# *Supplementary Material*

Title: **Arbuscular mycorrhizal fungi and rhizobium improve nutrient uptake and microbial diversity relative to dryland site-specific soil conditions**

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Table S1. Monthly mean temperature and precipitation from May to August during 2022 growing seasons at the two-dryland sites in Froid (DFS 1) and Sidney, Montana (DFS 2).

| | Mean temperature (°C) | | Mean precipitation (mm) | |
|---|---|---|---|---|
| Month | DFS1 | DFS2 | DFS1 | DFS2 |
| May | 11.00 | 12.00 | 62.50 | 143.10 |
| June | 17.00 | 18.00 | 61.20 | 68.00 |
| July | 21.00 | 22.00 | 142.70 | 45.60 |
| August | 22.00 | 22.00 | 10.70 | 3.60 |
| May -Aug | 17.75 | 18.50 | 69.28 | 65.08 |

Weather data obtained from North Dakota Agricultural Weather Network National Oceanic and Atmospheric Administration, monthly and precipitation data (http://www.ndsu.nodak.edu/weather-data-monthly.html). The weather stations, Froid MT 5S and Sidney MT 1NW, were co-located at the research sites DFS 1 Froid and DFS 2 Sidney, MT. Websites accessed 8 November 2023.

Table S2 – Characterization of the soil physicochemical analysis of the two contrasting dryland sites.

| Soil physico-chemical data | Dryland Site 1 | | Dryland Site 2 | |
|---|---|---|---|---|
| Available water supply | 0.17 | | 0.18 | |
| Soil Organic Matter (% LOI) | 1.50 | low | 2.50 | moderate |
| pH (1:1 pH rating) | 4.70 | strongly acidic | 6.30 | neutral |
| CEC/Sum of Cations me/100g | 12.83 | | 15.19 | |
| Nutrients*† | | | | |
| N | 28.33 | high | 7.06 | low |
| P | 73.00 | very high | 44.75 | high |
| K | 214.50 | very high | 277.88 | very high |
| S | 10.85 | medium | 7.26 | low |
| Ca | 482.50 | very high | 1636.75 | very high |
| Mg | 140.63 | very high | 396.88 | very high |
| Zn | 0.59 | medium | 0.72 | medium |
| Fe | 69.16 | very high | 36.51 | very high |
| Cu | 0.68 | very high | 0.90 | very high |
| Mn | 102.13 | very high | 27.94 | very high |

*measured in parts per million (ppm). † Soil fertility ratings for soil nutrients, Ward lab guide.

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Table S3– Pea nutrient requirement and baseline soil physicochemical analysis of the two contrasting dryland sites.

| Soil physico-chemical data | Pea nutrient requirement† | Dryland Site 1 | | Dryland Site 2 | |
|---|---|---|---|---|---|
| Available water supply | | 0.17 | | 0.18 | |
| Soil Organic Matter (% LOI) | | 1.50 | low | 2.50 | moderate |
| pH (1:1 pH rating) | neutral | 4.70 | strongly acidic | 6.30 | neutral |
| Bulk density | | 1.60 | | 1.60 | |
| CEC/Sum of Cations me/100g | | 12.83 | | 15.19 | |
| Nutrients (kg/ha) | | | | | |
| N | 168 | 272 | high | 68 | low |
| P | 50 | 701 | very high | 430 | very high |
| K | 157 | 2,054 | high | 2,668 | - high |

† Pea nutrient requirement to produce average yield of 1,364 kg/ha

Table S4 – Field management practices and chemical applications.

| Management practices | Category | Name | Active ingredient | Rate | Dryland site 1-Froid | Dryland site 2-Sidney |
|---|---|---|---|---|---|---|
| 1. Tillage | NA | NA | NA | NA | No tillage | No tillage |
| 2. Basal fertilization | Fertilizer | Phosphorus | P | 56 kg/ha | 5/15/2022 | 5/17/2022 |
| | Fertilizer | Muriate of Potash | K | 45 kg/ha | 5/15/2022 | 5/17/2022 |
| 3. Weed control | Herbicide | Basagran 5l | Bentazon | 12.8 oz/acre (897g/ha) | 6/27/2022 | 6/26/2022 |

