

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 custom data-collection software was used. Primary observations are from published sources (Safaie et al. 2018; the Global Coral-Bleaching Database, van Woesik & Kratochwill 2022). Environmental fields were obtained from public products: NOAA blended sea-surface winds, NOAA OISST, IBTrACS v4.01 storm tracks, and CMIP6 sfcWind accessed via the Pangeo Google-Cloud Zarr catalogue.

Data analysis All analysis was performed in R 4.6.0 and Python (≥ 3.9). Ordinal (cumulative-link) logistic models were fitted with the R package ordinal (2025.12-29); the Shapley decomposition, Mundlak within-between estimator, and bootstrap procedures were implemented in R. Carbonate-system calculations for the Box Upwelling-Diffusion model used seacarb 3.3.4. CMIP6 wind processing used Python (xarray, zarr, gcfsfs, pandas, numpy). All custom analysis code is openly available on GitHub (https://github.com/UAlbanyTRRE/corals_wind) and archived on Zenodo (<https://doi.org/10.5281/zenodo.20720763>), with a README documenting dependencies, installation, and reproduction.

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 source datasets are publicly available: in-situ bleaching records and thermal metrics from Safaie et al. (2018); the Global Coral-Bleaching Database from van Woesik & Kratochwill (2022); NOAA blended sea-surface winds; NOAA OISST; and IBTrACS v4.01 storm tracks. The two derived analysis datasets used to fit the models are provided as Supplementary Data (Table S1, SAF; Table S2, GLO). The reef-scale CMIP6 projected wind-change dataset (63,496 reef cells; SSP2-4.5 and SSP5-8.5) is archived on Zenodo (<https://doi.org/10.5281/zenodo.20721850>). No restrictions apply to data availability.

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	N/A
Reporting on race, ethnicity, or other socially relevant groupings	N/A
Population characteristics	N/A
Recruitment	N/A
Ethics oversight	N/A

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	Observational and modelling study, with no experimental manipulation. We analysed coral-bleaching severity in relation to sustained background wind speed using two independent published observational datasets, complemented by a steady-state ocean-carbonate box model and a CMIP6 multi-model wind-projection analysis. The analysis units are reef sites (1,195 in the global dataset; 81 in the in-situ dataset); the response is an ordered three- or five-level bleaching-severity index modelled by ordinal logistic regression.
Research sample	Existing datasets, not newly collected samples. The in-situ sample (SAF) is 81 event-resolved coral-bleaching observations from Safaie et al. (2018). The global sample (GLO) is 1,195 reef-site bleaching observations derived from the Global Coral-Bleaching Database (van Woesik & Kratochwill 2022), reduced to one record per 5 × 5 km reef site. These represent tropical/subtropical coral reefs worldwide; the two datasets were chosen for their contrasting design (precise event timing versus broad spatial coverage) so that agreement constitutes cross-dataset replication.
Sampling strategy	No sample-size calculation was performed; sample sizes are fixed by the available published records (n = 81 SAF; n = 1,195 GLO after reduction to one record per 5 × 5 km site). These sample sizes are sufficient because the wind association is estimated with narrow confidence intervals and reproduces across two independent datasets and across within-region (realm and basin) specifications.
Data collection	No primary data were collected by the authors. Bleaching observations were obtained from the published Safaie et al. (2018) and van Woesik & Kratochwill (2022) datasets. Environmental predictors were extracted from public products: NOAA blended sea-surface winds, NOAA OISST, IBTrACS v4.01 tropical-cyclone tracks, and CMIP6 sfcWind (Pangeo Google-Cloud Zarr catalogue).
Timing and spatial scale	The bleaching observations span the period covered by the source databases (largely 1980s–2020). Wind, SST and cyclone predictors were computed over antecedent windows (6- and 12-month) and a 1993–2020 climatological reference. The spatial unit of analysis is the 5 × 5 km reef site; gridded SST and wind predictors are at 0.25°. The CMIP6 wind-change analysis compares 2080–2099 against 1995–2014 across ~64,000 equal-area 5-km reef cells. No new sampling schedule applies, as the study uses existing records.

Data exclusions

For the global dataset, where a 5 × 5 km cell contained more than one record the earliest record was retained, to give one non-duplicated observation per site and to minimise the influence of prior thermal exposure and acclimation; this selection rule is pre-defined, and the wind contribution is unchanged when the most-severe or a randomly selected record per cell is used instead. Models were fitted on complete cases. No other exclusions were applied.

Reproducibility

This is not an experimental study, so there are no repeated experimental trials. Analytical reproducibility was verified in several ways: the wind contribution (Shapley share ≈18% GLO; ≈25% SAF) reproduces across two independent datasets; the global wind odds ratio is stable under a cluster bootstrap over 0.25° cells and under collapsing to one record per cell (Supplementary Note 7); and the within-region (realm and basin) analyses agree with the pooled result.

Randomization

Not relevant to this study.

Blinding

Not relevant to this study.

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

Methods

- | n/a | Involved in the study |
|-------------------------------------|--|
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Antibodies |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Eukaryotic cell lines |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Palaeontology and archaeology |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Animals and other organisms |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Clinical data |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Dual use research of concern |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Plants |

- | n/a | Involved in the study |
|-------------------------------------|---|
| <input checked="" type="checkbox"/> | <input type="checkbox"/> ChIP-seq |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Flow cytometry |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> MRI-based neuroimaging |

Plants

Seed stocks

N/A

Novel plant genotypes

N/A

Authentication

N/A