**Description of the data and file structure**

A randomized experiment in a PGR15 Conviron growth chamber was set up with the model plant Sudan-grass (Sorghum x drummondii) and 8 strains of the model AMF Rhizophagus irregularis, following established protocols. The 80 inoculated plant units consisted of 11 groups (4 homokaryon and 4 heterokaryon strains, a mixed group, a fungus-free planted control, and a plant-free control), each replicated 7 times. For 12 weeks, the chamber was pulsed weekly with isotopically labelled 13C-CO2 to track carbon (C) flow through the plant, AMF and soil. Plant biomass and soil samples were collected at harvest, and soil Mineral Associated Organic Matter (MAOM, the more stable C pool) and 13C fractions were analyzed using particle fractioning and Isotope Ratio Mass Spectrometry. Shoot samples from each plant were analyzed for nutrient concentration. In parallel, Sudan-grass roots colonized by each AMF heterokaryon were analyzed using droplet digital PCR (ddPCR) 13 to track differences in relative genome abundance. These data were analyzed in R to identify variation in host biomass, nutrient uptake, and soil C inputs among AMF strains.

**Information regarding** [**Ferguson\_2024\_Results.R**](https://github.com/rob-ferg/Ferguson-et-al_2024/blob/main/Ferguson_2024_Data.csv)

This script was generated in RStudio (Version 4.3.3). Required packages are listed at the top of the script.

For each statistical analysis, a figure was generated with the factors and response variable of interest, for visual inspection of the data. Below, preliminary tests were run to confirm the appropriate assumptions (ex: Shapiro-Wilk test, Levene's test), followed by the statistical test of interest (ex: ANOVA), then any post-hoc tests (ex: Tukey's HSD, Dunnet's test). Calculated p-values are reported below each test as comments.

At the bottom of the script, custom legends were generated for any figures that required them for clarification.

**Information regarding** [**Ferguson\_2024\_Data.csv**](https://github.com/rob-ferg/Ferguson-et-al_2024/blob/main/Ferguson_2024_Data.csv)

*Variables*

* Inoculation: Whether or not the host plant (Sudan-grass) was inoculated with an AMF strain (control = no AMF)
* Organization: The nuclear organization of the inoculated AMF strain (heterokaryon or homokaryon
* Clade: The clade of the inoculated AMF strain
* Strain: The abbreviation for the AMF strain identifier
* Replicate: Replicated pots were labeled 1-7
* Label: The specific combination of strain and replicate number
* Root\_DM: The root dry mass of the host plant at harvest
* Shoot\_DM: The shoot dry mass of the host plant at harvest
* Total\_DM: The total dry mass of the host plant at harvest
* R\_S\_Ratio: The root:shoot ratio of the host plant at harvest
* MR\_Root\_DM: The mycorrhizal response of host root dry mass at harvest (the value of a given replicate minus the AMF-free control group average)
* MR\_Shoot\_DM: The mycorrhizal response of host root dry mass at harvest (the value of a given replicate minus the AMF-free control group average)
* MR\_Total\_DM: The mycorrhizal response of host total dry mass at harvest (the value of a given replicate minus the AMF-free control group average)
* MR\_R\_S\_Ratio: The mycorrhizal response of host root:shoot ratio at harvest (the value of a given replicate minus the AMF-free control group average)
* Bulk\_Mycorrhizal\_C1: Total soil carbon inputs from the mycorrhizal system (fungus + plant), measured in "mg C per g of soil"
* Bulk\_Mycorrhizal\_C2: Total soil carbon inputs from the mycorrhizal system (fungus + plant), measured in "mg C per g of soil C"
* BulkMAOM\_Mycorrhizal\_C1: Total soil mineral associated organic carbon inputs from the mycorrhizal system (fungus + plant), measured in "mg C per g of mineral associated organic matter soil"
* BulkMAOM\_Mycorrhizal\_C2: Total soil mineral associated organic carbon inputs from the mycorrhizal system (fungus + plant), measured in "mg C per g of mineral associated organic carbon"
* Inc\_Mycorrhizal\_C1: Total post-incubation soil carbon inputs from the mycorrhizal system (fungus + plant), measured in "mg C per g of soil"
* Inc\_Mycorrhizal\_C2: Total post-incubation soil carbon inputs from the mycorrhizal system (fungus + plant), measured in "mg C per g of soil C"
* IncMAOM\_Mycorrhizal\_C1: Total post-incubation soil mineral associated organic carbon inputs from the mycorrhizal system (fungus + plant), measured in "mg C per g of mineral associated organic matter soil"
* IncMAOM\_Mycorrhizal\_C2: Total post-incubation soil mineral associated organic carbon inputs from the mycorrhizal system (fungus + plant), measured in "mg C per g of mineral associated organic carbon"
* Bulk\_SOC: Total estimated SOC in a sample from a given replicate pot
* Bulk\_MAOC: Total estimated MAOC in a sample from a given replicate pot
* Inc\_SOC: Total estimated SOC in an incubated sample from a given replicate pot
* Inc\_MAOC: Total estimated MAOC in an incubated sample from a given replicate pot
* Incubation\_effect\_C1: Amount of C (in mg C per g of soil) lost during incubation "Inc\_Mycorrhizal\_C1 - Bulk\_Mycorrhizal\_C1"
* Incubation\_effect\_C1\_MAOM: Amount of MAOC (mg C per g of mineral associated organic matter soil) lost during incubation "IncMAOM\_Mycorrhizal\_C1 - BulkMAOM\_Mycorrhizal\_C1"
* N\_Conc: Concentration of shoot nitrogen (in mg/g tissue) in a given host plant replicate
* S\_Conc : Concentration of shoot sulfur (in mg/g tissue) in a given host plant replicate
* P\_Conc: Concentration of shoot phosphorous (in mg/g tissue) in a given host plant replicate
* K\_Conc: Concentration of shoot potassium (in mg/g tissue) in a given host plant replicate
* Mg\_Conc: Concentration of shoot magnesium (in mg/g tissue) in a given host plant replicate
* B\_Conc: Concentration of shoot boron (in µg/g tissue) in a given host plant replicate
* Zn\_Conc: Concentration of shoot zinc (in µg/g tissue) in a given host plant replicate
* Mn\_Conc: Concentration of shoot manganese (in µg/g tissue) in a given host plant replicate
* Fe\_Conc: Concentration of shoot iron (in µg/g tissue) in a given host plant replicate
* Cu\_Conc: Concentration of shoot copper (in µg/g tissue) in a given host plant replicate
* Al\_Conc: Concentration of shoot aluminum (in µg/g tissue) in a given host plant replicate
* % Hyphae: Percent abundance of AMF hyphae in ink-vinegar stained roots of a given host plant replicate
* % Vesicles: Percent abundance of AMF vesicles in ink-vinegar stained roots of a given host plant replicate
* % Arbuscules: Percent abundance of AMF arbuscules in ink-vinegar stained roots of a given host plant replicate