Genetic Discontinuity Among Regional Populations of *Lophelia pertusa* in the North Atlantic Ocean

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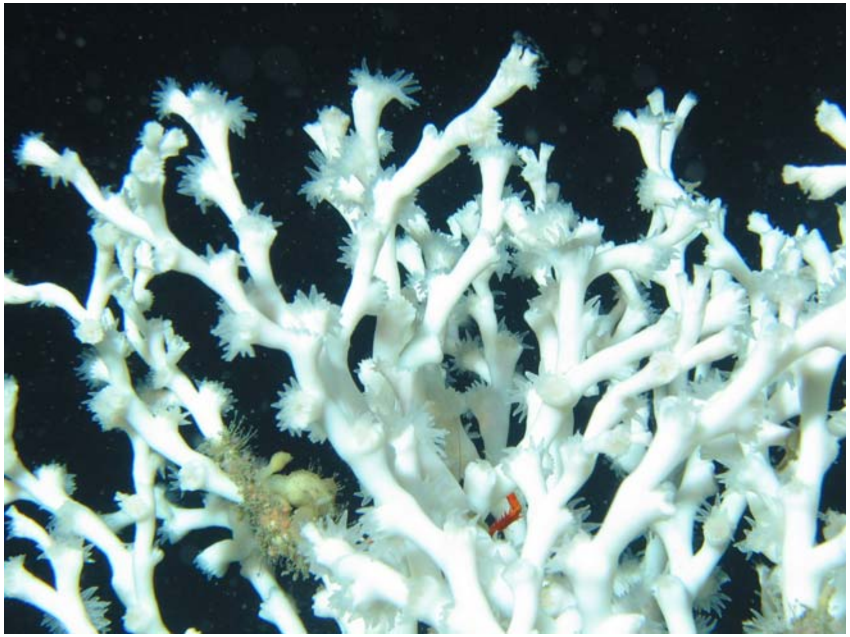
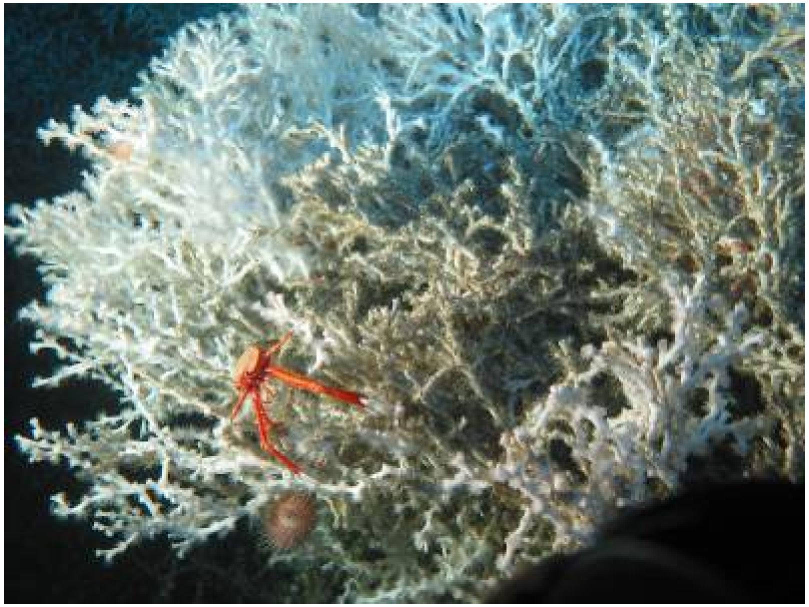
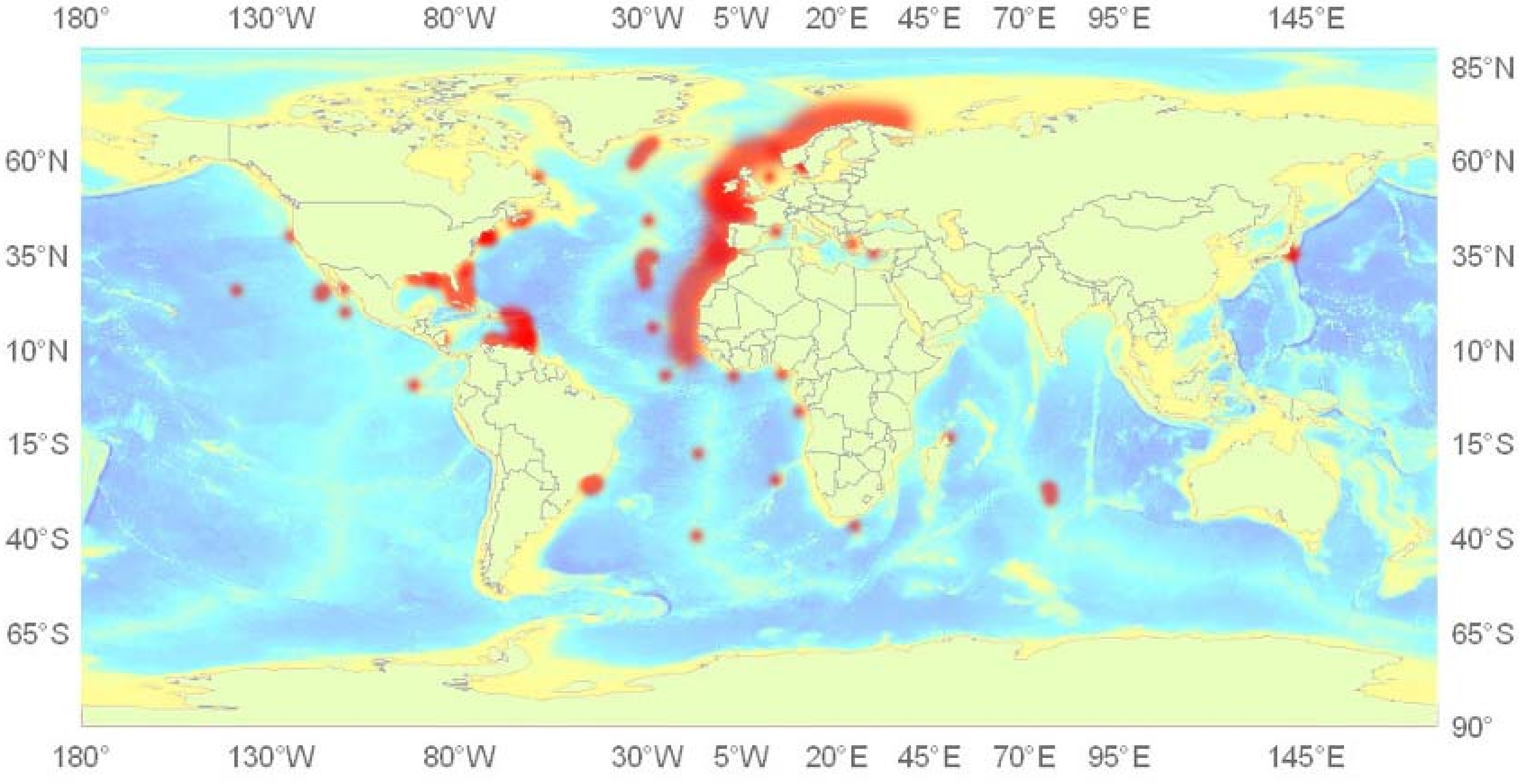
Lophelia pertusa (Linnaeus 1758)

- Deep-water scleractinian coral
- Monotypic genus
- Framework-building: habitat for ecologically diverse megafauna





