Lotus japonicus symbiosis signaling genes and their role in the establishment of root-associated bacterial and fungal communities

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Abstract

The wild legume *Lotus japonicus* engages in mutualistic symbiotic relationships with arbuscular mycorrhiza (AM) fungi and nitrogen-fixing rhizobia. Using plants grown in natural soil and community profiling of bacterial 16S *rRNA* genes and fungal internal transcribed spacers (ITS), we examined here the role of the *Lotus* symbiosis genes *RAM1*, *NFR5*, *SYMRK*, and *CCaMK* in structuring bacterial and fungal root-associated communities. We found host genotype-dependent community shifts in the root and rhizosphere compartments that were mainly confined to bacteria in *nfr5* or fungi in *ram1* mutants, whilst *symRK* and *ccamk* plants displayed major changes across both microbial kingdoms. We observed in all AM mutant roots an almost complete depletion of a large number of Glomeromycota taxa that was accompanied by a concomitant enrichment of Helotiales and *Nectriaceae* fungi, suggesting compensatory niche replacement within the fungal community. A subset of Glomeromycota whose colonization is strictly dependent on the common symbiosis pathway was retained in *ram1* mutants, indicating that *RAM1* is dispensable for intraradical colonization by some Glomeromycoyta fungi. However, intraradical colonization by certain Burkholderiaceae taxa is dependent on AM root infection, thereby revealing a microbial interkingdom interaction. Our findings imply a broad role for *Lotus* symbiosis genes in structuring the root microbiota.

Introduction

Mutualistic plant-microbe interactions are essential adaptive responses dating back to plant colonization of terrestrial habitats [1,2]. Endosymbiotic association with obligate arbuscular mycorrhizal (AM) fungi belonging to the phylum Glomeromycota is considered to have enabled early land plants to adapt to and survive harsh edaphic conditions by improving the acquisition of nutrients, especially phosphorus, and water from soil [3]. It is estimated that approximately 80% of extant plant species remain proficient in AM symbiosis (AMS), testifying to its importance for survival in natural ecosystems [4,5,6]. Another more recent endosymbiotic relationship has evolved between plants belonging to distinct lineages of flowering plants (Fabales, Fagales, Cucurbitales, and Rosales) and nitrogen-fixing members of the Burkholderiales, Rhizobiales or Actinomycetales, enabling survival on nitrogen-poor soils. These bacteria fix atmospheric nitrogen under the low oxygen conditions which are provided by plant root nodules.

Studies of mutant legumes deficient in both AM and RNS revealed that a set of genes defined as the common symbiotic signaling pathway (CSSP) are crucial for these symbioses. In the model legume *Lotus japonicus*, Nod factor perception by NFR1 and NFR5 activates downstream signaling through SYMRK, a malectin and leucine-rich repeat (LRR)-containing RLK [7], currently considered to be the first component of the CSSP. SYMRK associates with NFR5 through a mechanism involving intramolecular cleavage of the SYMRK ectodomain, thereby exposing its LRR domains [8]. Signaling from the plasma membrane is transduced to the nuclear envelope where ion channels [9,10], nuclear pore proteins [11,12,13] and cyclic nucleotide-gated channels [14] mediate symbiotic calcium oscillations. These calcium oscillations are interpreted by the calcium- and calmodulin-dependent protein kinase CCaMK, [15,16] that interacts with the DNA binding transcriptional activator CYCLOPS [17,18,19]. Several GRAS transcription factors (NSP1, NSP2, RAM1, RAD1) are activated downstream of CCAMK and CYCLOPS and determine whether plants engage in AMS or RNS symbiosis.

Plants establish the symbioses with AM fungi and nitrogen-fixing bacteria by selecting interacting partners from the taxonomically diverse soil biome. These interactions are driven by low mineral nutrient availability in soil and induce major changes in host and microbial symbiont metabolism [20,21]. Although RNS develops as localized events on legume roots, analysis of *Lotus* mutants impaired in their ability to engage in symbiosis with nitrogen-fixing bacteria revealed that these mutations do not only abrogate RNS, but also impact the composition of taxonomically diverse root- and rhizosphere-associated bacterial communities, indicating an effect on multiple bacterial

taxa that actively associate with the legume host, irrespective of their symbiotic capacity [22]. By contrast, the effect of AMS is known to extend outside the host *via* a hyphal network that can penetrate the surrounding soil and even indirectly affect adjacent plants [23]. In soil, fungal hyphae themselves represent environmental niches and are populated by a specific set of microbes [24]. Although the biology of AMF is well understood, the potential role of AMS on root-associated bacterial and fungal communities is currently unknown.

Here we used mutants impaired in RNS, AM, or both to address the role of symbiosis signaling genes in structuring bacterial and fungal root-associated communities in *Lotus* plants grown in natural soil. We show that genetic disruption of these symbioses results in significant host genotype-dependent microbial community shifts in the root and surrounding rhizosphere compartments. These changes were mainly confined to either bacterial or fungal communities in RNS- or AM-deficient plant lines, respectively, whereas mutants with defects in the CSPP revealed major changes in assemblages of the root microbiota across both microbial kingdoms.

Materials and Methods

Preparation and storage of soil

The soil batches used in this study were collected from Max Planck Institute for Plant Breeding Research agricultural field located in Cologne, Germany (50.958N, 6.865E) in the following seasons: CAS11-spring/autumn 2016, CAS12-spring 2017. The field had not been cultivated in previous years, no fertilizer or pesticide administration took place at the harvesting site. Following harvest, soil was sieved, homogenized and stored at 4 °C for further use.

Soil and plant material

All studied *L. japonicus* symbiosis-deficient mutants, *nfr5-2* [ref. 25], *ram1-2* [ref. 26], *symrk-3* [ref. 7] and *ccamk-13* [ref. 27], originated from the Gifu B-129 genotype.

Plant growth and harvesting procedure

The germination procedure of *L. japonicus* seeds included sandpaper scarification, surface sterilisation in 1% hypochlorite bleach (20 min, 60 rpm), followed by three washes with sterile water and incubation on wet filter paper in Petri dishes for one week (temperature: 20 °C, day/night cycle 16/8h, relative humidity: 60%). For each genotype and soil batch, six to eight biological replicas

were prepared by potting four plants in 7x7x9 cm pot filled with corresponding batch of soil (CAS11 soil six replicates, CAS12 soil eight replicated). Plants were incubated for ten weeks in the greenhouse (day/night cycle 16/8h, light intensity 6000 LUX, temperature: 20 °C, relative humidity: 60%), and were watered with tap water twice per week.

The block of soil containing plant roots was removed from the pot and adhering soil was discarded manually. Three sample pools were collected: complete root systems (harvested 1 cm below the hypocotyl), upper fragments of the root systems (4 cm-long, starting 1 cm below the hypocotyl) and lower root system fragments (harvested from 9 cm below; the latter two were collected from plants grown in the same pot (Fig. 1a). All pools were washed twice with sterile water containing 0.02% Triton X-1000 detergent and twice with pure sterile water by vigorous shaking for 1 min. The rhizosphere compartment was derived by collection of pellet following centrifugation of the first wash solution for 10 min at 1500 g. The nodules and visible primordia were separated from washed root pools of nodulating genotypes (WT and ram1-2) with a scalpel and discarded. In order to obtain the root compartment the root sample pools were sonicated to deplete the microbiota fraction attached to the root surface. It included 10 cycles of 30-second ultrasound treatment (Bioruptor NextGen UCD-300, Diagenode) for complete root systems and upper root fragments, while for the lower root fragments the number of cycles was reduced to three. All samples were stored at -80 °C for further processing. For AM colonisation inspection the whole root system of washed soil-grown plants was stained with 5% ink in 5% acetic acid solution and inspected for intraradical infection.

Generation of 16S rRNA and ITS2 fragment amplicon libraries for Illumina MiSeq sequencing

Root pool samples were homogenized by grinding in a mortar filled with liquid nitrogen and treatment with Precellys24 Tissue lyser (Bertin Technologies) for two cycles at 5600 rpm for 30 sec. DNA was extracted with the FastDNA Spin Kit for Soil, according to the manufacturer's protocol (MP Bioproducts). DNA concentrations were measured fluorometrically (Quant-iT™ PicoGreen dsDNA assay kit, Life Technologies, Darmstadt, Germany), and adjusted to 3.5 ng/µl. Barcoded primers targeting the variable V5-V7 region of the bacterial 16S rRNA gene (799F and 1193R, [28]) or targeting the ITS2 region of the eukaryotic ribosome (fITS7 and ITS4, [29,30]) were

used for amplification. The amplification products were purified, pooled and subjected to sequencing with Illumina MiSeq equipment.

Processing of 16S rRNA and ITS2 reads

All libraries from root fractionation experiments as well as from the main experiments were analyzed together. Due to a very low read count for 16S data in the first experiment in CAS11 soil, this library was not included in the final analysis. This resulted in an overall lower sample number for bacteria than for fungi (222 vs. 274 samples). All sets of amplicon reads were processed as recently described [31], using a combination of QIIME [32] and USEARCH tools [33]. For both datasets paired end reads were used. For ITS2 data, forward reads were kept, in case that no paired version was available. Main steps include quality filtering of reads, de-replicating, chimera detection and OTU clustering at a 97% threshold. 16S reads were filtered against the greengenes data base [34], whereas for ITS2 the reads where checked with ITSx [35] and compared against a dedicated ITS database to remove ITS sequences from non-fungal species. Taxonomic classification was done with uclust (assign_taxonomy from QIIME) for 16S OTUs and rdp classifier [36] for ITS2 OTUs. For the sake of consistency with NCBI taxonomic classification, the assignment of the ITS2 sequences was manually corrected so that that all OTUs assigned as Ilyonectria were assigned as belonging to the Sordariomycetes, Hypocreales and Nectriaceae, respectively. For 16S data, OTUs assigned as mitochondrial or chloroplast, were removed prior to analysis.

