The implications of intraspecific trait variation from fish sampled in Rhode Island salt ponds from June to October 2018

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

Contributors	Affiliation	Role
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Abstract
This dataset represents an archive of the fish functional trait data in the Northeast Atlantic Ocean from fish sampled in the Rhode Island salt ponds from June to October 2018.

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Coverage

Spatial Extent: **N**:41.5023 **E**:-71.4503 **S**:41.3311 **W**:-71.7689
Temporal Extent: 2018-06-12 - 2018-10-17

Methods & Sampling

Study system
We conducted this study within six coastal lagoons on the southern shore of Rhode Island: Green Hill (GH) Pond, Ninigret Pond (NP), Point Judith (PJ) Pond, Potter Pond (PP), Quonochontaug Pond (QP), and Winnapaug Pond (WP; Fig. S1.1). The fish communities in these ponds comprise mostly marine species, as all ponds are connected to the ocean via a breach way and recruits settle via larval dispersal. We focused on trait variation within and across species in 13 fish functional traits which represent three important functional roles: (1) energy acquisition, (2) locomotion, and (3) nutrient recycling (Villéger et al. 2017). We chose to examine fish communities, as they have been well studied in the functional trait literature, offering a comprehensive understanding of the functional roles fish provide and functionally meaningful traits to measure (Dumay et al. 2004, Mason et al. 2007, Villéger et al. 2010, 2017, Albouy et al. 2011, Stuart-Smith et al. 2013, Mouillot et al. 2013, Yeager et al. 2017, McLean et al. 2019).

Fish community collections
We sampled the six coastal pond fish communities monthly from June to October 2018 via 150-foot beach seine surveys in collaboration with the Rhode Island Department of Environmental Management. We targeted

38 species which accounted for 99.4% of total abundance across the surveys. We aimed to collect 20 individuals per species evenly distributed across their size range based on past survey data. Once collected from the seine net, fish were either transferred into seawater containers for excretion incubations or euthanized immediately via a seawater-clove oil (Eugenol extract, *Syzygium aromaticum*) mixture (IACUC protocol #: 18-0622R). Euthanized fish were held on ice before returning to the lab for morphometric analysis. We collected a total of 708 fish across 39 species and 26 families. We analyzed a subset of 200 fish for nutrient recycling traits, resulting in an average of 18.63 + 2.6 fish per species for energy acquisition and locomotion traits and an average of 7.48 + 0.91 fish per family for nutrient recycling traits.

Energy acquisition and locomotion traits
We took a series of five photos for each fish: (*i*) lateral full body, (*ii*) lateral head, (*iii*) lateral head with mouth protruded, (*iv*) ventral full body, and (*v*) anterior with mouth open, all with a ruler in shot for length standardization (Fig. S2.1a-e). Using ImageJ analysis, we measured 15 morphometrics which was used to calculate five energy acquisition traits: (oral gape surface, oral gape shape, oral gape position, protrusion, eye size) and five locomotion traits: (eye position, body transverse surface, body transverse shape, pectoral fin position, caudal peduncle throttling) (Table 1; Albouy et al. 2011). These continuous functional trait measurements have been commonly used in morphological studies on fishes and are connected to diet or movement (Sibbing and Nagelkerke 2000, Dumay et al. 2004, Mason et al. 2007, Villéger et al. 2010).

Nutrient recycling traits
We conducted excretion incubations for nutrient recycling traits, targeting 27 fish families (N = 1-3 species per family), which accounted for 99.7% of total abundance across the survey. Within each family, we targeted 10 individuals evenly distributed across their size range. Following the removal from the seine net each individual fish was placed directly into a 3L sterile plastic bag of seawater taken from the site before collection. Two 60mL 0.7 μm filtered water samples were taken from each plastic bag directly before and after each incubation trial, resulting in a pre-and post-incubation water sample for both N and P concentrations. Water samples were placed on ice and frozen immediately once returning from the field and kept in a -20°C freezer until processing. Each incubation lasted 30 minutes with bags placed in a larger cooler to ensure minimal stress. After incubations, fish were euthanized with a seawater-clove oil mixture.