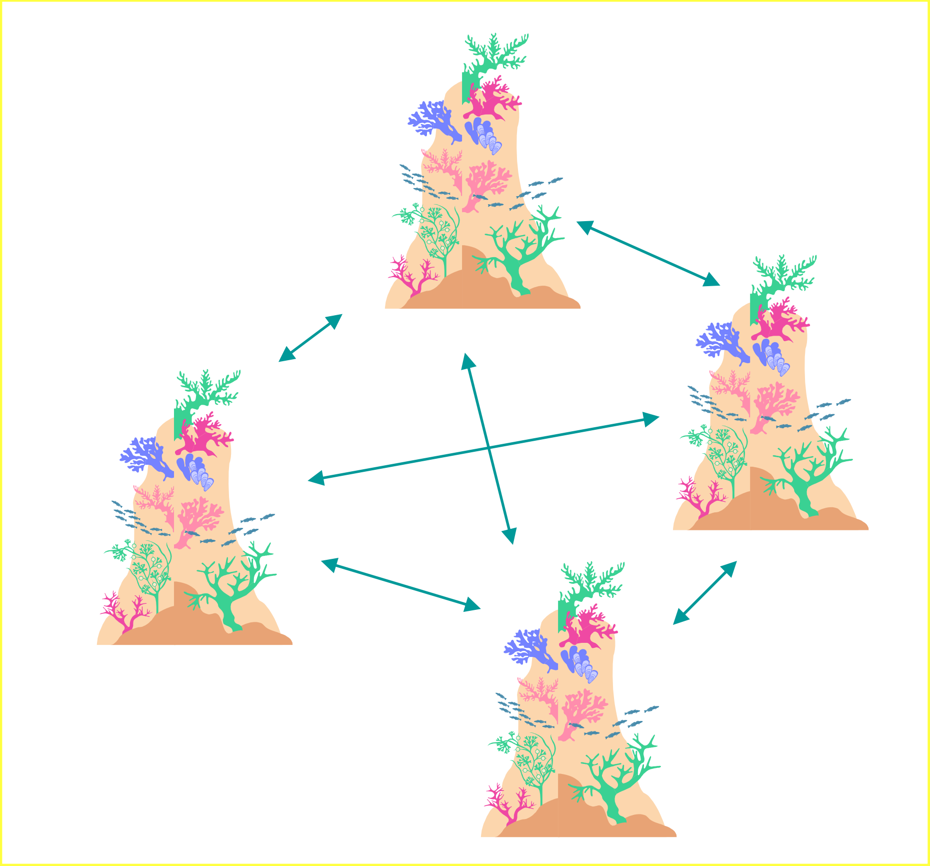
Lophelia pertusa Distribution



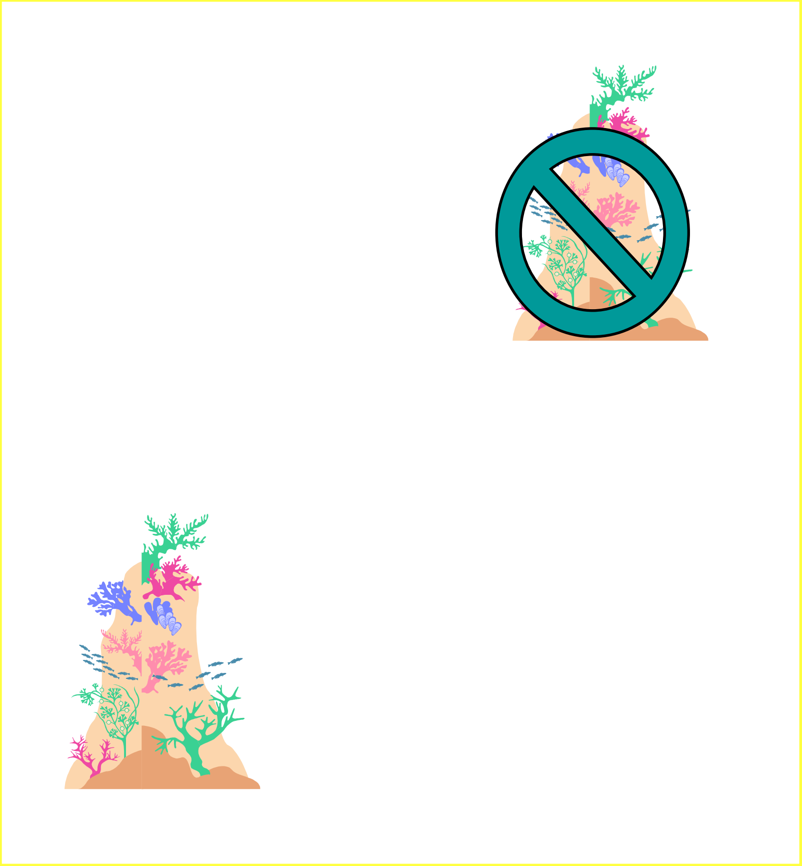
http://www.lophelia.org/images/jpeg/map_lopheliapertusa.jpg **after Freiwald et al. 2004**

Protection of Deep Reefs

- Resilience to disturbance depends on supply of new recruits



- ‘Connected’ reefs = higher resilience



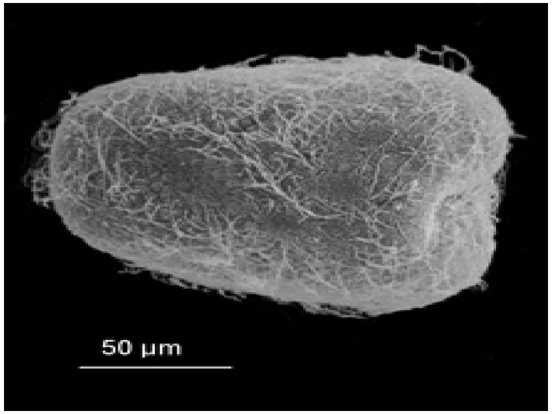
- Isolated reefs = less likely to recover

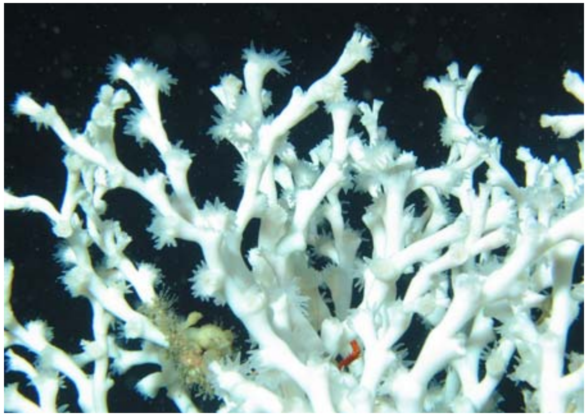
Protection of Deep Reefs

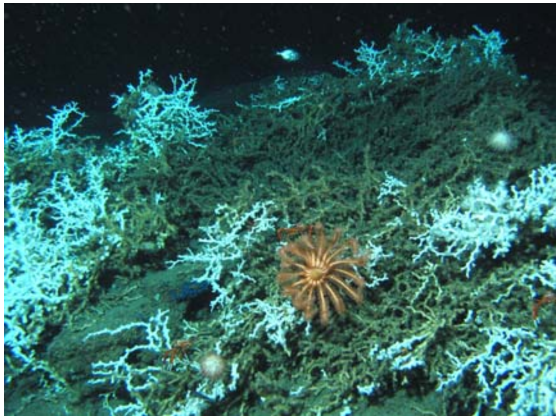
Realistic models of connectivity necessary for effective management of deep reefs

- <u>Sources</u> of larvae need protecting, whether local or external
- Difficult to directly follow larvae

