Divergent mycorrhizal lineages have different morphology and colonization rates in a model grass

Veronica Hoac, Gabriella Griffen, Rachel Hestrin
Stockbridge School of Agriculture, CAFE
University of Massachusetts Amherst

UMassAmherst
College of Natural Sciences
Center for Agriculture, Food, and the Environment

United States Department of Agriculture
National Institute of Food and Agriculture

Introduction

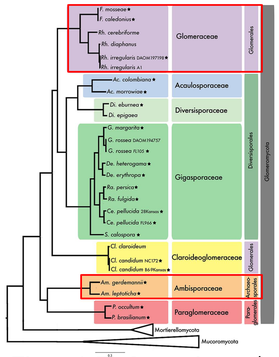


Figure 1. Phylogenetic tree.[4]

Background: Arbuscular mycorrhizal fungi (AMF) associate with the majority of terrestrial plant species. In exchange for photosynthates, these symbiotic fungi provide their hosts with mineral nutrients[1-3]. AMF span a range of phylogenetic diversity (Fig. 1), which corresponds with differences in mycorrhizal relationships, plant performance, and ecosystem function[1,3,4].

Research Objective: Assess colonization dynamics in mycorrhizal associations formed between the model grass *Brachypodium distachyon* and two divergent mycorrhizal lineages–*Archaeospora trappei* and *Rhizophagus intraradices*.

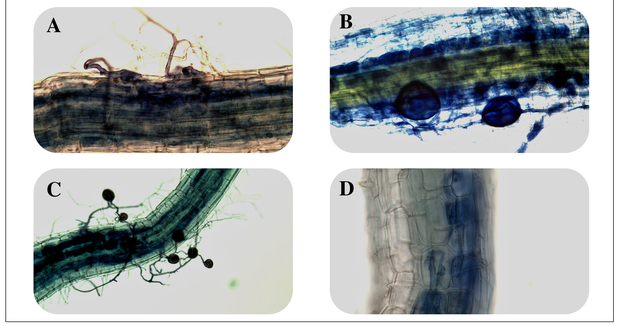
Hypothesis: Divergent mycorrhizal lineages have different colonization rates and morphologies.

Methods

Experimental Conditions: 50 *B. distachyon* plants were inoculated with *Ar. trappei* or *R. intraradices* and maintained in a growth chamber with controlled light, temperature, and humidity.

Analysis: Measured above and below ground plant biomass after 3 and 6 weeks of growth. Stained roots to assess mycorrhizal colonization. Quantified colonization with the Magnified Intersections Method[5]. Quantified fungal intraradical and extraradical hyphae (Fig. 2a), vesicles (Fig. 2b), chlamydospores (Fig. 2c), and intraradical hyphae (Fig. 2d).

Figure 2. Roots colonized by AMF.



Results

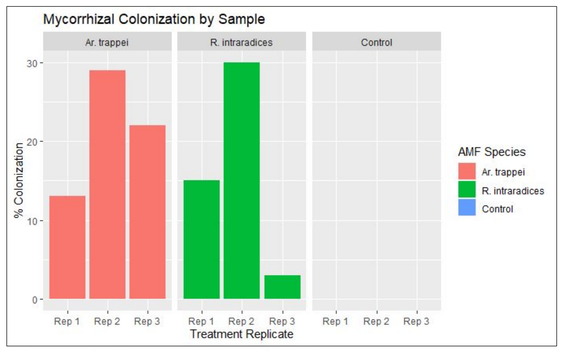


Figure 3. Proportion of each root system colonized by AMF at 3 weeks; each replicate is represented individually.

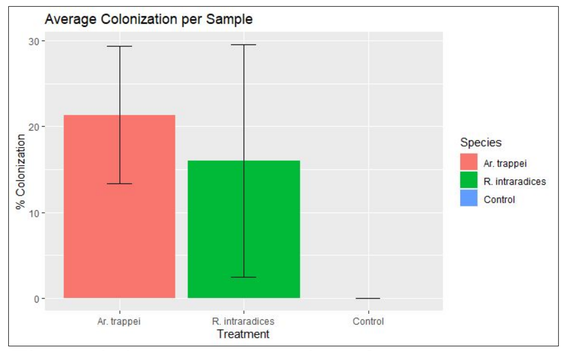


Figure 4. Average proportion of root system colonized by AMF at 3 weeks. Error bars represent the standard error (n = 3).

