nature portfolio

Corresponding author(s): Brook L. Nunn

Last updated by author(s): Feb 20, 2025

Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our Editorial Policies and the Editorial Policy Checklist.

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed
☐	☒ The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒ The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☐	☒ A description of all covariates tested
☐	☒ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒ A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☐	☒ For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☐	☒ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☐	☒ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☒	☐ Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	no code for data collection used.
Data analysis	All resulting proteomic search results, protein accession numbers and annotation files, lipid data, symbiont density and clade data, chlorophyll data and R code for plot generation and data analysis have been deposited in GitHub (https://github.com/Nunn-Lab/Publication-coral-resilience). The transcriptome was translated using Transdecoder v 2.0.1. Comet 2022.01 was used to search the DDA mass spectrometry files. Differential relative protein abundances for resilient vs. susceptible corals were determined for each timepoint (T1 and T2) using the QPROT-QSPEC package. To determine if categories of proteins were enriched in the resilient vs. susceptible coral cohorts at the two timepoints, a biological enrichment strategy that analyzes Gene Ontology (GO) categorical terms was used to compare sets of detected proteins (MetaGOmics). MetaGOmics software (version 0.2.0; https://www.yeastrc.org/metagomics) identified the lowest common ancestor on each peptide's functional Gene Ontology (GO) assignment. Sequencing was performed on an Ion Torrent PGM. All 16S rRNA gene amplicon sequence data, processing steps and code for quality control on the microbiome data and analysis are available on GitHub (https://github.com/tanyabrown9/Resilient_vs_Susceptible_Mcapitata). A logistic regression analysis was conducted to assess the relationship between the proportion of Durusdinium symbionts pre-bleaching and coral mortality post-bleaching. Supplementary data 1b included coral genets classified as either "resilient" (survived) or "susceptible" (died)

and their respective proportions of Durusdinium symbionts. Rows with missing data were excluded from the analysis. The binary outcome variable (mortality) was coded as 1 for "susceptible" and 0 for "resilient." The model was fitted using the glm function in R with a binomial family to account for the binary nature of the response variable. Statistical significance of the relationship was assessed using p-values for the proportion of Durusdinium symbionts as the predictor variable.

All other statistical analyses of microbial taxonomy were conducted using R 4.0.3. The top 10 bacterial families in each sample type were selected for taxonomic analysis. Significant differences between bacterial families, susceptibility, and timepoints were carried out using a nested ANOVA. The Benjamini-Hochberg FDR was used to control the false discovery rate. Microbiome Multivariate Association with Linear Models was performed on the 16S rRNA sequencing data using the R package MaAsLin266.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

All raw MS proteomic data and protein FASTA files used for searching can be accessed at PRIDE accession PXD021262, a public proteomic data repository. All resulting proteomic search results, protein accession numbers and annotation files, lipid data, symbiont density and clade data, chlorophyll data, and R code for plot generation and data analysis have been deposited in GitHub https://github.com/Nunn-Lab/Publication-coral-resilience(https://github.com/Nunn-Lab/Publication-coral-resilience). All 16S rRNA gene amplicon sequence data, processing steps, PICRUSt2 functional predictions, and code for quality control on the microbiome data and analysis are available on GitHub as well (https://github.com/tanyabrown9/Resilient_vs_Susceptible_Mcapitata). All study data are included in the article and/or as SI Datasets. All sequences used in this study are publicly available through NCBI GenBank and ProteomeXchange PRIDE. Accession numbers and annotations are provided as supplementary files (Datasets S1-3) and all supplemental datasets and files can be found in Figshare project 237383 (https://figshare.com/projects/Protein_signatures_predict_coral_resilience_and_survival_to_thermal_bleaching_events/237383).

Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	not relevant
Reporting on race, ethnicity, or other socially relevant groupings	not relevant
Population characteristics	not relevant
Recruitment	not relevant
Ethics oversight	not relevant

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☐ Life sciences ☐ Behavioural & social sciences ☒ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Ecological, evolutionary & environmental sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	Montipora capitata was experimentally bleached to examine molecular and physiological signatures of intrinsic differences between corals that recover (resilient) compared to those that die (susceptible). All corals were collected and monitored for eight months post-bleaching to identify genets exhibiting long-term resilience and survival. Using an integrated systems-biology approach that included quantitative proteomics, 16S rRNA of the microbiome, total lipids, symbiont community composition and density, we explored molecular-level mechanisms of tolerance in corals pre- and post-bleaching.

