

Reporting Summary

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Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
- ☐ ☒ An indication of 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 statistics 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
- ☐ ☒ Clearly defined error bars
State explicitly what error bars represent (e.g. SD, SE, CI)

Our web collection on [statistics for biologists](#) may be useful.

Software and code

Policy information about [availability of computer code](#)

Data collection

No software or code was used in the collection of community composition data. Trait data come from a variety of sources and information about software used is often not available. In some cases, ImageJ (various versions) was used to estimate leaf area.

Data analysis

All Bayesian analyses were done in either JAGS or Stan through R (v. 3.3.3) using the packages rjags (v. 4.6) or rstan (v2.14.1). The R package Taxonstand (v. 1.8) was used to clean species names and identify synonyms. The R package vegan (v. 2.4.6) was used in the ordination. All graphs were made using the R package ggplot2 (2009). Model equations are provided in the methods for all analyses. Model code (Stan) is provided for the two main analyses in the supplementary information.

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/reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research [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 list of figures that have associated raw data
- A description of any restrictions on data availability

Trait data

Data compiled through the Tundra Trait Team are publicly accessible (see data paper published in Global Ecology & Biogeography; Bjorkman et al. in press). The public TTT database includes traits not considered in this study as well as tundra species that do not occur in our vegetation survey plots, for a total of nearly 92,000 trait observations on 978 species. Additional trait data from the TRY trait database can be requested at try-db.org.

Composition data

Most sites and years of the vegetation survey data included in this study are available in the Polar Data Catalogue (ID # 10786_iso). Much of the individual site-level data has additionally been made available in the BioTIME database (Dornelas et al. 2018; <https://synergy.st-andrews.ac.uk/biotime/biotime-database/>).

References

Bjorkman, AD, IH Myers-Smith, SC Elmendorf, S Normand, HJD Thomas, et al. Tundra Trait Team: a database of plant traits spanning the tundra biome. Global Ecology and Biogeography. In press.
Dornelas, M, LH Antão, F Moyes, AE Bates, AE Magurran, et al. 2018. BioTIME: A database of biodiversity time series for the Anthropocene. Global Ecology and Biogeography. 27: 760-786.

Field-specific reporting

Please select 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/authors/policies/ReportingSummary-flat.pdf

Ecological, evolutionary & environmental sciences study design

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

Study description	The study involves plant community composition data at 117 sites around the Northern Hemisphere tundra biome. We used Bayesian hierarchical models for most analyses (plots nested within sites nested within regions). A region was defined as a WorldClim or CRU grid cell, depending on the analysis (across space or over time). We combined the community composition data with >50,000 trait observations from the TRY and TTT trait databases.
Research sample	We focused on vascular plant species as trait data are rarely available for bryophytes. Most repeat vegetation sampling occurred in permanent marked plots (2/3) while the remainder were randomly placed plots within a specific area. Most of the community composition data was previously archived at the Polar Data Catalogue (ID # 10786_iso); trait data are available through the TTT (fully public) and TRY (partially public) trait databases.
Sampling strategy	We included all available community composition and functional trait data. Thus, sample size was not predetermined but rather a maximum possible based on available data.
Data collection	Data was collected by many different people in many different locations (see authorship contribution statement).
Timing and spatial scale	Community composition data were collected between 1989 and 2015 at 117 tundra sites, including Arctic tundra sites in Alaska, Canada, Fennoscandia, Iceland, and Siberia, and alpine tundra sites in the Colorado Rockies and European Alps. The exact sampling dates vary by site. Trait data were collected between 1964 and 2016 (though the vast majority of trait data were collected since the 1990's).
Data exclusions	In order to ensure that comparisons among sites are not biased due to the method of vegetation survey, we included only sites which were surveyed using a method equivalent to percent cover. Trait data were "cleaned" - first by removing any impossible values (e.g., LDMC values greater than 1, plant height of 0) and then according to the algorithm described in the methods. The trait data cleaning code, along with the cleaned and uncleaned versions of the trait dataset, are publicly available as a GitHub repository (see Bjorkman et al. Global Ecology and Biogeography, in press).
Reproducibility	Our study was not experimental, but the large number of sampling sites (117) spread across the Northern Hemisphere tundra biome ensures good spatial replication.
Randomization	Our study does not include experiments, thus samples were not randomly allocated into experimental groups. We account for spatial and temporal non-independence of samples by using a hierarchical approach to analysis (plots nested within sites nested within regions).

Blinding

Group allocation was based on physical proximity only (plots within sites within regions). Vegetation surveys were not conducted with the goal of documenting trait change over time, thus bias in data collection is unlikely.

Did the study involve field work? ☒ Yes ☐ No

Field work, collection and transport

Field conditions	Field conditions varied by site. All sites from which community composition data were collected have mean summer (warmest quarter) temperatures of 10 degrees C or less.
Location	Community composition data were collected in 117 tundra sites spanning the Northern Hemisphere (including both Arctic and alpine tundra). Trait data were collected in hundreds of locations across the Northern Hemisphere.
Access and import/export	The appropriate data collection permits were obtained whenever necessary. The permits necessary varied among the different sites.
Disturbance	Vegetation sampling was non-destructive. In some cases, trait measurements required removing between 1 and 10 leaves from an individual plant.

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☒	☐ Unique biological materials
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☒	☐ Human research participants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging