Supplementary Methods

Amplicon library construction and sequencing

Sequencing libraries were created as described previously in Yergeau *et al*. (2015) based on a dual-indexed strategy following the "16S Metagenomic Sequencing Library preparation" Illumina guide (Part #15044223 Rev. B). Similar to qPCR analysis, for bacterial 16S rRNA gene the V3-V4 hypervariable region was amplified using the universal primers 520F (5'-AGCAGCCGCGGTAAT-3') and 799R (5'-CAGGGTATCTAATCCTGTT-3') (Edwards *et al*., 2008), and for fungi the ITS1 region was amplified using ITS1F (5'-CTTGGTCATTTAGAGGAAGTAA-3') and 58A2R (5'-CTGCGTTCTTCATCGAT-3') (Martin and Rygiewicz, 2005). Samples were pooled separately for fungi and bacteria and submitted for 2 × 250 bp Illumina MiSeq sequencing at the McGill University and Genome Québec Innovation Centre (Montréal, Canada). Sequence data were analysed following procedures described in Tremblay *et al*. (2015). Briefly, raw reads were controlled for quality. The remaining high-quality reads and free of sequencing adapters artifacts were dereplicated at 100% identity and clustered/denoised at 99% (DNAclust v3) (PMID:21718538). Clusters of less than three reads were discarded, and the remaining clusters were scanned for chimeras using UCHIME, first in de novo mode then in reference mode (Edgar *et al*., 2011). The remaining clusters were clustered at 97% identity (DNAclust v3) to produce OTUs. For 16S data types, taxonomy assignment of resulting OTUs was performed using the RDP classifier (Wang *et al*., 2007) with a modified Greengenes training set built from a concatenation of the Greengenes database v13_5 (DeSantis *et al*., 2006), and Silva eukaryotes 18S r128 (Quast *et al*., 2013). For ITS data, the taxonomic assignment was done with the RDP classifier using a training set generated from the Unite database (sh_refs_qiime_ver7_dynamic_20.11.2016) (Kõljalg *et al*., 2013). Raw data sets are available in the NCBI Sequence Read Archive (SRA) under the BioProject accession PRJNA526458.

References

Yergeau E, Bell TH, Champagne J, Maynard C, Tardif S, Tremblay J, Greer CW. Transplanting Soil Microbiomes Leads to Lasting Effects on Willow Growth, but not on the Rhizosphere Microbiome. *Front Microbiol* 2015;**6**:1436.

Tremblay J, Singh K, Fern A, Kirton ES, He S, Woyke T, Lee J, Chen F, Dangl JL, Tringe SG. Primer and platform effects on 16S rRNA tag sequencing. *Front Microbiol* 2015;**6**:771.

Wang Q, Garrity GM, Tiedje JM, Cole JR. Naive Bayesian classifier for rapid assignment of rRNA sequences into the new bacterial taxonomy. *Appl Environ Microbiol* 2007;**73**:5261–5267.

DeSantis TZ, Hugenholtz P, Larsen N, Rojas M, Brodie EL, Keller K, et al. Greengenes, a chimera-checked 16S rRNA gene database and workbench compatible with ARB. *Appl Environ Microbiol* 2006;**72**:5069–5072.

Quast C, Pruesse E, Yilmaz P, Gerken J, Schweer T, Yarza P, et al. The SILVA ribosomal RNA gene database project: improved data processing and web-based tools. *Nucleic Acids Res* 2013; **41**: 590–596.

Kõljalg U, Nilsson RH, Abarenkov K, Tedersoo L, Taylor AFS, Bahram M, et al. Towards a unified paradigm for sequence-based identification of fungi. *Mol Ecol* 2013; **22**: 5271–5277.