

# Abiotic and biotic data from Zostera Experimental Network (ZEN) 2014 surveys (ZEN 2 project)

**Website:** <https://www.bco-dmo.org/dataset/712069>

**Data Type:** Other Field Results

**Version:** 1

**Version Date:** 2016-09-26

## Project

» [Global biodiversity and functioning of eelgrass ecosystems \(Zostera Experimental Network 2\)](#) (ZEN 2)

Contributors	Affiliation	Role
<a href="#">Duffy, J. Emmett</a>	Smithsonian Institution (TMON)	Principal Investigator
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<a href="#">Stachowicz, John J.</a>	University of California-Irvine (UC Irvine)	Co-Principal Investigator
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## Abstract

This dataset includes biomass and diversity measurements of eelgrass communities from 50 sites across the Northern Hemisphere. The purpose was to study the plant and animal responses to top-down and bottom-up manipulations in eelgrass (*Zostera marina*) habitat.

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## Coverage

**Spatial Extent:** N:67.267 E:0.01 S:30.42 W:144

**Temporal Extent:** 2014-05-16 - 2014-09-29

## Methods & Sampling

Twenty meter square plots (2 meters apart) were sampled at 50 eelgrass meadows ("sites") in summer 2014. Abiotic parameters were quantified in situ and/or using local monitoring station data. The epifaunal community was quantified as in Duffy et al. 2015. Seagrass density was quantified in 20cm diameter rings, and dry mass from 20 cm diameter cores which captured all above ground mass, and below ground to a depth of 20 cm. A three centimeter section from each of 5 shoots per plot was quantified for leaf carbon and nitrogen (processed at the Virginia Institute of Marine Science), while another 3 cm section was utilized for plant genetic analyses (processed by J. Olsen at the University of Groningen). Additional details are included in the Zostera Experimental Network 2014 survey handbook protocol, available upon request.

Methodology is available from: J. Emmett Duffy, et al. Biodiversity mediates top-down control in eelgrass ecosystems: A global comparative-experimental approach. 2015. Ecology Letters 18:7 (696-705). [DOI:](#)

[10.1111/ele.12448](https://doi.org/10.1111/ele.12448).

## Data Processing Description

Data were aggregated and quality checked manually and through use of analysis scripts. Biotic values are site means.

### BCO-DMO Processing:

- added conventional header with dataset name, PI name, version date
- renamed some parameters to BCO-DMO standard
- replaced . with \_
- replaced special characters with ascii characters
- reformatted date from m/d/y to yyyy-mm-dd
- reduced digits to right of decimal
- sorted data by Latitude

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## Data Files

File
<b>ZEN2_survey_sorted.csv</b> (Comma Separated Values (.csv), 26.81 KB) MD5:6f1efa5e48fb9a66b9af7b21926e9ade
Primary data file for dataset ID 712069

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## Related Publications

Duffy, J. E., P.-O. Moksnes, and A. R. Hughes. (2013). Ecology of Seagrass Communities. Pages 271–297 in M. D. Bertness, J. F. Bruno, B. R. Silliman, and J. J. Stachowicz, editors. "Marine Community Ecology and Conservation". Sinauer Associates, Sunderland, Massachusetts. <https://isbnsearch.org/isbn/978-1605352282>  
*Results*

Duffy, J. E., Reynolds, P. L., Boström, C., Coyer, J. A., Cusson, M., Donadi, S., ... Stachowicz, J. J. (2015). Biodiversity mediates top-down control in eelgrass ecosystems: a global comparative-experimental approach. *Ecology Letters*, 18(7), 696–705. <https://doi.org/10.1111/ele.12448>  
*Results*

Reynolds, P. L., Richardson, J. P., & Duffy, J. E. (2014). Field experimental evidence that grazers mediate transition between microalgal and seagrass dominance. *Limnology and Oceanography*, 59(3), 1053–1064. <https://doi.org/10.4319/lo.2014.59.3.1053>  
*Results*

Whalen, M. A., Duffy, J. E., & Grace, J. B. (2013). Temporal shifts in top-down vs. bottom-up control of epiphytic algae in a seagrass ecosystem. *Ecology*, 94(2), 510–520. <https://doi.org/10.1890/12-0156.1>  
*Results*

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## Parameters

Parameter	Description	Units
Site_Code	Two letter code for the specific ZEN partner (25 total).	unitless

