

Database summarizing independent studies of nekton taxa associated with oyster reefs

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Project

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

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Abstract

This dataset summarizes independent studies of nekton taxa associated with oyster reefs off of the Atlantic and Gulf Coasts of the United States.

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Coverage

Temporal Extent: 1958 - 2018

Methods & Sampling

Literature review:

First, we determined the variety of reef characteristics reported by studies investigating nekton recruitment enhancement by oyster reefs using citations from the reference list of a recently completed meta-analysis (zu Ermgassen et al. 2016). We identified nekton families that were regularly reported at oyster reef and control habitats, including both resident (i.e., species that feed, breed, and shelter on reefs long after initial recruitment, Coen et al. 1999; Harding and Mann 2000) and transient (i.e., species that recruit to structured habitats but are more widely distributed across multiple habitats after recruitment, Harding and Mann 2001) reef-associated species. We also performed forward searches in Google Scholar on two published syntheses:

Peterson et al. (2003) and zu Ermgassen et al. (2016). We retained studies that met the following criteria: 1) authors quantified density or relative abundance of target nekton families at both oyster reefs (or experimental units that contained oyster shell and served as a mimic for reef habitat; e.g., Humphries et al. 2011) and unstructured mud or sand habitats within the same study; 2) restored reefs used oyster shell, including shell piles, cultch, bagged shell, or shell piles from other species (e.g., surf clams) if topped by oyster shell; 3) restored reefs were within the tidal extent of natural reefs (< 10 m deep relative to mean low water [MLW] at the base of the reef; Kennedy and Sanford 1999), 4) fishing gear(s) quantitatively censused juveniles; and 5) authors reported densities or abundances of target nekton by species or family.

Data Extraction:

We extracted densities or abundances, measures of spread (standard deviation or standard error), and sample sizes of each nekton species from oyster reefs and their paired unstructured control habitat patches. We extracted data for nine nekton families, including reef residents: toadfish (Batrachoididae), blennies (Blenniidae), gobies (Gobiidae), and skiliffish (Gobiesocidae, which were later removed due to limited data availability); and reef transients: grunts (Haemulidae), snappers (Lutjanidae), swimming crabs (Portunidae), drums (Sciaenidae), and porgies (Sparidae; Table 1 of Davenport et al. 2021). We normalized densities to mean individuals m⁻², abundances to mean individuals per sample (relative abundances), and measures of spread to one standard error of the mean (Appendix S2 of Davenport et al. 2021). We extracted tidal zone (subtidal or intertidal), reef type (restored or natural), restoration method (reefs restored with or without live oysters), and when available, reef size (standardized to m²), vertical relief (distance from bare sediment to the highest point on the reef, standardized to m), tidal elevation (at the base of the reef, in m relative to MLW), adult oyster density (individuals m⁻² > 75 mm in shell height, or specified as adult by the authors), and the year of restored reef construction, from which we calculated reef age (Appendix S1: Table 1; Appendix S2 of Davenport et al. 2021).

Data Processing Description

Analyses:

To compare nekton recruitment to oyster reefs versus unstructured control habitat, we calculated log response ratios (LRRs, Hedges et al. 1999) with 95% confidence intervals by family (Appendix S2 of Davenport et al. 2021). An LRR with CIs > 0 implies that nekton recruitment was enhanced by oyster reefs, an LRR with CIs < 0 implies the opposite, and an LRR with CIs that include 0 implies no difference in recruitment between oyster reef and control habitats. For each research question, we assessed data publication bias with funnel plots (Appendix S3 of Davenport et al. 2021) and data availability with mosaic and violin plots (Appendix S4 of Davenport et al. 2021).

To assess whether recruitment enhancement varied as a function of reef type (natural or restored) and nekton family, we conducted linear mixed model analyses separately for intertidal and subtidal reefs that included two categorical factors (reef type and nekton family) and their interaction as fixed effects, with study as a random effect. We conducted mixed model analyses separately by tidal zone since subtidal and intertidal habitats harbor different nekton communities (Lehnert and Allen 2002), and subtidal and intertidal oyster reefs are distributed unevenly in our database: intertidal reefs are more prevalent on the Atlantic coast and subtidal reefs are more common in the Gulf of Mexico (Fig. 1; Appendix S1: Table S1 of Davenport et al. 2021). Furthermore, the reef characteristics in our database differed across tidal zones (Appendix S4: Fig. S1-S12 of Davenport et al. 2021). We removed any family that was represented by fewer than three independent studies and/or fewer than 10 independent LRRs ("NA" on Fig. 2 of Davenport et al. 2021). Results of randomization and resampling in support of these criteria are presented in Appendix S5 of Davenport et al. (2021).