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Table S5 – Microbial dependency (%) data showing the microbial inoculants' contribution to aboveground biomass, grain yield and overall plant growth at two dryland sites.

| Treatment | Biomass MD% | Grain MD% | Plant MD% |
|---|---|---|---|
| Microbial Inoculant (M) | | | |
| Control | 0 | 0 | 0 |
| AMF | -2.54 | 10.86 | 8.32 |
| Rhizobium | 1.51 | 2.70 | 4.21 |
| AMF+ Rhizobium | 1.16 | 10.65 | 11.81 |
| Dryland Site (S) | | | |
| Site 1 | -0.05 | 9.55 | 9.50 |
| Site 2 | 0.11 | 2.56 | 2.67 |
| M x S | | | |
| 1_Control_DFS 1 | 0.00 | 0.00 | 0.00 |
| 2_AMF_DFS 1 | -2.75 | 26.92 | 24.58 |
| 3_Rhizobium_DFS 1 | 3.68 | 2.08 | 5.76 |
| 4_AMF+Rhizobium_DFS 1 | -1.53 | 9.19 | 7.66 |
| 5_Control_DFS 2 | 0.00 | 0.00 | 0.00 |
| 6_AMF_DFS 2 | -2.75 | -5.20 | -7.94 |
| 7_Rhizobium_DFS 2 | -1.53 | 3.32 | 2.66 |
| 8_AMF+Rhizobium_DFS 2 | 3.85 | 12.12 | 15.97 |
| | | | |
| Significance | | | |
| Nonparametric: Wilcoxon/KruskalWallis Test | ns‡ | AMF+Rhizobium_DFS 2 ≠ Control in both sites (*P*=0.0075, z=2.67401) | ns |

* Significant P≤0.05.

**Significant P≤0.001.

† Means followed by different lowercase letters within a column are significantly different at $P \leq 0.05$ and P≤0.001.

‡ Not significant.

Table S6 – Effect of microbial inoculations on plant biomass and grain nutrient content (% by mass) at two dryland sites.

| Treatment | Plant biomass | | | Pea grain | | | |
|---|---|---|---|---|---|---|---|
| | Carbon | Nitrogen | Protein | Carbon | Nitrogen | Phosphorus | Protein |
| Microbial Inoculant | | | | | | | |
| Control | 42.80 | 1.43 | 8.92 | 41.76b | 4.27 | 0.43 | 26.66 |
| AMF | 42.70 | 1.47 | 9.18 | 42.04a | 4.27 | 0.44 | 26.03 |
| Rhizobium | 42.90 | 1.49 | 9.32 | 41.91ab | 4.28 | 0.43 | 26.75 |
| AMF+ Rhizobium | 42.50 | 1.50 | 9.35 | 42.03a | 4.31 | 0.43 | 26.95 |
| Dryland Site | | | | | | | |
| Site 1 | 42.60 | 2.16a | 13.52a | 42.54a | 4.72a | 0.40b | 29.47a |
| Site 2 | 42.85 | 0.78b | 4.86b | 41.34b | 3.80b | 0.47a | 23.73b |
| Significance | | | | | | | |
| M | ns‡ | ns | ns | * | ns | ns | ns |
| S | ** | ** | ** | ** | ** | ** | ** |
| M x S | ns | ns | ns | ** | ns | ns | ns |

* Significant P≤0.05.

**Significant P≤0.001.

† Means followed by different lowercase letter within a column are significantly different at $P \leq 0.05$ and P≤0.001.

‡ Not significant.

