

## 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 software was used to collect data. All datasets are downloaded from the original sources.

Data analysis All data analysis was conducted using R (version 4.2.1, program for statistical computing, [www.R-project.org](http://www.R-project.org)). Key R packages used in this study include ggplot2 (v3.5.1), lme4 (1.1.33), lmerTest(v3.1.3), ppcor (v1.1) and agricolae (v1.3.5). The code scripts for reproductivity have been archived on Zenodo: <https://doi.org/10.5281/zenodo.13854273>. The code for the deviation of Amax from the FLUXNET2015 database can be accessed at: <https://github.com/trevorkeenan/inhibitionPaperCode>. The code for modelling optimality-based Vcmax can be accessed at: <https://github.com/chongya/SVOM>.

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 dataset of FLUXNET2015 flux sites under the CC-BY-4.0 policy is publicly available for download at <http://fluxnet.fluxdata.org>. Remote-sensing canopy structure data from the MODIS MCD43A and MOD15A2H products are freely accessible at <https://lpdaac.usgs.gov/products/mcd43a3v006/> and <https://lpdaac.usgs.gov/products/mod15a2hv006/>. BESS flux products are publicly available at <https://www.environment.snu.ac.kr/data/>. PFT-based Vcmax25C is derived from TRY trait database at <https://www.try-db.org/TRYWeb/dp.php>.

## 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](https://www.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 derive Amax from light response curves of half-hourly or hourly eddy-covariance carbon fluxes obtained from more than 200 FLUXNET2015 flux sites. We examine the correlation between Amax and growth temperature when averaged over different time windows to identify the most relevant time scale for thermal acclimation, as indicated by peak correlation. Finally, we evaluate a biochemical model of canopy-scale C3 photosynthesis, incorporating recent advances in parameterizing temperature dependence acclimation and modelled optimality-based leaf photosynthetic capacity, to assess its ability to reproduce the observed thermal acclimation rates.
Research sample	Half-hourly and hourly net ecosystem exchanges of CO2 and their corresponding environmental conditions were collected from all sites listed on FLUXNET2015. MODIS LAI and fPAR data were also collected for each site.
Sampling strategy	We attempted to derived Amax from all FLUXNET2015 sites under the CC-BY-4.0 policy, though failed on three sites due to missing data variable and mismatched time periods with MODIS.
Data collection	All data were downloaded from their original source through the URLs provided in the data availability statement. The raw data were collected and processed by site PIs. The FLUXNET community standardized the flux data by ONEFlux.
Timing and spatial scale	We focused on the period between 2002 and 2014 when MODIS data were available and overlapped with FLUXNET2015. Daily fAPAR and LAI for each site were derived by interpolating the 8-day MODIS MOD15A2H products. We chose the growing seasons identified by fPAR and air temperature and well-watered conditions according to an aridity index (ET/PET).
Data exclusions	Sites are excluded if data are unavailable during the MODIS period from 2002 onwards (e.g. US-LWW and US-Me4) or if the uncertainty estimation is missing (e.g. CA-Man).

Reproducibility

Randomization

Blinding

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	Included 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 type="checkbox"/>	<input checked="" type="checkbox"/> Plants

### Methods

n/a	Included 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

## Dual use research of concern

Policy information about [dual use research of concern](#)

### Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

No	Yes
<input checked="" type="checkbox"/>	<input type="checkbox"/> Public health
<input checked="" type="checkbox"/>	<input type="checkbox"/> National security
<input checked="" type="checkbox"/>	<input type="checkbox"/> Crops and/or livestock
<input checked="" type="checkbox"/>	<input type="checkbox"/> Ecosystems
<input checked="" type="checkbox"/>	<input type="checkbox"/> Any other significant area

### Experiments of concern

Does the work involve any of these experiments of concern:

No	Yes
<input checked="" type="checkbox"/>	<input type="checkbox"/> Demonstrate how to render a vaccine ineffective
<input checked="" type="checkbox"/>	<input type="checkbox"/> Confer resistance to therapeutically useful antibiotics or antiviral agents
<input checked="" type="checkbox"/>	<input type="checkbox"/> Enhance the virulence of a pathogen or render a nonpathogen virulent
<input checked="" type="checkbox"/>	<input type="checkbox"/> Increase transmissibility of a pathogen
<input checked="" type="checkbox"/>	<input type="checkbox"/> Alter the host range of a pathogen
<input checked="" type="checkbox"/>	<input type="checkbox"/> Enable evasion of diagnostic/detection modalities
<input checked="" type="checkbox"/>	<input type="checkbox"/> Enable the weaponization of a biological agent or toxin
<input checked="" type="checkbox"/>	<input type="checkbox"/> Any other potentially harmful combination of experiments and agents

# Plants

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Seed stocks

N/A

Novel plant genotypes

N/A

Authentication

N/A