To evaluate the effects of restored reef characteristics (i.e., reef size, vertical relief, and age) on recruitment enhancement, we focused on restored reefs only, and performed linear mixed effect regression models with orthogonal polynomials (first and second order) for the continuous reef characteristics as fixed effects, and study as a random effect. We conducted separate analyses for each reef characteristic, nekton family, and tidal zone. We did not model families represented by fewer than three independent studies and/or 10 independent LRRs covering different values of the reef characteristics (e.g., reef sizes, vertical reliefs, or ages; "insufficient data" in Figs. 3-8 of Davenport et al. 2021), and results are not reported or plotted for models that did not converge. Since not all families were represented at all values of each reef characteristic (e.g., all vertical reliefs or sizes), we performed separate analyses for each family and included all available data (but for combined-family approaches, see Appendix S2 (Davenport et al. 2021) for methods and Appendix S5 of Davenport et al. 2021 for results). We also examined the influence of tidal elevation on recruitment enhancement for each family using linear mixed effect regression models with orthogonal polynomials (first and second order) for tidal elevation as a fixed effect and study as a random effect (Appendix S5 of Davenport

et al. 2021). Where models indicated that predictor variables are on substantially different scales (i.e. reef size) we rescaled using natural log transformation.

All models were weighted by sample size (Appendix S2 of Davenport et al. 2021). All analyses were conducted in R 3.6.1 (R Core Team, 2019) on the RStudio IDE 1.2.1335 (RStudio Team, 2019).

BCO-DMO processing description:

- Adjusted field/parameter names to comply with BCO-DMO naming conventions;
- Missing data identifier 'NA' replaced with 'nd' (BCO-DMO's default missing data identifier);
- Added a conventional header with dataset name, PI names, version date;
- Removed commas from the "embayment" column;
- Rounded oys_fish, con_fish, and LRR to 3 decimal places;
- Replaced "Humphries 2011" with "Humphries et al. 2011" in the study_name column.

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Data Files

File
meta-analysis_data.csv (Comma Separated Values (.csv), 299.71 KB) MD5:b17911f3a1764001b6fb56cb681ecac0
Primary data file for dataset ID 845755

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Related Publications

Coen, Loren D., Mark W. Luckenbach, and Denise L. Breitburg. "The Role of Oyster Reefs as Essential Fish Habitat: A Review of Current Knowledge and Some New Perspectives." In American Fisheries Society Symposium, 22:438–54, 1999.

Methods

Davenport, T. M., Hughes, A. R., Ermgassen, P. S. E., & Grabowski, J. H. (2021). Recruitment enhancement varies by taxonomic group and oyster reef habitat characteristics. *Ecological Applications*, 31(5). Portico. <https://doi.org/10.1002/eap.2340>

Results

Harding, J. M., & R. Mann. "Oyster Reefs as Fish Habitat: Opportunistic Use of Restored Reefs by Transient Fishes." *Journal of Shellfish Research* 20, no. 3 (2001): 951–59., *Methods*

Methods

Harding, JM and Mann, Roger L., Estimates of naked Goby (*Gobiosoma bosc*), striped blenny (*Chasmodes bosquianus*) and Eastern oyster (*Crassostrea virginica*) larval production around a restored Chesapeake Bay oyster reef (2000). *Bulletin of Marine Science*, 66(1), 29-45. <https://scholarworks.wm.edu/vimsarticles/1527>

Methods

Hedges, L. V., Gurevitch, J., & Curtis, P. S. (1999). THE META-ANALYSIS OF RESPONSE RATIOS IN EXPERIMENTAL ECOLOGY. *Ecology*, 80(4), 1150–1156. doi:[10.1890/0012-9658\(1999\)080\[1150:tmaorr\]2.0.co;2](https://doi.org/10.1890/0012-9658(1999)080[1150:tmaorr]2.0.co;2)

Results

Humphries, A. T., La Peyre, M. K., Kimball, M. E., & Rozas, L. P. (2011). Testing the effect of habitat structure and complexity on nekton assemblages using experimental oyster reefs. *Journal of Experimental Marine Biology and Ecology*, 409(1-2), 172–179. doi:[10.1016/j.jembe.2011.08.017](https://doi.org/10.1016/j.jembe.2011.08.017)

Methods

Kennedy, V. S., & Sanford, L. P. (1999). The morphology and physical oceanography of unexploited oyster reefs in North America. *Oyster Reef Habitat Restoration: A Synopsis and Synthesis of Approaches*. Virginia Institute of Marine Science Press, Gloucester Point, VA, 25-46.