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Table S7 – Effect of microbial inoculants on carbon sequestered/stored in the harvested plant biomass and grains at two dryland sites.

| Treatment | Biomass | | | Grain | | | Total C sequestered (kg/ha) |
|---|---|---|---|---|---|---|---|
| | yield (kg/ha) | C concentration | C content (kg/ha) | yield (kg/ha) | C concentration | C content (kg/ha) | |
| Microbial Inoculant | | | | | | | |
| Control | 3146.89 | 0.4280 | 1346.43 | 1287.48 | 0.417615b | 536.69 | 1883.13 |
| AMF | 3004.30 | 0.4270 | 1282.19 | 1300.15 | 0.420349a | 544.15 | 1826.34 |
| Rhizobium | 3117.00 | 0.4290 | 1337.09 | 1288.03 | 0.419117ab | 536.40 | 1873.48 |
| AMF+ Rhizobium | 3154.65 | 0.4246 | 1340.46 | 1388.12 | 0.420333a | 578.66 | 1919.12 |
| Dryland Site | | | | | | | |
| Site 1 | 2916.21b | 0.4256 | 1241.48b | 834.55b | 0.4253a | 355.06b | 1596.54b |
| Site 2 | 3295.21a | 0.4284 | 1411.60a | 1797.35a | 0.4133b | 742.89a | 2154.49a |
| Significance | | | | | | | |
| M | ns‡ | ns | ns | ns | * | ns | ns |
| S | * | ns | * | ** | ** | ** | ** |
| M x S | ns | ns | ns | * | ns | * | ns |

* Significant P≤0.05.

**Significant P≤0.001.

† Means followed by different lowercase letter within a column are significantly different at $P \leq 0.05$ and P≤0.001.

‡ Not significant.

Table S8 – Effect of microbial inoculants on plant N and P nutrient uptake at two dryland sites.

| Treatment | N uptake in biomass | N uptake in grains | N uptake whole plant | P uptake in grains |
|---|---|---|---|---|
| Microbial Inoculant | | | | |
| Control | 43.74 | 53.22 | 96.95 | 5.93946 |
| AMF | 43.29 | 52.55 | 95.85 | 6.19661 |
| Rhizobium | 46.12 | 52.78 | 98.90 | 5.65876 |
| AMF+ Rhizobium | 45.21 | 57.00 | 102.21 | 6.17326 |
| Dryland Site | | | | |
| Site 1 | 63.67a | 39.42b | 102.79 | 3.37656b |
| Site 2 | 25.81b | 68.36a | 94.17 | 8.60748a |
| Significance | | | | |
| M | ns‡ | ns | ns | ns |
| S | ** | ** | ns | ** |
| M x S | ns | ns | ns | ns |

* Significant P≤0.05.

**Significant P≤0.001.

† Means followed by different lowercase letter within a column are significantly different at $P \leq 0.05$ and P≤0.001.

‡ Not significant.

Table S9 –Effect of microbial inoculation on soil organic residual NPK (kg/ha) after pea cropping.

| .Soil nutrient residual | N | P | K |
|---|---|---|---|
| Microbial inoculants (M) | | | |
| Control | 40.90 | 130.80 | 1,358.40 |
| AMF | 58.44 | 124.80 | 1,334.40 |
| Rhizobium | 46.56 | 96.00 | 1,194.00 |
| AMF+ Rhizobium | 41.28 | 120.00 | 1,327.00 |
| Sites (S) | | | |
| Dryland site 1 | 68.16a | 162.60a | 1,204.40b |
| Dryland site 2 | 25.44b | 73.20b | 1,401.60a |
| Significance | | | |
| M | ns‡ | ns | ns |
| S | ** | ** | * |
| M x S | ns | ns | ns |

* Significant P≤0.05 **Significant P≤0.001 ‡ Not significant

† Means followed by different lowercase letter within a column are significantly different at $P \leq 0.05$ and P≤0.001.