Statistical analysis

For calculating Shannon diversity indices, OTU tables were rarefied to 1000 reads. Significant differences were determined using ANOVA (aov function in R) and post-hoc Tukey test (TukeyHSD in R, $p<0.05$). For calculating Bray Curtis distances between samples, OTU tables were normalized using cumulative sum scaling (CSS, [37]). Bray-Curtis distances were used as input for principal coordinate analysis (PCoA, cmdscale function in R) plots and as input for constrained analysis of principal coordinate (CPCoA, capscale function, vegan package in R). For the latter, the analysis was constrained by genotypes (each mutant and WT separately) and corrected for the effect of soil type and experiment (using the “Condition” function). This analysis has been repeated with OTU tables from which OTUs that represent known plant symbionts (Phyllobacteriaceae for 16S and Glomeromycota for ITS2) were removed before normalization, distance calculation and CPCoA. A previously described approach was used to draw ternary plots and for respective

enrichment analysis [22]. Fold change of OTUs between wild type and mutant plants was calculated as followed. Samples showing a read count <5000 were removed. OTUs with mean RA >0.1% across all root or rhizosphere samples, respectively, were kept for analysis. Fold change in RA from WT to mutants was calculated over all WT samples for nfr5-2, ram1-2 and symrk-3, whereas the change to ccamk-13 was only calculated with WT samples from experiments where ccamk-13 mutants were present. To avoid zeros in calculation the RA of OTUs missing from samples was set to 0.001%. The significance of differences in abundance was tested using the Kruskal-Wallis test ($p<0.05$).

Results

Root fractionation protocol affects the composition of associated bacterial communities

Earlier physiological studies have shown that only cells of a specific developmental stage, located in the root elongation zone, respond to Myc and Nod factors, mount symbiotic calcium oscillations and enable epidermal infection by rhizosphere-derived fungal and bacterial symbionts [38,39].To explore spatial organization of root-associated bacterial and fungal communities along the longitudinal axis, we collected samples of the upper and lower root zones as well as the entire root system of six-week-old Gifu wild-type plants, grown in Cologne soil (2 to 5 cm and >9 cm of the root system, respectively; Fig. 1A; [40]). Microbial assemblages of these three root endosphere compartments were compared to the communities in the corresponding rhizosphere fractions, i.e. soil tightly adhering to the respective root zones, and with the bacterial biome present in unplanted Cologne soil. 16S rRNA gene amplicon libraries of the V5-V7 hypervariable region and gene libraries of the Internally Transcribed Spacer 2 (ITS2) region of the eukaryotic ribosome were generated by amplification [28,29,30]. Information on the number and relative abundance of operational taxonomic units (OTUs) in each compartment was used to calculate α (Shannon index; within sample diversity) and β-diversity (Bray-Curtis distances; between samples diversity), OTU enrichment and taxonomic composition. In bacteria we observed a gradual decrease in α-diversity from unplanted soil to the rhizosphere and to the root endosphere compartments, a trend which was similar for each longitudinal root fraction. This suggests that winnowing of root commensals from the highly complex soil biome occurs in all tested root zones (Fig. S1A). Similar overall results were obtained for the fungal dataset (Fig. S1B), but the decrease in diversity from unplanted soil towards the rhizosphere was mild or even lacking. The latter finding is similar to that of a recent study of root-associated fungi in non-mycorrhizal *A. thaliana* sampled at three natural sites [31]. Analyses of taxonomic composition and β-diversity revealed striking differences in the endosphere

and rhizosphere compartments associated with the upper and lower root longitudinal fractions. The composition of bacterial and fungal taxa of the whole root closely resembled that of the upper root fraction (Fig. 1B), with only low numbers of OTUs differentially abundant between these two compartments (Fig. 1C and 1D). Additionally, we observed a higher sample-to-sample variation in the taxonomic profiles of the lower root zone compared to the upper whole root fractions (Fig. 1B). This greater community variation in the developmentally younger region of *L. japonicus* roots might reflect a nascent root microbiota or greater variation in root tissue and adherent rhizosphere samples that we recovered from this root zone by our fractionation protocol. Based on the finding that whole root and upper root compartments host comparable bacterial communities and given their greater stability we decided to use the former for further analyses.

Host genes needed for symbioses determine bacterial and fungal community composition of *L. japonicus* root and rhizosphere

For root microbiota analysis, we cultivated wild-type (ecotype Gifu) *L. japonicus* and *nfr5-2*, *symrk-3*, *ccamk-13* and *ram1-2 (nfr5, symrK, ccamk* and *ram1,* from thereof*)* mutant genotypes in parallel in two batches of Cologne soil, to account for batch-to-batch and seasonal variation at the sampling site. *nfr5-2* mutant plants are impaired in rhizobial Nod factor perception and signaling, which prevents initiation of infection thread formation [25]. Mutations in *SymrK* and *CcamK* affect the common symbiosis pathway downstream of Nod or Myc factor perception, abrogating infection either by nitrogen fixing rhizobia or AM fungi [7,27]. The RAM1 transcription factor controls arbuscule formation, and while *ram1-2* mutants of *L. japonicus* are indistinguishable from wild type and permit incipient AM fungus infection, fungal colonization is terminated with the formation of stunted symbiotic structures [26]. All plant genotypes appeared healthy (Fig. 2A-E), but the shoot length and shoot fresh weight of all mutant plants was significantly reduced in comparison to wild type (Fig. 2F and 2G), suggesting that genetic disruption of either AM or *Rhizobium* symbiosis is detrimental for the fitness of plants grown in natural soil. Whereas all defects in nitrogen-fixing symbiosis, validated by the absence of root nodules in *nfr5-2*, *symrk-3* and *ccamk-13* genotypes (Fig. 2C-E, Table S1), resulted in similarly severe impacts on plant growth (Fig. 2F and 2G), both shoot length and shoot fresh weight were significantly reduced in *ram1-2* plants, although the effects were less severe and these plants still formed nodules and, unlike wild-type and *nfr5-2*, showed impairment in AM symbiosis (Table S1) and a less severe, but significant reduction of both shoot length and shoot fresh weight in comparison to wild type.

In order to determine the impact of rhizobial and AM symbiosis on root microbiota assembly, we characterized fungal and bacterial communities of unplanted Cologne soil, rhizosphere, and root compartments of all aforementioned *L. japonicus* genotypes at bolting stage. Visible nodules and root primordia were removed from the roots of nodulating wild type and *ram1*-2 genotypes prior to sample processing for community profiling. We amplified the V5-V7 hypervariable region of the bacterial 16S rRNA gene and the ITS2 region of the eukaryotic ribosome. High-throughput sequencing of these amplicons yielded 22,761,657 16S and 21,228,781 ITS reads, distributed in 222 and 274 samples, respectively, which were classified into 5,780 and 3,361 distinct microbial OTUs. Analysis of α-diversity revealed a general reduction of complexity from unplanted soil to rhizosphere and lastly in root compartments for bacterial communities, whereas the complexity of fungal communities was largely similar for the latter two compartments (Fig. S2A and S2B), which is consistent with a recent study of *A. thaliana* root-associated fungal communities [31]. Bacterial α-diversity was slightly elevated in the *nfr5*-2 genotype in rhizosphere and root compartments in comparison to all other genotypes (Fig. S2A). Fungal communities were similarly diverse in the rhizosphere of all tested plant genotypes, but their diversity in the root compartment was significantly and specifically reduced in all three AM mutants (*ccamk*-13, *ram1*-2, and *symrk-3*; Fig. S2B).

Analysis of β-diversity using Principal Coordinate Analysis (PCoA) of Bray-Curtis distances showed a significant effect of soil batch on soil-resident bacterial and fungal communities (Fig. S2C and D). In order to account for this technical factor and assess the impact of the different host compartment and genotypes in community composition, we performed a Canonical Analysis of Principle Components Coordinates (CAP; [41]). This revealed a clear differentiation of bacterial and fungal communities in the tested plant genotypes in both root and rhizosphere compartments, with the host genotype explaining as much as 7.61% of the overall variance of the 16S rRNA, and 13.5% of ITS2 data (Fig. 3; $P<0.001$). The rhizosphere compartments of wild type and *ram1-2* were found to harbor similar bacterial communities, but were separate from those of *symrk-3* and *ccamk-13* (Fig. 3A). Further, the rhizosphere communities of each of these four plant genotypes were found to be significantly different from that of *nfr5* (Fig. 3A). A similar trend was observed for fungal communities, except that wild-type and *ram1* rhizosphere communities were clearly separated from each other (Fig. 3C). In the root compartment we found bacterial consortia that were distinctive for each of the five plant genotypes (Fig. 3B). A pronounced host genotype effect was also found for the root-associated fungal communities, but in this case the communities of wild-type and *nfr5* clustered together, indicating a high similarity (Fig. 3D). *L. japonicus* is

nodulated by members of *Mesorhizobium loti* belonging to the Phyllobacteriaceae family, and engages in AM symbiosis with Glomeromycota fungi. The plant genotypes included in this study differed in their capacity to accommodate nitrogen-fixing bacteria and/or AM fungi inside roots, and, consequently, the lack of these symbionts alone might explain the microbial community separation observed by CAP analysis (Fig. 3). To test whether these symbiotic microbes are the sole drivers of the observed community separations, we repeated the CAP analysis after *in silico* removal of *Phyllobacteriaceae* sequencing reads for bacterial communities, and of Glomeromycota reads for the fungal assemblages. Interestingly, although this reduced the community variance explained by host genotype across the dataset (Fig. S3 compared to Fig. 3), overall patterns of β-diversity remained unaltered, suggesting that other community members besides root nodule and arbuscular mycorrhizal symbionts contribute to the plant genotype-specific community shifts. Collectively, our analyses of *L. japonicus* symbiotic mutants grown in natural soil show that lack of AM and/or RNS symbioses has a significant effect on plant growth and on the structures of bacterial and fungal communities associated with legume roots.

Loss of symbiosis affects specific bacterial and fungal families of the root microbiota

Comparison of bacterial family abundance between wild type and mutants lacking RNS and/or AM symbiosis identified significant changes in *Comamonadaceae*, *Phyllobacteriaceae*, *Methylophilaceae*, *Cytophagaceae* and *Sinobacteracea* in the rhizosphere compartment (Fig. 4A; top 10 most abundant families). The abundance of *Comamonadaceae* and *Phyllobacteriaceae* also differed significantly in the root compartment of RNS mutants compared to wild type. *Streptomycetaceae* and *Sinobacteraceae* relative abundances were specifically affected by loss of *Nfr5*, whereas *Anaeroplamataceae* and *Burkholderiaceae* abundances were affected by the lack of AM symbiosis in *symrk* and *ccamk* plants (Fig. 4A). The relative abundances of the same two families were also significantly reduced in *ram1* roots, suggesting that active AM symbiosis influences root colonization by a subset of bacterial root microbiota taxa.

Six out of the ten most abundant fungal families in the rhizosphere compartment of *Lotus* plants belonged to Ascomycota (Fig. 4B). By contrast, the root endosphere was dominated by numerous families of Glomeromycota, which were found to be almost fully depleted from the rhizosphere and root compartments of *ram1*, *symrk* and *ccamk* mutants, indicating that absence of AM symbiosis predominantly affects Glomeromycota and does not limit root colonization or rhizosphere association by other fungal families. However, depletion of Glomeromycota in the AM mutant roots was accompanied by an increase in the relative abundance of Ascomycota members belonging to

Nectriaceae in both rhizosphere and root compartments and by an increased abundance of unclassified *Helotiales*, *Leotiomycetes*, and *Sordariomycetes* in the root compartment only (Fig. 4B).

Closer inspection of the microbial community shifts at the OTU level identified 45 bacterial OTUs and 87 fungal OTUs enriched in the roots of symbiosis mutants compared to those of wild type (Fig. 5), and 60 bacterial OTUs and 30 differentially abundant fungal OTUs in the rhizosphere samples (Fig. S4). The absence of RNS in *nfr5-2* roots affected the relative abundance of multiple OTUs (n=27 in the root, n=23 in the rhizosphere) belonging to diverse taxa. Many of these OTUs (n=18 in the root, n=16 in the rhizosphere) showed a similar differential relative abundance in *symrk-3* and/or *ccamk-13* mutants when compared to wild type (Fig.5A), indicating that their contribution to the *Lotus* root communities outside of nodules is affected by active nitrogen fixing symbiosis. Impairment of both AM and RNS symbioses in *symrk* and/or *ccamk* mutants resulted in opposite changes in the relative root abundances of OTUs belonging to specific Burkholderiales families. Depletion of OTUs belonging to *Burkholderiaceae* (n=5) was accompanied by the enrichment of OTUs from other Burkholderiales families (*Oxalobacteraceae* [n=3], *Comamonadadaceae* [n=2], and *Methylophilaceae* [n=2]; Fig. 5A). Only three of the above-mentioned *Burkholderiaceae* OTUs were depleted in *ram1* roots, suggesting that their enrichment in *Lotus* roots is dependent on functional AM symbiosis.

Analysis of the ITS2 amplicon sequences from root samples identified a large number of Glomeromycota OTUs (n=39); thus, *Lotus* Gifu roots grown in natural soil accommodate a phylogenetically diverse community of AM fungi (Fig. 5B). The majority of these fungal OTUs (n=31) were depleted in *symrk-3*, *ccamk-13* and *ram1-2* mutant roots, indicating that their enrichment is dependent on a functional AM symbiosis pathway. Their intraradical colonization appears to be independent of *RAM1*, as 12 OTUs assigned to Glomeromycota or to unknown taxa, nine of which define a Glomeromycota sublineage, were depleted in *symrk-3* and *ccamk-13* but not in *ram1-2* roots. A reduced abundance of Glomeromycota OTUs in the endosphere compartment was accompanied by an increased abundance of Ascomycota members, especially of members belonging to the *Nectriaceae* (8 OTUs) and *Helotiales* (7 OTUs) families, suggestive of a mutually exclusive occupancy of the intraradical niche. In sum, our results reveal that in natural soil CSSP symbiotic genes are essential for root colonization by a wide range of Glomeromycota fungi; further, these genes significantly affect the abundances of multiple bacterial taxa, predominantly belonging to the Burkholderiales and Rhizobiales orders.

Discussion

Here, we investigated the role of host AM and/or RNS genes in establishing structured bacterial and fungal communities in the rhizosphere and endosphere compartments of *L. japonicus* grown in natural soil. Impairment of RNS in *nfr5-2* or AMS in *ram1-2* plants had a significant impact on root microbiota structure, which was mainly confined to the composition of bacterial or fungal communities, respectively.

The shift between the root-associated microbial communities of wild type and *nfr5-2* mutant is in line with both the qualitative and quantitative findings of a previous report on the *Lotus* bacterial root microbiota (Fig. 3A and B in this study; [22]). However, here we observed an enhanced rhizosphere effect in both wild type and *nfr5-2* plants, leading also to a less prominent community shift in this compartment (Fig. S5). These differences in rhizosphere bacterial composition are likely caused by a soil batch effect and, to a lesser extent, possibly also the use of different sequencing platforms (Illumina *versus* 454 pyrosequencing). The nearly unaltered fungal community composition in *nfr5* mutant plants compared to wild type (only 3 out of 39 Glomeromycota OTUs differentially abundant) suggests that NFR5 is dispensable for fungal colonization of *L. japonicus* roots. This finding, together with a massive shoot biomass reduction of *nfr5* plants in natural soil (~4-fold; Fig. 2), further reveals that intraradical colonization by soil-derived fungal endophytes is robust against major differences in plant growth.

A recent microbial multi-kingdom interaction study in *A. thaliana* showed that bacterial commensals of the root microbiota are crucial for the growth of a taxonomically wide range of fungal root endophytes. These antagonistic interactions between bacterial and fungal root endophytes are essential for plant survival in natural soil [31]. We have shown here that an almost complete depletion of diverse Glomeromycota taxa from roots of each of the three AM mutants was accompanied by an enrichment of OTUs belonging to the families *Nectriaceae* and Helotiales (Fig. 4). We speculate that the increased relative abundance of these taxa is caused by intraradical niche replacement as a compensatory effect following the exclusion of Glomeromycota symbionts from the root compartment. Previous mono-association experiments have shown that isolates belonging to *Nectriaceae* and Helotiales can have either mutualistic or pathogenic phenotypes [42,43,44]. Given that all plant genotypes were free of disease symptoms when grown in natural soil (Fig. 2), we speculate that the complex shifts in the composition of the bacterial root microbiota in *nfr5-2, symRK-3,* and *ccamk-13* mutants did not affect the capacity of bacterial endophytes to prevent pathogenic fungal overgrowth. Of note, Helotiales root endophytes were also enriched in

roots of healthy *Arabis alpina*, a non-mycorhyzal plant species and relative of *A. thaliana*, and contribute to phosphorus nutrition of the host when grown in extremely phosphorus-impoverished soil [45]. The enrichment of Helotiales in *Lotus* AM mutants is therefore consistent with potential niche replacement by other fungal lineages to ensure plant nutrition in nutrient-impoverished soils. Although the proposed compensatory effect in AM mutants will need further experimental testing in phosphorus-depleted soils, our hypothesis is consistent with the only mild impairment in plant growth in *ram1-2* mutants (Fig. 2).

We identified three bacterial OTUs, all belonging to the *Burkholderiaceae* family, that are significantly depleted in the roots of each of the three AM mutants compared to wild type. Interestingly, members of the Glomeromycota have been found to contain intracellular endosymbiotic bacteria [46], some belonging to the order Burkholderiales [47]. This finding suggests that these bacteria are either endosymbionts of Glomeromycota fungi that are excluded from the roots of the AM defective genotypes or that their intraradical colonization is indirectly mediated by AM infection. The small changes in the bacterial root microbiota in *ram1-2* plants, which were mainly limited to depletion of the three aforementioned Burkholderia OTUs, revealed that root-associated bacterial community structure is remarkably robust against major changes in the composition of root-associated fungal communities (Fig. 5).

