nature portfolio

Corresponding author(s): Giulia M. Marchioro

Last updated by author(s): 18 June 2026

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	Field photophysiological measurements were collected using a Diving-PAM II fluorometer (Walz GmbH, Germany) and a MINI-SPEC spectroradiometer. Confocal microscopy images were acquired using a Zeiss LSM 780 confocal microscope and processed using ZEN Black software (v14.0.16.201, Carl Zeiss). Symbiodiniaceae ITS2 sequence data were processed using SymPortal.
Data analysis	All statistical analyses were performed in R software (version 4.1.0; R Core Team, 2021)

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

The temperature datasets supporting this study are publicly available through the published shallow-to-mesophotic longitudinal monitoring datasets repository maintained by P. Bongaerts and collaborators (https://github.com/pimbongaerts/monitoring).

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	*Use the terms sex (biological attribute) and gender (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design; whether sex and/or gender was determined based on self-reporting or assigned and methods used.* *Provide in the source data disaggregated sex and gender data, where this information has been collected, and if consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected.* *Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.*
Reporting on race, ethnicity, or other socially relevant groupings	*Please specify the socially constructed or socially relevant categorization variable(s) used in your manuscript and explain why they were used. Please note that such variables should not be used as proxies for other socially constructed/relevant variables (for example, race or ethnicity should not be used as a proxy for socioeconomic status).* *Provide clear definitions of the relevant terms used, how they were provided (by the participants/respondents, the researchers, or third parties), and the method(s) used to classify people into the different categories (e.g. self-report, census or administrative data, social media data, etc.)* *Please provide details about how you controlled for confounding variables in your analyses.*
Population characteristics	*Describe the covariate-relevant population characteristics of the human research participants (e.g. age, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."*
Recruitment	*Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.*
Ethics oversight	*Identify the organization(s) that approved the study protocol.*

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	This study investigated bleaching susceptibility in the coral Madracis pharensis across a depth gradient during the 2023 Caribbean acute thermal stress event. The study examined the relationships among colony health status, dominant Symbiodiniaceae type, host fluorescence characteristics, and symbiont physiological traits.
Research sample	The study focused on colonies of the Caribbean reef-building coral Madracis pharensis from Snake Bay, Curaçao (12.139° N, 68.998° W). Colonies were surveyed for bleaching status at 10, 20, and 40 m depth during the 2023 Caribbean mass bleaching event. Colonies collected for physiological and genetic analyses originated from 10 and 20 m depth, whereas information on Symbiodiniaceae associations at 40 m depth was obtained from previously published observations from the same reef (Frade et al., 2008a). This species was selected because it spans a broad depth range and exhibits strong depth-related structuring of host and symbiont communities.
Sampling strategy	Bleaching prevalence was assessed through field surveys of Madracis pharensis colonies at 10, 20, and 40 m depth in Snake Bay, Curaçao, during November–December 2023. A total of 135 colonies were surveyed (10 m, n = 55; 20 m, n = 48; 40 m, n = 32). Physiological, genetic, and confocal microscopy analyses were conducted on 44 colonies collected from 10 m (n = 12) and 20 m (n = 32). Colonies from 40 m depth were not collected for laboratory analyses; but information on Symbiodiniaceae associations at this depth was obtained from a previously published study conducted at the same reef site (Frade et al., 2008a). The temperature datasets supporting this study are publicly available through the published shallow-to-mesophotic longitudinal monitoring datasets repository maintained by P. Bongaerts and collaborators (https://github.com/pimbongaerts/monitoring).
Data collection	Field surveys, photographic documentation, and physiological measurements were conducted by SCUBA diving at Snake Bay,

