

Abstract

Most land plants including the cereal model crop maize acquire nutrients directly from the rhizosphere through their roots and indirectly through mutualistic interactions with arbuscular mycorrhizal fungi (AMF). AMF extend extraradical hyphae (ERH) beyond the rhizosphere into the hyphosphere, accessing nutrient patches unreachable for roots. Due to the limited ability of AMF to e.g. mineralize soil organic phosphorus, they rely on interactions with other microbes in the hyphosphere and on their hyphal surface (hyphoplane). However, whether roots and hyphae assemble distinct bacterial and fungal communities and to what extent soil management and plant genotypic variations affect those communities is largely unknown.

To study host genotype x microbiota x soil interactions, we investigated the bacterial and fungal communities in root- and hyphae-associated compartments sampled from four genotypically distinct maize lines grown under varying phosphorus (P) and nitrogen (N) fertilization in three consecutive field studies using automated ribosomal intergenic spacer analysis (ARISA) and amplicon sequencing. To investigate spatial relationships in maize mycorrhizosphere compartments, we developed a half-automated sieving and sucrose centrifugation (SSC) method with high throughput to obtain the hyphoplane from natural loamy field soil.

The bacterial and fungal communities inhabiting the root endosphere and rhizosphere differed remarkably in diversity and structure from those found in the hyphoplane and hyphosphere. Soil P and N fertilization, and to a lesser extent plant genotype, affected the microbial communities throughout all compartments, indicating that changes in the plant genotype are transmitted to community assembly by ERH. The knock-out of the mycorrhizal phosphate (Pi) transporter PHT1;6, which leads to a dysfunctional mycorrhizal Pi uptake pathway (MPU), had the strongest effects on the growth and nutrient content of maize and on the composition of the bacterial community on the hyphoplane among the four plant genotypes investigated. The loss of MPU more strongly shaped fungal and bacterial communities in the root endosphere than in the rhizosphere, hyphoplane, and hyphosphere, but left ERH length unchanged. The ERH length was affected by soil pH, soil fertilization, and the plant growth stage. Furthermore, we found a correlation between ERH length, plant biomass, plant P levels, and fungal root colonization, providing initial evidence for a feedback loop between intraradical and extraradical fungal hyphae in response to soil nutrient conditions, impacting plant biomass and nutrient levels reciprocally. However, this feedback loop may be disrupted in *pht1;6* mutants. We further identified bacterial and fungal genera consistently enriched at the hyphoplane and those that are more abundant under conditions favoring the arbuscular mycorrhizal symbiosis (AMS), and therefore potentially relevant for hyphoplane community assembly and AMS.

Overall, our results highlight that hyphae recruit specific fungal and bacterial communities to the hyphoplane, whose assembly is influenced by the host's ability to take up Pi via the MPU pathway and by soil fertilization.