Table S10. Alpha and beta diversity of pea rhizosphere soils as influenced by microbial inoculants at two dryland conditions, MT 2022.

| Diversity metrics | Microbial Inoculants (M) | Dryland Sites (S) | M X S |
|---|---|---|---|
| Bacterial and archaeal community (16S rRNA) | | | |
| † Alpha diversity | | | |
| Observed ASVs | 0.029 | 0.143 | 0.008 |
| Shannon index | 0.041 | 0.354 | 0.017 |
| ‡Beta diversity | 0.637 / $R^2$=0.065 | 0.001 / $R^2$=0.314 | 0.001* / $R^2$=0.436 |
| Fungal community (ITS) | | | |
| † Alpha diversity | | | |
| Observed ASVs | 0.409 | 1.02e-07 | 0.003 |
| Shannon index | 0.852 | 0.00004 | 0.043 |
| ‡Beta diversity | 0.998/ $R^2$=0.027 | 0.001* / $R^2$=0.484 | 0.001* / $R^2$=0.551 |

* Significant P≤0.05.

** Significant P≤0.001.

† Alpha diversity metrics, a qualitative measure of microbial richness using observed species richness and Shannon diversity index

‡ Beta diversity metrics, a quantitative measure of community dissimilarity using Bray Curtis Index (statistical method: permutational analysis of variance (PERMANOVA).

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Table S11 - Influence of microbial inoculants at two dryland sites on the most abundant (relative sequences abundance > 1% of all bacterial sequences) bacterial taxa on pea rhizosphere soil.

| Taxonomic group | Microbial Inoculants (M) | | | | Dryland Site (S) | | Significance P value | | |
|---|---|---|---|---|---|---|---|---|---|
| **Phylum** | Control | AMF | Rhizobium | AMF+ Rhizobium | Site 1 | Site 2 | M | S | M*S |
| Actinobacteria | 0.35964b | 0.32322b | 0.43008a | 0.35661b | 0.35426 | 0.38052 | * | ns‡ | ns |
| Proteobacteria | 0.25526 | 0.22502 | 0.24957 | 0.28519 | 0.25726 | 0.25026 | ns | ns | ns |
| Acidobacteria | 0.13851 | 0.22504 | 0.13422 | 0.1437 | 0.15621 | 0.16453 | ns | ns | ns |
| Chloroflexi | 0.07418 | 0.04076 | 0.06432 | 0.06324 | 0.06401 | 0.05724 | ns | ns | ns |
| Bacteroidetes | 0.07443 | 0.04453 | 0.04102 | 0.05335 | 0.04092b | 0.06574a | ns | * | ns |
| WPS2 | 0.03683 | 0.06741 | 0.03226 | 0.03739 | 0.08694a | -2.10E-17b | ns | ** | ns |
| Firmicutes | 0.02311 | 0.03897 | 0.02457 | 0.02579 | 0.00792b | 0.0483a | ns | ** | ns |
| Thaumarchaeota | 0.01374 | 0.01959 | 0.01177 | 0.0145 | 0.00963 | 0.02017 | ns | ns | ns |
| Nitrospirae | 0.00886 | 0.0081 | 0.0016 | 0.00555 | -4.30E-18b | 0.01206a | ns | ** | ns |
| Planctomycetes | 0.00857 | 0.00204 | 0.00594 | 0.00685 | 0.0105a | 0.0012b | ns | ** | ns |
| **Order** | | | | | | | | | |
| Propionibacteriales | 0.11409 | 0.10717 | 0.13561 | 0.13655 | 0.05045b | 0.19626a | ns‡ | * | ns |
| Solibacterales | 0.06859 | 0.10651 | 0.08728 | 0.09069 | 0.09694 | 0.07959 | ns | ns | ns |
| Betaproteobacteriales | 0.09407 | 0.06969 | 0.096 | 0.0898 | 0.07107 | 0.10371 | ns | ns | ns |
| Micrococcales | 0.06667 | 0.07355 | 0.08214 | 0.07485 | 0.08638 | 0.06223 | ns | ns | ns |
| Solirubrobacterales | 0.06814 | 0.05818 | 0.08691 | 0.05131 | 0.08252 | 0.04975 | ns | ns | ns |
| Rhizobiales | 0.05325 | 0.07277 | 0.05797 | 0.0571 | 0.04594b | 0.0746a | ns | * | ns |
| Acetobacterales | 0.05777 | 0.05516 | 0.0584 | 0.05663 | 0.1029a | 0.01108b | ns | ** | ns |