Paleontological and phylogenomic studies established the ancestral origin of genetic signatures enabling AM symbiosis in land plants [1,48]. In monocots and dicots, the extended AM fungal network is primarily recognized as a provider of nutrients, particularly phosphorus [49,50], but the positive impact of AM symbiosis on the host transcends nutrient acquisition [51]. Additionally, phylogenomic studies of the symbiotic phosphate transporter PT4 suggest that this trait evolved late and therefore that phosphorus acquisition might not have been the (only) driving force for the emergence of AM symbiosis [48]. *SymRK* and *Ram1* were identified in the genomes of liverworts, but evolution of *CCaMK* predated the emergence of all land plants, as shown by its presence and conserved biochemical function in advanced charophytes [48]. Together, these findings raise questions regarding the forces driving the evolution of signaling genes enabling intracellular symbioses in land plants. Our study shows that in *L. japonicus*, simultaneous impairment of AM and RN symbioses in *symRK-3* and *ccamk*-13 plants had a dramatic effect on the composition of both bacterial and fungal communities of the legume root microbiota (Fig. 5). Importantly, mutation of *CcamK* and *SymrK* led to an almost complete depletion of a large number of fungal OTUs, mostly belonging to Glomeromycota, indicating that in *Lotus*, these genes predominantly control

384 the colonization of roots by this particular fungal lineage. The finding that *ram1-2* mutants show
385 retained accommodation for a subset of fungal root endophytes (n=13; Fig. 5B, and Fig 4B) whose
386 colonization is dependent on an intact common symbiosis pathway is not surprising based on the
387 capacity of these mutants to enable fungal colonization but not to sustain a full symbiotic
388 association [26], and indicates that *RAM1* is dispensable for the intraradical colonization of these
389 Glomeromycota fungi. Alternatively, these fungal root endophytes may engage in commensal
390 rather than mutualistic relationships with *L. japonicus* independently of the AM symbiosis pathway
391 as is the case for multiple species of commensal non-symbiotic rhizobia [22,52]. For instance,
392 given that *ram1*-2 mutants specifically block AM arbuscule differentiation but not root colonisation
393 [26], it is conceivable that the Glomeromycota taxa colonizing this plant genotype may not form
394 arbuscules during root colonization.

395 Legumes have evolved the capacity to recognize and accommodate both types of intracellular
396 symbionts, and the large effect of CSSP genes on associated microbiota seen in the present work
397 could reflect a legume-specific trait. However, in rice, which does not engage in symbiotic
398 relationships with nodulating rhizobia, mutants lacking *CCaMK* were also found to display
399 significant changes in root-associated bacterial communities that could be mainly explained by
400 depletion of Rhizobiales and Sphingomonadales lineages [53]. Thus, our findings based on
401 comparative microbiota analysis of *Lotus ccamk* and *ram1* mutants suggest a broader role for
402 common symbiosis signaling genes in microbiota assembly. Future studies on orthologous genes
403 in basal land plants will contribute to a better understanding of the role of symbiotic signaling in the
404 evolution of plant-microbiota associations.

405

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411 **Conflict of interest**

412 The authors declare no conflict of interests.

413 **Data availability**

414 All sequencing reads will be uploaded to the European Nucleotide Archive (ENA). Code and
415 relevant data files (e.g. OTU tables) will be made public via GitHub.

416

417

418 **References**

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Main Figures

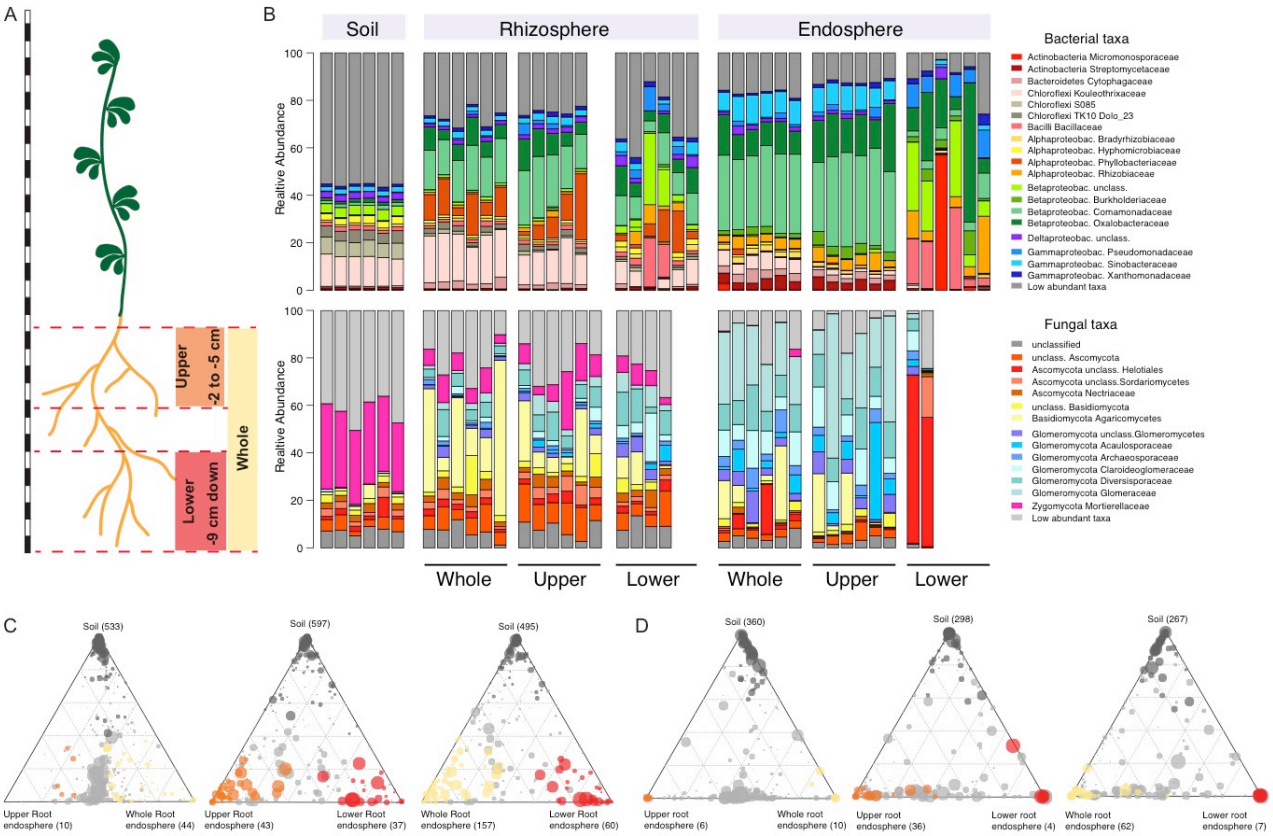

Fig1, **Bacterial & fungal community profile for different root fractions of *L. japonicus***.
A) Cartoon showing the length of the three different root fractions. B) Community profile showing the relative abundance of bacterial (upper panel) and fungal (lower panel) families across compartments and fractions (only samples with >5000 (bacteria) or >1000 (fungi) reads are shown, taxa having average RA < 0.1 (bacteria) or <0.15 (fungi) across all samples are aggregated as low-abundant.). C) Ternary plots showing bacterial OTUs that are enriched in the endosphere of specific root fractions, compared to the soil samples. B) Ternary plots showing fungal OTUs that are enriched in the endosphere of specific root fractions, compared to the soil samples. Circle size corresponds to RA across all fractions. Dark grey circles denote OTUs that are enriched in soil, light grey circles always represent OTUs that are not enriched in any of the fractions.