Methods

Lehnert, R. L., & Allen, D. M. (2002). Nekton use of subtidal oyster shell habitat in a Southeastern U.S. estuary. *Estuaries*, 25(5), 1015–1024. doi:[10.1007/bf02691348](https://doi.org/10.1007/bf02691348)

Methods

Peterson, C. H., Grabowski, J. H., & Powers, S. P. "Estimated Enhancement of Fish Production Resulting from Restoring Oyster Reef Habitat: Quantitative Valuation." *Marine Ecology Progress Series* 264 (2003): 249-64. <https://doi.org/10.3354/meps264249>.

Methods

R Core Team (2019). R: A language and environment for statistical computing. R v3.5.1. R Foundation for Statistical Computing, Vienna, Austria. URL <https://www.R-project.org/>
Software

RStudio Team (2019). RStudio: Integrated Development for R. RStudio, Inc., Boston, MA. URL <http://www.rstudio.com/>.
Software

zu Ermgassen, P. S. E., Grabowski, J. H., Gair, J. R., & Powers, S. P. (2015). Quantifying fish and mobile invertebrate production from a threatened nursery habitat. *Journal of Applied Ecology*, 53(2), 596-606. doi:[10.1111/1365-2664.12576](https://doi.org/10.1111/1365-2664.12576)

Methods

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Parameters

Parameter	Description	Units
line_no	number assigned to each line (row) in the dataset	NA
author	first author's surname	NA
pub_year	year study was published, or unpublished data were made available to us	NA
study_name	shorthand name of the study; e.g. Smith et al. 2000	NA
study	separate number assigned to each study, in the order they were entered in the dataset	NA
exp_no	Letter representing the experiment within a study (in order it was entered). A = first experiment of the study. B = second experiment of the study, and so on. Experiments include different locations, sampling gear, experimental comparisons within a study.	NA
rep_no	Number assigned to a replicate within an experiment in the order they were entered into the dataset. 1 = first replicate of the experiment in a study, 2 = second replicate of an experiment within a study, and so on. Replicates represent repeated sampling events such as those repeated by year, season, or month.	NA
rep_id	Unique identifier for each replicate that is a concatenation of study, exp.no and rep.no.	NA
taxon	A common name for the nekton family.	NA
LH_cat	Categorical level of association with the oyster reef habitat. Resident: species that feed, breed, and shelter on reefs long after initial recruitment, Coen et al. 1999; Harding and Mann 2000). Transient: species that recruit to structured habitats but are more widely distributed across multiple habitats after recruitment, Harding and Mann 2001.	NA
family	scientific family name	NA
scientific_name	scientific species name	NA

oys_fish	density or relative abundance of fish species at oyster habitat	density (per meters squared), or relative abundance (e.g. fish per trap)
se_oys_fish	spread of fish density or relative abundance at oyster habitats	1 standard error of the mean
con_fish	density or relative abundance of fish species at control (mud or sand) habitat	density (per meters squared), or relative abundance (e.g. fish per trap)
se_con_fish	spread of fish density or relative abundance at control habitats	1 standard error of the mean
SI	subtidal or intertidal designation. S = oyster habitat is subtidal; I = oyster habitat is intertidal	NA
Con	restored or natural oyster habitat designation. Y = oyster habitat is constructed (restored); N = oyster habitat is natural	NA
Reef_size_m2	reported area of oyster habitat	meters squared
Height_m	maximum height of oyster habitat off of the seafloor	meters
Reef_age_yr	age of the oyster habitat (e.g. reef) in years when the replicate sample was taken. Calculated from sample.yr - con.yr. Reported as NA if multiple sampling years are pooled in a replicate.	year
tidal_elev_m_MLW	tidal elevation relative to mean low water (positive values are above MLW; negative values below MLW)	meters
LRR	Log Response Ratio of nekton density in oyster vs control habitat	NA
n_oys_ind	number of independent replicates in space used to construct the LRR	NA
n_time_ind	number of independent replicates in time used to construct the LRR	NA
n_rep_ind	total number of independent replicates at oyster habitat (product of n.oys.ind and n.time.ind). Used to weight experiment by sample size	NA
sample_yr	year samples taken at both oyster and control	year
con_yr	year the oyster habitat (e.. Reef) was constructed	year
ocean	ocean basin, ATL = Atlantic. GOM = Gulf of Mexico	NA
lat_dd	latitude in decimal degrees of either the most northern patch sampled per row (= individual study, substudy and replicate for a species), or the center in the case of a very large (>500m ²) oyster reef	decimal degrees
long_dd	longitude in decimal degrees of either the most northern patch sampled per row (= individual study, substudy and replicate for a species), or the center in the case of a very large (>500m ²) oyster reef	decimal degrees
state	US state (in state abbreviations) the samples were taken	NA
embayment	name of embayment inside which sampling is completed. If control is elsewhere, embayment refers to where the oyster treatment is located	NA

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.

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Funding

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

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