| **Order** | Control | AMF | Rhizobium | AMF+ Rhizobium | Site 1 | Site 2 | M | S | M*S |
|---|---|---|---|---|---|---|---|---|---|
| Frankiales | 0.060a | 0.0284c | 0.07489a | 0.04422ab | 0.03272b | 0.07112a | * | ** | ns |
| Chitinophagales | 0.07443 | 0.05335 | 0.04453 | 0.04102 | 0.04092b | 0.06574a | ns | * | ns |
| Uncultured bacterium | 0.03683 | 0.06741 | 0.03226 | 0.03739 | 0.08694a | -2.10E-17b | ns | ** | ns |
| Elsterales | 0.0368b | 0.0274b | 0.02551b | 0.06897a | 0.01848b | 0.06087a | * | * | * |
| Acidobacteriales | 0.0235b | 0.0613a | 0.01577b | 0.02857b | 0.05927a | 0.00529b | * | ** | ns |
| Thermomicrobiales | 0.0371 | 0.02738 | 0.02721 | 0.02945 | 0.00333b | 0.05724a | ns | ** | ns |
| Bacillales | 0.02311 | 0.03897 | 0.02457 | 0.02579 | 0.00792b | 0.0483a | ns | ** | ns |
| Gaiellales | 0.0291 | 0.02535 | 0.03131 | 0.0264 | 0.05608a | -3.50E-18b | ns | ** | ns |
| **Genus** | | | | | | | | | |
| uncultured bacterium | 0.14048 | 0.13688 | 0.12272 | 0.17982 | 0.2202a | 0.0698b | ns‡ | * | ns |
| Nocardioides | 0.10011 | 0.08104 | 0.10245 | 0.11032 | 0.04745b | 0.14952a | ns | * | ns |
| Bryobacter | 0.06859 | 0.10651 | 0.08728 | 0.09069 | 0.09694 | 0.07959 | ns | ns | ns |
| uncultured | 0.0919 | 0.08109 | 0.04496 | 0.06138 | 0.08143 | 0.05823 | ns | ns | * |
| Pseudarthrobacter | 0.04773 | 0.05247 | 0.06399 | 0.0477 | 0.04844 | 0.05751 | ns | ns | ns |
| Blastococcus | 0.0602 | 0.02839 | 0.07489 | 0.04422 | 0.03272b | 0.0711a | * | ** | ns |
| Conexibacter | 0.04512 | 0.03362 | 0.05427 | 0.03204 | 0.08252a | 2.08E-17b | ns | ** | ns |
| Acidiphilium | 0.03438 | 0.03739 | 0.04175 | 0.03859 | 0.06498a | 0.0111b | ns | ** | ns |
| Bradyrhizobium | 0.0237 | 0.04127 | 0.03026 | 0.02984 | 0.02436 | 0.03817 | ns | ns | ns |
| uncultured Acidobacteria | 0.02606 | 0.06366 | 0.0149 | 0.02001 | 0.01939 | 0.04293 | ns | ns | ns |
| uncultured Chloroflexi | 0.04166 | 0.02301 | 0.03142 | 0.02667 | 0.0126 | 0.04878 | ns | ns | ns |

