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Reporting Summary

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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
<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. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P 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 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 software was used for data collection.

Data analysis The MATLAB code (R2024a) to run the eco-evolutionary model is accessible on the lead author's GitHub profile at https://github.com/liamlachs/REEFMOD-PALAU_v2.1, with a stable version archived on Zenodo at <https://doi.org/10.5281/zenodo.20528898>. R code (version 4.0.2) used to analyse eco-evolutionary model results are freely available on Zenodo at <https://doi.org/10.5281/zenodo.20392804>

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](#)

Processed datasets for this study and R code (version 4.0.2) used to analyse eco-evolutionary model results are freely available on Zenodo at <https://doi.org/10.5281/zenodo.20392804>

Research involving human participants, their data, or biological material

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Reporting on sex and gender

Reporting on race, ethnicity, or other socially relevant groupings

Population characteristics

Recruitment

Ethics oversight

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	A simulation-based analysis comparing spatial conservation strategies of coral meta-populations in Palau, Western Pacific (bounding box: [134.1, 6.9, 134.8, 8.1]). Coral projections were generated using a mechanistic eco-evolutionary model of coral meta-populations that includes coral demography, evolution of heatwave tolerance through natural selection, future selective pressure from marine heatwaves under contrasting emissions scenarios (SSP1-2.6, SSP2-4.5), and either protection or restoration measures.
Research sample	Heatwave impacts were driven by accumulated heat stress (Degree Heating Weeks) derived from the satellite record for the past timeseries and from statistically downscaled daily sea surface temperatures projections from 5 global circulation models across the likely range of equilibrium climate sensitivity for future projections.
Sampling strategy	For each conservation action and emissions scenario, simulations were bootstrapped to capture stochasticity of the system. Results primarily focus on Palau-wide averages across the 95 meta-populations.
Data collection	No field data was collected. The model is parameterised based on published rates of coral demography, ecology, and evolutionary potential. Heatwave exposure was based on the NOAA CoralTemp v3.1 dataset and future projections from the Coupled Model Intercomparison Project 6 (CMIP6) as per Lachs et al. 2024 (Natural selection could determine whether Acropora corals persist under expected climate change, Science)
Timing and spatial scale	All heatwave stress data is based on daily SSTs at 5km spatial resolution. Connectivity is based on a model with 250m resolution
Data exclusions	The CMIP6 model NorESM2-LM was excluded due to misrepresenting the observed heatwave exposure gradient, leaving an ensemble of 5 GCMs
Reproducibility	All code and data are available, allowing the full reproduction of results.
Randomization	Coral recruitment, larval dispersal, background coral mortality and heatwave-driven coral mortality were simulated with the addition of randomly generated noise (i.e., random draws between zero and one and actions based on supercedence). The model code includes 10 different random seed settings used to initialise MATLAB's random number generator. This allows for the reproduction of the same sequence of random numbers used in each scenario.
Blinding	N/A

Did the study involve field work? ☐ Yes ☒ No

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

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.