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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	The locations of plant occurrences were obtained from the Global Biodiversity Information Facility (https://www.gbif.org/developer/occurrence#search) using the rgbif package in R (https://cran.r-project.org/web/packages/rgbif/index.html).
Data analysis	The t-tests were done using Origin 2021. The linear regressions between the phytolith concentration in rice and wheat and the temperature at the sampling points were completed using Origin 2021. The maps were drawn using R 4.3.1. Sequence alignment was performed using MEGA (https://www.megasoftware.net), and the evolutionary tree was constructed using the Reltime and the Neighbor-Joining methods.

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

Data available within the article or its supplementary materials.

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	This study did not involve sex and gender.
Reporting on race, ethnicity, or other socially relevant groupings	This study did not involve race, ethnicity, or other socially relevant groupings.
Population characteristics	This study did not involve population characteristics
Recruitment	This study did not involve human participants.
Ethics oversight	This study did not involve human participants.

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 first designed an experiment that investigated the effect of Si on rice – a model Si-accumulating species – experiencing high and low temperature stress. Each treatment contained five biological replicates. We then analyzed the present-day variation in Si concentrations in the plant kingdom to see whether this was related to current Earth's temperatures (including 19932 occurrences, see Table S2 for details). We also used wheat and rice samples collected along climatic gradients to test whether Si intraspecific variation was linked to air temperature (including 475 wheat individuals and 279 rice individuals). Finally, we constructed evolutionary trees of plant Si transporter proteins and analyzed the relationship between periods of high- and low-Si plant differentiation and corresponding Earth history temperatures (including 45 families of angiosperms and 555 species of five major families; see Tables S3 and S4 for details).
Research sample	The leaf silicon concentrations of different species, families, and orders were obtained from data published by de Tombeur et al. (2023) in Trends in Ecology & Evolution (https://doi.org/10.1016/j.tree.2022.11.002). Taxonomic information was corrected using the NCBI database (www.ncbi.nlm.nih.gov). Wheat and rice were collected from the main production areas of China. Homologous sequences of proteins related to Si transport were searched by BLASTp on NCBI (https://blast.ncbi.nlm.nih.gov). The dataset of historic climate change over the last 200 Ma was obtained from the literature in Annual Review of Earth and Planetary Sciences and Earth-Science Reviews (https://doi.org/10.1146/annurev-earth-081320-064052, https://doi.org/10.1016/j.earscirev.2021.103503). The evolutionary time data for both high- and low-Si families were obtained from the Angiosperm Phylogeny Website (www.mobot.org/MOBOT/research/APweb/) and literature in Nature Plants (https://doi.org/10.1038/s41477-019-0421-0).
Sampling strategy	Leaf silicon concentrations of about 1800 species were obtained from de Tombeur's database, the largest database of leaf silicon concentrations integrating studies from the past 30 years (also containing all the information about silicon from the TRY Plant Trait Database). For the analysis of distribution temperature, we first selected 10 orders with high and low mean leaf Si concentrations. Then, the location of 1000 occurrences was randomly selected within each order from the Global Biodiversity Information Facility. After data cleaning, the final 19932 location will be used for subsequent analyses. The sample size is already large enough to reflect the different distribution temperatures of high and low silicon plants.

	For field sampling, we collected 475 wheat individuals from 95 sampling sites and 279 rice individuals from 93 sampling sites. The distribution of the sampling sites is 87.513–121.680 °E and 19.487–43.991 °N, which corresponds to the main harvesting regions of wheat and rice in China. This collection ensures that the sample size is large enough for various analyses and experiments and can well represent the characteristics of different geographical environments in the main production area. At the same time, such collection not only meets research needs but also takes into account considerable human, material, and time costs. For the differentiation time of high and low silicon plants, we not only analyzed 45 families, but considering that Asteraceae, Orchidaceae, Fabaceae, Rubiaceae, and Poaceae are the five largest families of angiosperms, we analyzed each of these families separately to emphasize the applicability of our conclusions (see Table S4 for details).
Data collection	The data were collected and recorded in Excel by Zhihao Pang, Wenjuan Li, and Enqiang Zhao from Yongchao Liang's Laboratory.
Timing and spatial scale	Rice and wheat collections were made from June to October 2021, which matched their harvest seasons.
Data exclusions	From the 20,000 plant occurrences obtained from GBIF, data with missing latitude and longitude information were eliminated. The final 19,932 occurrences were used for subsequent analysis.
Reproducibility	For the experiments on the effects of high and low temperatures on rice growth, all our replicates were similar to the results reported in the manuscript.
Randomization	Contained in this manuscript are controlled experiments using plants, including comparing the effects of high and low temperatures on plants, and the distribution and evolutionary timing of high and low silicon plants, so no randomization was required.
Blinding	This manuscript only involves plant research, therefore there is no need for blinding.

Did the study involve field work? ☒ Yes ☐ No

Field work, collection and transport

Field conditions	Rice and wheat collections were carried out from July to October 2021, with temperatures at the time of sampling ranging from 20-28°C and no rainfall in the week prior to sampling.
Location	The distribution of the sampling sites is 87.513-121.680 °E and 19.487-43.991 °N, which corresponds to the main harvesting regions of wheat and rice in China.
Access & import/export	Rice and wheat collections have been reported to the local Department of Agriculture. No import or export was involved in this study.
Disturbance	This study had a negligible impact on food production at the sampling sites and caused no disturbance to the agro-ecosystem.

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	Rice seeds (Oryza sativa L. cv. Nipponbare) are from the China Rice Data Center of the China National Rice Research Institute (https://www.ricedata.cn/variety/varis/602979.htm).
Novel plant genotypes	This study did not involve novel plant genotypes.
Authentication	This study did not involve authentication.