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| **Genus** | Control | AMF | Rhizobium | AMF+ Rhizobium | Site 1 | Site 2 | M | S | M*S |
|---|---|---|---|---|---|---|---|---|---|
| uncultured bacterium | 0.14048 | 0.13688 | 0.12272 | 0.17982 | 0.2202a | 0.0698b | ns‡ | * | ns |
| Nocardioides | 0.10011 | 0.08104 | 0.10245 | 0.11032 | 0.04745b | 0.14952a | ns | * | ns |
| Bryobacter | 0.06859 | 0.10651 | 0.08728 | 0.09069 | 0.09694 | 0.07959 | ns | ns | ns |
| uncultured | 0.0919 | 0.08109 | 0.04496 | 0.06138 | 0.08143 | 0.05823 | ns | ns | * |
| Pseudarthrobacter | 0.04773 | 0.05247 | 0.06399 | 0.0477 | 0.04844 | 0.05751 | ns | ns | ns |
| Blastococcus | 0.0602 | 0.02839 | 0.07489 | 0.04422 | 0.03272b | 0.0711a | * | ** | ns |
| Conexibacter | 0.04512 | 0.03362 | 0.05427 | 0.03204 | 0.08252a | 2.08E-17b | ns | ** | ns |
| Acidiphilium | 0.03438 | 0.03739 | 0.04175 | 0.03859 | 0.06498a | 0.0111b | ns | ** | ns |
| Bradyrhizobium | 0.0237 | 0.04127 | 0.03026 | 0.02984 | 0.02436 | 0.03817 | ns | ns | ns |
| uncultured Acidobacteria | 0.02606 | 0.06366 | 0.0149 | 0.02001 | 0.01939 | 0.04293 | ns | ns | ns |
| uncultured Chloroflexi | 0.04166 | 0.02301 | 0.03142 | 0.02667 | 0.0126 | 0.04878 | ns | ns | ns |
| Bacillus | 0.02311 | 0.03897 | 0.02457 | 0.02579 | 0.00792b | 0.0483a | ns | ** | ns |
| Solirubrobacter | 0.02303 | 0.02457 | 0.03264 | 0.01927 | 1.73E-17b | 0.0498a | ns | * | ns |
| Massilia | 0.03641 | 0.00797 | 0.02941 | 0.02226 | 0.02306 | 0.02496 | ns | ns | ns |
| Rhizobacter | 0.0203 | 0.0181 | 0.02523 | 0.02187 | 0.00666b | 0.0361a | ns | * | ns |
| RB41 | 0.02639 | 0.01818 | 0.0217 | 0.01775 | -3.50E-18b | 0.0420a | ns | * | ns |
| Microlunatus | 0.00559 | 0.02204 | 0.02698 | 0.01761 | -6.90E-18b | 0.0361a | ns | ** | ns |
| Nitrosospira | 0.0156 | 0.01188 | 0.01966 | 0.01818 | 0.00318b | 0.0295a | ns | ** | ns |

* Significant P≤0.05; **Significant P≤0.001; † Means followed by different lowercase letter within a column are significantly different at $P \leq 0.05$; and ‡ Not significant.

Table S12 - Influence of microbial inoculants at two dryland sites on the most abundant (relative sequences abundance > 1% of all fungal sequences) fungal taxonomic group level phylum, order and genera on pea rhizosphere soil.

| Taxonomic group | Microbial Inoculants (M) | | | | Dryland Site (S) | | Significance P value | | |
|---|---|---|---|---|---|---|---|---|---|
| **Phylum** | Control | AMF | Rhizobium | AMF+ Rhizobium | Site 1 | Site 2 | M | S | M*S |
| Ascomycota | 2106 | 2147.4 | 2016.6 | 2205.6 | 2198.35 | 2039.45 | ns‡ | ns | ns |
| Basidiomycota | 572.4 | 470.1 | 646.8 | 433.1 | 607.75 | 453.45 | ns | ns | ns |
| Mortierellomycota | 254.1 | 292.6 | 274.6 | 224.1 | 150.25b | 372.45a | ns | * | ns |
| Chytridiomycota | 88.8 | 135.5 | 84.1 | 160.7 | 71.95b | 162.6a | ns | * | ns |
| unidentified | 53.4 | 29.6 | 46.3 | 46.9 | 48.4 | 39.7 | ns | ns | ns |
| Not_Assigned | 23.8 | 24.3 | 38.9 | 34.8 | 17.65b | 43.25a | ns | * | ns |
| Mucoromycota | 12.5 | 11.5 | 3.7 | 5.8 | 16.65a | 0.10b | ns | * | ns |
| **Order** | | | | | | | | | |
| Hypocreales | 524.4 | 499.7 | 505.6 | 547.1 | 486.75 | 551.65 | ns‡ | ns | ns |
| Eurotiales | 495.9 | 387.4 | 379.6 | 428.2 | 652.9a | 192.65b | ns | ** | ns |
| Unidentified | 285.4 | 432.1 | 357.1 | 459.8 | 337.9 | 429.3 | ns | ns | ns |
| Mortierellales | 254.1 | 292.6 | 274.6 | 224.1 | 150.25b | 372.45a | ns | * | ns |
| Filobasidiales | 308.6 | 191.1 | 294.3 | 205.5 | 350a | 149.75b | ns | ** | ns |
| Pleosporales | 272.7 | 233.2 | 246.8 | 219.6 | 122.3b | 363.85a | ns | ** | ns |
| Thelebolales | 169.4 | 247.6 | 233.5 | 175.1 | 255.65 | 157.15 | ns | ns | ns |
| Sordariales | 126.4 | 177.6 | 140.4 | 167.9 | 225.35a | 80.8b | ns | ** | ns |
| Not Assigned | 132.6 | 137.4 | 175.9 | 129.6 | 71.55b | 216.2a | ns | * | ns |