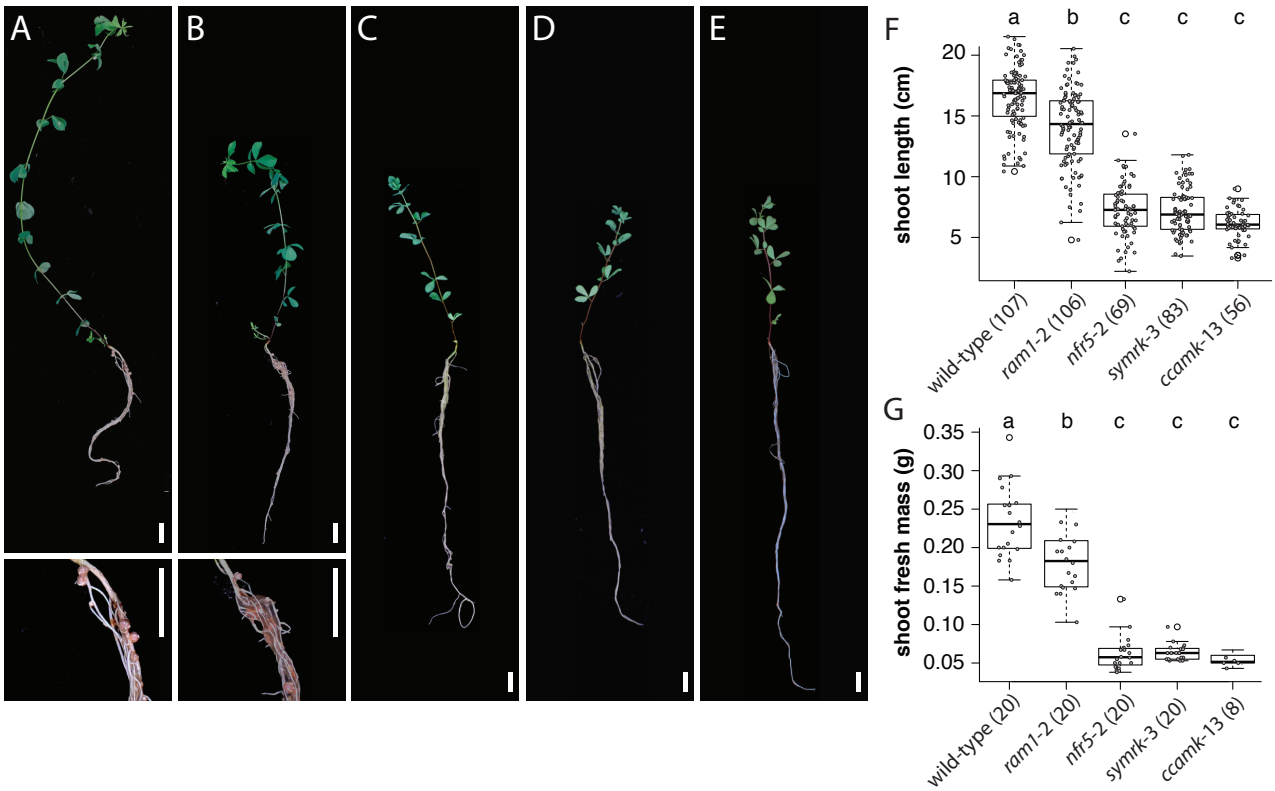

Fig2, **Phenotypes of WT and mutant plants**. Images depicting *L. japonicus* wild-type (A) and symbiosis-deficient mutant plants: *ram1-2* (B), *nfr5-2* (C), *symRK-3* (D) and *ccamk-13* (E). Insets show close-up view of nodules. Scale bars correspond to 1 cm. F) Boxplots display the shoot length for the identical set of genotypes presented in (A-E). G) Boxplots displaying the shoot fresh mass. Letters above plots correspond to groups based on Tukey's HSD test ($P<0.05$). Number of samples are indicated in brackets.

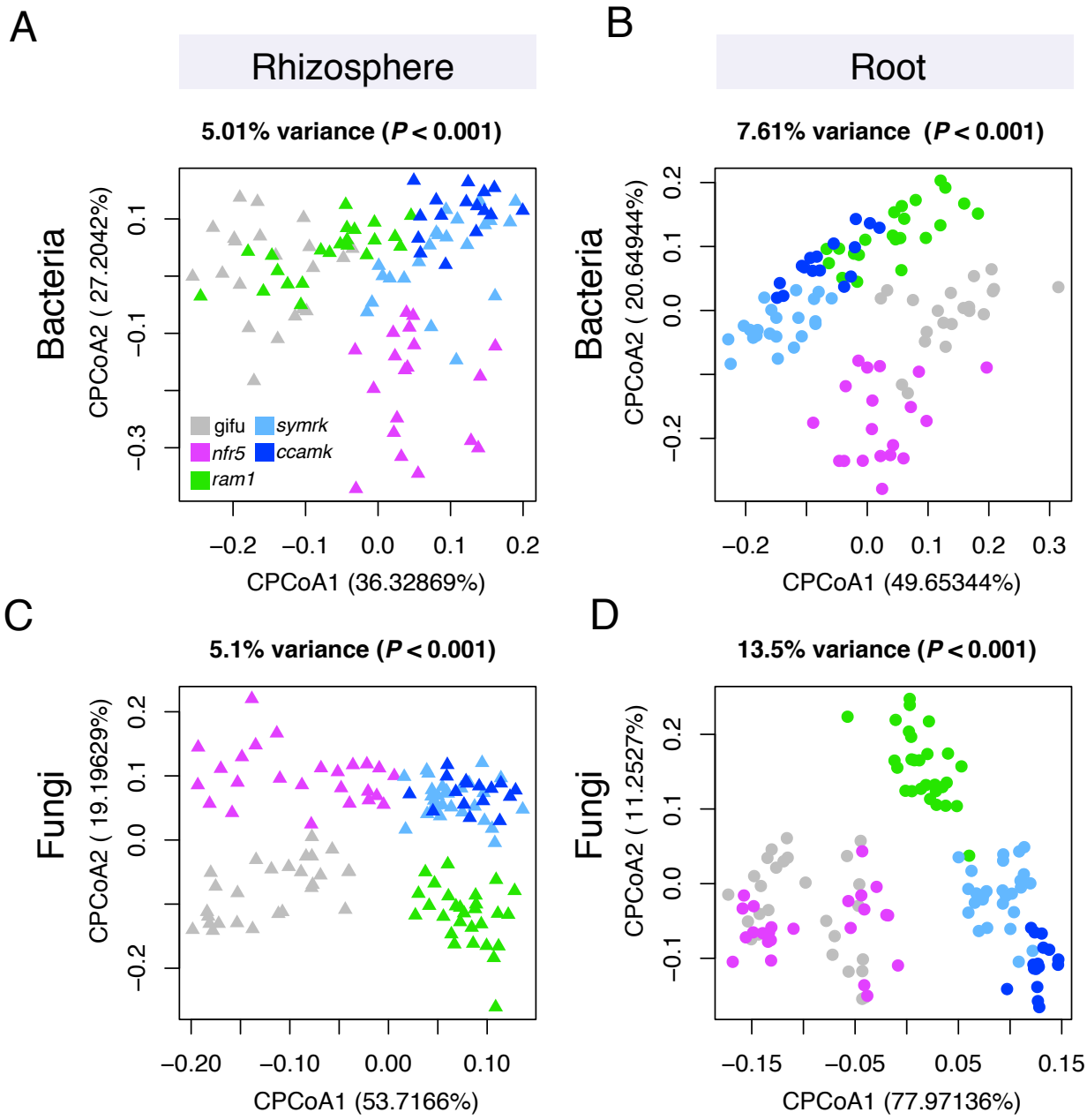

Fig3, **Constrained PCoA analysis showing genotype effect on microbial communities.** A) Constrained PCoA plots for bacterial datasets showing rhizosphere samples (n = 100) and B) root samples (n = 100). C) Constrained PCoA plots for fungal datasets showing only rhizosphere samples (n = 124) and D) root samples (n = 122).