Indirect estimates of connectivity via population genetic analyses



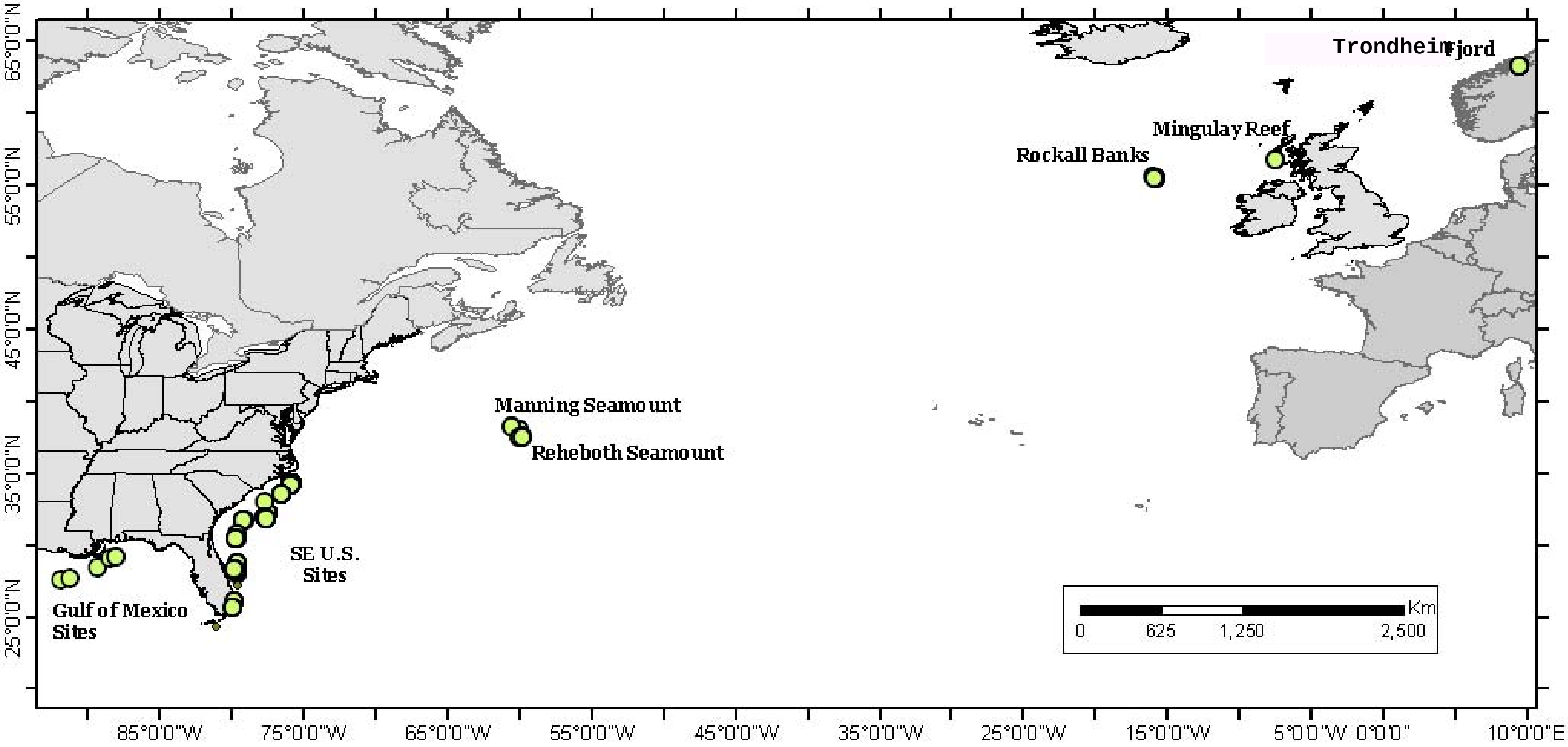




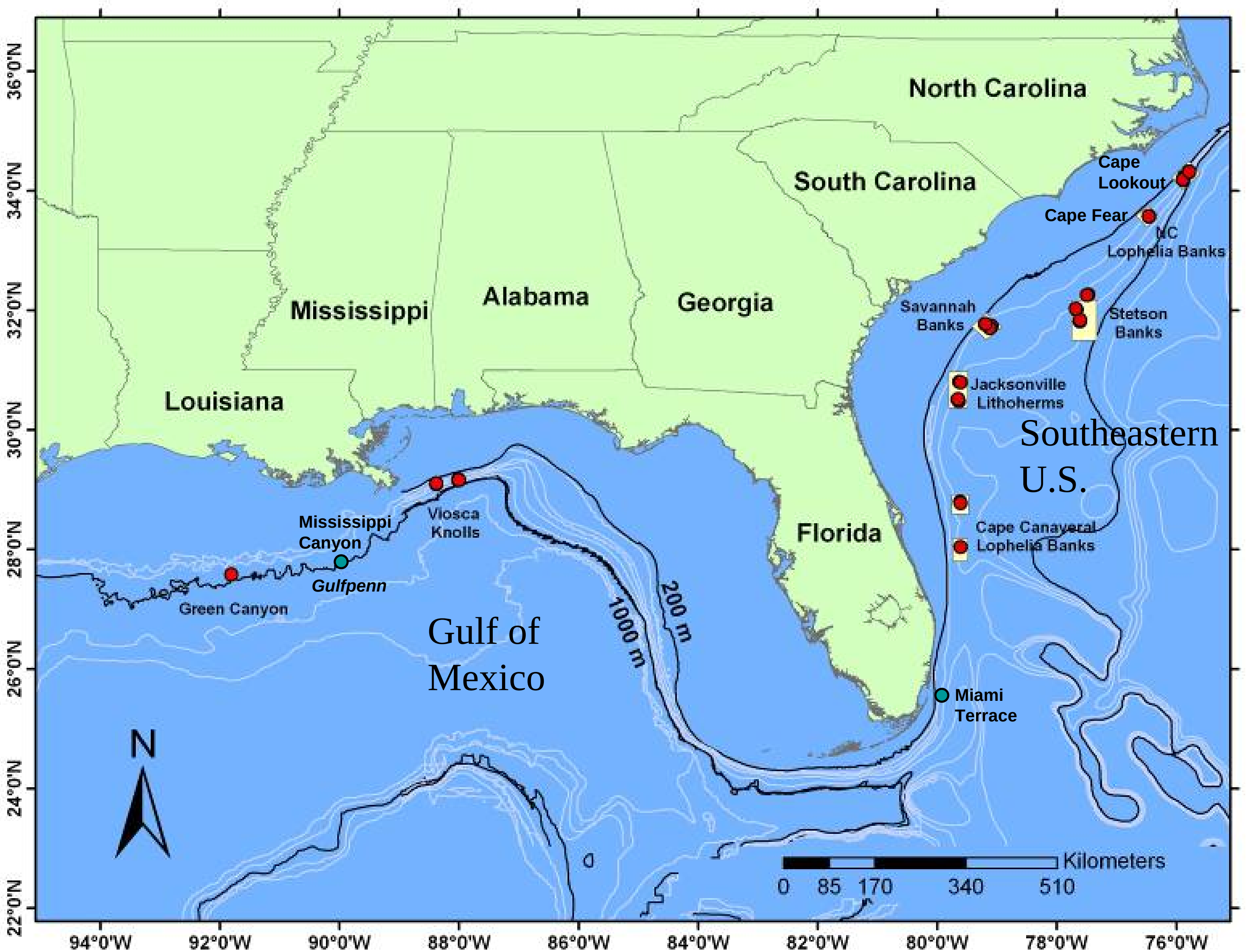
Objectives

- Use suite of *Lophelia pertusa* microsatellite markers to quantify genetic diversity
- Assess genetic connectivity in *Lophelia pertusa* across:
  - local (several km) to vast (>8000km) spatial scales
  - habitat types (continental slope, fjords, seamounts)
  - depths (140–1600 m)

