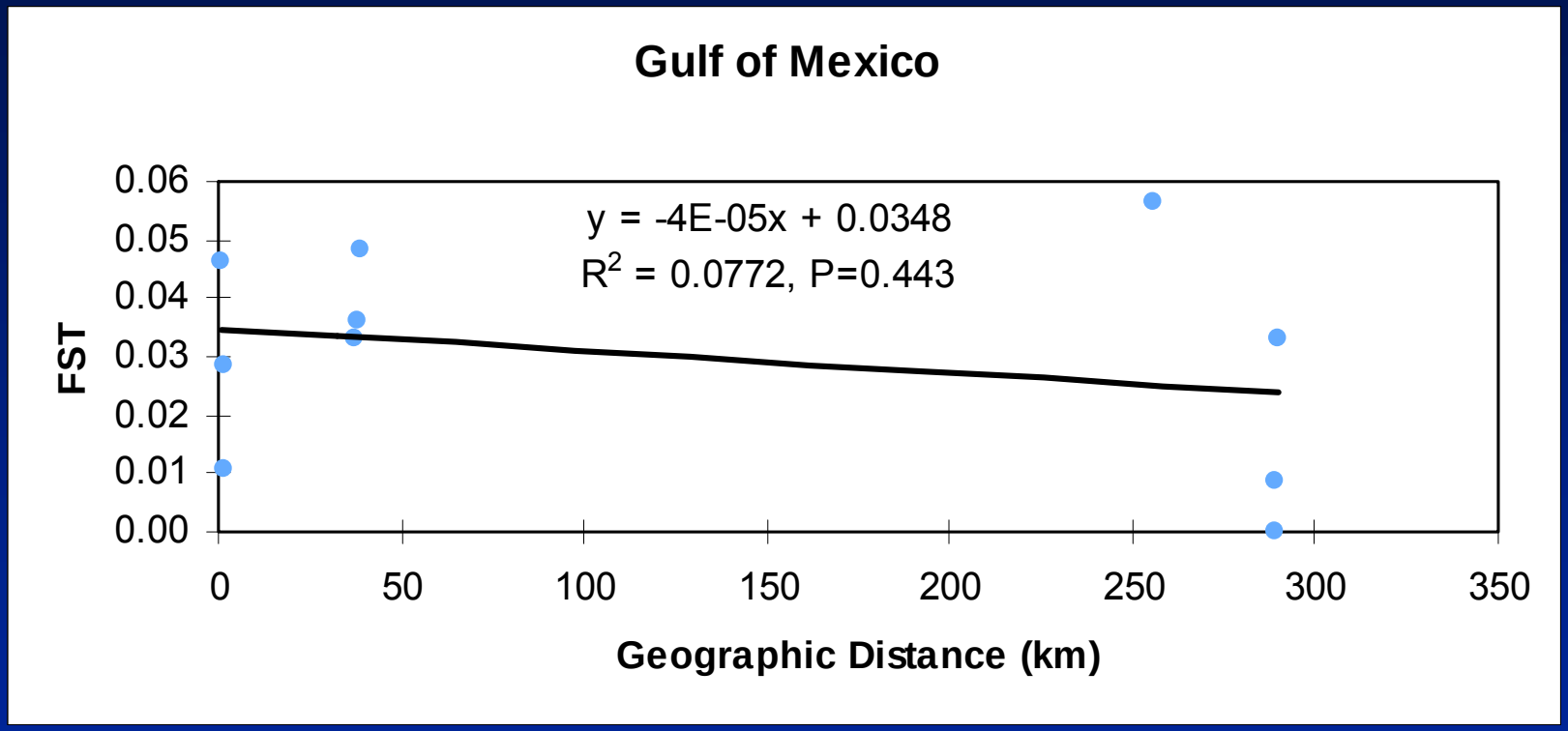
Note: Significant when genetic distance=chord

Isolation by Distance – SAB



Note: NOT significant when genetic distance=chord

Isolation by Distance – Gulf



Note: NOT significant when genetic distance=chord

Preliminary Conclusions

- Each *Lophelia* population – substantial genetic diversity
- Low levels of clonal reproduction detected – varies with site
- Significant genetic structuring (populations ≠ panmictic)
  - Private alleles
  - High genetic (chord) distances between all pops
  - AMOVAs significant
  - Significant differences in allele frequencies, esp. between regions
- YET … Some cohesion between populations regionally
  - SOME low F_{ST}
  - Geographic pattern complex
- Gene flow: Low to moderate within regions, but generally localized

Preliminary Conclusions II

- Weak Isolation by Distance at large spatial scales (>500 km)
  - Suggestive of maximum dispersal distance?
  - Hydrodynamic processes – inhibit migration?
- Phylogeographic breaks
  - Gulf and SAB
  - Trans-Atlantic
- On-going lab work
  - More genotyping
  - More microsatellite markers

Implications for *Lophelia* Conservation

- Good news: a lot of genetic diversity in *Lophelia*
  - potential for adaptive evolution
- Gulf *Lophelia:* areas especially worthy of protection
  - VK 826 = substantial and highly complex genetic variation
  - VK 862 = most isolated (genetically unique
- ‘Other’ news: lots of genetic structuring detected
  - ALL populations unique, relationships complex
  - Loss of ANY population = substantial loss of genetic diversity
- Most effective management of *Lophelia:* REGIONAL reserve networks

Recommendations

- Additional Sampling
  - Missing ‘piece of the puzzle’ = West Florida Shelf
  - Sampling along transects
    - Spatial autocorrelation: fine scale limits of connectivity
  - Additional samples from Western Gulf, Gulf Penn
- Compare *Lophelia* genetic structure with:
  - *Lophelia* morphologies
  - Microbes
  - Patterns of reproduction
  - Models of local currents

Sincere Thanks!

- Funding
  - USGS Outer Continental Shelf Ecosystem Program and sponsored by Minerals Management Service
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- Logistics
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  - Continental Shelf Associates *Lophelia* scientists: S. Viada, C. Fisher, E. Cordes, S. Brooke, W. Schroeder
  - S. Marion, B. Lubinski, C. Callahan, M. Eackles, J. Switzer, A. Quattrini, M. Partyka, R. Toonen, L. Baird, A. Howard
- Samples: J. Murray Roberts, A. Davies, E. Cordes, C. Fisher, W. Schroeder

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