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## Different Arbuscular Mycorrhizal Fungi Cocolonizing on a Single Plant Root System Recruit Distinct Microbiomes

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Plant roots are usually colonized by various arbuscular mycorrhizal (AM) fungal species, which vary in morphological, physiological, and genetic traits. This colonization constitutes the mycorrhizal nutrient uptake pathway (MP) and supplements the pathway through roots. Simultaneously, the extraradical hyphae of each AM fungus is associated with a community of bacteria. However, whether the community structure and function of the microbiome on the extraradical hyphae differ between AM fungal species remains unknown. In order to understand the community structure and the predicted functions of the microbiome associated with different AM fungal species, a splitroot compartmented rhizobox cultivation system, which allowed us to inoculate two AM fungal species separately in two root compartments, was used. We inoculated two separate AM fungal species combinations, (i) *Funneliformis mosseae* and *Gigaspora margarita* and (ii) *Rhizophagus intraradices* and *G. margarita*, on a single root system of cotton. The hyphal exudate-fed, active microbiome was measured by combining <sup>13</sup>C-DNA stable isotope probing with MiSeq sequencing. We found that different AM fungal species, which were simultaneously colonizing a single root system, hosted active microbiomes that were distinct from one another. Moreover, the predicted potential functions of the different microbiomes were distinct. We conclude that the arbuscular mycorrhizal fungal component of the system is responsible for the recruitment of distinct microbiomes in the hyphosphere. We found that arbuscular mycorrhizal fungi cocolonizing on single plant roots recruit their own specific microbiomes, which should be considered in evaluating plant microbiome form and function. Our findings demonstrate the importance of understanding trophic interactions in order to gain insight into the plant-AM fungus-bacterium symbiosis