North Atlantic *Lophelia* Collections

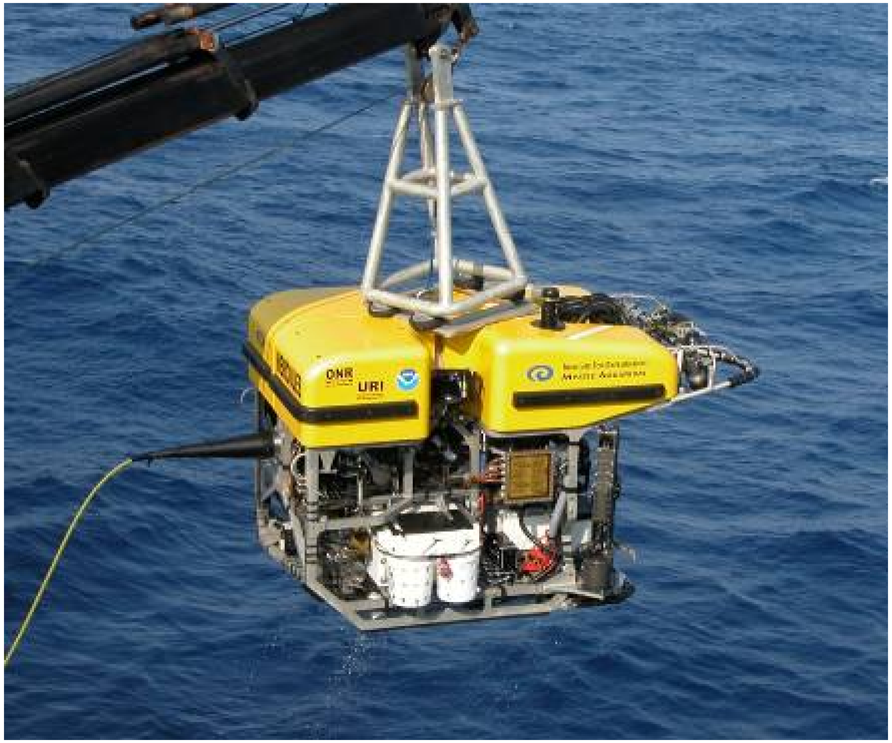


Western North Atlantic *Lophelia* Collections



Lophelia Sample Collection

- Manned submersibles
  - Johnson-Sea-Link I & II: western North Atlantic
- Hercules ROV: New England seamounts
- Box cores, ROV, eastern North Atlantic



Characteristics of *Lophelia* Markers

(401 samples genotyped)

Name	Repeat	No. Alleles
*Lpe*A5	AAC	12
*Lpe*C44	GATA	57
*Lpe*C52	GATA	31
*Lpe*C61	GATA	43
*Lpe*C120	GATA	37
*Lpe*C142	GATA	35
*Lpe*C151	GATA	17
*Lpe*D3	TGAC	69
*Lpe*D5	TGAC	47
Total		348
Avg. alleles/locus		38.7

P_{ID}=4.3 X 10^{-5} → 15 % clones → 341 unique samples

Markers described in Morrison et al. 2008.

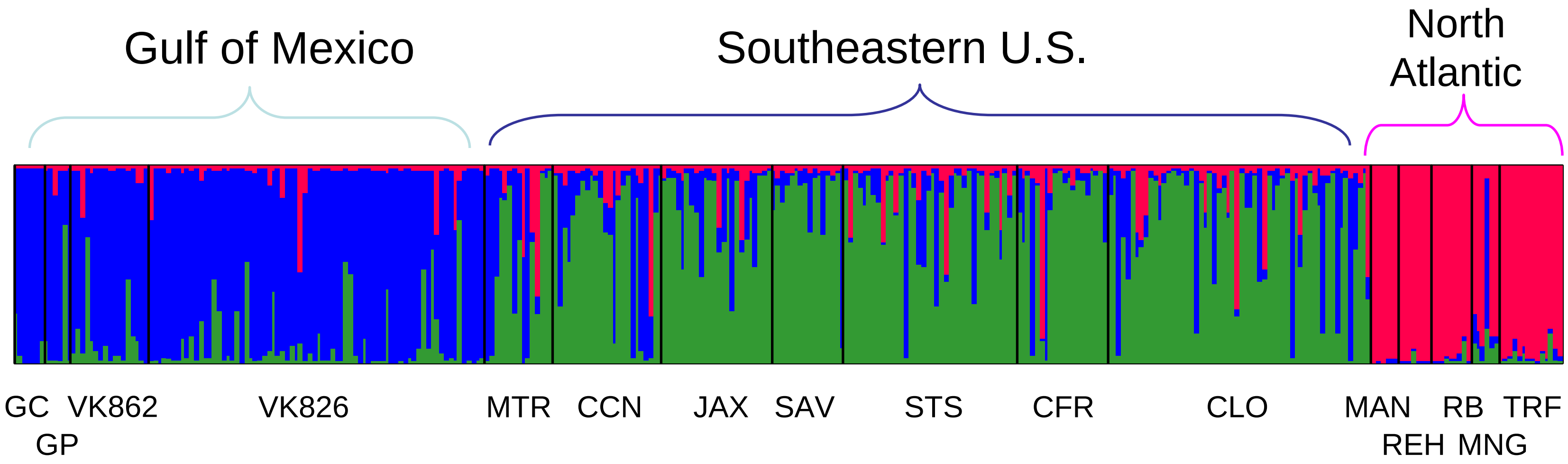
Measures of Population Structure

- ‘Populations’ defined a priori:
  - ‘Private’ alleles = unique to population
  - Genetic distance (chord) - degree of shared heredity between pairs of populations
  - *F*- and *R*-statistics, AMOVA: allocation of genetic variation among vs. within populations

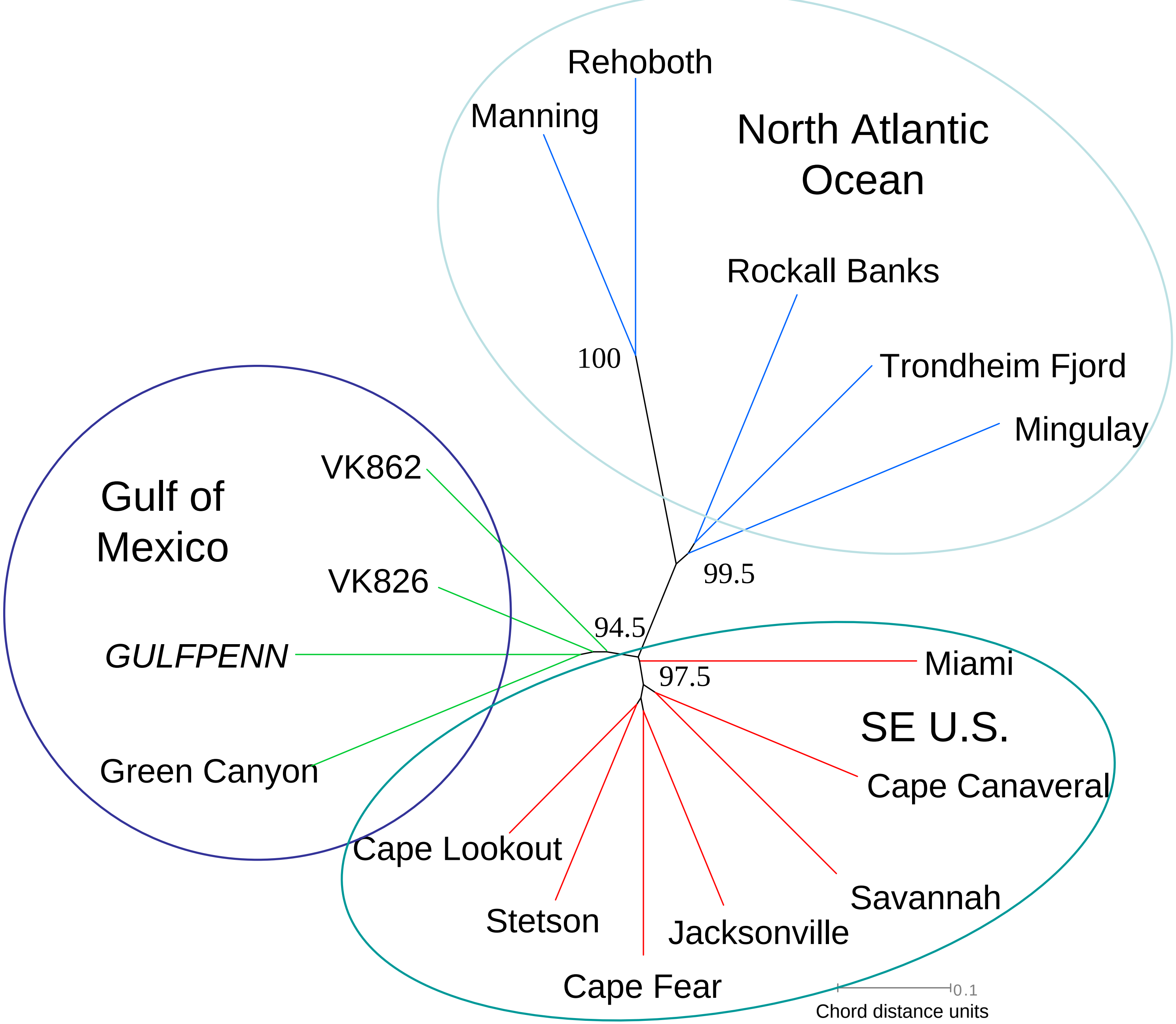
- Analysis ‘defines’ populations
  - Bayesian assignment of individuals to clusters (*K*)
    - STRUCTURE software (Pritchard et al. 2000)