We analyzed all water samples for concentrations of ammonium ($NH4+$) and phosphate ($PO43-$) using two spectra-photometric assays of phenolhypochlorite (Solórzano 1969) and molybdenum blue (Murphy and Riley 1962) methods as modified by (Whiles et al. 2009). We calculated the difference between pre-and post-incubation water samples for both N and P concentrations to quantify the N and P contribution for each fish, (Fig. S2.1f-g). Lastly, we took the ratio of change of N to P for each fish to calculate the N:P functional trait.

All references to figures and tables are from Yeager, M. E. and A.R. Hughes. The implications of intraspecific trait variation for functional diversity. Diversity and Distributions. In Review.

Data Processing Description

Generalized additive model fitting
We fit generalized additive models (GAMs) to the 13 functional traits (response variables) with species or length as predictor variables to hindcast the functional traits of fish from past surveys collected by the Rhode Island Department of Environmental Management. GAMs model a response variable (e.g., functional trait) as the sum of nonlinear functions from different predictor variables such as species and fork length (Hastie and Tibshirani 1990). We utilized thin-plate penalized regression splines, which adds a penalty to the smoother function to avoid overfitting (Wood and Augustin 2002). Penalty weights were optimized using the generalized cross validation score which minimizes the root mean square error of the model fit to the data and balances model complexity with goodness-of-fit. To run all models, we used the function 'gam' of the mgcv R package (R Development Core Team 2013). We used the GAMs fit to each functional trait (Appendix S3 for model fits) to hindcast the functional traits of 30 fish species for which we had fork length data across 6 years and 6 ponds of survey data. This generated functional trait information for a total of 81,337 fish.

Intra- vs. interspecific trait distance analysis
We measured the Bray-Curtis dissimilarity within (intraspecific) and across (interspecific) species within functional trait space by constructing a dissimilarity matrix across every species-length combination using the function 'vegdist' within the vegan R package. We then tested for mean differences in intra- vs. interspecific distances across the total community using a two-sample T- test and differences in their distributions via a Kolmogorov-Smirnov (ks) test.

Functional diversity analysis

We examined three well-studied functional diversity metrics which measure diversity in multivariate trait space and can accommodate both continuous and qualitative traits (Villéger et al. 2008): Functional Richness (FRic), Functional Evenness (FEve), and Functional Divergence (FDiv). For each community, all species were plotted in functional trait space. FRic measures the total trait space filled by the community and is the area of the 'convex hull', or minimal polygon drawn to encompass all species and is scaled by total FRic across all communities. FEve is the evenness of abundance across trait space and is measured as the linearized distance of minimum spanning tree, which is a tree that connects all species in trait space with the minimum sum of branch length. Lastly, FDiv measures how community's abundances are distributed in the volume of trait space occupied. This metric is calculated as the deviations from the mean circle drawn though the species in trait space (which represents the mean distance to the centroid for each community). The higher abundance that is greater than the mean, the larger the FDiv. We used the Distance-based Functional Diversity Indices, 'dbFD', function in the FD R package (R Development Core Team 2013) to calculate all three metrics across all pond communities in two ways: (1) with traits averaged across species (as is most common in the literature; Mouillot et al. 2007, 2013, Villéger et al. 2010, 2012, Albouy et al. 2011, McLean et al. 2019) and (2) with intraspecific variation included. When using species averages, the functional trait by species matrix and the abundance by site matrix had a row and a column, respectively, for the species average. In contrast, when intraspecific variation was explicitly included, the functional trait matrix and the abundance matrix had a row and column, respectively, for each species-length combination.

For each functional diversity metric, we used simple regression to determine whether the slope relating the functional diversity metric with vs. without intraspecific trait information was significantly different from 1. Specifically, we ran a forced linear regression (intercept of zero) between the functional diversity metrics for each community calculated with vs. without intraspecific information and then determined whether the slope of the regression differed from 1 using a one-sample t-test: $t = \text{slope} - 1 \, SE_{\text{slope}}$. A significant slope means that functional diversity computed with intraspecific variation differs from that computed without intraspecific variation (i.e., including intraspecific trait information significantly alters the functional diversity metric).

