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Reporting Summary

Nature Research 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 Research policies, see Authors & Referees and the Editorial Policy Checklist.

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	Spectra Vista PC data acquisition software for collecting leaf-level spectra; Headwall Photonics Hyperspec III software for collecting imaging spectroscopy data with the mobile tram; Agilent ChemStation software for HPLC data collection.
Data analysis	R version 3.3.2; R packages ape 3.3, vegan 2.4-1, plsRglm 1.1.1, ade4 1.7-4, FD 1.0-12, picante 1.6-2, spectrolab 0.0.2; the R script for calculating qD(TM) is available at https://github.com/ShanKothari/DecomposingFD; ENVI 5.2 image processing software for extracting reflectance spectra from imaging spectroscopy data; Agilent ChemStation software for analysing HPLC data.

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

Spectral and biomass data that support the findings of this study (Figs. 1-3; Supplementary Figs. 3-10) are available from EcoSIS (https://ecosis.org) and the Cedar Creek Ecosystem Science Reserve (http://www.cedarcreek.umn.edu/research/data). The tram dataset is available from the LP DAAC (doi: 10.5067/Community/Headwall/HWHYPCCMN1MM.001).

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	Reflectance spectra of plants were collected using a portable spectrometer with a leaf clip and an imaging spectrometer mounted on an automated tram system, respectively. We tested if more spectrally dissimilar species were more functionally dissimilar and more distantly related, and investigated the degree to which the spectral diversity of plant communities predicted aboveground productivity, a critical ecosystem function.
Research sample	Leaf-level spectra were collected in 35 plots and imaging spectrometry data were collected in 27 plots in the Cedar Creek Biodiversity experiment in East Bethel, Minnesota. This subset of plots is annually sampled for aboveground biomass and covers all initially planted diversity levels. The experiment was seeded in the summers of 1994 and 1995 with 1, 2, 4, 8 or 16 grassland–savannah perennial species selected from a pool of 18 species: 4 C4 and 4 C3 grasses, 4 legumes, 4 forb species and 2 tree species. Plots measure 9 m × 9 m. We included the 17 most abundant species in our study: Achillea millefolium L., Agropyron smithii Rydb., Amorpha canescens Pursh, Andropogon gerardii Vitman, Asclepias tuberosa L., Koeleria cristata auct. non Pers. p.p., Lespedeza capitata Michx., Liatris aspera Michx., Lupinus perennis L., Monarda fistulosa L., Panicum virgatum L., Petalostemum candidum (Willd.) Michx., Petalostemum purpureum (Vent.) Rydb., Poa pratensis L., Schizachyrium scoparium (Michx.) Nash, Solidago rigida L. and Sorghastrum nutans (L.) Nash.
Sampling strategy	To capture species variability within each plot, we visually divided each plot into nine 3 m x 3 m subplots and measured the most abundant species in 4 to 8 subplots per plot (4 subplots for 1 and 2 species plots, 6 subplots for 6 species plots, and 8 subplots for 8 or 16 species plots). To capture spectral variability within individuals, we took either three or five spectral measurements of different leaves per individual depending on plant height, three measurements for individuals < 30 cm and five measurements for individual >=30 cm (see Methods). The plots sampled with the mobile tram system were the same as for the leaf-level data collection, with the exception of six plots in which tram data collection failed due to technical difficulties and two plots were no data were collected because of time and weather constraints.
Data collection	Leaf-level spectra were collected by A.K.S, Brett Fredericksen and Ian Carriere using a spectrometer covering the wavelength region 340–2500 nm and a leaf clip. The tram data were collected by R.W. and J.A.G. using an imaging spectrometer covering the wavelength region 400–990 nm, mounted on an automated tram system designed by J.A.G. (see Methods).
Timing and spatial scale	Leaf-level data were collected between July, 2nd and July, 22nd 2015. Tram data were collected between July, 23rd and July, 30th 2014 and between July, 8th and July, 26th 2015, respectively. The timing of spectral data collection on the ground matched the timing of airborne imaging spectrometer campaigns that are part of the Dimensions of Biodiversity project “Linking remotely sensed optical diversity to genetic, phylogenetic and functional diversity to predict ecosystem processes”. We collected spectral data at the leaf level and the proximal canopy level (at around 3 m above ground). Aboveground productivity was measured and predicted at the plant community scale.
Data exclusions	No data were excluded from the analyses.
Reproducibility	Spectral, functional and phylogenetic diversity of plant communities was calculated using three different methods which all provided consistent results: 1) abundance-weighted functional trait dispersion qD(TM) (Scheiner, S. M., Kosman, E., Presley, S. J. & Willig, M. R., 2016), 2) non-abundance-weighted qD(TM) and 3) functional dispersion FDis (Laliberte & Legendre, 2010). Spectra collected with the mobile tram are not a true replicate of spectra collected with a leaf clip. However, the tram data were collected in the same research plots as the leaf-level spectra, and albeit the tram measures spectral reflectance at a different scale, the total amount of variability in aboveground productivity explained by spectral diversity calculated from the tram data was comparable.

Randomization	Species composition of the plots was determined by random draws of 1, 2, 4, 8, or 16 species from a pool of 18 species. For the leaf-level sampling, we visually divided each plot into nine 3 m x 3 m subplots and collected spectral data within a randomly placed 1 m x 1 m grid in 4 to 8 subplots (see Methods). We measured four randomly selected individuals of the most abundant species per subplot. For the imaging spectrometer data analysis, we extracted 1,000 vegetation pixels per imaged plot at random. To predict foliar chemistry from leaf-level spectra, we calibrated partial least squares regression (PLSR) models for a set of 14 leaf traits. Models were tenfold cross-validated 500 times and model coefficients were averaged for predictions (see Methods).
Blinding	NA; there were no treatments assigned and data were not grouped.

Did the study involve field work? ☒ Yes ☐ No

Field work, collection and transport

Field conditions	All data were collected under dry weather conditions. Tram data were collected under sunny skies.
Location	All data were collected at the Cedar Creek Ecosystem Science Reserve in East Bethel, Minnesota, USA (45.403000, -93.190000).
Access and import/export	All sampling efforts were coordinated with Cedar Creek staff.
Disturbance	We did not step into the plots and always set up our equipment outside of the plots. For leaf-level data acquisition, we visually divided each plot into nine subplots and collected spectra in four to eight subplots; the centre subplot was always excluded to prevent disturbance.

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