Bayesian Clustering

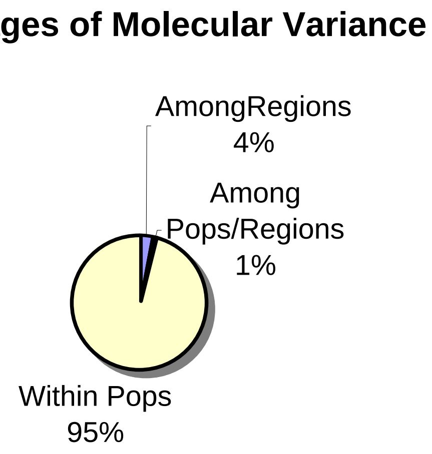
STRUCTURE, *K*=3



Evolutionary Relationships among *Lophelia* Localities

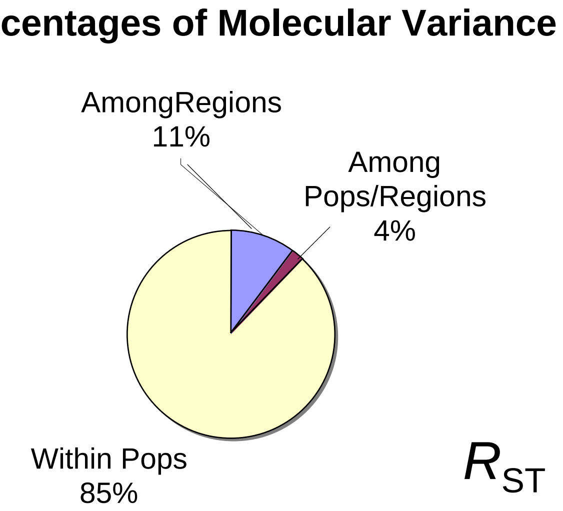


AMOVA Results: 3 Clusters


Percentages of Molecular Variance

$F_{ST} = 0.047$

$P < 0.0001$*


Percentages of Molecular Variance

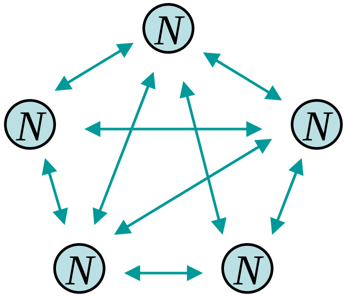
$R_{ST} = 0.153$

$P < 0.0001$*

AMOVA Results: Within Regions

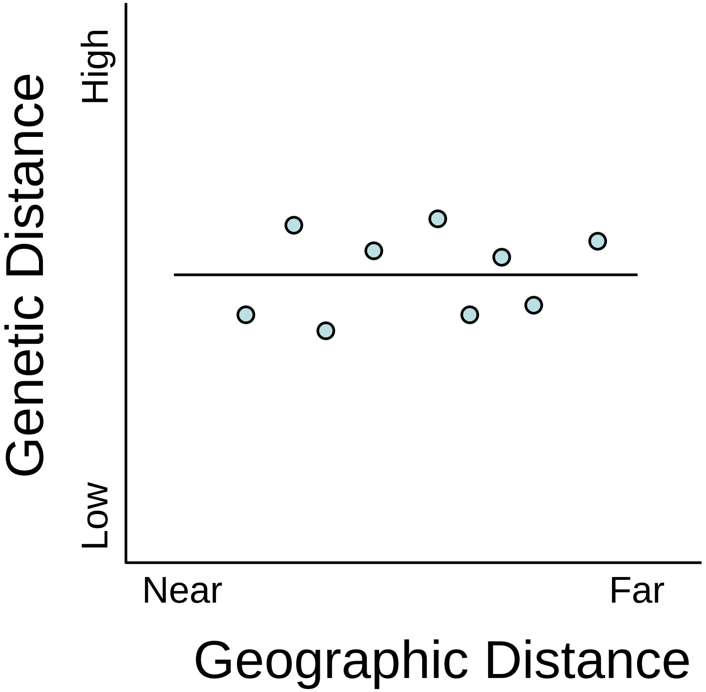
Cluster	F_{ST}	*P* value
North Atlantic	0.085	< 0.0001*
SE U.S.	0.006	< 0.015*
Gulf of Mexico	0.007	< 0.010*

Mechanisms underlying patterns?



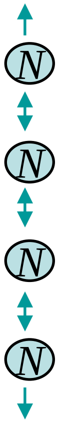
Island Model

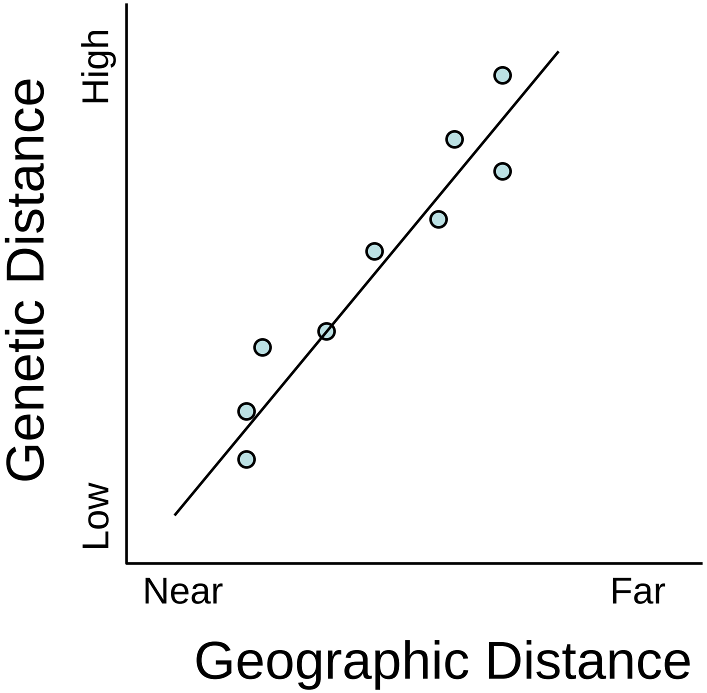
(Wright 1969)