Site	The 2 letter ZEN Site.Code followed by the subsite A or B (50 total)	unitless
Subsite	Designation of the ZEN sub-site (A or B; except for LI where it is 1 or 2).	unitless
Subsite_Name	The partner-provided name for their subsite (50 total).	unitless
Ocean	Two choices: Atlantic or Pacific	unitless
Coast	Combination of Basin and Ocean. Four choices: East.Atlantic; West.Atlantic; East.Pacific; West.Pacific	unitless
Basin	Location along the ocean basin margin. Two choices: East or West.	unitless
Latitude	Latitude of the site of deployment in decimal degrees	decimal degrees
Longitude	Longitude of the site of deployment in decimal degrees	decimal degrees
Sampling_Time	Two choices 1 or 2. Internal coding to differentiate for sites which conducted two separate sampling efforts.	unitless
Month	Calendar month in which the sampling occurred.	unitless
Date_Collected	Specific date the specific measurement was collected for a given variable. Format: yyyy-mm-dd	unitless
Temperature_C	Seawater temperature in degrees Celsius taken in the middle of the seagrass canopy height at low tide during sampling. Appropriate local monitoring station data substituted if in situ data not available.	degrees Celsius
Salinity_ppt	Salinity (in ppt) taken in the middle of the seagrass canopy height at low tide during sampling. Appropriate local monitoring station data substituted if in situ data not available.	parts per thousand
Day_length_hours	Length (in hours) of daylight for the day on which the sampling was conducted using date-calendar.	hours
GenotypicRichness	Genotypic richness (G-1/N-1) of <i>Zostera marina</i> from one shoot per plot. Provided by J.Olsen. Genotypic richness ranges from 0 (all individuals the same) to 1 (all individuals different) and is a measure of the number of distinct genotypes. (Genotype = a clone.) Genotypes are multilocus with 8 16 or 24 loci involved.	unitless
AllelicRichness	Allelic richness ( $\hat{A}$ ) of <i>Zostera marina</i> from one shoot per plot. Provided by J.Olsen. Interpretation: the average number of alleles per locus; normalized to 7 genets.	unitless
Inbreeding	Inbreeding coefficient (FIS) of <i>Zostera marina</i> from one shoot per plot. Provided by J.Olsen.	unitless
Mean_Shoots_Zmarina_per_m2	Mean density of <i>Zostera marina</i> shoots per square meter (from sampling hoops or other methods)	shoots per square meter

SD_Shoots_Zmarina_per_m2	Standard deviation of the number of Zostera marina shoots per square meter	shoots per square meter
SE_Shoots_Zmarina_per_m2	Standard error of the number of Zostera marina shoots per square meter	shoots per square meter
Mean_Site_Std_Periphyton	Mean standardized loading of periphyton (g dried periphyton/dry g Zostera)	unitless
SD_Site_Std_Periphyton	Standard deviation of Mean.Site.Std.Periphyton	unitless
SE_Site_Std_Periphyton	Standard error of Mean.Site.Std.Periphyton	unitless
Mean_Site_Std_SessileInvertebrate	Mean standardized loading of sessile invertebrates	grams dry sessile invertebrates/dry grams Zostera
SD_Site_Std_SessileInvertebrate	Standard deviation of Mean.Site.Std.SessileInvertebrate	grams dry sessile invertebrates/dry grams Zostera
SE_Site_Std_SessileInvertebrate	Standard error of Mean.Site.Std.SessileInvertebrate	grams dry sessile invertebrates/dry grams Zostera
Mean_Site_Std_TotalEpibiota	Mean standardized loading of total epibiota (periphyton + sessile invertebrates) on Zostera marina	grams total dried epibiota/dry grams Zostera
SD_Site_Std_TotalEpibiota	Standard deviation of Mean.Site.Std.TotalEpibiota	grams total dried epibiota/dry grams Zostera
SE_Site_Std_TotalEpibiota	Standard error of Mean.Site.Std.TotalEpibiota	grams total dried epibiota/dry grams Zostera
Sheath_Width_cm	Mean widest measurement of the leaf sheath	centimeters
Sheath_Length_cm	Mean length of the longest intact sheath; from the meristem to the top of the sheath	centimeters
Longest_Leaf_Length_cm	Mean length from the meristem to the tip of the longest leaf	centimeters
SD_Sheath_Width_cm	Standard deviation of Sheath.Width.cm	centimeters
SD_Sheath_Length_cm	Standard deviation of Sheath.Length.cm	centimeters
SD_Longest_Leaf_Length_cm	Standard deviation of Longest.Leaf.Length	centimeters
SE_Sheath_Width_cm	Standard error of Sheath.Width.cm	centimeters
SE_Sheath_Length_cm	Standard error of Sheath.Length.cm	centimeters
SE_Longest_Leaf_Length_cm	Standard error of Longest.Leaf.Length	centimeters
Below_Zmarina_g	Mean dry belowground mass (g) of Zostera marina per square meter	grams/meter <sup>2</sup>
Below_OtherSeagrass_g	Mean dry belowground mass (g) of seagrass species excluding Zostera marina per square meter	grams/meter <sup>2</sup>
Above_Zmarina_g	Mean dry aboveground mass (g) of Zostera marina per square meter	grams/meter <sup>2</sup>
Above_OtherSeagrass_g	Mean dry aboveground mass (g) of seagrass species excluding Zostera marina per square meter	grams/meter <sup>2</sup>

