

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
<input type="checkbox"/>	<input checked="" type="checkbox"/> The exact sample size (<i>n</i>) for each experimental group/condition, given as a discrete number and unit of measurement
<input type="checkbox"/>	<input checked="" type="checkbox"/> A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
<input type="checkbox"/>	<input checked="" type="checkbox"/> The statistical test(s) used AND whether they are one- or two-sided <i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>
<input type="checkbox"/>	<input checked="" type="checkbox"/> A description of all covariates tested
<input type="checkbox"/>	<input checked="" type="checkbox"/> A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
<input type="checkbox"/>	<input checked="" type="checkbox"/> 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)
<input type="checkbox"/>	<input checked="" type="checkbox"/> For null hypothesis testing, the test statistic (e.g. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
<input checked="" type="checkbox"/>	<input type="checkbox"/> For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
<input type="checkbox"/>	<input checked="" type="checkbox"/> For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
<input type="checkbox"/>	<input checked="" type="checkbox"/> Estimates of effect sizes (e.g. Cohen's <i>d</i> , Pearson's <i>r</i>), 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	<ul style="list-style-type: none">Google Earth Engine (GEE) JavaScript API: Used for retrieving and processing climate and hydrological data from TerraClimate, and reflectance data from Copernicus Sentinel-2 and Landsat. Custom scripts written in JavaScript were used within the GEE API for data processing, cloud masking, and vegetation indices calculations. These scripts can be shared upon request or deposited in a repository (e.g., GitHub) upon acceptance.AppEEARS Tool: Used to access ECOSTRESS data (Online platform at https://lpdaacsvc.cr.usgs.gov/appeears).
Data analysis	<ul style="list-style-type: none">R Programming Language: Version 4.3.0.Packages Used: MuMIn for stepwise model selection; lme4 and nlme for Linear Mixed Effects Models (LMMs); phia for interaction testing; ggeffects for model predictions; spdep for spatial autocorrelation analysis; sf and gstat for geospatial analyses and Kriging; stats for PCA and correlation analyses.Custom R scripts were written for model fitting, residual diagnostics, and statistical analyses. These include spatial autocorrelation analysis, Kriging interpolation, and PCA visualisation. The scripts can be shared with editors and reviewers upon request and will be deposited in a public repository (e.g., GitHub) for community use following manuscript acceptance.

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 datasets used in this study are publicly available and were accessed as follows:

- Community-Weighted Mean (CWM) SLA Data: Obtained from previously published data in Aguirre-Gutierrez et al. (In press), available from Google Earth Engine (GEE).
- ECOSTRESS Data: Retrieved via the AppEEARS tool (<https://lpdaacsvc.cr.usgs.gov/appeears>).
- TerraClimate Data: Accessed through the Google Earth Engine (https://developers.google.com/earth-engine/datasets/catalog/IDAHO_EPSCOR_TERRACLIMATE).
- Copernicus Sentinel-2 Data: Accessed via the Google Earth Engine (https://developers.google.com/earth-engine/datasets/catalog/COPERNICUS_S2_SR).
- Landsat 5, 7, and 8 Data: Accessed via the United States Geological Survey (USGS) Earth Resources Observation and Science (EROS) Center (<https://www.usgs.gov/landsat-missions/landsat-collection-2>).

Data supporting the findings of this study are available from the corresponding author upon reasonable request. Custom scripts used to process and analyse the data will be deposited in a public repository (e.g., GitHub) upon acceptance of the manuscript. For any additional inquiries regarding data access or use, please contact the corresponding author.

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

Not relevant to this study.

Reporting on race, ethnicity, or other socially relevant groupings

Not relevant to this study.

Population characteristics

Not relevant to this study.

Recruitment

Not relevant to this study.

Ethics oversight

Not relevant to this study.

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

This study investigates the relationship between leaf-level traits, particularly specific leaf area (SLA), and spectral reflectance stability across Amazonian and Cerrado vegetation types. The quantitative analysis examines community-weighted means (CWM) of SLA in relation to spectral indices, climatic, and hydrological variables.

Study Design:

Treatment Factors and Interactions:

Primary factors include SLA, climatic variables (e.g., temperature, precipitation, water deficit), hydrological variables (e.g., evaporative stress index, evapotranspiration, water use efficiency), and seasonality (dry and wet).

Interactions between SLA and season, as well as between SLA and hydrological variables, were tested.

Design Structure:

The design is hierarchical and includes spatial and temporal nesting.

