



L. Timm  
Email: ltimm004@fiu.edu  
Office: 305-919-4101

# Diversity and connectivity of a mesopelagic shrimp as proxies for ecosystem health and recovery in the Gulf of Mexico

Timm, L & Bracken-Grissom, H

Florida International University, 3000 NE 151<sup>st</sup> St. MSB 330, North Miami, FL 33181



H. Bracken-Grissom  
Email: hbracken@fiu.edu  
Office: 305-919-4190

## Introduction

The ability to measure genetic diversity and connectivity can be very powerful for predicting population recovery after a disturbance, especially in marine environments<sup>1,2</sup>. These genetic measurements will be used to diagnose the health and resilience of the Gulf of Mexico (GoM) across small spatial and temporal scales. Applying a next-generation sequencing (NGS) technique to *Acantheephyra purpurea* (Fig 1), a mesopelagic shrimp collected from the GoM, we will be able to gauge the health and resilience of mid-water crustaceans – a group of great ecological and economical importance.



Fig 1. *Acantheephyra purpurea*. Photo credit: A) D. Fenolio; B) T. Y. Chan.

## Objectives

1. Investigate intraspecific diversity within *Acantheephyra purpurea* to inform estimates of ecosystem health
2. Analyze the impacts of distance on connectivity within/between basins and its effect on genetic recovery
3. Characterize fluctuations in diversity and connectivity over a range of timescales and across geographic distances
4. Compare pre- and post-spill diversity and connectivity measurements
5. Identify and classify selection pressures on *A. purpurea* as a means to infer historical diversity and connectivity

## Why ddRADseq?

Our research utilizes a cutting-edge NGS technique: double-digest Restriction-site Associated DNA sequencing (ddRADseq; Fig 2). This approach allows us to:

- Analyze a huge portion of the genome
- Discover very fine-scale diversity
- Identify even small amounts of gene flow
- Characterize selective pressures

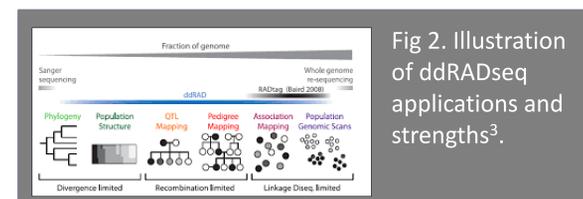


Fig 2. Illustration of ddRADseq applications and strengths<sup>3</sup>.

## Preliminary Results

Samples have been collected from the GoM and the western Atlantic (Table 1; Fig 4). The first lane of ddRADseq libraries have been sent for sequencing. This multiplexed sample includes a test library prepared from eight shrimp collected during the DP01 and DP02 cruises. *Acantheephyra purpurea* has been hypothesized to have a very large genome (roughly 3X that of humans). The results of our enzyme trials confirm this (Fig 3; Table 2).

Year	GoM	Bear Seamount
2011	7	0
2014	0	48
2015	56	0

Table 1. A list of samples collected from the GoM and Bear Seamount, 2011-present