Stepping Stone Model

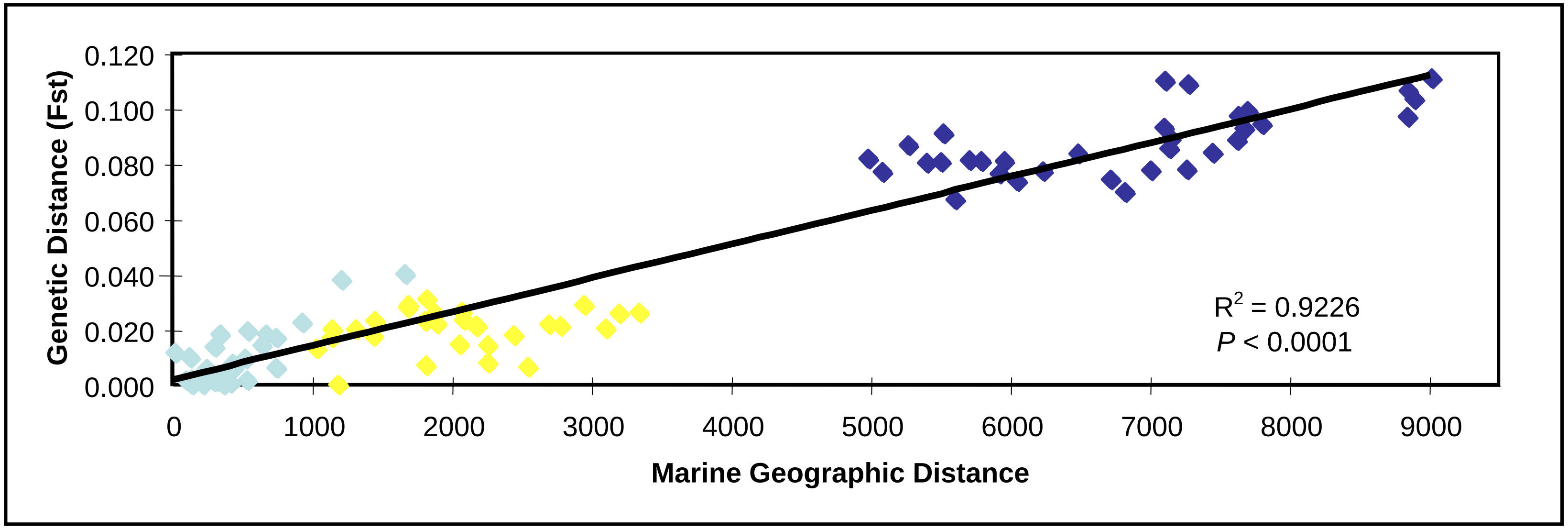
(Slatkin 1987)





“Isolation By Distance”