Ecosystem function analysis
We calculated ecosystem function as the total biomass of the fish community within each pond and year. As with the functional trait dataset, we constructed a GAM with species and length as explanatory variables to calculate biomass from past survey data, based on the biomass (g) that was measured at the same time as the functional trait data collections. We then summed total biomass for each unique pond-year combination to generate an estimate of ecosystem function for each pond community through time. Using simple regression, we tested for relationships between FRic with or without intraspecific trait information and ecosystem function comparing the fit and slope between the two models.

BCO-DMO processing description:
- Converted dates to YYYY-MM-DD format
- Adjusted field/parameter names to comply with BCO-DMO naming conventions
- Missing data identifier 'NA' and '#DIV/0!' replaced with 'nd' (BCO-DMO's default missing data identifier)
- Added a conventional header with dataset name, PI names, version date
- Replaced positive "Narrow River" longitude values with negative values to correct for error in original spreadsheet

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Data Files

File
functional_trait_data_rhode_island_salt_pond_survey-1.csv (Octet Stream, 109.94 KB) MD5:f1484b398abe0c84206683e14f385f13
Primary data file associated with dataset 870857, version 1.

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Related Publications

Albouy, C., Guilhaumon, F., Villéger, S., Mouchet, M., Mercier, L., Culioli, J., Tomasini, J., Le Loc'h, F., & Mouillot, D. (2011). Predicting trophic guild and diet overlap from functional traits: statistics, opportunities and

limitations for marine ecology. Marine Ecology Progress Series, 436, 17–28.
https://doi.org/10.3354/meps09240
Methods

Dumay, O., Tari, P. S., Tomasini, J. A., & Mouillot, D. (2004). Functional groups of lagoon fish species in Languedoc Roussillon, southern France. Journal of Fish Biology, 64(4), 970–983.
https://doi.org/10.1111/j.1095-8649.2004.00365.x
Methods

Hastie, T. J., and R. J. Tibshirani. 1990. Generalized additive models. Chapman & Hall, London.
Methods

Mason, N. W. H., Lanoiselée, C., Mouillot, D., Irz, P., & Argillier, C. (2007). Functional characters combined with null models reveal inconsistency in mechanisms of species turnover in lacustrine fish communities. Oecologia, 153(2), 441–452. https://doi.org/10.1007/s00442-007-0727-x
Methods

McLean, M., Mouillot, D., Lindegren, M., Villéger, S., Engelhard, G., Murgier, J., & Auber, A. (2019). Fish communities diverge in species but converge in traits over three decades of warming. Global Change Biology, 25(11), 3972–3984. Portico. https://doi.org/10.1111/gcb.14785
Methods

Mouillot, D., Dumay, O., & Tomasini, J. A. (2007). Limiting similarity, niche filtering and functional diversity in coastal lagoon fish communities. Estuarine, Coastal and Shelf Science, 71(3–4), 443–456.
https://doi.org/10.1016/j.ecss.2006.08.022
Methods

Mouillot, D., Graham, N. A. J., Villéger, S., Mason, N. W. H., & Bellwood, D. R. (2013). A functional approach reveals community responses to disturbances. Trends in Ecology & Evolution, 28(3), 167–177.
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Methods

Murphy, J., & Riley, J. P. (1962). A modified single solution method for the determination of phosphate in natural waters. Analytica Chimica Acta, 27, 31–36. doi:10.1016/s0003-2670(00)88444-5
https://doi.org/10.1016/S0003-2670(00)88444-5
Methods

RCore Team (2013). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria (http://www.R-project.org/)
Software

SOLÓRZANO, L. (1969). DETERMINATION OF AMMONIA IN NATURAL WATERS BY THE PHENOLHYPOCHLORITE METHOD 1 1 This research was fully supported by U.S. Atomic Energy Commission Contract No. ATS (11-1) GEN 10, P.A. 20. Limnology and Oceanography, 14(5), 799–801.
doi:10.4319/lo.1969.14.5.0799
Methods

Sibbing, F. A., & Nagelkerke, L. A. J. (2000). Reviews in Fish Biology and Fisheries, 10(4), 393–437.
https://doi.org/10.1023/a:1012270422092 https://doi.org/10.1023/A:1012270422092
Methods

