

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](#).

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
<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. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
<i>Give P 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 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 in this study

Data analysis
 Qiime: <http://qiime.org/>
 Usearch: <https://www.drive5.com/usearch/>
 RDP: <https://rdp.cme.msu.edu/classifier/classifier.jsp>
 R: <https://www.r-project.org/>
 R, vegan package: <https://www.rdocumentation.org/packages/vegan/versions/2.4-2>
 Code & raw data: <https://github.com/ththi/European-Root-Suppl>

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. 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

Sequencing data, european transect at ENA: ERP115101
 Sequencing data, transplant experiment at ENA: ERP115102

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	Spatial and temporal monitoring of the <i>Arabidopsis thaliana</i> root microbiota in 17 European sites across three successive years. Effect of soil origin and location were uncoupled in a reciprocal transplant experiment between two <i>A. thaliana</i> populations in northern and southern Europe to test the contribution of edaphic and climatic conditions to root microbiota variation and local plant adaptation at large spatial scale.
Research sample	Roots and associated soil fractions (soil, rhizosphere, rhizoplane, root) were harvested from flowering <i>Arabidopsis thaliana</i> and co-occurring grasses (Poaceae family) at 17 natural sites in spring 2015, 2016, and 2017 (n = 1,125 samples in total). For the reciprocal transplant experiment, soil and whole root samples (root with rhizoplane microbes) were harvested from <i>A. thaliana</i> at fruit maturation and include 8 different genotype-soil-location combinations (n = 131 samples in total). On the host side, we scored plant survival, fecundity (number of fruits per reproducing plant), and estimated overall fitness (number of fruits per seedling planted) across 1,008 plant individuals.
Sampling strategy	Plants were harvested with their surrounding soil, transferred in pots and transported to the laboratories of collaborators within less than 24 hours after harvesting. In the laboratory, plant compartments were separated using a custom protocol. No sample-size calculation was previously performed. Due to limited plants availability in some sites and to maintain population stability across years, a maximum of 16 <i>A. thaliana</i> individuals were harvested per site and year. Four pooled plants were considered as one technical replicate and four (<i>A. thaliana</i>) and three (for grasses) technical replicates were taken per site and year. For the reciprocal transplant experiment, six to twelve soil samples were harvested for each of the eight combinations of soil, location and genotype (n = 72), as well as three to twelve whole root samples per condition (n = 59).
Data collection	Isolation of DNA from soil and root samples, as well as library preparation are described in the Methods section. Bacterial, fungal and oomycetal communities were profiled using primer pairs targeting the V2V4 and V5V7 regions of the bacterial 16S rRNA gene, the ITS1 and ITS2 segments of the fungal ITS, and the ITS1 segment of the oomycetal ITS, resulting in the sequencing of 5,625 microbial community profiles for the European transect and 393 for the reciprocal transplant experiment. Sequencing was performed using an in-house MiSeq device. In the common garden experiment, <i>A. thaliana</i> fitness was obtained by scoring survival after winter, flowering time and number of siliques per individual (n = 1,008 plant individuals).
Timing and spatial scale	Plants were harvested along a latitudinal gradient (up to 3500 km) from Sweden to Spain. Across European sites (n = 17), all plants were harvested at the flowering stage from February to May in 2015, 2016 and 2017. The difference in harvesting time reflects that fact that not all populations flower at the same time across Europe. For example, plants at German sites were sampled in March, whereas those at Swedish sites were sampled in May. Note that plants at each site were harvested at one specific date and a similar time frame was selected every year to assess year-to-year variation. The reciprocal transplant include two geographically distant sites in Sweden and Italy in which plants were harvested at fruit maturation in April (Italy) and May (Sweden) 2016.
Data exclusions	Very few samples where 16S rRNA or ITS sequences did not meet predetermined quality checks (i.e. low quality or low read counts) were excluded.
Reproducibility	All attempts to repeat the same sampling strategies across years were successful.
Randomization	<i>A. thaliana</i> and grasses were randomly harvested across sites to maximize the representation of the samples taken. In the common garden experiment, seedlings were transplanted in blocks of 6x7 cells in a checkerboard design and randomly harvested for microbiota analysis.
Blinding	Blinding was not relevant for this study as plants were harvested regardless of their phenotypical state.
Did the study involve field work?	☒ Yes ☐ No

Field work, collection and transport

Field conditions	Soil chemical properties were determined for each site and yearly average air temperature and humidity data were obtained from public online sources (see Supplementary Table 1)
Location	GPS coordinates and information of natural sites and reciprocal transplant sites can be found in the Supplementary Table 1
Access and import/export	Collaborators of each country were contacted in order to identify natural sites and access them. Harvested samples were then transported to the laboratory and, once fractionated, shipped to the MIPZ in Cologne in dry ice.

Disturbance

Soil was disturbed when plants and soil were harvested at each site. In order to minimize disturbance, holes made were covered with surrounding soil. To maintain plant population stability across years, a maximum of 16 *A. thaliana* individuals were harvested per site and year

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
☐	☒ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

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

Animals and other organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research

Laboratory animals

The study did not involve laboratory animals

Wild animals

The study did not involve wild animals

Field-collected samples

Plant and soil samples collected from natural sites

Ethics oversight

Since no animals were used in this study, no ethical approval or guidance was required

Note that full information on the approval of the study protocol must also be provided in the manuscript.