

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 (<i>n</i>) 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 <i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>
☒	☐ 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. <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 <i>P</i> values as exact values whenever suitable.</i>
☒	☐ 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 <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	By using car packages, we calculated variance inflation factor (VIF) for community diversity and leaf nutrients, then removed factors with VIF > 5 to avoid multicollinearity. LMER were implemented by using lme4 and lmerTest packages in R environment. The glm was performed using the edgeR package in R environment. Based on the maximum likelihood method and the minimum evolution method, we generated microbial phylogenetic trees of all core OTUs using FASTTREE. Then phylogenetic trees were annotated and visualized using iTOL software. MST was calculated using the NST package in the R environment, and function nst.panova was used to test whether the difference between green and yellow leaves was significant. MST indices for microbial communities were visualized using ggplot2.
Data analysis	We will provide the code in a community repository after our paper were accepted.

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](#)

Raw reads were deposited into the NCBI Sequence Read Archive (SRA) database (Accession Number: SRP342019).

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

Reporting on race, ethnicity, or other socially relevant groupings

Population characteristics

Recruitment

Ethics oversight

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	Using amplicon sequencing of 16S rRNA and ITS genes, we examined the composition and diversity of microbial communities from young (green) to old (yellow) leaves of rubber trees. A total of 144 samples (green leaves and yellow leaves) were collected over the course of the experiment (September 2019 for rainy season and December 2020 for dry season).
Research sample	Our research sample is young and old rubber tree leaves.
Sampling strategy	A total of six study sites encompassing major plantations were chosen from Danzhou, Wanning, and Ledong Districts on Hainan Island and from Jinghong, Menglun, and Mengpeng Districts in Xishuangbanna. At each site, three plots separated by 5-15 km in distance were selected for sampling. In each sampling plot, leaf samples were collected from three trees separated from one another by approximately 100 m. Green and yellow leaves were collected in the same time from branches 2 m away from the center of the trunk and 12 m above the ground (Figure S1D). Leaves were selected from each of the four cardinal directions (i.e., north, south, east, and west) and all sampled leaves from the three trees were mixed respectively for green or yellow leaves to form a single composite sample. A total of 72 leaves were collected in the two seasons (i.e., rainy season and dry season), and a total of 144 samples were collected over the course of the experiment (September 2019 for rainy season and December 2020 for dry season).
Data collection	Same to above.
Timing and spatial scale	Leaf samples were collected over the course of the experiment (September 2019 for rainy season and December 2020 for dry season).
Data exclusions	No data were excluded from the analysis.
Reproducibility	Our findings can be reproducibility. We believe that resampling and analysis will get similar results.
Randomization	Not applicable. We mixed all leaf samples (different site, different season) together.

Blinding

Not applicable.

Did the study involve field work?

☒ Yes☐ No

Field work, collection and transport

Field conditions

Rubber plantation is the most economically important agroecosystem in tropical China. We selected study sites on Hainan Island and in Xishuangbanna region where rubber plantations account for nearly one fourth and one third of the vegetated area, respectively.

Location

Hainan province and Xishuangbanna of Yunnan province, south China.

Access & import/export

We have got the permission from the farmer.

Disturbance

Almost no disturbance.

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

Methods

- | | |
|-------------------------------------|--|
| 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 |

- | | |
|-------------------------------------|---|
| n/a | Involved in the study |
| ☒ | ☐ ChIP-seq |
| ☒ | ☐ Flow cytometry |
| ☒ | ☐ MRI-based neuroimaging |

Plants

Seed stocks

We used rubber tree leaves not seed.

Novel plant genotypes

Not applicable.

Authentication

Not applicable.