

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 (<i>n</i>) 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 <i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>
☒	☐ 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
☒	☐ 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 <i>d</i> , Pearson's <i>r</i>), 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	GG Macros software was developed by our group and distributed free-of charge on the group's website: https://home.physics.wisc.edu/gilbert/software/ . The software runs in Igor Pro 8. GG Macros was developed to analyze synchrotron spectroscopy data acquired using Photo Emission Electron Microscopy (PEEM). Myriad Maps, described in Schmidt et al. 2024, are built using GG Macros v1.0.0 in Igor Pro 8.
Data analysis	Code was developed to analyze the Myriad Maps produced from data and is described in this publication, accessible on GitHub and Zenodo with DOI: https://doi.org/10.5281/zenodo.18175786 . Code built using MATLAB R2023b is designed to extract the precursor proportion from MM as a function of distance from the coral skeleton edge. These precursor proportions are then used to perform in the analysis in this publication. A series of exponential fitting functions using Scipy 1.10.1, Pandas 2.0.1, and Numpy 1.24.3 packages were written in Python 3.11.3 and displayed using Matplotlib 3.7.1. All code is accessible in the corresponding Zenodo/Github DOI.

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 precursor proportions generated in this work from MMs and Stylophora pistillata coral nubbin growth data have been deposited in the data.xlsx file available on Zenodo and GitHub 57 with DOI <https://doi.org/10.5281/zenodo.18175786> and is source data to reproduce Fig. 2C,D, Fig. 3B,C, Fig. 4 B,C, Fig. 5B, Supplementary Figs 2, 4, 5, 6, Table 1, and Supplementary Tables 3, 4, and 5. The data used to produce MMs is available with no restricted access and can be obtained by contacting the corresponding author of this work at any period after publication of this work.

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

Life sciences study design

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

Sample size

No a priori sample-size calculation was performed. Sample sizes were constrained to by the experimental limitations of the PEEM instrument. A total of 28 50 × 50 µm regions of fresh forming coral skeleton were collected. Rigorous data exclusion criteria led to a final analysis sample size of 8 regions from 4 different coral skeletons. Although the number of regions was not predetermined, all analyses were conducted on a pixel-resolved basis, with ~10⁶ pixels per region, providing a large effective sample size for statistical analysis. Conclusions are based on consistent patterns observed across multiple regions of independent skeleton surfaces.

Data exclusions

Data exclusion criteria were used to determine the final 8 regions of the analysis. The criteria consisted of three parts. The first step was to produce MMs for all areas and confirm that each area exhibited a presence of precursor phases. Many regions consisted entirely of mature aragonite presumably because they had already crystallized fully at the time of analysis, thus, they had to be excluded. Secondly, two stacks and therefore 2 MMs were acquired and processed for each region, to determine the energy landscape of all pixels in that region. If any phase transitions from the 1st to the 2nd Stack went thermodynamically uphill, in any pixels of an region, that region was excluded from this analysis. This second step is a measure of the acquisition quality at PEEM. A third and final step to select final regions for this analysis was to

examine the precursor abundance deeper ($> 4 \mu\text{m}$) into the coral skeleton. Any regions where one or more precursors increased as a function of distance from the edge were excluded. This only occurred in a few regions and in those regions the reason for precursor increase may have been the presence of centers of calcification (CoCs) near the edge. The first two criteria existed before finalizing regions for the analysis. The third criteria regarding CoCs was developed after identifying the pattern of increasing precursor proportion within several nonuniform, isolated precursor heavy areas deep inside the forming coral skeletons.

Replication	The findings of each area were tested several times with different tools, and all arrived at the same final finding except in one experimental group. The findings of the mature aragonite group are found to exponentially rise just as all other experimental groups, but during the analysis were also found to logarithmically rise at comparable R2 values to exponential growth. These results can be reproduced using available data and software provided in the linked coding repositories on GitHub and Zenodo.
Randomization	Coral skeletons used in the analysis were separated into groups by pH, one group at pH 8.05 and one group at pH 7.2. For each 50 x 50 micron region, each precursor phase was treated as its own experimental group: ACCH2O, ACC, CCHH, MHC, and aragonite groups. All were analyzed separately and found to demonstrate the same exponential decay/growth findings.
Blinding	Blinding was not performed because the analysis did not involve a subjective outcome assessment. All findings per region were based on automated, pixel-resolved classification and quantitative image analysis using predefined criteria applied uniformly across all samples. Data selection and exclusion were based solely on objective presence of the precursor phases being analyzed, PEEM acquisition quality, and removal of regions with potential CoCs.

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	Stylophora Pistillata coral nubbins sampled from continuously growing skeletons.
Wild animals	The study did not involve wild animals.
Reporting on sex	No sex-based analysis was performed in this work.
Field-collected samples	The study did not involve samples collected from the field.
Ethics oversight	Ethics guidance and procedures from the Centre Scientifique de Monaco and the Lawrence Berkeley National Laboratory, respectively, were followed for this analysis.

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, mosaicism, off-target gene editing) were examined.