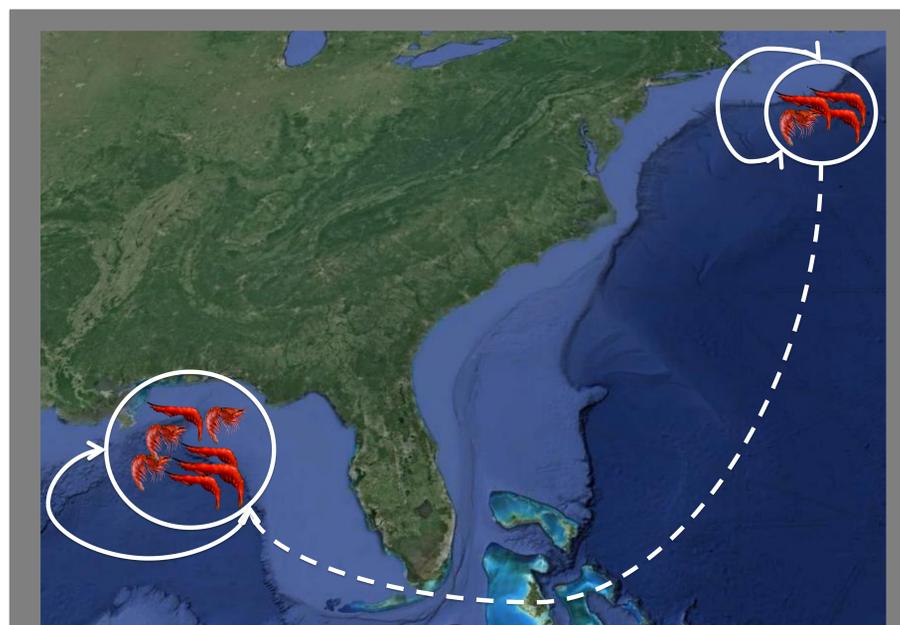


Fig 3. Map of collection sites from the GoM and Bear Seamount in the western Atlantic. Circles indicate sites included in diversity calculations. Solid arrows indicate hypothesized self-recruitment of individuals. Dotted arrows indicate hypothesized inter-basin connectivity

Enzyme Combination	180-220bp		270-330bp		360-440bp	
	# of fragments	Samples/Lane	# of fragments	Samples/Lane	# of fragments	Samples/Lane
EcoRI + NlaIII	701,457	10	584,156	11	527,418	13
EcoRI + SphI	1,790,027	4	1,350,418	5	901,794	7
MluCI + NlaIII	888,087	8	892,528	7	895,887	7
MluCI + SphI	1,053,295	6	584,673	11	43,777,037	15
MspI + NlaIII	919,255	8	656,757	11	561,245	15
MspI + SphI	301,503	28	199,878	43	188,813	45

Table 2. ddRADseq calculations based on Bioanalyzer results, including estimated number of fragments resulting from digestion and the estimated number of samples that can be sequenced per HiSeq lane (assuming 30X coverage).

## Acknowledgments

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## Methods

Using GoM and Bear Seamount samples collected between 2010-2011 and 2015-2017, we will quantify changes in diversity and connectivity over different timescales and across oceanic basins using ddRADseq (Fig 5).

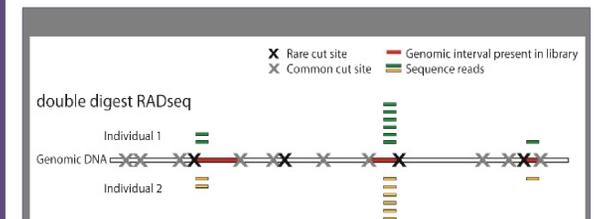


Fig 5. Illustration of ddRADseq technique<sup>3</sup>.

## Anticipated Results

1. Homogeneous diversity given the lack of obvious barriers in the GoM
2. Small degree of isolation-by-distance, as the Gulf Loop Current mixes the majority of the GoM
3. Large fluctuations in diversity immediately following the spill (2010-2011), stabilizing over time (2012-2017) – a timeline of recovery
4. Highest diversity in pristine (Atlantic) samples, post-spill diversity increasing annually (if not semi-annually); majority of connectivity differences attributable to seasonal variation; classify GoM as genetically “open” or “closed” with respect to the Atlantic
5. Classifying past selection events and recoveries can be powerful for predicting GoM resilience

## Ongoing Work

- Samples continue to be collected from the GoM twice annually.
- Enzyme trials continue.
- Other shrimp species are being considered for ddRADseq analysis, such as *Sergia robusta* (Fig 6).



Fig 6. *Sergia robusta*, a dendrobranchiate shrimp

- Preliminary analyses of test libraries will begin in late spring.

## Literature Cited

1. Cowen & Sponaugle, 2009. *Ann Rev Mar Sci.* 1, 443-466.
2. Hellberg et al., 2002. *Bull Mar Sci.* 70(1S), 273-290.
3. Peterson et al., 2012. *PLOS ONE.* 7(5), e37135.