Research sample	For this study we used the coral Montipora capitata. This species is locally abundant and a dominant reef-building coral in Hawai'i, United States. It is a small-polyp species (ca. 0.8 mm) that grows in branching and plating forms, or it can exhibit both morphologies in a single colony. Only the branching form was collected for this study. M. capitata is a resilient species with the ability to perform heterotrophic plasticity.
Sampling strategy	Seventy-four Montipora capitata (approximately 30 cm in diameter) were collected from Moku O Lo'e island (patch reef) located in Kāne'ohe Bay, O'ahu, Hawai'i (21.428°N, 157.792°W) in August 2017. Corals were brought to shore and acclimated in flow-through outdoor tanks at the Hawaii Institute of Marine Biology (HIMB) for two weeks at ambient conditions (28°C). At the time of collection, corals were divided in two pieces to compare physiological performance for the same genets with/without exposure to thermal stress. Individual colonies were collected more than 3 m apart and although no genetic analyses were conducted, they were considered to be different genets. Ten Montipora capitata coral genets were randomly selected from those that survived and those that died 3 months after the thermal exposure for downstream molecular level analyses.
Data collection	Field data was collected manually, either by snorkeling on the reef or by recording observations from the experimental tanks. Field data was collected by Tanya Brown, Lisa Rodrigues, Jeremy Axworthy and Jacqueline Padilla-Gamiño. Symbiont counts were obtained by separating the algae from the symbionts using centrifugation and symbiont pellets were homogenized prior to being counted using a hemocytometer. Chlorophyll a was extracted with 100% acetone and absorbance was measured with a light spectrophotometer. Chlorophyll a and symbiont densities were standardized to grams of ash-free dry weight (gdw) of coral tissue. This data was collected by Callum Backstrom and Jeremy Axworthy, managed by Lisa Rodrigues and Jacqueline Padilla-Gamiño. To obtain lipids whole fragments (tissue plus skeleton) were crushed and digested in a 2:1 chloroform:methanol solution, sequentially washed in a 0.88% KCl solution, dried under grade 5.0 N 2 gas to a constant weight and standardized to ash-free gdw of coral tissue. This data was collected by Lisa Rodrigues Microbial data was collected by preparing DNA libraries, high-throughput sequencing and bioinformatics processing. The processed data was analyzed to identify microbial species and diversity patterns. Microbial data was collected by Tanya Brown and Jesse Zaneveld. All proteomic samples were prepared by by Brook Nunn and Emma Timmins Schiffman and data is automatically collected on the mass spectrometer. This was managed by Brook Nunn.
Timing and spatial scale	Field and experimental data was collected from August 2014 to September 2015. Photographs to assess coral health in the field were collected every week throughout the experiment. Coral samples were collected at the beginning of the thermal stress experiment, three weeks after the end of the experiment. Branches from twelve (six resilient and six susceptible) M. capitata corals were collected at two time points: 1) August 30, 2017, after temperature acclimation in the tanks but before corals were bleached (T1) and 2) on October 1, 2017, 24 hours after bleached corals were gradually returned to ambient temperature (T2). All coral samples were collected 1 cm from the tip of a branch and snap frozen immediately in liquid nitrogen.
Data exclusions	No data was excluded.
Reproducibility	Reproducibility of experimental findings was assessed with preliminary studies.
Randomization	The two halves from each colony were randomly assigned to one of three outdoor flow-through tanks for the ambient temperature control group or one of three tanks for the bleaching treatment group. Throughout the experiment, corals were randomly rotated among tanks weekly to minimize any tank effects. Protein analyses completed included mass spectrometry based proteomics. Samples were prepped in randomized batches and then analyzed on the mass spectrometer in randomized order.
Blinding	Blinding was not relevant to our study because the study relied on directly measurable, quantitative data (e.g., temperature, genetic sequencing, lipids, chlorophyll, etc), subjective biases from researchers or participants is minimal. In our study there was no risk of observer bias.

Did the study involve field work? ☒ Yes ☐ No

Field work, collection and transport

Field conditions	Seawater temperature was around 28 +/- 0.9 ◦C.
Location	Samples were collected from the inner lagoon of Kaneohe Bay, surrounding the Hawai'i Institute of Marine Biology (HIMB, 21.428 ◦N, 157.792 ◦W). Samples were collected at 1-3 m depth.
Access & import/export	This research was conducted under Hawai'i Department of Land and Natural Resources Special Activity Permit No. 2018-46.
Disturbance	To minimize disturbance in the reef, we set the racks for the field experiments in areas where coral abundance was low.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Plants

Seed stocks	not relevant
Novel plant genotypes	not relevant
Authentication	not relevant