

Seed counts from a survey of the shallow and deep zones at four different sites in Massachusetts, USA in 2019

Website: <https://www.bco-dmo.org/dataset/847088>

Data Type: Other Field Results

Version: 1

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Project

» [RUI: Collaborative Research: Trait differentiation and local adaptation to depth within meadows of the foundation seagrass *Zostera marina*](#) (ZosMarLA)

Contributors	Affiliation	Role
Hughes, A. Randall	Northeastern University	Principal Investigator
Rauch, Shannon	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract

This dataset includes seed counts from a survey of the shallow and deep zones at four different sites in Massachusetts, USA in 2019. The four sites were West Beach in Beverly (N 42.55921, W 70.80578), Curlew Beach in Nahant (N 42.42009, W 70.91553), Lynch Park in Beverly (N 42.42009, W 70.91553), and Niles Beach in Gloucester (N 42.59711, W 70.65592).

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Coverage

Spatial Extent: N:42.59711 E:-70.65592 S:42.42009 W:-70.9155

Temporal Extent: 2019-08 - 2019-08

Methods & Sampling

We conducted surveys of four different eelgrass beds in Massachusetts in mid-August of 2019. The four sites were West Beach in Beverly (N 42.55921, W 70.80578), Curlew Beach in Nahant (N 42.42009, W 70.91553), Lynch Park in Beverly (N 42.42009, W 70.91553), and Niles Beach in Gloucester (N 42.59711, W 70.65592). Surveys were done in both the shallow and deep zone. These zones were defined as being along the respective edges of the eelgrass beds. The exact depths of the zones varied from bed to bed.

During the surveys, we collected flowering shoots from within 0.25 m² quadrats every 2 m along a 30 m transect (that would be extended for each quadrat that had no eelgrass). Any flowering shoots found within the quadrats were taken and their seeds counted. This led to there being up to 25 flowering shoots per depth per site.

Data Processing Description

Data Processing:

We analyzed the number of seeds per flowering shoot at all four sites using a GLM with a negative binomial regression and independent and interactive effects of depth and site.

Statistical analyses were conducted using R Statistical Software v. 3.6.0 (R Core Team 2019). Negative binomial regression was done using the `glm.nb` function in the MASS package (Venables and Ripley 2002). We used a significance level of $\alpha = 0.05$ for all of our analyses.

BCO-DMO Processing:

- renamed fields to conform with BCO-DMO naming conventions.

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Data Files

File
seed_counts.csv (Comma Separated Values (.csv), 2.45 KB) MD5:0b6af764e1eb2bae8e789876daa674f1
Primary data file for dataset ID 847088

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Related Publications

R Core Team (2019). R: A language and environment for statistical computing. R v3.6.0. R Foundation for Statistical Computing, Vienna, Austria. URL <https://www.R-project.org/>
Software

Venables, W. N., & Ripley, B. D. (2002). Modern applied statistics with S (4th ed., Ser. Statistics and computing). Springer. URL: <http://www.stats.ox.ac.uk/pub/MASS4> <https://isbnsearch.org/isbn/0-387-95457-0>
Methods

Von Staats, D. A., Hanley, T. C., Hays, C. G., Madden, S. R., Sotka, E. E., & Hughes, A. R. (2020). Intra-Meadow Variation in Seagrass Flowering Phenology Across Depths. *Estuaries and Coasts*, 44(2), 325–338.
doi:[10.1007/s12237-020-00814-0](https://doi.org/10.1007/s12237-020-00814-0)
Results

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Parameters

Parameter	Description	Units
Site	The location of sample collection. DC (Curlew Beach), WB (West Beach), NB (Niles Beach), or LP (Lynch Park).	unitless
ID	A unique identification number given to each flowering shoot for which seeds were counted.	unitless
Depth	SH (shallow zone) or DP (deep zone).	unitless
Seed_Count	The number of mature seeds per flowering shoot.	Number of seeds per flowering shoot

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Project Information

RUI: Collaborative Research: Trait differentiation and local adaptation to depth within meadows of the foundation seagrass *Zostera marina* (ZosMarLA)

NSF Award Abstract:

Understanding how species cope with spatial variation in their environment (e.g. gradients in light and temperature) is necessary for informed management as well as for predicting how they may respond to change. This project will examine how key traits vary with depth in common eelgrass (*Zostera marina*), one of the most important foundation species in temperate nearshore ecosystems worldwide. The investigators will use a combination of experiments in the field and lab, paired with fine-scale molecular analyses, to determine the genetic and environmental components of seagrass trait variation. This work will provide important information on the microevolutionary mechanisms that allow a foundation species to persist in a variable environment, and thus to drive the ecological function of whole nearshore communities. The Northeastern University graduate and Keene State College (KSC) undergraduate students supported by this project will receive training in state-of-the-art molecular techniques, as well as mentorship and experience in scientific communication and outreach. A significant portion of KSC students are from groups under-represented in science. Key findings of the research will be incorporated into undergraduate courses and outreach programs for high school students from under-represented groups, and presented at local and national meetings of scientists and stakeholders.

Local adaptation, the superior performance of "home" versus "foreign" genotypes in a local environment, is a powerful demonstration of how natural selection can overcome gene flow and drift to shape phenotypes to match their environment. The classic test for local adaptation is a reciprocal transplant. However, such experiments often fail to capture critical aspects of the immigration process that may mediate realized gene flow in natural systems. For example, reciprocal transplant experiments typically test local and non-local phenotypes at the same (often adult) life history stage, and at the same abundance or density, which does not mirror how dispersal actually occurs for most species. In real populations, migrants (non-local) often arrive at low numbers compared to residents (local), and relative frequency itself can impact fitness. In particular, rare phenotypes may experience reduced competition for resources, or relative release from specialized pathogens. Such negative frequency dependent selection can reduce fitness differences between migrants and residents due to local adaptation, and magnify effective gene flow, thus maintaining greater within-population genetic diversity. The investigators will combine spatially paired sampling and fine-scale molecular analyses to link seed/seedling trait variation across the depth gradient at six meadows to key factors that may drive these patterns: local environmental conditions, population demography, and gene flow across depths. The team will then experimentally test the outcome of cross-gradient dispersal in an ecologically relevant context, by reciprocally out-planting seeds from different depths and manipulating relative frequency in relation to both adults and other seedling lineages. The possible interaction between local adaptation and frequency-dependence is particularly relevant for *Zostera marina*, which represents one of the best documented examples of the ecological effects of genetic diversity and identity. Further, a better understanding of seagrass trait differentiation is not simply a matter of academic interest, but critical to successful seagrass restoration and conservation.

This award reflects NSF's statutory mission and has been deemed worthy of support through evaluation using the Foundation's intellectual merit and broader impacts review criteria.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1851043

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