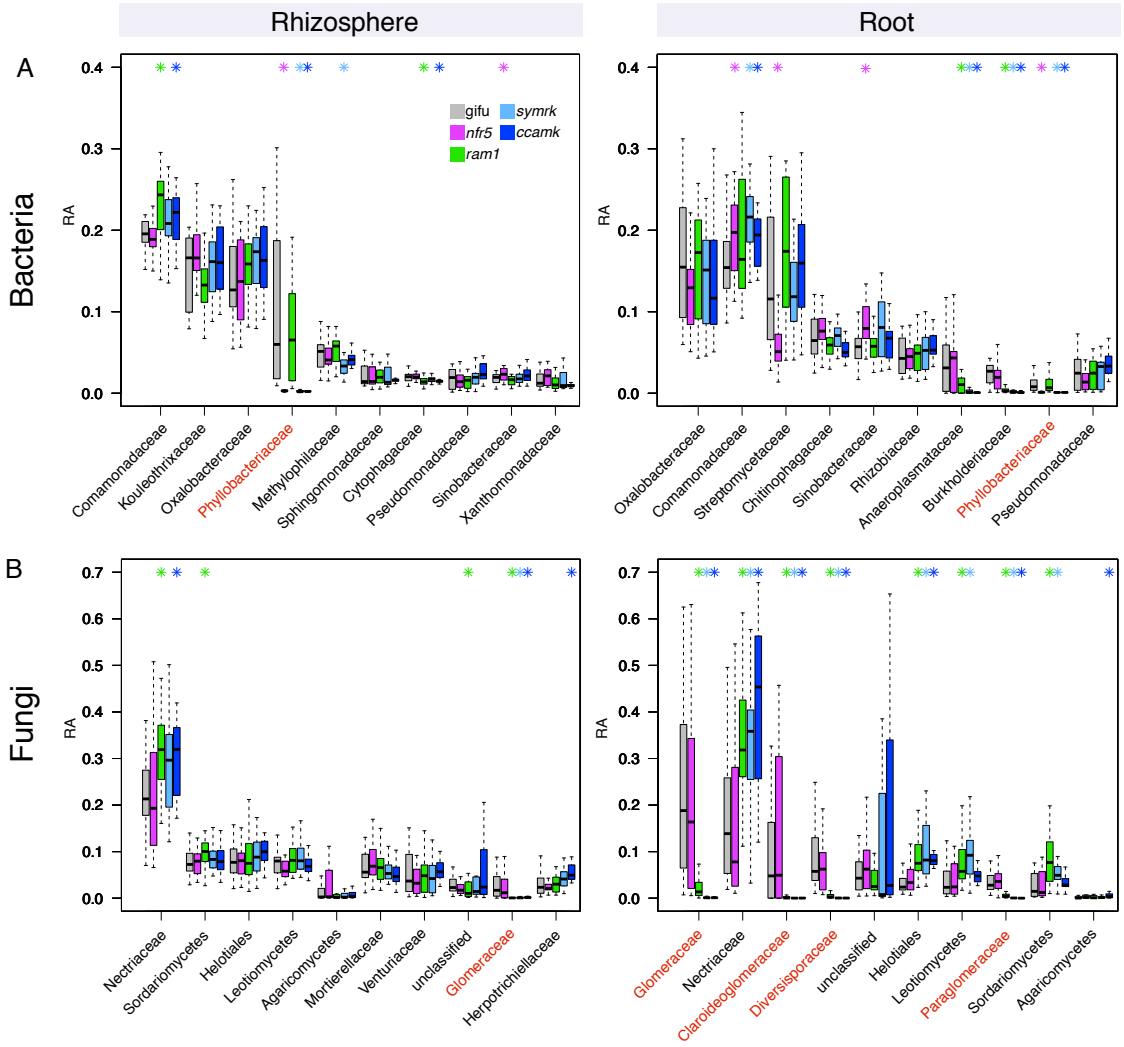

Fig4, **Relative abundance for main microbial taxa across plant compartments and genotypes**. A) RA for bacterial families in rhizosphere (left panel) and root compartment (right panel). B) RA for fungal families in rhizosphere (left panel) and root compartment (right panel). Taxa are sorted in decreasing order according to their average RA in wt plants (only first 10 most abundant taxonomical groups are shown). RA in wt as well as in the respective mutants is displayed. Significant differences compared to wt are marked with an asterisk in the color of the mutant ($P<0.05$, Kruskal-Wallis test). Families that include known symbionts are marked in red (Phyllobacteriaceae for bacteria and Glomeromycetes for Fungi). For some fungal taxa the next higher rank is shown, when no family level information was available.

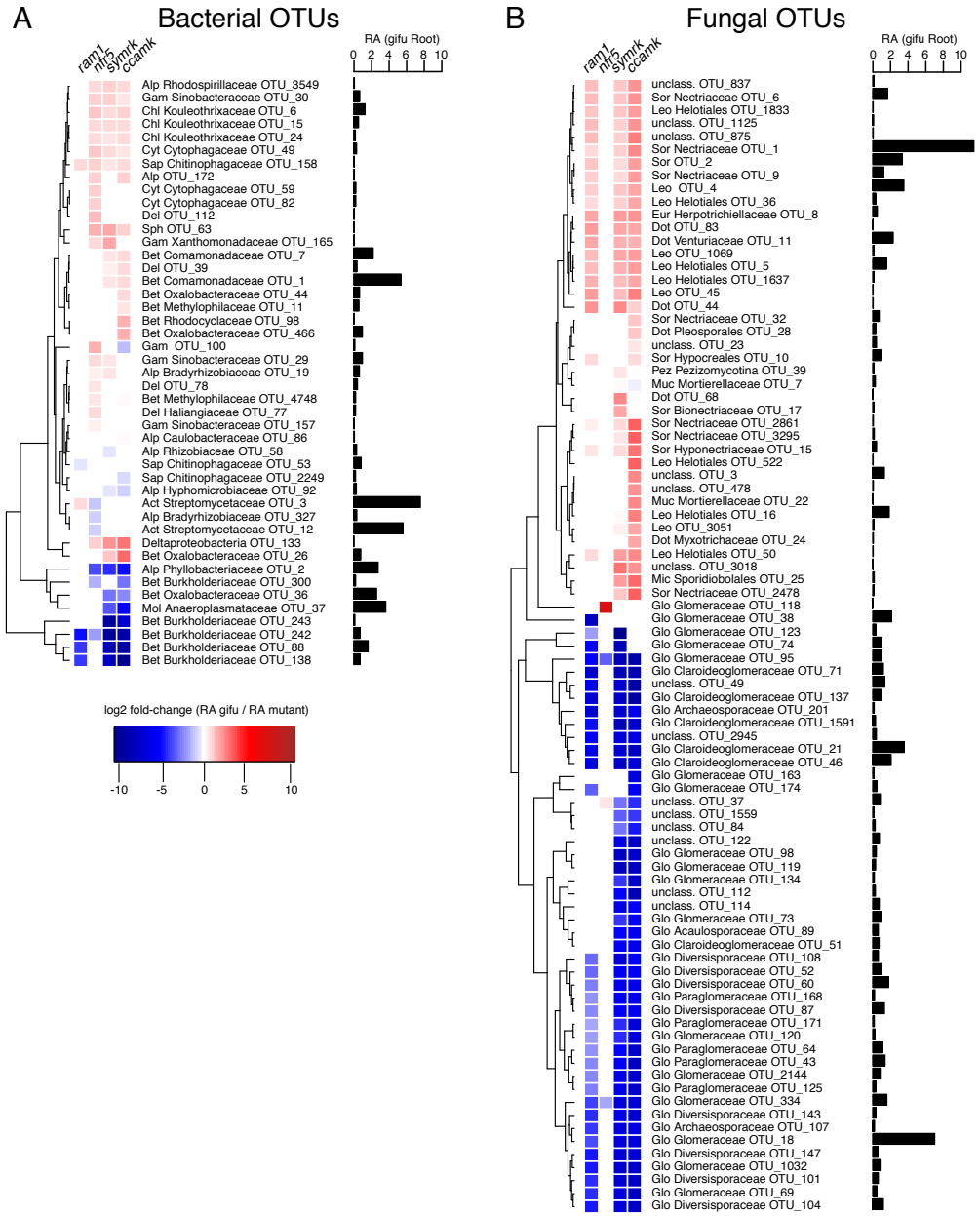

Fig5, **Differential abundance analysis for root associated OTUs**.
A) Bacterial OTUs that are differentially abundant in the roots of mutants compared to wt roots. B) fungal OTUs that are differentially abundant in the roots of mutants compared to wt roots. Only OTUs that have an average RA > 0.1% across all root samples, including mutants, are considered here. For each OTU the fold change in RA from wt to mutant is indicated ($P < 0.05$, Kruskal-Wallis test). Next to each OTU the RA in wt roots is indicated. Phylum and family asscociation (if available) is given for each OTU (Bacterial phyla: Del=Deltaproteobactria, Gem=Gemm-1 , Chl=Chloroflexi, Bet=Betaproteobacteria, Alp=Alphaproteobacteria, Gam=Gammaproteobacteria, Cyt=Cytophagia, Sap=Saprospirae, Ped=Pedosphaerae, Sph= Sphingobacteria, Mol= Mollicutes ; Fungal phyla: Sor=Sordariomyctes, Dot=Dothideomycetes, Mic= Microbotryomycetes, Ust=Ustilaginomycetes, Eur=eurotiomycetes, Leo=Leotiomycetes, Aga=Agaricomycetes, Glo=Glomeromyctes, Pez=Pezizomycota, Muc=Mucoromycotina).

685 **Supplementary Figures**
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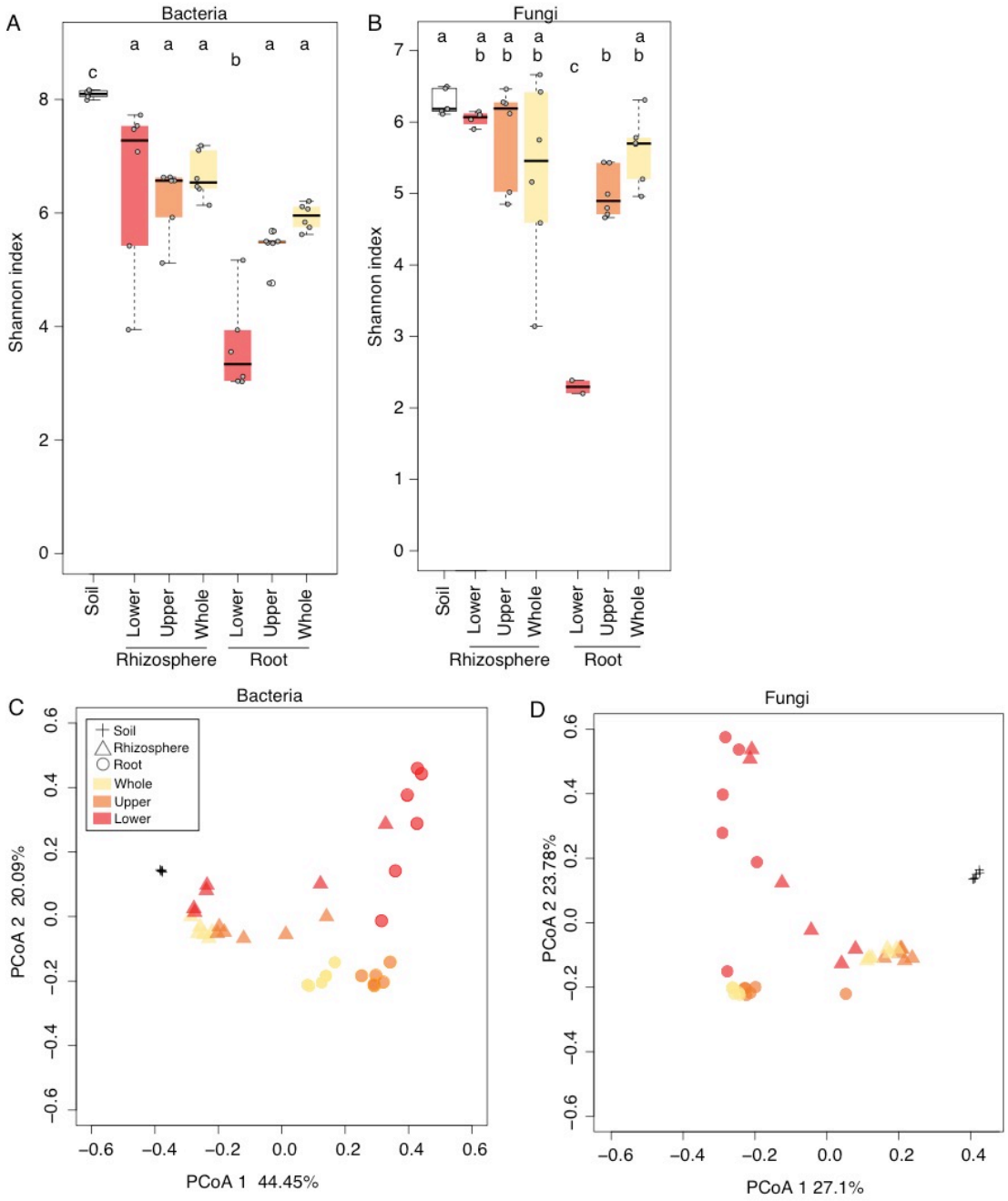

