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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	PhenoCam imagery and data processed as described in Richardson et al. (2018) Scientific Data 5: 180028. Links to processing code on GitHub are contained in this paper.
Data analysis	Data analysis conducted in SAS v9

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

All data are publicly available. PhenoCam imagery is publicly available through the project web page (http://phenocam.sr.unh.edu), and the phenological data sets used in this study are available through the SPRUCE data portal, https://doi.org/10.3334/CDIAC/spruce.045 and https://doi.org/10.3334/CDIAC/spruce.044.

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	There are 10 experimental enclosures. The experiment uses a regression-based design, with 5 levels of warming from +0 (control) to +9 °C, in 2.25 °C increments. Thus each level of warming is replicated twice. The temperature treatments are crossed with a CO2 treatment, so that at each level of warming, one replicate receives ambient CO2 and the other replicate receives elevated CO2. Thus 5 of the 10 enclosures receive elevated CO2. Treatments were randomly assigned, and treatments were independently applied to each enclosure. Thus an enclosure is an experimental unit. For further details, see Hanson et al (2017) Biogeosciences 14: 861-883. Our analysis treats temperature as a continuous variable and CO2 as a class variable with two levels (elevated and ambient). In testing for temperature effects, we evaluate both linear and breakpoint models, as described in Methods. In testing CO2 effects, we include both CO2 and a CO2 x temperature interaction effect.
Research sample	Observations were conducted at the species level within each enclosure. Because most species were found in each of the 10 enclosures, we consider the sample size to be n = 10. An exception is Larix, which was not visible in the camera imagery for one enclosure. Hence for this species, n = 9 for the camera data.
Sampling strategy	Statistical methods were not used to predetermine sample size. The range of temperatures applied was selected to ensure that at least the warmest enclosures exceed model-based projections of future temperature increase expected by 2100. Financial considerations precluded additional replication at each level of warming.
Data collection	Phenological ground observations were conducted by WRN and RRH, with data recorded (was a particular phenophase observed, yes or no?) on a pre-printed form for each enclosure ADR transcribed the data and determined phenological transition dates, based on the first "yes" observation following a series of "no" observations. PhenoCam imagery was recorded automatically every 30 minutes from 4 am to 10 pm, following standard PhenoCam procedures (as described in Richardson et al. (2018) Scientific Data). ADR drew the masks used to define the three vegetation types for which data was extracted. Automated image processing and extraction of phenological transition dates follows Richardson et al (2018) Scientific Data.
Timing and spatial scale	Phenological ground observations were conducted in Spring 2016 (April to July) and Spring and Autumn 2017 (April to December), at approximately weekly intervals. While twice-weekly surveys would have been ideal, and would have enabled more precise identification of transition dates, the observers had other duties at the site which made more frequent observations impossible. Ground observations represent the consensus across multiple individuals of a species within each enclosure. PhenoCam imagery was recorded automatically every 30 minutes from 4 am to 10 pm, beginning August 2015. Here we use data through December 2017 but note that image acquisition is ongoing.
Data exclusions	For the ground observations of phenology, the rationale for excluding some phenophases from the analysis is described in Methods. Briefly, for certain phenophases for certain species, the observers felt either that (1) the phenophase was difficult to observe reliably or (2) the species was not sufficiently well distributed for the observations to be robust. No individual data points were excluded. No data were excluded from PhenoCam observations.
Reproducibility	Due to costs, full replication of the experiment was not feasible. Instead, we show that the observed patterns are consistent from year-to-year over the 2.5 y (to date) of the experiment, and consistent between ground observations and PhenoCam data. The experiment is scheduled to run for 10 y.
Randomization	17 permanent plots were established within the SPRUCE S1 bog in 2012. Assignment of the experimental treatments to 10 of these permanent plots was random. See Hanson et al. (2017) Biogeosciences for additional details.
Blinding	Blinding is not feasible. It is impossible for observers not to be aware of the temperature treatments in each enclosure.

Did the study involve field work? ☒ Yes ☐ No

Field work, collection and transport

Field conditions	The historic climate at the site is subhumid continental: mean annual temperature is 4°C, mean annual precipitation is 750 mm, and extreme temperatures range from –38 °C to +30 °C. Temperatures in the warmest (+9 °C) enclosures exceed those in the

	control (+0 °C) enclosures by the target amount. Temperatures in the control enclosures exceed ambient temperatures by 1-2 ° C.
Location	The SPRUCE experiment is conducted at the Marcell Experimental Forest, near Grand Rapids, Minnesota, USA ((47° 30.171' N, 93° 28.970' W), on land owned by the US Forest Service.
Access and import/export	The SPRUCE experiment is a collaborative effort between DOE's Oak Ridge National Laboratory (operated by UT-Battelle) and the US Forest Service's (USFS) Northern Research Station, conducted under a memorandum of understanding between UT-Battelle and the Forest Service dated 11/03/2009. DOE completed an Environmental Assessment (DOE/EA-1764) and DOE and USFS determined that the "proposed action is not a major federal action that would significantly affect the quality of the human environment within the meaning of the National Environmental Protection Act (NEPA) of 1969". Therefore, based on the "finding of no significant impact", the preparation of an Environmental Impact Statement was not necessary.
Disturbance	A geotechnical site survey was completed in 2011 by American Engineering Testing, Inc. (report 07-05001). Prior to the installation of the experimental enclosures, a network of raised boardwalks was constructed to minimize disturbance and damage to the site. Within each enclosure a circular boardwalk permits access to vegetation without trampling or further disturbance. Potential artifacts associated with the construction of the enclosures are discussed by Hanson et al. (2017) Biogeosciences.

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