nature portfolio

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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	Trait data was collected from published databases and other publicly available sources. The references to these sources can be found at GEUS Dataverse "Trait datasets AMD14-204_CASQ", https://doi.org/10.22008/FK2/P1RJDV, which includes: AMD14-204_denoised_rbcL_traits.txt, AMD14_204_18S_allshorts_traits_unicellular.txt, and AMD14_204_18S_allshorts_traits_multicellular.txt. Private URLs are shared in the submitted manuscript file for review as well: https://dataverse.geus.dk/privateurl.xhtml?token=ca067e7a-b151-4422-bedc-a76f4b45099e
Data analysis	Code for the processing and analysis of the data can be found at GEUS Dataverse "Trait datasets AMD14-204_CASQ", https://doi.org/10.22008/FK2/P1RJDV, which includes both code and input files in zip-compressed folders 1-4. A private URL is also shared in the submitted manuscript file for review: https://dataverse.geus.dk/privateurl.xhtml?token=ca067e7a-b151-4422-bedc-a76f4b45099e

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

Trait data as well as raw DNA-sequencing data and corresponding tag-files for demultiplexing are available at GEUS Dataverse for 18S https://doi.org/10.22008/FK2/P1RJDV and rbcL https://doi.org/10.22008/FK2/Y3EHFJ and traits https://doi.org/10.22008/FK2/P1RJDV. Private URLs are also shared in the submitted manuscript file for review (18S: https://dataverse.geus.dk/privateurl.xhtml?token=3def1a9b-f328-4020-8a1d-85bec5a1bcaa; rbcL: https://dataverse.geus.dk/privateurl.xhtml?token=aa9d3a6c-9b4e-4d9c-b624-55c014e63189).

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	NA
Reporting on race, ethnicity, or other socially relevant groupings	NA
Population characteristics	NA
Recruitment	NA
Ethics oversight	NA

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	We selected 38 sediment depths from the core, spanning the past ~8.3 thousand years and applied DNA metabarcoding using the ~110 bp-short eukaryote marker 18S_allshorts and the 76 bp-short diatom-specific marker diat_rbcl76. Taxonomic assignments were linked with functional trait annotations derived from published databases and literature reviews. Specifically, we studied the diversity responses of functional groups and functional trait modalities to latitudinal-zone temperature reconstructions and sea ice conditions.
Research sample	We took 38 samples along a 734cm long sediment marine core and applied sedimentary ancient DNA (sedaDNA) metabarcoding. We took 3 samples from each depth (biological replicates) and performed 2 PCRs for each replicate, resulting in 6 PCR-replicates per depth. During all procedures, negative controls were included and sequenced.
Sampling strategy	A maximum of ~0.5g sediment was used for each DNA extraction, which is the limit of input for the kit we were using. As we cannot homogenize more material per depth prior to extraction, we decided to take three samples per depth to cover any potential heterogeneity or patchiness of preserved DNA across the core diameter. A total of 38 sample depths were chosen along the core, resulting in one sample each median ~12cm with a temporal resolution of median ~171 years, which is appropriate to identify long-term responses of biodiversity to climatic changes in the past.
Data collection	Functional annotations of taxonomically assigned and quality filtered ASVs are based on compiled trait information from a mix of sources (databases, research papers, and books), but largely built upon Ramond et al. for protists and Fragoso et al. for diatoms.
Timing and spatial scale	The sediment core AMD14-204_CASQ covers a time frame of ~9000 years. As the lowermost depths were mostly barren of any microfossils, we focused our study on the past ~8,300 years. An update age-depth model is presented in the Supplement. This sediment core covers a single site, yet the signal is likely more regional.
Data exclusions	As we focused on marine ecosystem changes, we removed amplicon sequence variants (ASVs) assigned to land plants. Furthermore, fungi were the largest source for contamination in our data. As the core was opened in 2014, this also likely compromised the fungal composition by active growth. For these reasons, we disregarded fungi in our analyses.

Reproducibility	We took 3 samples from each depth (biological replicates) and performed 2 PCRs for each replicate, resulting in 6 PCR-replicates per depth.
Randomization	NA
Blinding	We use sample codes during lab work, but since we always have to work from old towards young to prevent contamination from younger to older samples, it is not strictly blinded.

Did the study involve field work? ☒ Yes ☐ No

Field work, collection and transport

Field conditions	Fieldwork was carried on board the ship CCGS Amundsen.
Location	Melville Bay: Latitude: 73.261050, Longitude: -57.899780, Date/Time: 2014-07-28T00:00:00; water depth: 987.0 m
Access & import/export	Fieldwork was carried on board the CCGS Amundsen. Access & import/export: the fieldwork was carried out in compliance with local and international laws, and all relevant permissions were obtained from Amundsen Science. We note that the collection of this record precedes the adoption of the Nagoya protocol in 2014 and the later related legislation adopted by the Greenland Government in 2016.
Disturbance	No disturbances were caused.

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	NA
Novel plant genotypes	NA
Authentication	NA