Macroalgae_g	Mean dry mass (g) of macroalgae per square meter (based on seagrass core collections)	grams/meter <sup>2</sup>
TOTAL_Seagrass_Biomass	Mean dry mass (g) of all seagrass (below + above)	grams
Total_Seagrass_Biomass_Above	Mean dry mass (g) of all aboveground seagrass mass	grams
Total_Seagrass_Biomass_Below	Mean dry mass (g) of all belowground seagrass mass	grams
SD_Below_Zmarina_g	Standard deviation of Below.Zmarina.g	grams
SD_Below_OtherSeagrass_g	Standard deviation of Below.OtherSeagrass.g	grams
SD_Mean_Above_Zmarina_g	Standard deviation of Above.Zmarina.g	grams
SD_Above_OtherSeagrass_g	Standard deviation of OtherSeagrass.g	grams
SD_Macroalgae_g	Standard deviation of Macroalgae.g	grams
SD_Mean_Total_Seagrass_Biomass_Above	Standard deviation of Mean.Total.Seagrass.Biomass.Above	grams
SD_Mean_Total_Seagrass_Biomass_Below	Standard deviation of Mean.Total.Seagrass.Biomass.Below	grams
SE_Below_Zmarina_g	Standard error of Below.Zmarina.g	grams
SE_Below_OtherSeagrass_g	Standard error of Below.OtherSeagrass.g	grams
SE_Mean_Above_Zmarina_g	Standard error of Above.Zmarina.g	grams
SE_Above_OtherSeagrass_g	Standard error of OtherSeagrass.g	grams
SE_Macroalgae_g	Standard error of Macroalgae.g	grams
SE_Mean_Total_Seagrass_Biomass_Above	Standard error of Mean.Total.Seagrass.Biomass.Above	grams
SE_Mean_Total_Seagrass_Biomass_Below	Standard error of Mean.Total.Seagrass.Biomass.Below	grams
Mean_Leaf_PercN	Mean leaf percent nitrogen in the young growth <i>Zostera marina</i> tissue	percent
Mean_Leaf_PercC	Mean leaf percent carbon in the young growth <i>Zostera marina</i> tissue	percent
SD_Mean_Leaf_PercN	Standard deviation of Mean.Leaf.PercN	percent
SD_Mean_Leaf_PercC	Standard deviation of Mean.Leaf.PercC	percent
SE_Mean_Leaf_PercN	Standard error of Mean.Leaf.PercN	percent
SE_Mean_Leaf_PercC	Standard error of Mean.Leaf.PercC	percent
Mean_Epifaunal_Richness	Mean richness of epifauna per plot. Richness counts based on lowest taxonomic resolution identified per specimen (primarily species level)	unitless
SE_Epifaunal_Richness	Standard error of Mean.Epifaunal.Richness	unitless
SD_Epifaunal_Richness	Standard deviation of Mean.Epifaunal.Richness	unitless
Mean_Mesograzer_Richness	Mean richness of epifauna per plot identified as mesograzer taxa. Richness counts based on lowest taxonomic resolution identified per specimen (primarily species level)	unitless
SE_Mesograzer_Richness	Standard error of Mean.Mesograzer.Richness	unitless
SD_Mesograzer_Richness	Standard deviation of Mean.Mesograzer.Richness	unitless