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689 **Supp Fig1, Alpha and beta diversity across root fractions.**
690 A) Shannon diversity index for 16S amplicon data, soil (n=6), lower (n=6), upper (n=6), whole root
691 fractions (n=6), and respective rhizosphere samples (n=6 each) B) Shannon diversity index for
692 ITS2 amplicon data, soil (n=6), lower (n=2), upper (n=6), whole root fractions (n=6), and
693 respective rhizosphere samples (n=6 each, except lower, n=4) (ANOVA with Tukey's post hoc
694 test, $P<0.05$). C) Principal coordinate analysis of Bray-Curtis distances for bacterial data. D)
695 Principal coordinate analysis of Bray-Curtis distances for fungal data.
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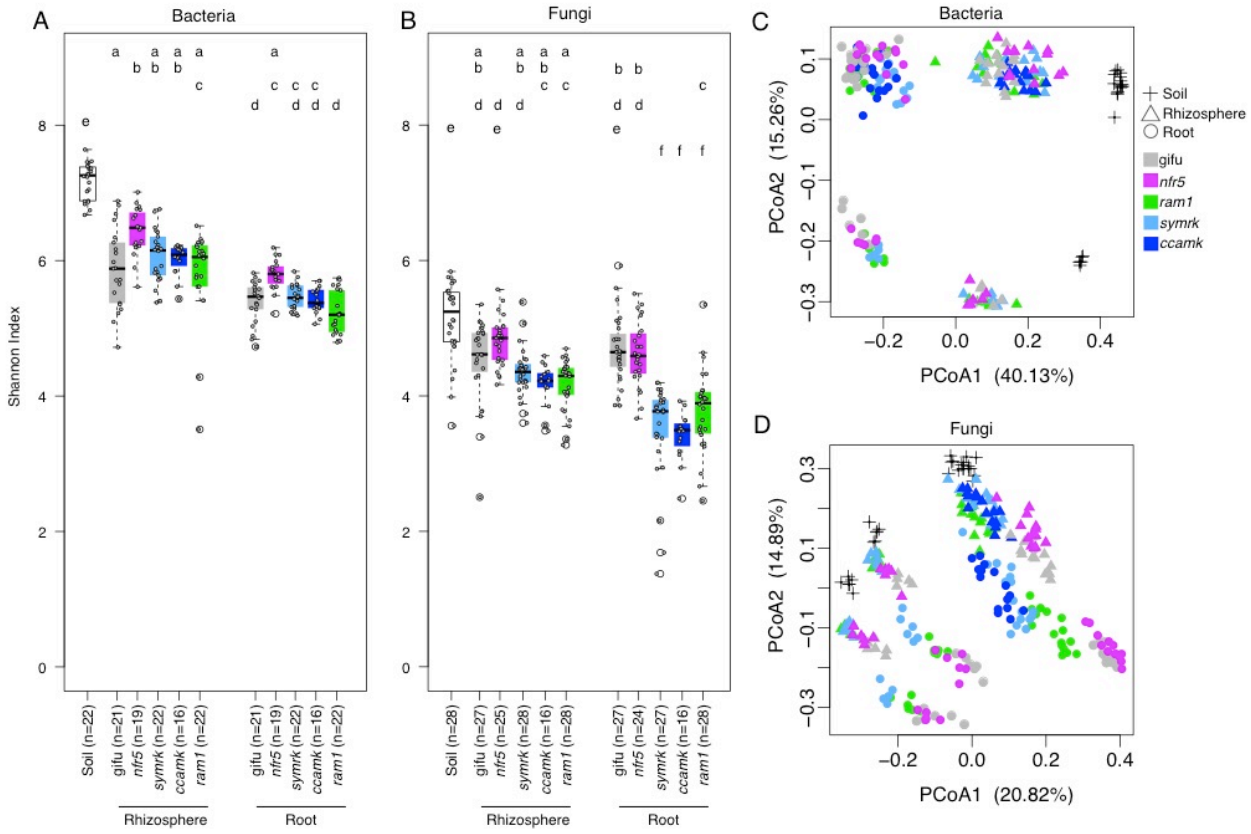
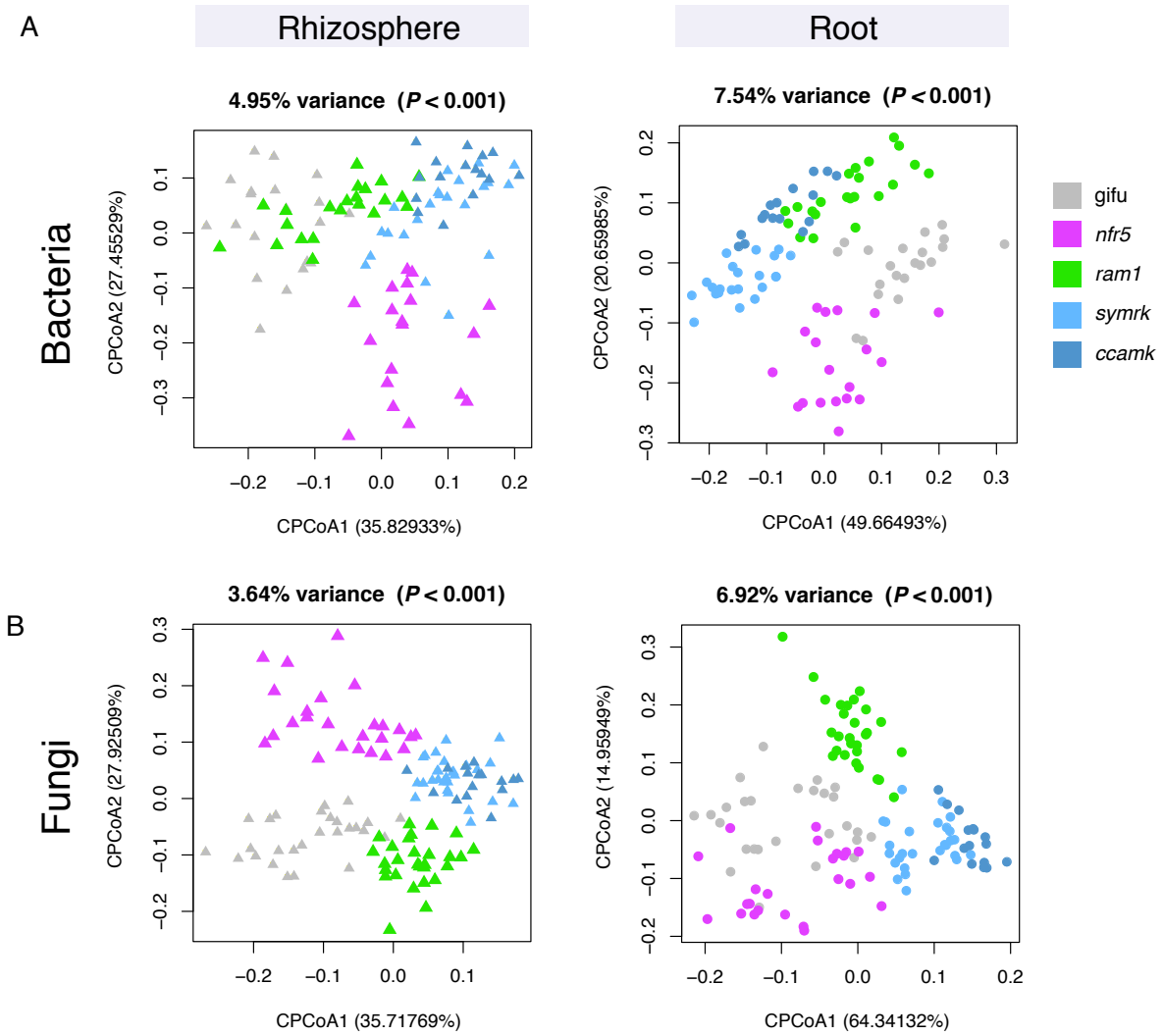
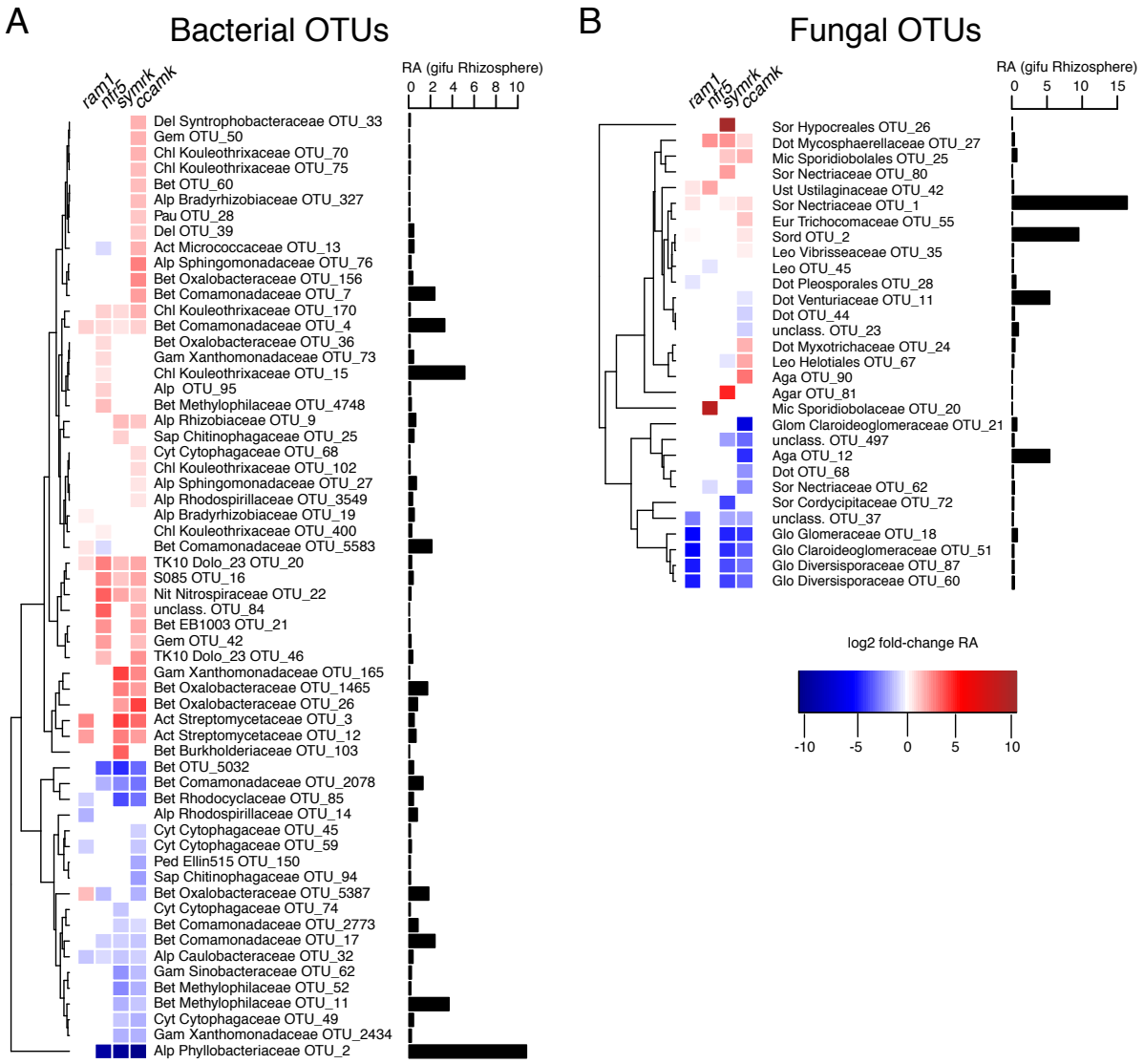


