Genetic Connectivity among *Lophelia pertusa* Reefs in the Gulf of Mexico

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Genetics Areas of Study

- *Lophelia* connectivity/population genetics
- Deep coral transcriptomics
- Scleractinian coral phylogeny
- Community genetics—*Lophelia* associates
- Galatheid crab phylogeny
Lophelia Reef Connectivity

• Effective protection of deep reefs
  – Requires knowledge of directions and distances that mobile juvenile stage (coral larvae) travel
• Larval movement (dispersal) influenced by
  – Physical factors: topography and currents
  – Biological factors: larval duration and behavior
• Larval dispersal difficult to measure
  – Dispersal homogenizes genetic signatures between reefs
  – Indirect estimates of larval dispersal (i.e. reef connectivity) through comparisons of genetic profiles
Lophelia Connectivity Study Objectives

• Use microsatellite markers to quantify local and regional patterns of genetic variation in *Lophelia*
  – Assess patterns of connectivity between natural reef areas, wreck and rig sites

• Interpret genetics results in relation to environmental variables
  – Long-term instruments
  – Loop Current studies
Lophelia I Discoveries

- *L. pertusa* reefs regionally isolated
  - Regional reserve networks
- Within regions: patterns complex
  - Nonrandom mating: self-recruitment
  - Regional cohesion: some larvae disperse

Morrison et al., Conservation Genetics, in press
Lophelia I

Gulf of Mexico: 100 samples, 3 sites
Lophelia II Sample Collection

- Viosca Knoll
- Garden Banks
- Mississippi Canyon
- West Florida
Lophelia Sample Collection
Lophelia Sample Collection
Manned Submersibles

• Johnson-Sea-Link I & II, (HBOI): 7 cruises
Lophelia Sample Collection
Remotely Operated Vehicles

• Remotely Operated Vehicles (ROVs)
  – Jason2 (WHOI): 2 cruises, C. Fisher, E. Cordes
  – Kraken II (U. of Connecticut): 1 cruise, S. Ross
Bayesian Clustering

STRUCTURE, $K=2$

Gulf of Mexico

Southeastern U.S.

439 individuals, 8 microsatellite loci
Evolutionary Relationships Among Locales

Neighbor-joining phylogram, chord distances
Maximum Likelihood Assignment Tests
Gulf of Mexico *Lophelia*

$F_{ST}$ range 0 - 0.008, average = 0.003
## Maximum Likelihood Assignment Tests Shipwreck *Lophelia*

<table>
<thead>
<tr>
<th>Pop</th>
<th>Garden Banks</th>
<th>MC751</th>
<th>VK906</th>
<th>VK862</th>
<th>VK826</th>
<th>WFL</th>
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<tbody>
<tr>
<td>GulfPenn</td>
<td>2</td>
<td>3</td>
<td>4</td>
<td>3</td>
<td>0</td>
<td>4</td>
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<tr>
<td>GulfOil</td>
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<td>1</td>
<td>0</td>
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<td>4</td>
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</table>

*Gulf Oil*
Lophelia Connectivity Conclusions

• Gulf and Atlantic Lophelia populations regionally isolated
  – Attenuation of gene flow
    • Currents through Florida Straits?
    • Inhospitable environment?
  – Regional reserve networks

• Gulf: Weak genetic structuring
  – Connectivity generally high
  – Natural reefs = important larval sources
  – Lophelia larvae disperse far and/or reefs spaced adequately
  – VK862 = most unique

• Lophelia conservation = Good news!
  – Replenishment of reefs by new recruits
  – *Given adequate time and conditions
Lophelia Connectivity Next Steps

• Approximately 80 samples to genotype
  – Viosca Knolls
  – West Florida

• Fine-scale relatedness
  – Heterozygote deficits – Wahlund effect
  – Viosca Knoll (Gulf)
  – Cape Canaveral (Atlantic)

• Additional sampling
  – Gulf Platforms
  – Caribbean, Bahamas
Deepwater Horizon Incident
MC-338: *Madrepora*, brown substance
Coral Transcriptomics

• Sub-lethal, chronic effects of exposure to oil and dispersants
  – Alterations in gene expression
  – Shifts away from normal homeostasis at cellular and molecular levels

• Examine transcriptomes
  – Set of all RNA molecules present at particular time
  – Identify genes (or gene systems) actively expressed

• Important first step in gene discovery
• Correlate with known stress-related physiological pathways
• Provide benchmarks of transcript abundances in RNAs
• Biomarkers and improved diagnostic tools for long-term monitoring
Coral Transcriptomics – Methods

• Next-generation 454 (Roche) sequencing
  – cDNA library
  – Roche 454 GS Junior next-generation sequencer
  – *De novo* transcriptome assembly
  – Annotate genes
    • Identify by matches to GenBank databases (e.g. BLASTX)
    • Matches to other corals EST databases (e.g. SymBioSys)

• Compare pre- and post-spill sequencing runs
  – *Lophelia* and *Madrepora*

• Compare genes expressed by both deep corals
**Lophelia Transcriptome**

<table>
<thead>
<tr>
<th>Lophelia cDNA</th>
<th>Count</th>
<th>Avg. Length</th>
<th>Bases</th>
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<tbody>
<tr>
<td>Reads</td>
<td>147,347</td>
<td>399 bp</td>
<td>58,711,188</td>
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<tr>
<td>Matched</td>
<td>142,920</td>
<td>400</td>
<td>57,187,244</td>
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<tr>
<td>Contigs</td>
<td>555</td>
<td>537</td>
<td>298,516</td>
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<tr>
<td>Singletons</td>
<td>4,427</td>
<td>344</td>
<td>1,523,944</td>
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</table>

cDNA library from pre-spill Gulf samples
## Madrepora Transcriptome

<table>
<thead>
<tr>
<th>Lophelia cDNA</th>
<th>Count</th>
<th>Avg. Length</th>
<th>Bases</th>
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<tbody>
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<td>Contigs</td>
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<tr>
<td>SNPs</td>
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cDNA library from post-spill MC 338 sample
Coral Transcriptomics – Future

• Baselines for future long-term monitoring
• *Madrepora* samples – GC852 (similar depth to MC338)
• Laboratory challenges: light crude oil, dispersants
  – Exposed vs. unexposed *Lophelia*
  – RNA-Seq, Ion Torrent
  – Compare and quantify expression patterns
• Additional markers generated for connectivity
  – Microsatellites
  – Single Nucleotide Polymorphisms (SNPs)
  – Neutral vs. adaptive population differences
Acknowledgments

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  – Woods Hole Oceanographic Institute, Jason2 ROV team; R/V Ron Brown
  – UCONN, KrakenII ROV team; R/V Cape Hatteras
  – Genetics Lab: R. Johnson, D.K. Coykendall, T. L. King

• Samples:
  – S. Ross, S. Brooke, E. Cordes, C. Fisher, W. Schroeder, J. Reed, C. Messing

http://fl.biology.usgs.gov/DISCOVRE