Mean_Total_Abund	Mean total abundance of epifauna per plot sample: counts of animals per dry mass of the plants they were collected from	# animals/grams plant
SE_Total_Abund	Standard error of Mean.Total.Abund	# animals/grams plant
SD_Total_Abund	Standard deviation of Mean.Total.Abund	# animals/grams plant
Mean_Total_Abund_Mesograzers	Mean total abundance of epifauna per plot sample identified as mesograzer taxa	# animals/grams plant
SE_Total_Abund_Mesograzers	Standard error of Mean.Total.Abund.Mesograzers	# animals/grams plant
SD_Total_Abund_Mesograzers	Standard deviation of Mean.Total.Abund.Mesograzers	# animals/grams plant
Mean_Std_Total_Abund	Mean total abundance of epifauna per plot sample standardized by the total dry mass (g) of macrophytes from which the sample was collected	# animals/grams plant
SE_Std_Total_Abund	Standard error of Mean.Std.Total.Abund	# animals/grams plant
SD_Std_Total_Abund	Standard deviation of Mean.Std.Total.Abund	# animals/grams plant
Mean_Std_Total_Abund_Mesograzers	Mean total abundance of epifauna per plot sample identified as mesograzer taxa; standardized by the total dry mass (g) of macrophytes from which the sample was collected	# animals/grams plant
SE_Std_Total_Abund_Mesograzers	Standard error of Mean.Std.Total.Abund.Mesograzers	# animals/grams plant
SD_Std_Total_Abund_Mesograzers	Standard deviation of Mean.Std.Total.Abund.Mesograzers	# animals/grams plant
Site_Epifaunal_Richness	Total richness of epifauna at the site. Richness counts based on lowest taxonomic resolution identified per specimen (primarily species level)	unitless
Site_Mesograzer_Richness	Total richness of epifauna identified as mesograzer taxa at the site. Richness counts based on lowest taxonomic resolution identified per specimen (primarily species level)	unitless
epifauna_max_size	Maximum sieve size (mm) of epifauna collected at the site	millimeters
epifauna_med_size	Median sieve size (mm) of epifauna collected at the site	millimeters
mesograzers_max_size	Maximum sieve size (mm) of epifauna identified to be mesograzer taxa collected at the site	millimeters
mesograzers_med_size	Median sieve size (mm) of epifauna identified to be mesograzer taxa collected at the site	millimeters

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## Instruments

<b>Dataset-specific Instrument Name</b>	
<b>Generic Instrument Name</b>	Automated DNA Sequencer
<b>Generic Instrument Description</b>	General term for a laboratory instrument used for deciphering the order of bases in a strand of DNA. Sanger sequencers detect fluorescence from different dyes that are used to identify the A, C, G, and T extension reactions. Contemporary or Pyrosequencer methods are based on detecting the activity of DNA polymerase (a DNA synthesizing enzyme) with another chemoluminescent enzyme. Essentially, the method allows sequencing of a single strand of DNA by synthesizing the complementary strand along it, one base pair at a time, and detecting which base was actually added at each step.

<b>Dataset-specific Instrument Name</b>	
<b>Generic Instrument Name</b>	CHN Elemental Analyzer
<b>Generic Instrument Description</b>	A CHN Elemental Analyzer is used for the determination of carbon, hydrogen, and nitrogen content in organic and other types of materials, including solids, liquids, volatile, and viscous samples.

<b>Dataset-specific Instrument Name</b>	
<b>Generic Instrument Name</b>	Refractometer
<b>Dataset-specific Description</b>	Used to measure salinity
<b>Generic Instrument Description</b>	A refractometer is a laboratory or field device for the measurement of an index of refraction (refractometry). The index of refraction is calculated from Snell's law and can be calculated from the composition of the material using the Gladstone-Dale relation. In optics the refractive index (or index of refraction) $n$ of a substance (optical medium) is a dimensionless number that describes how light, or any other radiation, propagates through that medium.

<b>Dataset-specific Instrument Name</b>	
<b>Generic Instrument Name</b>	Temperature Logger
<b>Dataset-specific Description</b>	HOBO Pendant temperature loggers
<b>Generic Instrument Description</b>	Records temperature data over a period of time.