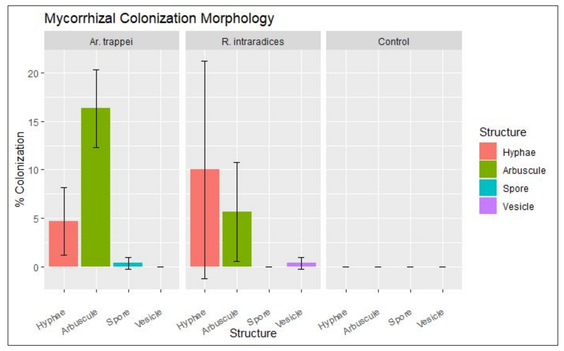


Figure 5. Variation in mycorrhizal morphology observed in roots at 3 weeks. Error bars represent the standard error (n = 3).

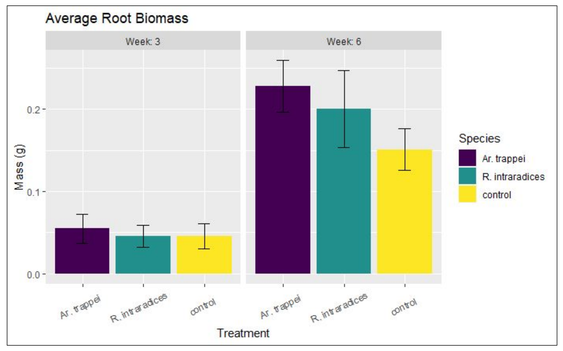


Figure 6. Root biomass of uninoculated control plants and plants inoculated with AMF. Error bars represent the standard error (n = 3).

Results

The two divergent mycorrhizal lineages–*Archaeospora trappei* and *Rhizophagus intraradices*–exhibited different colonization dynamics. At 3 weeks, fungal colonization was highly variable across replicate plants inoculated with each AMF lineage (Fig. 3). Averaged, *Ar. trappei* colonized 18.75% of inoculated root systems, while *R. intraradices* colonized 16.00% (Fig. 4). The two AMF lineages also produced different proportions of distinct morphological features (Figs 2&5). Roots inoculated with *Ar. trappei* contained spores and a higher proportion of arbuscules compared to hyphae, while *R. intraradices* produced vesicles and a lower proportion of arbuscules to hyphae (Fig. 5). As expected, the uninoculated control plants showed no signs of mycorrhizal colonization or other fungal infections. At week 3, there were no significant differences between root biomass of inoculated or uninoculated plants. At week 6, however, the biomass of roots inoculated with *Ar. trappei* was greater than that of uninoculated control plants (Fig. 6).

Discussion

Conclusions: Although differences in total colonization rates were not statistically significant at 3 weeks, *Ar. trappei* appeared to colonize roots more rapidly and form more arbuscules at 3 weeks compared to *R. intraradices*. Arbuscules are the primary site of resource exchange between AMF and roots. This may explain why the biomass of roots inoculated with *Ar. trappei* was greater than the biomass of uninoculated roots, while the biomass of roots inoculated with *R. intraradices* was not significantly different. These findings contrast with previous reports that more anciently diverging AMF lineages provide less benefit to plants than more recently diverging lineages[1,3]. It is possible that contextual differences (e.g., nutrient availability, absence of other biotic interactions, etc.) are responsible for these contrasting results. Analysis of a wider set of biotic and abiotic variables, as well as analysis of samples collected from later timepoints will help to characterize different colonization dynamics and effects on plant performance.

Future Directions:

- Investigate colonization dynamics at later timepoints
- Confirm fungal identity with DNA sequencing
- Quantify fungal effects on plant biomass and root architecture
- Characterize root & mycorrhizal exudate profiles and functional capacity

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