



Plant host and soil origin influence fungal and bacterial assemblages in the roots of woody plants

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Background

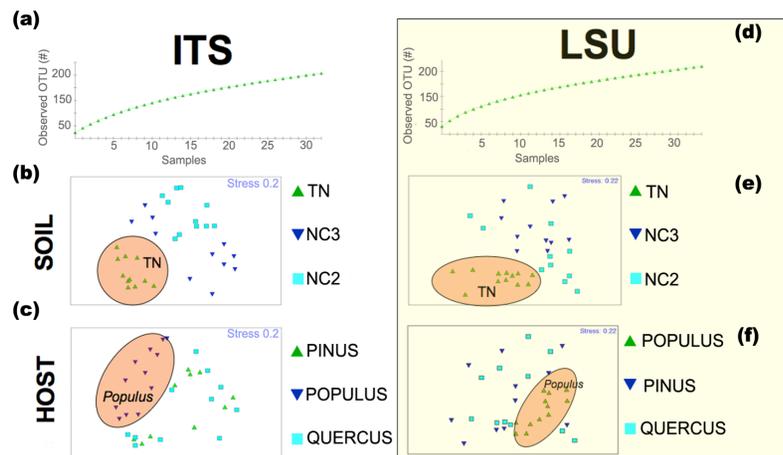
A trap-plant bioassay experiment was designed to decouple effects of host-preference and soil origin on the development of microbial communities in plant roots. Fungal and bacterial communities were profiled from *Populus*, *Quercus* and *Pinus* roots by multiplex 454 amplicon pyrosequencing of 4 loci (ITS, 18S, 28S & 16S rDNA).

Science

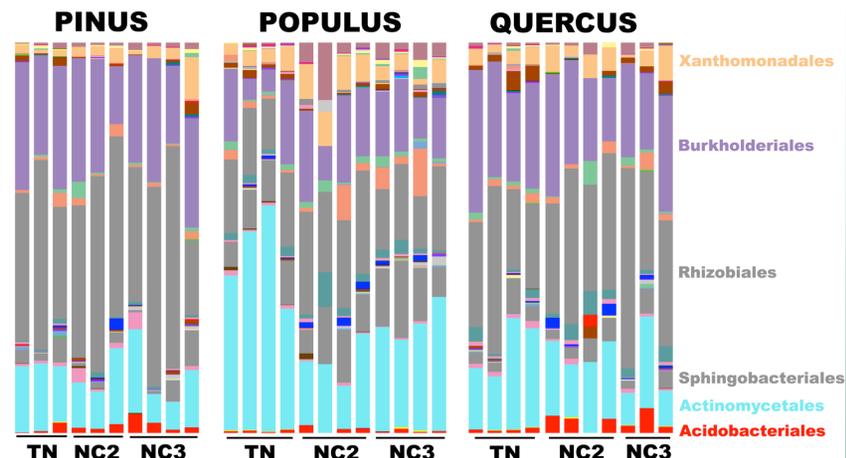
- ITS and LSU were commensurate in detecting fungal diversity and identifying dominant fungal taxa (OTUs).
- A high diversity (but low sequence abundance) of arbuscular mycorrhizas in the Glomeraceae and Paraglomaceae were detected on *Populus*, while *Quercus* and *Pinus* root systems were depauperate in arbuscular mycorrhizal taxa.
- Soil origin has a greater effect on the structure of fungal communities in roots than do effects of different host genera, however, bacterial communities in plant roots are more tightly structured by plant host than soil origin.

Significance

- The trap-plant bioassay, coupled with high-throughput multi-locus sequencing, provides a powerful experimental approach for decoupling complex ecological questions.



Rarefaction and principal coordinate ordination of fungal communities based on (a-c) ITS1 and (d-f) 28S (LSU) present a similar view of fungal root communities and their diversity. In particular, fungal communities in TN soils segregate cleanly from those in NC soils, while communities in the two NC soils are more intermixed. Similarly, fungal communities of *Populus* segregate from fungal communities of *Pinus* and *Quercus*.



Higher level taxonomic assignments of bacteria detected based on 16S rDNA. Samples are separated by host and soils. Taxonomic ranks for abundant taxa are labeled on the right.

Bonito et al. (2014) Plant host and soil origin influence fungal and bacterial assemblages in the roots of woody plants. *Molecular Ecology*. 23: 3356-3370.