<b>Dataset-specific Instrument Name</b>	
<b>Generic Instrument Name</b>	Thermal Cycler
<b>Generic Instrument Description</b>	A thermal cycler or "thermocycler" is a general term for a type of laboratory apparatus, commonly used for performing polymerase chain reaction (PCR), that is capable of repeatedly altering and maintaining specific temperatures for defined periods of time. The device has a thermal block with holes where tubes with the PCR reaction mixtures can be inserted. The cycler then raises and lowers the temperature of the block in discrete, pre-programmed steps. They can also be used to facilitate other temperature-sensitive reactions, including restriction enzyme digestion or rapid diagnostics. (adapted from <a href="http://serc.carleton.edu/microbelife/research_methods/genomics/pcr.html">http://serc.carleton.edu/microbelife/research_methods/genomics/pcr.html</a> )

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## Deployments

### ZEN2\_2014

<b>Website</b>	<a href="https://www.bco-dmo.org/deployment/659814">https://www.bco-dmo.org/deployment/659814</a>
<b>Platform</b>	eelgrass_beds_global
<b>Start Date</b>	2014-05-16
<b>End Date</b>	2014-09-29
<b>Description</b>	eelgrass community studies

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## Project Information

### Global biodiversity and functioning of eelgrass ecosystems (Zostera Experimental Network 2) (ZEN 2)

**Website:** <http://zenscience.org>

**Coverage:** 20+ sites located throughout the northern hemisphere

#### *Description from NSF award abstract:*

This research will produce the second generation of a global collaborative research project, the Zostera Experimental Network (ZEN), to quantify the interacting influences of environmental forcing, biodiversity, and food-web perturbations on structure and functioning of eelgrass (*Zostera marina*) beds, the foundation of important but threatened coastal ecosystems worldwide. Partners at 40 sites in 14 countries will conduct parallel, standardized field sampling of producer and consumer biomass and diversity, and measure grazing and predation rates, to produce a global map of biodiversity, biomass distribution among trophic levels, and ecosystem processes in eelgrass habitats. Partners at a subset of core sites will conduct factorial experiments to characterize the interaction of nutrient loading, predator loss, and biogenic habitat structure (eelgrass density) in mediating producer growth and trophic processes in eelgrass. Finally, guided by the results from mechanistic experiments, the global field data will be used to test specific hypotheses about impacts of climate warming, nutrient loading, and declining biodiversity on eelgrass ecosystems via structural equation modeling, a uniquely powerful approach to dissecting complex interacting networks of causality. The proposed research will characterize in unprecedented detail how environmental forcing, biodiversity, and food-web processes interact to mediate functioning of a coastal ecosystem on a global scale. There are four general objectives:



1. Quantify linkages between eelgrass genetic diversity, growth, and provision of animal habitat;
2. Quantify the influence of eelgrass habitat structure on consumer-prey interactions, secondary production, and trophic transfer;
3. Identify mechanisms for the influence of grazer diversity on algal control;
4. Develop a global map of grazing and predation intensity to assess the relative importance of bottom-up and top-down forcing in eelgrass beds.

This program's integrated characterization of biodiversity, ecosystem state variables, and process rates across the globe is arguably unique in any marine system. It builds on promising results from the first generation of ZEN to allow for the first time a rigorous analysis of links between biodiversity and ecosystem functioning in a natural system on a global scale. As part of this analysis, the proposed research will provide the most comprehensive analysis yet of the controversial question of the relative importance of bottom-up and top-down forcing in seagrass ecosystems, an issue of fundamental importance to management and conservation.

Seagrasses and the many ecosystem services they provide are declining worldwide. This project's data on higher trophic levels and food-web interactions will provide a valuable and overdue complement to the many monitoring programs around the world that focus primarily on seagrasses and water quality, and will ultimately be made available to parameterize and test models of threatened seagrass ecosystems at a higher level of resolution ecological reality than previously possible. The success of the *Zostera* Experimental Network (ZEN) is evidenced by the continuation of all but one partner in the second generation (ZEN 2), and recruitment of nearly the same number of new partners to this global collaboration. This research will solidify and expand this network by more than doubling the number of participating sites, collaborating with parallel European Union and Japanese efforts, and integrating the world's largest and most successful seagrass restoration project at the Virginia Coast LTER site.

*Note:* This is an NSF-funded Collaborative Research project.

Also see: [ZEN project](#) BCO-DMO page.

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## Funding

Funding Source	Award
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1336206</a>
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1336741</a>
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1336905</a>

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