

# Microsatellite genotypes of marine bryozoan from shallow seagrass habitats in St. Teresa, Florida, USA in June 2017

**Website:** <https://www.bco-dmo.org/dataset/893165>

**Data Type:** Other Field Results

**Version:** 1

**Version Date:** 2023-04-05

## Project

» [Consequences of kin structure in benthic marine systems](#) (Marine kin structure)

Contributors	Affiliation	Role
<a href="#">Burgess, Scott</a>	Florida State University (FSU)	Principal Investigator, Contact
<a href="#">Bueno, Marília M.</a>	Florida State University (FSU)	Scientist
<a href="#">Powell, Jackson</a>	Florida State University (FSU)	Student
<a href="#">Heyl, Taylor</a>	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

## Abstract

We integrate a series of experiments to study how dispersal affects the density and relatedness of neighbors, and how the density and relatedness of neighbors in turn affects fitness. In a marine bryozoan, microsatellite genetic markers identified very few half sibs (and no full sibs) in adults from the natural population, and rarely close enough to directly interact.

## Table of Contents

- [Coverage](#)
- [Dataset Description](#)
  - [Methods & Sampling](#)
  - [Data Processing Description](#)
- [Data Files](#)
- [Related Publications](#)
- [Related Datasets](#)
- [Parameters](#)
- [Project Information](#)
- [Funding](#)

## Coverage

**Spatial Extent:** Lat:29.9 Lon:-84.5

**Temporal Extent:** 2016-12-15

## Methods & Sampling

At our field sites in the shallow seagrass habitats near the Florida State University Coastal and Marine Laboratory (FSUCML) in St. Teresa, Florida, USA (29° 54' N, 84° 30' W), multiple *B. neritina* colonies are commonly found attached to the same blade of seagrass, often contacting each other at times of the year when densities are highest. In December 2016, we randomly selected 15 blades of seagrass containing adult colonies within a roughly 10-50 meter area immediately east of the FSUCML. Sampled seagrass blades were roughly 2 – 5 meters from each other. Each sampled blade contained between 2 to 11 adult colonies (median = 4), which were all genotyped at 16 microsatellite loci, following methods described in Burgess et al. (2019). We collected and genotyped an additional 53 randomly selected colonies from the same general area to provide a more precise estimate of the population allele frequencies used to estimate relatedness. In total, there were 127 individuals in the sample, of which 74 were the focal individuals from the 15 blades of seagrass. Our focal populations contain the S1 haplotype of the cytochrome oxidase c subunit I (COI) gene, and do not include cryptic species.

We used the program COLONY (Version 2.0.6.6., Build 20200830) to identify pairs of individuals with a full- or half-sib relationship using a sibship reconstruction analysis. Sibship reconstruction requires no a-priori knowledge of the relationships in the sample of individuals, and uses a clustering algorithm to arrange individuals into families based on Mendelian rules of allele inheritance. Given the time of year and the size of colonies that were collected, the sample was considered to consist of a single cohort (i.e., no parent-offspring relationships in the sample). We used the full sample of 127 individuals to increase the confidence in identifying family clusters, but focus on the 74 individuals sampled from known seagrass blades.

For all runs in COLONY, the parameter settings used were: allele frequency unknown and not updated, monoecious, no inbreeding, diploid, male and female polygamy, no clones, full sibship scaling, weak sibship prior of 1, long length of run, full-likelihood with high precision, allelic drop out and false allele rate of 0.0001. We carried out 5 runs using different seed numbers to check the reliability of the results. Only full- and half-sibs that were equal to or above a certain probability (0.8, 0.9, or 0.95) in all 5 replicate runs were considered to be reliably estimated.

## Data Processing Description

### BCO-DMO Processing Description:

- Adjusted field/parameter names to comply with BCO-DMO naming conventions

[ [table of contents](#) | [back to top](#) ]

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## Data Files

File
<b>microsatellite_genotypes-1.csv</b> (Comma Separated Values (.csv), 17.12 KB) MD5:4936979461ea6686c3284a9b37929d55
Primary data file for dataset 89316, version 1.

[ [table of contents](#) | [back to top](#) ]

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## Related Publications

Burgess, S. C., Powell, J., & Bueno, M. (2022). Dispersal, kin aggregation, and the fitness consequences of not spreading sibling larvae. *Ecology*, 104(1). Portico. <https://doi.org/10.1002/ecy.3858>  
*Results*

[ [table of contents](#) | [back to top](#) ]

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## Related Datasets

### IsRelatedTo

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Burgess, S., Powell, J., Bueno, M. M. (2023) **Aggregation kin versus nonkin experiments in marine bryozoans from shallow seagrass habitats in St. Teresa, Florida, USA in June 2017**. Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2023-04-04 doi:10.26008/1912/bco-dmo.893150.1 [[view at BCO-DMO](#)]

Burgess, S., Powell, J., Bueno, M. M. (2023) **Dispersal distance in a marine bryozoan in shallow seagrass habitats in St. Teresa, Florida, USA, between October and December 2017**. Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2023-04-03 doi:10.26008/1912/bco-dmo.893092.1 [[view at BCO-DMO](#)]

Burgess, S., Powell, J., Bueno, M. M. (2023) **Marine bryozoan aggregation experiments in shallow seagrass habitats in St. Teresa, Florida, USA in May 2017**. Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2023-04-04 doi:10.26008/1912/bco-

dmo.893115.1 [[view at BCO-DMO](#)]