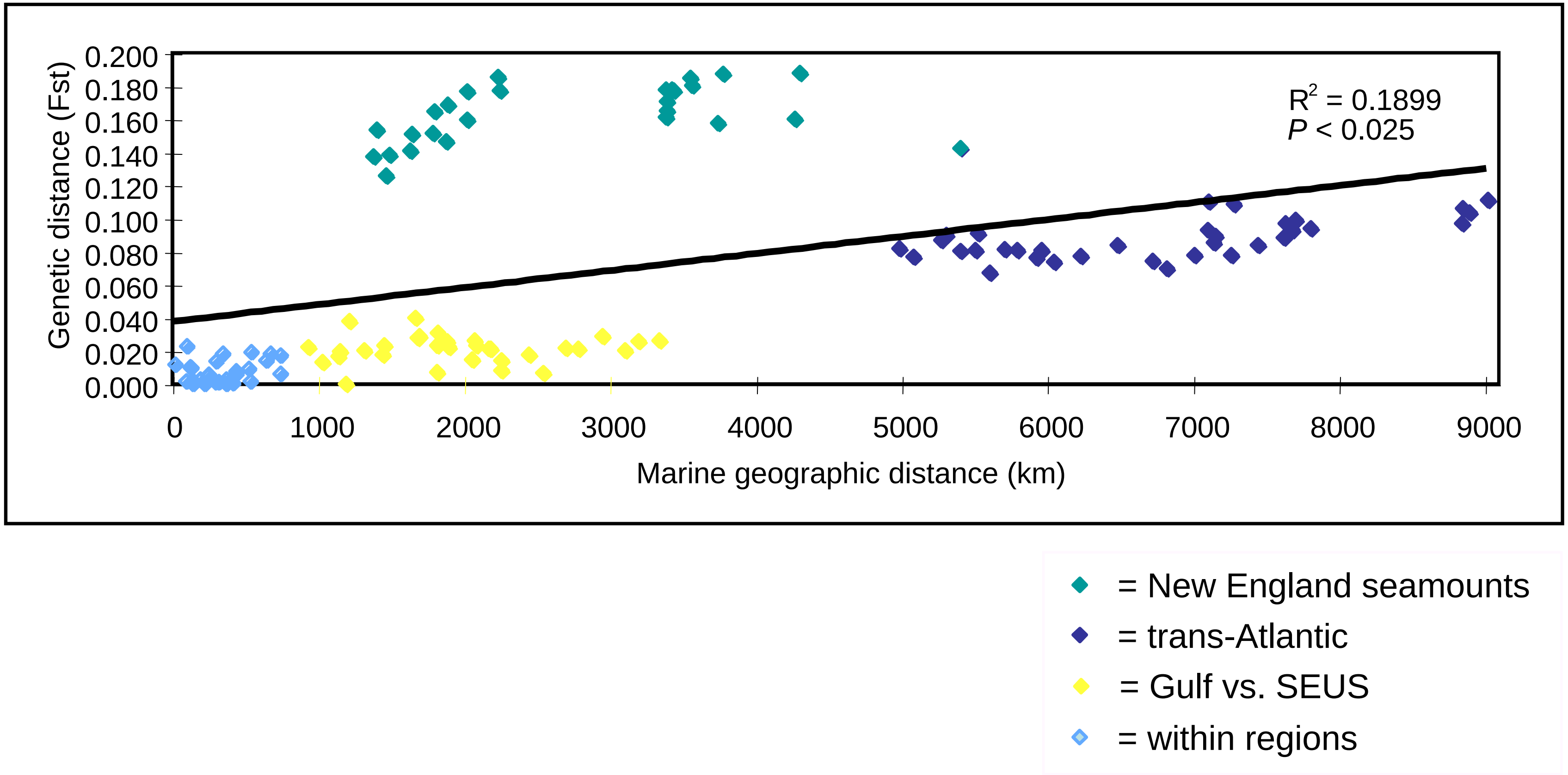
Mantel Test: Isolation by Distance



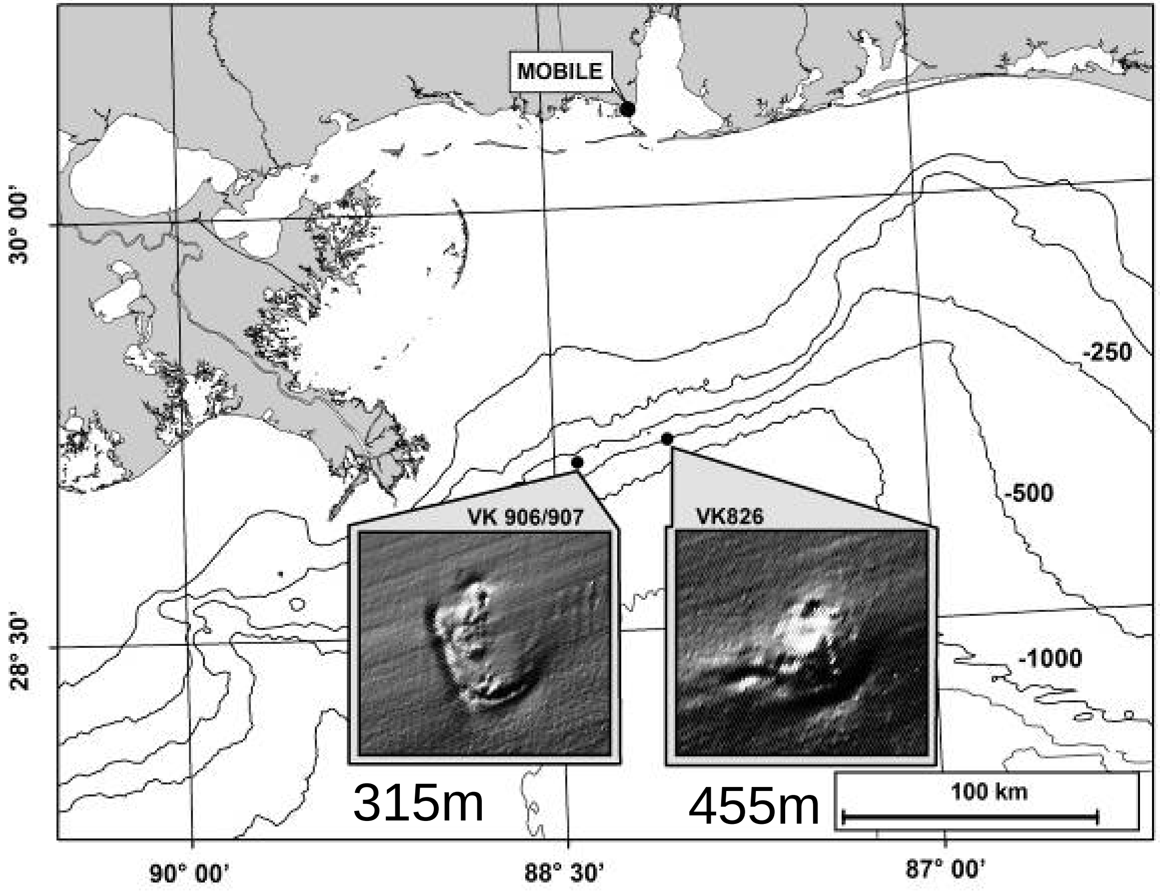
◆ = trans-Atlantic
◆ = Gulf vs. SEUS
◇ = within regions

<u>Within regions:</u>
Weak IBD pattern in North Atlantic and SEUS
No IBD in Gulf of Mexico