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| **Order** | Control | AMF | Rhizobium | AMF+ Rhizobium | Site 1 | Site 2 | M | S | M*S |
|---|---|---|---|---|---|---|---|---|---|
| Coniochaetales | 97.8 | 98.4 | 65.8 | 104.9 | 9.1b | 174.35a | ns | ** | ns |
| Helotiales | 106.2 | 85.1 | 62.1 | 96.5 | 16.7b | 158.25a | ns | * | ns |
| Chaetothyriales | 75.8 | 88.6 | 85.5 | 85.1 | 73.9 | 93.6 | ns | ns | ns |
| Holtermanniales | 57.5 | 54.6 | 59.7 | 34.9 | 101.5a | 1.85b | ns | ** | ns |
| Tremellales | 34.5 | 36.4 | 56.5 | 49.6 | 86.6a | 1.9b | ns | ** | ns |
| Capnodiales | 45 | 30.6 | 50.7 | 40.2 | 41.1 | 42.15 | ns | ns | ns |
| Chaetosphaeriales | 9.2 | 10.8 | 29.6 | 51.1 | 0.8b | 49.55a | ns | * | ns |
| Others | 19.7 | 16.9 | 18.4 | 22.1 | 15.25 | 23.3 | ns | ns | ns |
| Xylariales | 23.4 | 13.4 | 17.1 | 17.6 | 20.6 | 15.15 | ns | ns | ns |
| Orbiliales | 5.4 | 33.9 | 4.1 | 8.3 | 24.25 | 1.6 | ns | ns | ns |
| Rhizophlyctidales | 22.1 | 9 | 9.4 | 5.5 | 17.8a | 5.2b | ns | * | ns |
| **Genus** | | | | | | | | | |
| unidentified | 425.8 | 539.1 | 440.3 | 592.8 | 366.75b | 632.25a | ns‡ | * | ns |
| Mortierella | 333.2 | 323.4 | 316.5 | 277 | 262.35b | 362.7a | ns | * | ns |
| Hamigera | 247.2 | 285.1 | 268.9 | 214.8 | 135.55b | 372.45a | ns | ** | ns |
| Not Assigned | 336.4 | 211.7 | 207.4 | 254.4 | 504.95a | -2.00E-13b | ns | * | ns |
| Pseudogymnoascus | 203.9 | 222 | 236.8 | 189.9 | 134.2 | 292.1 | ns | ns | ns |
| Naganishia | 169.4 | 247.6 | 233.5 | 175.1 | 255.65a | 157.15b | ns | ** | ns |
| Penicillium | 199.4 | 120.3 | 223.1 | 113.1 | 281.5 | 46.45 | ns | ns | ns |