Stuart-Smith, R. D., Bates, A. E., Lefcheck, J. S., Duffy, J. E., Baker, S. C., Thomson, R. J., Stuart-Smith, J. F., Hill, N. A., Kininmonth, S. J., Airoldi, L., Becerro, M. A., Campbell, S. J., Dawson, T. P., Navarrete, S. A., Soler, G. A., Strain, E. M. A., Willis, T. J., & Edgar, G. J. (2013). Integrating abundance and functional traits reveals new global hotspots of fish diversity. Nature, 501(7468), 539–542. https://doi.org/10.1038/nature12529
Methods

Villéger, S., Brosse, S., Mouchet, M., Mouillot, D., & Vanni, M. J. (2017). Functional ecology of fish: current approaches and future challenges. Aquatic Sciences, 79(4), 783–801. https://doi.org/10.1007/s00027-017-0546-z
Methods

Villéger, S., Mason, N. W. H., & Mouillot, D. (2008). NEW MULTIDIMENSIONAL FUNCTIONAL DIVERSITY INDICES FOR A MULTIFACETED FRAMEWORK IN FUNCTIONAL ECOLOGY. Ecology, 89(8), 2290–2301.
https://doi.org/10.1890/07-1206.1
Methods

Villéger, S., Miranda, J. R., Hernández, D. F., & Mouillot, D. (2010). Contrasting changes in taxonomic vs. functional diversity of tropical fish communities after habitat degradation. Ecological Applications, 20(6), 1512–

1522. https://doi.org/[10.1890/09-1310.1](https://doi.org/10.1890/09-1310.1)
Methods

Whiles, M. R., Huryn, A. D., Taylor, B. W., & Reeve, J. D. (2009). Influence of handling stress and fasting on estimates of ammonium excretion by tadpoles and fish: recommendations for designing excretion experiments. Limnology and Oceanography: Methods, 7(1), 1–7. Portico. https://doi.org/[10.4319/lom.2009.7.1](https://doi.org/10.4319/lom.2009.7.1)
Methods

Wood, S. N., & Augustin, N. H. (2002). GAMs with integrated model selection using penalized regression splines and applications to environmental modelling. Ecological Modelling, 157(2–3), 157–177. https://doi.org/10.1016/s0304-3800(02)00193-x https://doi.org/10.1016/S0304-3800(02)00193-X
Methods

Yeager, L. A., Deith, M. C. M., McPherson, J. M., Williams, I. D., Baum, J. K., & Belmaker, J. (2017). Scale dependence of environmental controls on the functional diversity of coral reef fish communities. Global Ecology and Biogeography, 26(10), 1177–1189. Portico. https://doi.org/[10.1111/geb.12628](https://doi.org/10.1111/geb.12628)
Methods

Yeager, M. E. and A.R. Hughes. The implications of intraspecific trait variation for functional diversity. Diversity and Distributions. In Review.
Results

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Parameters

Parameter	Description	Units
Date	date organism was collected in format: YYYY-MM-DD	unitless
Pond	name of pond where the organism was collected	unitless
Latitude	latitude of the pond	decimal degrees
Longitude	longitude of the pond; negative values = west	decimal degrees
Scientific_name	scientific name of the organism to lowest taxonomic level possible	unitless
Common_name	common name of the organism	unitless
Biomass	weight of organinsm	grams
Standard_length	length of the fish from mouth to caudaul peduncle	millimeters
Fork_length	length of the fish from mouth to center of forked caudual fin	millimeters
Oral_gape_surface	ratio of mouth suface to body surface	unitless
Oral_gape_shape	ratio of mouth depth to mouth width	unitless
Oral_gape_position	ratio of mouth position	unitless
Protrusion	length the fish's jaw protudes when feeding	millimeters
Eye_size	ratio of eye depth to head depth	unitless
Eye_Position	ratio of eye height to head depth	unitless
Body_transversal_shape	ratio of body depth to body width	unitless
Body_transversal_surface	surface area of the fish's transversal plane	mm2 per gram
Pectoral_in_position	ratio of height of pectoral fin to body depth	unitless
Caudal_peduncle_throttling	ratio of the width of the caudal peduncle to the height of the caudal fin	unitless
Concentration_of_NH4	concentration of ammonia (NH4) from individual's excretion	Micromoles (uM)
Concentration_of_PO4	concentration of phosphate (PO4) from individual's excretion	Micromoles (uM)
N_P_ratio	ratio of NH4 to PO4 concentration	unitless

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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.

Funding

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