Response of *Lonicera maackii* to soil chemistry and fungal communities.

This project aims at disentangling the relative contribution of soil physico-chemistry and fungal communities in driving *Lonicera maackii* performance. In 2019, we sampled 50 soil inocula, from 5 distinct sites, and grew *Lonicera maackii* in these inocula in a growth chamber, for 12 weeks.

We measured shoot dry mass, root length and average diameter, and root fungal colonization as response variables.

In parallel, for each inoculum, we measured soil physico-chemistry and extracted DNA from ~250mg soil to characterize fungal community structure using Illumina MiSeq technology (PE250bp), with amplicons targeting the ITS2 region (primers = gITS7 [fwd] and ITS4 [rev]). Data are provided as follows:

1. Soil properties, fungal root colonization and *Lonicera* performance are all included in the file lonicera.txt. *Lonicera* growth data is averaged for pseudo-replicates belonging to the same inoculum, but raw data for all pseudo-replicates separately are available in raw.growth.txt.

2. Soil fungal community structure can be found in the file comm.txt, where row names are inocula ID and number within each cell are the number of reads found in each inoculum for the corresponding column (fungal sequence variant). The 7-levels taxonomy, under the form of a table with rows corresponding to columns in `comm.txt` is provided in the `taxa.txt`. We also provide raw sequence files within the sequence read archives (SRA) under the `BioProject # PRJNA1049398`. The SRR numbers associated with all samples can be found in our file `SRRs.txt`.

METADATA

Below are found metadata for each individual data file. All files are organized in a tabular format, so we explain in the metadata the meaning of all column titles, and relevant information as to how that particular piece of information was collected in the project.

File 1: comm.txt

COLUMN TITLE	EXPLANATION	NOTES
ASV1, ASV2, ASV...	Amplicon sequence variants (i.e., unique non-chimeric sequences identified in the study)	The content of each cell represents the number of sequence reads found for each of these fungal taxa (ASVs) in each corresponding soil inoculum (rows).

In this file, only samples with at least 5000 reads are kept for downstream analyses, ending up in keeping 32 samples out of our 50 samples overall.

File 2: lonicera.txt

COLUMN TITLE	EXPLANATION	NOTES
Site	The site at which the inoculum (row) has been collected.	Inocula have been collected in 5 sites (5 sites $\times$ 10 inocula per site = 50 inocula overall). All these sites were forested areas with different histories, times since *Lonicera* invasion and dominant canopy species.

COLUMN TITLE	EXPLANATION	NOTES
Inoculum	Unique soil inoculum used in the experiment	Consisted of raw live (i.e., unsterilized) soil.
masse.tige	Dry shoot mass (g)	Measured by harvesting *Lonicera* aboveground biomass after 12 weeks of growth in the inoculum, and drying at 65C to constant weight.
l.racines	Total root length (m)	Measured by washing roots free of soil, and scanning them on a flatbed scanner. Root length was estimated using WinRhizo
diam.racines	Average root diameter (mm)	Based on root images acquired as described above, average diameter was estimated by WinRhizo
arb	Arbuscules colonization frequency (%)	Based on the gridline intersect method of McGonigle et al. (1990), we estimated the frequency of root colonization by *Arum*-type arbuscules, after staining in ink-vineagar (5% v/v)
coils	Coils colonization frequency (%)	These were differentiated from arbuscules by the visible presence of interwoven hyphae (as opposed to a dichotomous branching pattern for *Arum*-type arbuscule).
ves	Vesicles colonization frequency (%)	Again with the gridline intersect method, colonization frequency of roots by arbuscular mycorrhizal (AM) vesicles was estimated
nonmyc	Non-mycorrhizal structure colonizaiton frequency (%)	Any fungal (or Oomycota) structure that could be clearly established to be non-AM fungal, or not belonging to a dark septate endophyte (see below), was recorded in this category. This includes regularly septate hyphae but not thick melanized hyphae appearing as DSE, and structures looking like *Olpidium* chlamydospores, or oomycete oospores...
dse	Dark septate endophytes root colonization frequency (%)	In this category were included fungal structure with relatively large hyphal diameter, regular septation, melanized brown appearance and a clear diagnostic feature was the presence of either linear chains, or tufts of microsclerotia. Recognizing that some dark septate endophytes can also stain heavily with ink (and not appear as brownish melanized hyphae), our estimate is not intended to be a clear guild-level colonization estimate, but rather a morphology/appearance-based estimation of different categories of non-AM fungal structures, along with "nonmyc".
pH	soil pH	Measured in a 1:2 mixture ratio (v/v) with distilled water
ammonium	NH_4-N	Estimated by colorimetry following an extraction from soil using 2N KCl
nitrate	NO_3-N	Estimated by colorimetry following an extraction from soil using 2N KCl
phosphore	orthophosphates	Estimated using a Mehlich-III extraction and a colorimetric test (Murphy-Riley approach with blue molybdate complex)
wsa	Water-stable aggregates (%)	Percentage of 250 $\mu\textrm{m}$ - 1mm aggregates stable to water immersion cycles as tested in a Yoder's apparatus.
mo	% Organic matter	Percent organic matter estimated as loss on ignition at 350°C

File 3: taxa.txt

COLUMN TITLE	EXPLANATION	NOTES
Kingdom	Kingdom	The Kingdom to which all fungal ASVs (rows) belong. ASVs are placed in the same order (rows) as columns in `comm.txt`.
Phylum	Phylum	The phylum to which the ASV belongs. NA means the naive Bayesian classifier was not able to confidently assign a value for that particular level.
Class	Class	The class to which the ASV belongs. NA means the naive Bayesian classifier was not able to confidently assign a value for that particular level.
Order	Order	The Order to which the ASV belongs. NA means the naive Bayesian classifier was not able to confidently assign a value for that particular level.
Family	Family	The Family to which the ASV belongs. NA means the naive Bayesian classifier was not able to confidently assign a value for that particular level.
Genus	Genus	The Genus to which the ASV belongs. NA means the naive Bayesian classifier was not able to confidently assign a value for that particular level.
Species	Species	The Species to which the ASV belongs. NA means the naive Bayesian classifier was not able to confidently assign a value for that particular level.

Bioinformatics

Before proceeding with statistical analyses, we first processed raw `.fastq` sequence files using the R package `dada2`. First, we quality-filtered sequences in order to [.....]

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[..............]
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Then, we proceeded with paired-end merging:

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[..............]
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Next, we removed potential chimeras:

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[..............]
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Finally, we assigned taxonomy using the UNITE database, version **XYZ**. Because of the size of the database, we had to submit this last job to a supercomputer using the following SLURM job:

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To correct for uneven sequencing depth per sample, we conducted sequence rarefaction in R:

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