High-resolution analysis in Nova Xavantina (5 plots segmented into 448 subplots of 10 × 10 m).

Coarser resolution analysis for the Amazon biome (130 plots in 44 regions, with 100 × 100 m resolution).

Experimental Units and Replicates:

	<p>Nova Xavantina: 441 subplots (10 × 10 m), with repeated measurements across months and seasons.</p> <p>Amazon Biome: 130 plots (100 × 100 m) across 44 regions, with repeated measurements for each region across months and years. Replicates include 3–5 individuals per species for SLA measurement and repeated sampling across temporal scales.</p> <p>This structure enables the evaluation of spatial and temporal variations in SLA and reflectance stability across diverse environmental conditions.</p>
Research sample	<p>The research sample includes 135 sites: 5 in Nova Xavantina, Brazil, representing diverse Cerrado-Amazon transition vegetation types, and 130 across 44 regions in the Amazon biome. Nova Xavantina sites were chosen for their detailed tree inventories and trait data, while Amazon sites were selected for their wide geographic and environmental diversity, enabling a broad assessment of SLA and spectral reflectance relationships. Sites were positioned below 400 m elevation and away from anthropogenic disturbances to capture natural vegetation responses to environmental gradients. This sampling ensures both high-resolution local analysis and regional-scale generalisability.</p>
Sampling strategy	<p>The sampling procedure included selecting 135 sites based on pre-existing vegetation data, environmental diversity, and minimal anthropogenic disturbance.</p> <p>Nova Xavantina: Five plots were chosen to represent various Cerrado-Amazon transition vegetation types. Subplots (10 × 10 m) were created to align with Sentinel-2 resolution, resulting in 448 subplots for analysis.</p> <p>Amazon Biome: 130 plots across 44 regions were selected from Sullivan et al. and Aguirre-Gutierrez et al. data, with 100 × 100 m resolution.</p> <p>Sample Size Determination:</p> <p>No formal sample size calculation was performed. Sample sizes were determined based on the availability of high-quality vegetation and spectral data, ensuring geographic coverage and ecological diversity. The rationale was to achieve robust representation of vegetation responses across spatial and environmental gradients while aligning with existing datasets.</p>
Data collection	<p>Field Data Collection:</p> <p>In Nova Xavantina, detailed vegetation data were collected in 2014–2015. Over 3,300 individual trees with a diameter of ≥10 cm at breast height were inventoried. Trait measurements were conducted on 3–5 replicate individuals per dominant species, focusing on sun-exposed branches. Measurements included SLA and other functional traits. Field data were collected by a research team led by specialists in tropical vegetation ecology.</p> <p>Remote Sensing Data:</p> <p>Sentinel-2 and Landsat Data: Satellite reflectance data were processed using the Google Earth Engine (GEE) platform. Spectral indices (e.g., NDVI, EVI) and coefficients of variation (CV) were derived using custom scripts.</p> <p>ECOSTRESS Data: Hydrological variables were obtained from the AppEEARS tool.</p> <p>TerraClimate Data: Historical climatic data were extracted from the GEE data catalogue.</p> <p>All data collection was conducted by trained researchers using standardised protocols to ensure accuracy and reproducibility.</p>
Timing and spatial scale	<p>Field Data:</p> <p>Nova Xavantina vegetation inventory was conducted in 2015, with trait measurements taken between March and May 2014.</p> <p>Remote Sensing Data:</p> <p>Sentinel-2 data were collected for 2019.</p> <p>ECOSTRESS hydrological data were collected from January 2019 to December 2022, aggregated into monthly means.</p> <p>TerraClimate data spanned from 1984 to 2022, summarised as monthly and decadal averages.</p> <p>Landsat time series covered 1984–2022, with seasonal and decadal summaries.</p> <p>Spatial Scale:</p> <p>Nova Xavantina: High-resolution data from 5 plots segmented into 448 subplots (10 × 10 m).</p> <p>Amazon Biome: Coarser resolution data from 130 plots across 44 regions (100 × 100 m).</p> <p>Rationale:</p> <p>Sampling was designed to align with vegetation trait measurement periods and ensure sufficient temporal resolution for capturing inter- and intra-annual variability in vegetation responses. Spatial scales were chosen to match plot sizes with satellite data resolution and to ensure regional representativeness.</p>
Data exclusions	<p>Some data were excluded from the analysis based on the following criteria:</p> <p>Remote Sensing Data:</p> <p>Satellite images with >5% cloud cover or low-quality pixels were excluded to ensure reliable spectral reflectance measurements. Sentinel-2 and Landsat data outside the specified timeframes (2019 for Sentinel-2 and 1984–2022 for Landsat) were not used.</p> <p>Field Data:</p> <p>Trait measurements from shaded branches were excluded to focus on sun-exposed branches, which directly influence spectral reflectance.</p> <p>Sites with anthropogenic disturbances or elevations >400 m were excluded to ensure natural vegetation responses were analysed.</p> <p>Rationale:</p> <p>These exclusions were necessary to maintain data quality, avoid bias, and ensure alignment with the study's objectives of evaluating natural vegetation responses under consistent environmental conditions.</p>
Reproducibility	<p>Standardised Protocols:</p> <p>Field data collection followed established protocols for vegetation inventory and trait measurement, ensuring consistency across sites.</p> <p>Remote sensing data were processed using documented and reproducible workflows in Google Earth Engine and R.</p>

