

Database of published habitat restoration studies from 1995, 2005, and 2015

Website: <https://www.bco-dmo.org/dataset/747668>

Data Type: Other Field Results, document

Version: 1

Version Date: 2018-09-04

Project

» [CAREER: Linking genetic diversity, population density, and disease prevalence in seagrass and oyster ecosystems](#) (Seagrass and Oyster Ecosystems)

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Abstract

Database of published habitat restoration studies from 1995, 2005, and 2015.

Table of Contents

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

Coverage

Temporal Extent: 1995 - 2015

Dataset Description

We systematically searched 27 international general science, conservation, and restoration-specific journals for published studies in 3 representative years (1995, 2005, 2015). Once studies were identified (N=559), we examined each individually to determine whether it was an empirical restoration (i.e., including a specific restoration action for which data were collected) or not. For empirical restorations, we identified the ecosystem, the habitat within the ecosystem, if the restoration project involved the active planting or translocation of target species, and how many, and whether the restoration included a biodiversity component (i.e., consideration of taxonomic richness, diversity, or composition). Finally, for those studies including a biodiversity component, we examined the stage of restoration incorporating biodiversity (design/implementation or monitoring/response), and the level of biodiversity (genetic, species, functional, or trophic).

Data Processing Description

In our targeted analysis of specific journals, we then tested whether the proportion of empirical restorations varied by year (1995, 2005, 2015) or by journal, using a binomial generalized linear model (GLM) with logit link, with each study categorized as empirical (181 studies) or not empirical (378 studies). Within the 181 empirical studies, we evaluated whether the proportion of studies including a biodiversity component differed across years, ecosystem, or habitat within ecosystem, again using a binomial GLM with logit link. Finally, we examined whether the proportion of studies including biodiversity (108 studies) in the design / implementation stage vs.

in the monitoring stage varied across ecosystems or habitats within ecosystems using a binomial GLM with logit link. All analyses were conducted in R Studio.

BCO-DMO Processing Notes:

- added conventional header with dataset name, PI name, version date
- modified parameter names to conform with BCO-DMO naming conventions
- removed special characters from Authors field.
- replaced commas with semi-colons in the Authors field.

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

Data Files

File
hab_res.csv (Comma Separated Values (.csv), 48.82 KB) MD5:32a772bab08c21ea5d8ee27b8839062c
Primary data file for dataset ID 747668

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

Related Publications

Hughes, A. R., Grabowski, J. H., Leslie, H. M., Scyphers, S., & Williams, S. L. (2017). Inclusion of Biodiversity in Habitat Restoration Policy to Facilitate Ecosystem Recovery. *Conservation Letters*, 11(3), e12419.

doi:[10.1111/conl.12419](https://doi.org/10.1111/conl.12419)

Results

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Methods

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

Parameters

Parameter	Description	Units
ID	Unique numerical identifier for each study	unitless
Journal	Journal the study was published in	unitless
Year	Year of publication	unitless
Authors	Abbreviated author list of publication	unitless
Empirical	Binomial variable categorizing each study as an empirical restoration study: 0 = not empirical; 1 = empirical	unitless
Not_empirical	Binomial variable categorizing each study as non empirical restoration study or not: 1 = not empirical; 0 = empirical	unitless
Ecosystem	Categorical variable describing focal ecosystem of the study: terrestrial; estuarine/marine; freshwater	unitless
Biodiversity	Binomial variable categorizing each study as having a biodiversity component: 0 = no; 1 = yes	unitless
No_biodiversity	Binomial variable categorizing each study as not having a biodiversity component: 0 = yes; 1 = no	unitless
Biodiversity_in_design	Binomial variable categorizing each study as having a biodiversity component in the design phase of the restoration: 0 = no; 1 = yes	unitless
Biodiversity_in_monitoring	Binomial variable categorizing each study as having a biodiversity component in the monitoring phase of the restoration: 0 = no; 1 = yes	unitless
Genetic_diversity	Binomial variable for whether the biodiversity component included genetic diversity: yes or no	unitless
Species_diversity	Binomial variable for whether the biodiversity component included species diversity: yes or no	unitless
Functional_diversity	Binomial variable for whether the biodiversity component included functional diversity (number or composition of functional groups): yes or no	unitless
Trophic_diversity	Binomial variable for whether the biodiversity component included trophic diversity (number or composition of trophic levels): yes or no	unitless
Species_actively_transplanted	Binomial variable for whether species were actively added or transplanted during the restoration process: yes or no	Number of species
Total_number_species_restored	If species were actively transplanted; the total number of species reported to have been restored across the entire project	Number of species
Max_number_species_restored_per_plot_patch	If species were actively transplanted; the maximum number of species planted in a given plot or patch	Number of species

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

Project Information

CAREER: Linking genetic diversity, population density, and disease prevalence in seagrass and oyster ecosystems (Seagrass and Oyster Ecosystems)

Coverage: Coastal New England

NSF Award Abstract:

Disease outbreaks in the ocean are increasing, causing losses of ecologically important marine species, but the factors contributing to these outbreaks are not well understood. This 5-year CAREER project will study disease prevalence and intensity in two marine foundation species - the seagrass *Zostera marina* and the Eastern oyster *Crassostrea virginica*. More specifically, host-disease relationships will be explored to understand how genetic diversity and population density of the host species impacts disease transmission and risk. This work will pair large-scale experimental restorations and smaller-scale field experiments to examine disease-host relationships across multiple spatial scales. Comparisons of patterns and mechanisms across the two coastal systems will provide an important first step towards identifying generalities in the diversity-density-disease relationship. To enhance the broader impacts and utility of this work, the experiments will be conducted in collaboration with restoration practitioners and guided by knowledge ascertained from key stakeholder groups. The project will support the development of an early career female researcher and multiple graduate and undergraduate students. Students will be trained in state-of-the-art molecular techniques to quantify oyster and seagrass parasites. Key findings from the surveys and experimental work will be incorporated into undergraduate courses focused on Conservation Biology, Marine Biology, and Disease Ecology. Finally, students in these courses will help develop social-ecological surveys and mutual learning games to stimulate knowledge transfer with stakeholders through a series of workshops.

The relationship between host genetic diversity and disease dynamics is complex. In some cases, known as a dilution effect, diversity reduces disease transmission and risk. However, the opposite relationship, known as the amplification effect, can also occur when diversity increases the risk of infection. Even if diversity directly reduces disease risk, simultaneous positive effects of diversity on host density could lead to amplification by increasing disease transmission between infected and uninfected individuals. Large-scale field restorations of seagrasses (*Zostera marina*) and oysters (*Crassostrea virginica*) will be utilized to test the effects of host genetic diversity on host population density and disease prevalence/intensity. Additional field experiments independently manipulating host genetic diversity and density will examine the mechanisms leading to dilution or amplification. Conducting similar manipulations in two marine foundation species - one a clonal plant and the other a non-clonal animal - will help identify commonalities in the diversity-density-disease relationship. Further, collaborations among project scientists, students, and stakeholders will enhance interdisciplinary training and help facilitate the exchange of information to improve management and restoration efforts. As part of these efforts, targeted surveys will be used to document the perceptions and attitudes of managers and restoration practitioners regarding genetic diversity and its role in ecological resilience and restoration.

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

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1652320

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