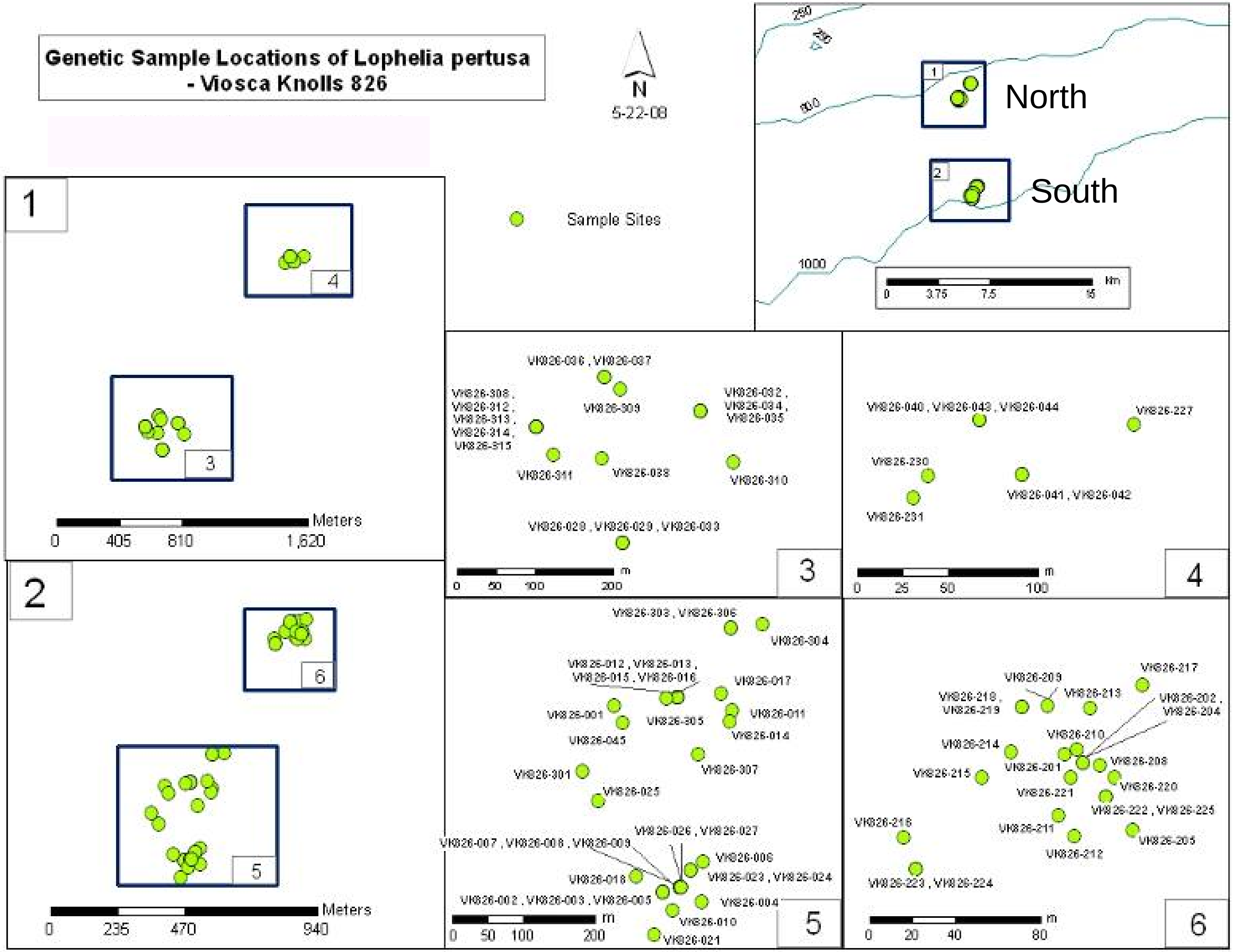
Mantel Test: Isolation by Distance



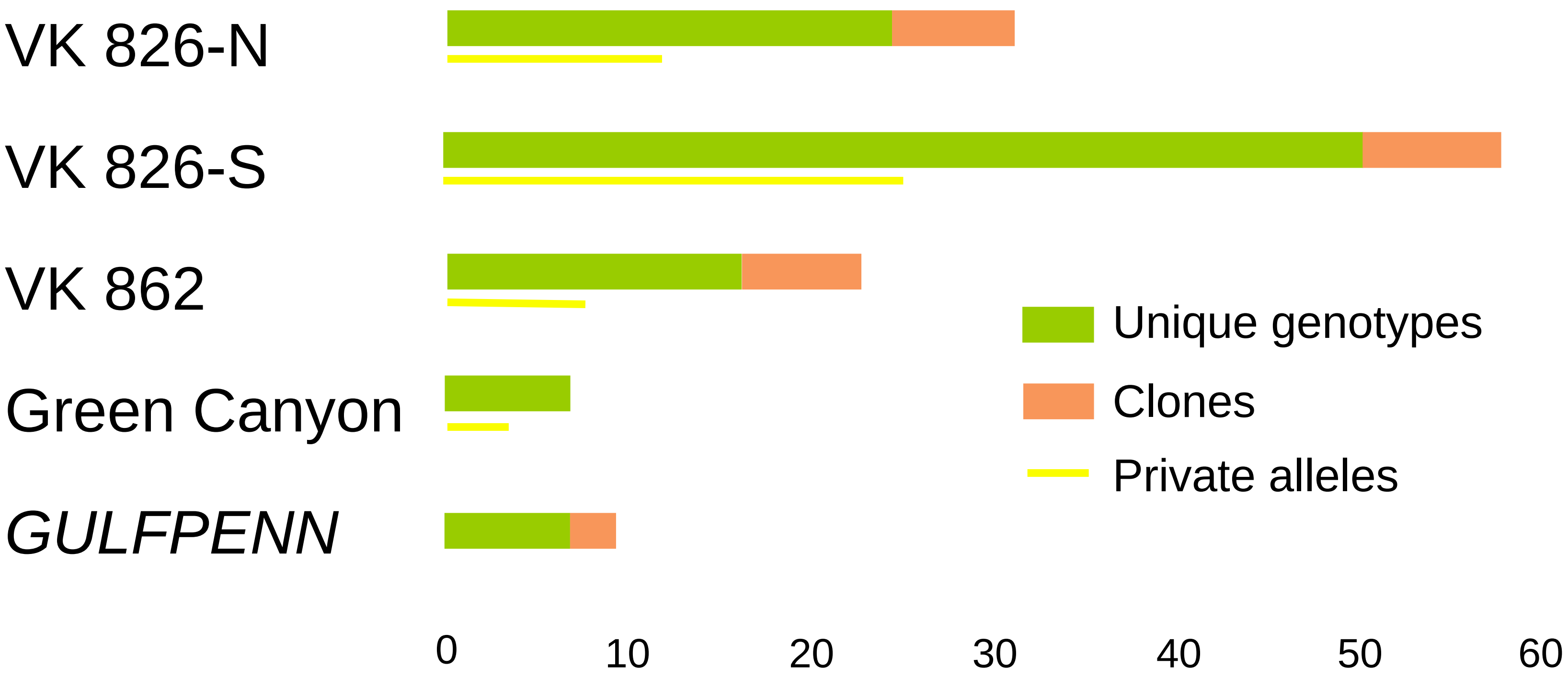
Locations of Viosca Knoll Sites



Genetic Sample Locations of Lophelia pertusa - Viosca Knolls 826



Genetic Characterization of Gulf *Lophelia*



Total *N*: 128 (19% clones, 50 private alleles)

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

F_{ST}

R_{ST}

Site	GC	GP	VK862	VK826N	VK826S
Green Canyon		0.000	0.020	0.000	0.012
Gulfpenn	0.000		0.008	0.000	0.001
VK-862	0.111	0.087		0.014	0.012
VK-826 N	0.035	0.000	0.056		0.008
VK-826 S	0.026	0.007	0.026	0.003	

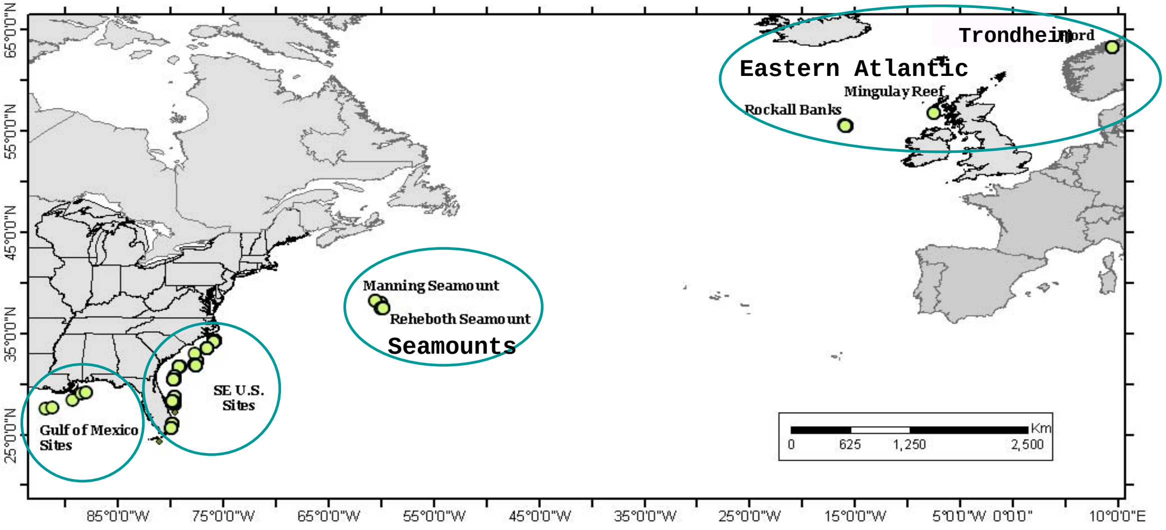
Maximum Likelihood Assignment Tests

Gulf of Mexico *Lophelia*

Pop	Green Canyon	*Gulfpenn*	VK862	VK826	Correct assign
GC	*0*	0	0	7	0%
GP	0	*0*	0	6	0%
VK862	1	2	*6*	8	35%
VK826	8	9	7	*50*	68%
54% correctly assigned to collection site					

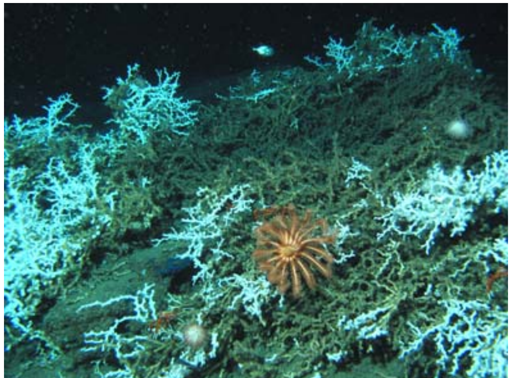
Conclusions – Broad Scale

- Regional breaks in connectivity
- Highest level hierarchical structuring = 3 genetic clusters
  - Gulf of Mexico
  - Southeastern U.S.
  - North Atlantic (New England seamounts and eastern North Atlantic)
- New England seamounts highly differentiated (4 clusters)
- Isolation by distance
- Depth
- Concordance with biogeographic patterns of DW scleractinian species diversity (Cairns and Chapman 2002)



Conclusions – Gulf of Mexico

- Moderate clonality
- Weak genetic structuring, moderate gene flow
  - VK-862 = most unique
  - VK-826 = important larval source
- Pattern of gene flow in Gulf of Mexico:
  - East to West
- *Gulfpenn Lophelia*
  - origins in Gulf of Mexico, likely from VK-826
  - Multiple recruits (unique genotypes, not fragmentation)



Conservation Implications

- Substantial genetic diversity
  - Potential for adaptation
  - Loss of any reef area = loss of genetic diversity
- Majority of recruitment localized
- Sporadic long-distance dispersal
  - New recruits unlikely to replenish destroyed reefs in short term (years)
- Restricted gene flow between regions/clusters
  - Regional reserve networks

Considerations for Future Studies

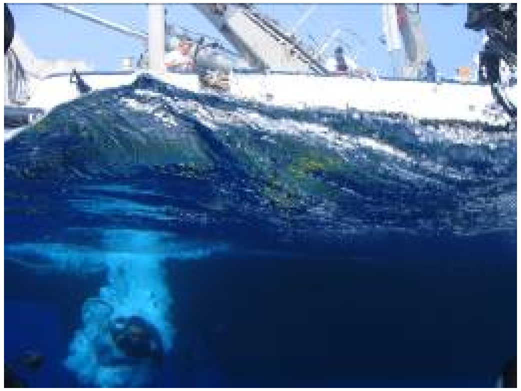
- Increase sample sizes (W. Gulf), add sites (wrecks)
- Increase geographic representation
  - West FL slope
  - Pourtales Terrace
  - Caribbean

- Intermediate to Broad scale: ‘Seascape’ Genetic Analyses
  - ➢ Understand physical processes and limits to dispersal
  - Multi-locus genotypes
  - Geographic information (lat/long coordinates) per sample
  - Oceanographic data for physical environments (broad and fine-scale)

- Fine scale: define ‘neighborhood size’
  - ➢ Are individuals more closely related than random mating?
  - ➢ Heterozygote deficits?
  - Multi-locus genotypes
  - Geographic information (lat/long coordinates)

- Compare patterns of connectivity
  - Associated megafauna
  - Scleractinian corals (e.g. *Madrepora oculata*)
  - Octocorals, Antipatharians

Acknowledgments



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- Logistics
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- Samples: J. Murray Roberts, A. Davies, E. Cordes, C. Fisher, W. Schroeder, J. Reed, C. Messing

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