Burgess, S., Powell, J., Bueno, M. M. (2023) **Postsettlement performance in kin groups from shallow seagrass habitats in St. Teresa, Florida, USA in November and December 2017**. Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2023-04-04 doi:10.26008/1912/bco-dmo.893158.1 [[view at BCO-DMO](#)]

[ [table of contents](#) | [back to top](#) ]

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## Parameters

Parameter	Description	Units
Sample	Unique code for each individual colony	unitless
Group	Unique code indicating which seagrass blade colonies were sampled from. Blank entries indicate colonies that were randomly sampled, each from different seagrass blades	unitless
Locus_1323_Allele_1	Allele 1 at locus 1323	unitless
Locus_1323_Allele_2	Allele 2 at locus 1323	unitless
Locus_231_Allele_1	Allele 1 at locus 231	unitless
Locus_231_Allele_2	Allele 2 at locus 231	unitless
Locus_7294_Allele_1	Allele 1 at locus 7294	unitless
Locus_7294_Allele_2	Allele 2 at locus 7294	unitless
Locus_4717_Allele_1	Allele 1 at locus 4717	unitless
Locus_4717_Allele_2	Allele 2 at locus 4717	unitless
Locus_689_Allele_1	Allele 1 at locus 689	unitless
Locus_689_Allele_2	Allele 2 at locus 689	unitless
Locus_4166_Allele_1	Allele 1 at locus 4166	unitless
Locus_4166_Allele_2	Allele 2 at locus 4166	unitless
Locus_284_Allele_1	Allele 1 at locus 284	unitless
Locus_284_Allele_2	Allele 2 at locus 284	unitless
Locus_3595_Allele_1	Allele 1 at locus 3595	unitless
Locus_3595_Allele_2	Allele 2 at locus 3595	unitless
Locus_157_Allele_1	Allele 1 at locus 157	unitless
Locus_157_Allele_2	Allele 2 at locus 157	unitless
Locus_2664_Allele_1	Allele 1 at locus 2664	unitless
Locus_2664_Allele_2	Allele 2 at locus 2664	unitless
Locus_7402_Allele_1	Allele 1 at locus 7402	unitless
Locus_7402_Allele_2	Allele 2 at locus 7402	unitless
Locus_568_Allele_1	Allele 1 at locus 568	unitless
Locus_568_Allele_2	Allele 2 at locus 568	unitless
Locus_1671_Allele_1	Allele 1 at locus 1671	unitless
Locus_1671_Allele_2	Allele 2 at locus 1671	unitless
Locus_590_Allele_1	Allele 1 at locus 590	unitless
Locus_590_Allele_2	Allele 2 at locus 590	unitless
Locus_12984_Allele_1	Allele 1 at locus 12984	unitless
Locus_12984_Allele_2	Allele 2 at locus 12984	unitless
Locus_1314_Allele_1	Allele 1 at locus 1314	unitless
Locus_1314_Allele_2	Allele 2 at locus 1314	unitless

[ [table of contents](#) | [back to top](#) ]

## Project Information

### Consequences of kin structure in benthic marine systems (Marine kin structure)

### **NSF Award Abstract:**

In marine systems, the production, dispersal, and recruitment of larvae are crucial processes that rebuild depleted adult stocks, facilitate changes in species geographic ranges, and modify the potential for adaptation under environmental stress. Traditionally, the tiny larvae of bottom-associated adults were thought to disperse far from their parents and from each other, making interactions among kin improbable. However, emerging evidence is challenging this view: larval dispersal does not always disrupt kin associations at settlement, and a large fraction of invertebrate diversity on the seafloor contains species in which most larvae disperse short distances. Limited dispersal increases the potential for interactions among kin, which has important consequences for individual fitness across many generations, and therefore the productivity of populations and the potential for adaptation. But when these consequences occur, and how exactly they manifest, remains largely unexplained. The key challenge now is to explain and predict when kin associations are likely to occur, and when they are likely to have positive or negative ecological consequences. Therefore, the key questions addressed by this research are: 1) how and when do kin associations arise and persist, and 2) what are the consequences of living with kin for survival, growth, and reproduction. This concept-driven research combines genomic approaches with experimental approaches in lab and field settings using an experimentally-tractable and representative invertebrate species. The project trains and mentors PhD students and a postdoctoral scholar at Florida State University (FSU). Field and laboratory activities are developed and incorporated into K-12 education programs and outreach opportunities at FSU.

The spatial proximity of relatives has fundamentally important consequences at multiple levels of biological organization. These consequences are likely to be particularly important in a large range of benthic marine systems, where competition, facilitation, and mating depend strongly on the proximity and number of neighbors. However, explaining and predicting the occurrence, magnitude, and direction of such effects remains challenging. Emerging evidence suggest that the ecological consequences of kin structure are unlikely to have a straight-forward relationship with dispersal potential. Therefore, it is crucial to discover new reasons for when kinship structure occurs and why it could have positive, negative, or neutral ecological consequences. This research aims to provide a new understanding of how dispersal and post-settlement processes generate spatial kin structure, how population density and relatedness influence post-settlement fitness, and how the relatedness of mating partners influences the number and fitness of their offspring (inbreeding and outbreeding). The research combines genomic approaches, experimental progeny arrays, and manipulative experiments in field and lab settings to test several hypotheses that are broadly applicable across species. By focusing on an experimentally tractable species to test broadly applicable hypotheses, the project achieves generality and a level of integration that has been difficult to achieve in previous work.

[ [table of contents](#) | [back to top](#) ]

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## **Funding**

Funding Source	Award
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1948788</a>

[ [table of contents](#) | [back to top](#) ]