Supp Fig2, Alpha and beta diversity across plant compartments and genotypes.
A) Shannon diversity indices for the bacterial (16S amplicon) dataset. B) Shannon diversity indices for the fungal (ITS2 amplicon) dataset (ANOVA with Tukey's post hoc test, P<0.05) C) Principal coordinate analysis of Bray-Curtis distances for the bacterial dataset (n=222). D) Principal coordinate analysis of Bray-Curtis distances for the fungal dataset (n=274).

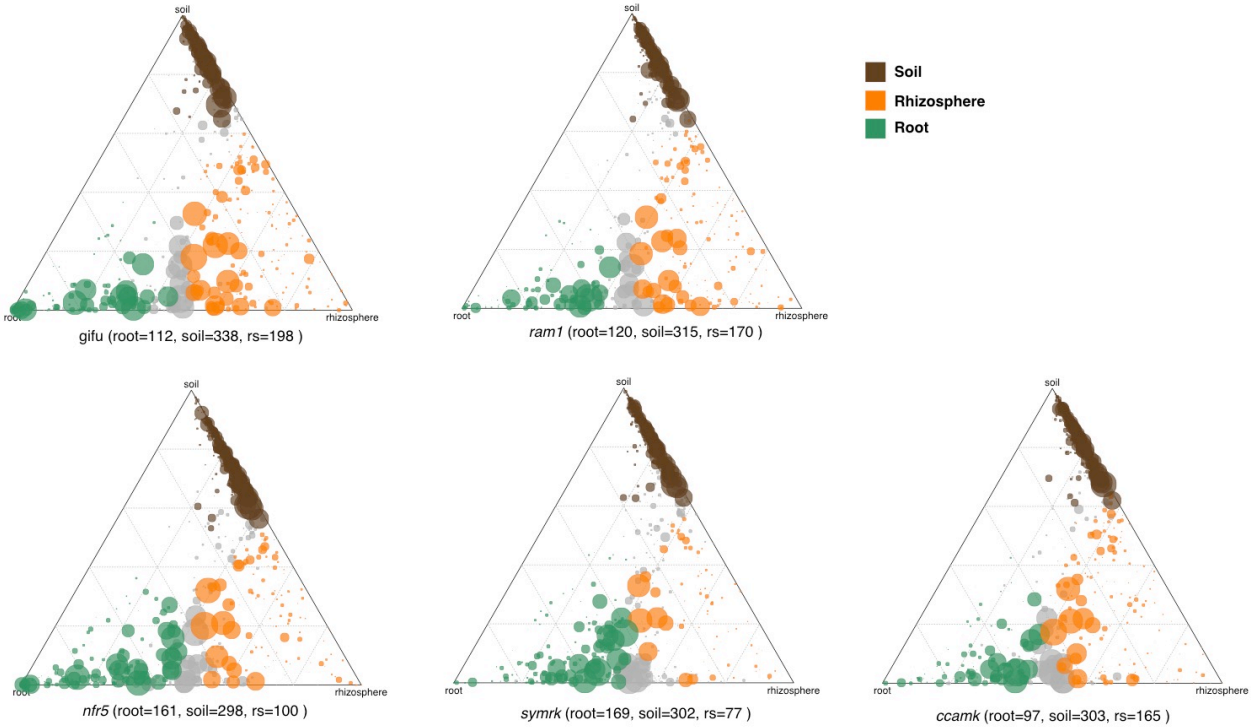


Supp Fig3, CPCoA, showing the same results as Fig3, but without known symbionts. Results are separated by compartments. Datasets were constrained by genotype, and filtered for effects of experiments and soil type. A) Bacterial dataset from which OTUs belonging to the Phyllobacteriaceae were removed before analysis (root n=100, rhizosphere n=100). B) Fungal dataset from which OTUs belonging to the Glomeromycota were removed before analysis (root n=122, rhizosphere n=124).



Supp Fig4, Differential abundance analysis for rhizosphere-associated OTUs showing enrichment and depletion in mutants.

A) bacterial OTUs that are differentially abundant in the rhizosphere of mutants compared to wt. B) fungal OTUs that are differentially abundant in the rhizosphere of mutants compared to wt. Only OTUs that have an average RA > 0.1% across all rhizosphere samples, including mutants, are considered here. For each OTU, the fold change in RA from wt to mutant is indicated ($P < 0.05$, Kruskal-Wallis test). Next to each OTU the RA in wt rhizosphere is indicated. Phylum and family asscociation is given for each OTU (Bacterial phyla: Del=Deltaproteobacteria, Gem=Gemm-1 , Chl=Chloroflexi, Bet=Betaproteobacteria, Alp=Alphaproteobacteria, Gam=Gammaproteobacteria, Cyt=Cytophagia, Sap=Saprospirae, Ped=Pedosphaerae, Sph= Sphingobacteria, Mol= Mollicutes ; Fungal phyla: Sor=Sordariomyctes, Dot=Dothideomycetes, Mic= Microbotryomycetes, Ust=Ustilaginomycetes, Eur=Eurotiomycetes, Leo=Leotiomycetes, Aga=Agaricomycetes, Glo=Glomeromyctes, Pez=Pezizomycota, Muc=Mucoromycotina).



Supp fig5, Ternary plots showing compartment-enriched bacterial OTUs. Separately for wt and mutant plants. Below each plot the number of enriched OTUs for each compartment is shown.

Supp table1, Symbiotic phenotype of *Lotus japonicus* wild-type and mutants grown in Cologne soil (*n=5*)

Genotype	WT(Gifu)	*nfr5-2*	*ram1-2*	*symrk-2*	*ccamk-13*
Colonization (% of root system with intraradical colonisation)	60-70	60-70	10	0	0
Arbuscules	present	present	present	none	none
Nodulation (% of roots with nodules)	100	0	100	0	0