Data Quality Control:

Cloud masking and pixel quality checks were applied to remote sensing data to ensure reliability.

Statistical diagnostics (e.g., residual analysis, spatial autocorrelation tests) verified model robustness.

Code Availability:

Custom scripts for data processing and analysis will be deposited in a public repository (e.g., GitHub) upon acceptance, enabling independent replication.

Cross-validation:

Analyses were cross-validated by comparing outputs across multiple temporal and spatial resolutions (e.g., Nova Xavantina vs. Amazon plots).

Documentation:

All methods, datasets, and analyses are fully documented, including software versions and parameters used, ensuring reproducibility by other researchers.

Randomization

Field sampling was stratified by dominant vegetation types and basal area dominance to ensure ecological representativeness rather than random sampling. In Nova Xavantina, tree species contributing most to basal area were prioritised, with 3–5 replicates sampled per species.

For remote sensing analyses, randomization was not applicable as data were collected systematically across defined spatial plots (10 × 10 m for Nova Xavantina; 100 × 100 m for the Amazon biome). Analyses accounted for spatial and temporal variation using hierarchical and mixed-effects models to mitigate potential biases.

Blinding

Blinding was not applicable to this study as the data collection and analysis were based on field measurements and remotely sensed data, which do not involve subjective assessments or treatments requiring concealment. All analyses were conducted objectively using predefined protocols and computational methods to ensure unbiased results.

Did the study involve field work? ☒ Yes ☐ No

Field work, collection and transport

Field conditions

The fieldwork was conducted in Nova Xavantina, Brazil, a region characterised by a tropical savanna climate with distinct dry and wet seasons:

Temperature: Average annual temperature ranges from 24°C to 28°C.

Rainfall: Annual precipitation averages 1,200–1,500 mm, with most rainfall occurring during the wet season (November to April).

Elevation: Sites were located below 400 m.

Vegetation Types: Included rocky cerrado, typical cerrado, woody cerrado, and semi-deciduous forest, representing the Cerrado-Amazon transition zone.

These conditions were ideal for studying functional traits and vegetation responses under natural environmental gradients.

Location

Nova Xavantina, Brazil: Located in the Cerrado-Amazon transition zone at approximately –52.352 W, –14.708 S.

Access & import/export

Fieldwork in Nova Xavantina adhered to all local and national regulations regarding habitat access and sample collection. Necessary permissions were obtained from relevant authorities and institutions managing the study areas.

No biological samples were exported or imported as the study relied on field-measured functional traits and publicly available remote sensing datasets. Data collected in the field were digitised and securely stored in compliance with local and international data-sharing policies. Remote sensing data were accessed from open-source platforms such as Google Earth Engine, ensuring full compliance with international research standards.

Disturbance

The study caused minimal disturbance to the environment.

Fieldwork: Tree measurements and leaf sampling involved collecting small branches or leaves from a limited number of individuals per species (3–5 replicates), ensuring no long-term harm to vegetation.

Site Access: Field teams adhered to established trails and avoided damaging understory vegetation or soil structure during data collection.

Remote Sensing: Relied entirely on satellite data, causing no physical disturbance to the habitats studied.

Efforts were made to minimise disturbance by using non-destructive sampling methods and limiting fieldwork activities to what was necessary for the study's objectives.

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	Involvement 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	Involvement 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

Seed stocks	Not applicable to this study.
Novel plant genotypes	Not applicable to this study.
Authentication	Not applicable to this study.