Data collection	Curaçao, during November–December 2023. Colony bleaching status was assessed visually in situ. Photochemical efficiency and fluorescence measurements were collected using a Diving-PAM II fluorometer and MINI-SPEC spectroradiometer. Coral fragments were collected for genetic, physiological, and confocal microscopy analyses. Samples for physiological and genetic analyses were flash-frozen in liquid nitrogen, transported to Vienna, Austria in liquid nitrogen and dry ice, and stored at −80°C upon arrival. Samples for microscopy were fixed in 4% paraformaldehyde (PFA), transported at 4°C, and maintained at 4°C until processing.
Timing and spatial scale	Data collection was conducted between November and December 2023 at Snake Bay, Curaçao (12.139° N, 68.998° W). Temperature records used to calculate Degree Heating Weeks were obtained from long-term monitoring datasets spanning 2022–2023.
Data exclusions	No data were excluded from confocal microscopy or physiological analyses in general, except Chl- c2 measurements, which were below detection limits and then were excluded. Non-Symbiodiniaceae sequences were removed using mothur, BLAST+, and Minimum Entropy 475 Decomposition. Only profiles supported by >200 reads were retained.
Reproducibility	Biological replication consisted of independent coral colonies sampled across depths, with each colony representing a biological replicate. For confocal microscopy analyses, nine tissue sections were examined per colony, and measurements were averaged across sections to obtain a single value for each colony prior to statistical analysis.
Randomization	Not relevant to this study as we sampled from naturally occurring populations across depth, and no experimental treatments were done.
Blinding	Not relevant to this study as we sampled from naturally occurring populations across depth, and no experimental treatments were done.

Did the study involve field work? ☒ Yes ☐ No

Field work, collection and transport

Field conditions	Fieldwork was conducted during November–December 2023, coinciding with the 2023 Caribbean mass bleaching event. Seawater temperatures exceeded 30°C across all monitored depths (10, 20, and 40 m) during the sampling period.
Location	Field surveys and coral sampling were conducted at Snake Bay, Curaçao (12.139° N, 68.998° W), Southern Caribbean. Colonies were were collected at 10 ± 3 m and 20 ± 3 m depth.
Access & import/export	Samples were exported from Curaçao and transported by air to Vienna, Austria, in compliance with all applicable regulations. Samples were exchanged between the CARMABI Institute (CITES# AN001) and the Natural History Museum Vienna (Naturhistorisches Museum Wien, CITES #AT017). Government-approved CITES documentation is enclosed here. All samples were collected in Curaçao (former Netherlands Antilles) under the collecting permits provided to CARMABI by the Curaçaoan Government (CARMABI 2022/21467 – copy included). The samples were formerly archived in CARMABI's collection under number CAR-SCLER-80-2760 to CAR-SCLER-80-3689. Samples designated for physiological and genetic analyses were transported in liquid nitrogen dry shippers and on dry ice in proper containers. Samples fixed in 4% paraformaldehyde were transferred to phosphate-buffered saline (PBS) following fixation and transported at ambient temperature. To prevent leakage during transport, Falcon tube containing the samples were sealed with Parafilm and placed in sealed boxes within checked luggage.
Disturbance	Disturbance to the reef was minimized by collecting only small coral fragments required for the analyses and by avoiding unnecessary contact with the reef substrate and other animals.

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

Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

Laboratory animals	This study did not involve laboratory animals.
Wild animals	The study involved colonies of the reef-building coral Madracis pharensis surveyed and sampled in their natural habitat at Snake Bay, Curaçao (12.139° N, 68.998° W) during November–December 2023. Colonies were photographed and small fragments were collected by SCUBA divers for physiological, genetic, and microscopy analyses.
Reporting on sex	Sex was not determined and was therefore not included as a variable in the study design or analyses.
Field-collected samples	Coral fragments were collected from colonies at 10 ± 3 m and 20 ± 3 m depth. Samples designated for physiological and genetic analyses were flash-frozen in liquid nitrogen immediately after collection and stored at −80°C until processing. Samples intended for microscopy were fixed in 4% paraformaldehyde at 4°C for 6 h and subsequently stored in PBS until further processing. Samples were transported to Vienna, Austria, in liquid nitrogen and dry ice. Upon arrival, samples for genetics and physiological measurements were stored at −80°C , while samples fixed in PBS were stored at 4°C until further processing.
Ethics oversight	Coral sampling was conducted under permits issued by the relevant authorities in Curaçao.

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

Plants

Seed stocks	*Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.*
Novel plant genotypes	*Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.*
Authentication	*Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosiacism, off-target gene editing) were examined.*