| **Genus** | Control | AMF | Rhizobium | AMF+ Rhizobium | Site 1 | Site 2 | M | S | M*S |
|---|---|---|---|---|---|---|---|---|---|
| Gibberella | 156.1 | 167.9 | 156.5 | 167.7 | 133.55b | 190.55a | ns | * | ns |
| Fusicolla | 150.6 | 109.4 | 178.3 | 149 | 122.15b | 171.5a | ns | ** | ns |
| Fusarium | 115.1 | 132.4 | 118.6 | 129.9 | 161.35a | 86.65b | ns | ** | ns |
| Clonostachys | 86.5 | 69.1 | 88 | 107 | 24.65b | 150.65a | ns | * | ns |
| Chrysanthotrichum | 83.2 | 96.5 | 58.1 | 96.7 | 102.35a | 64.9b | ns | ** | ns |
| Solicoccozyma | 43.4 | 90 | 69.4 | 95.5 | 149.15a | 4.26E-14b | ns | * | ns |
| Knufia | 95.7 | 54.6 | 58.5 | 78.5 | 41b | 102.65a | ns | * | ns |
| Trichoderma | 45.3 | 56.3 | 57.8 | 55.2 | 43.05b | 64.25a | ns | * | ns |
| Coniochaeta | 59.9 | 67.5 | 40.8 | 42.5 | 74.95a | 30.4b | ns | ** | ns |
| Holtermanniella | 41.9 | 57.6 | 36.7 | 71.1 | 5.85b | 97.8a | ns | ** | ns |
| Saitozyma | 57.5 | 54.6 | 59.7 | 34.9 | 101.5a | 1.85b | ns | ** | ns |
| Sclerostagonospora | 33.9 | 35.9 | 56.5 | 49.4 | 86.6 | 1.25 | ns | * | ns |
| Neosetophoma | 47.8 | 39.4 | 39.3 | 39.1 | 23.4 | 59.4 | ns | ** | ns |

* Significant P≤0.05.

**Significant P≤0.001.

† Means followed by different lowercase letter within a column are significantly different at $P \leq 0.05$.

‡ Not significant

Table S13 – Bacterial and archaeal taxonomic difference between inoculated microbial communities and the control obtained from heat tree analysis, using the median abundance and non-parametric Wilcoxon Rank Sum test (Foster et al., 2017).

| tax_rank | tax_name | log2_median_ratio | median_diff | mean_diff | wilcox_p_value |
|---|---|---|---|---|---|
| **Dryland Site 1** | | | | | |
| **AMF vs Control** | | | | | |
| o__D_3 | Elsterales | Inf | -0.02564 | -0.02667 | 0.00729 |
| o__D_3 | Xanthomonadales | Inf | -0.02564 | -0.03795 | 0.00729 |
| f__D_4 | uncultured | Inf | -0.02564 | -0.02667 | 0.00729 |
| f__D_4 | Rhodanobacteraceae | -1.442820656 | -0.02564 | -0.03795 | 0.00729 |
| g__D_5 | uncultured_bacterium | Inf | -0.02564 | -0.02667 | 0.00729 |
| s__D_6 | uncultured_bacterium | Inf | -0.02564 | -0.02667 | 0.00729 |
| c__D_2 | Chloroflexia | Inf | -0.01026 | -0.01231 | 0.00729 |
| p__D_1 | Chloroflexi | Inf | -0.09231 | -0.06256 | 0.020008 |
| s__D_6 | uncultured_bacterium | Inf | -0.01026 | -0.01231 | 0.024251 |
| o__D_3 | Elev_1554 | Inf | -0.00513 | -0.00718 | 0.024808 |
| f__D_4 | uncultured_Chloroflexi_bacterium | Inf | -0.03077 | -0.02154 | 0.024808 |
| f__D_4 | uncultured_bacterium | Inf | -0.00513 | -0.00718 | 0.024808 |
| g__D_5 | uncultured_Chloroflexi_bacterium | Inf | -0.03077 | -0.02154 | 0.024808 |
| g__D_5 | uncultured_bacterium | Inf | -0.00513 | -0.00718 | 0.024808 |
| s__D_6 | uncultured_Chloroflexi_bacterium | Inf | -0.03077 | -0.02154 | 0.024808 |
| s__D_6 | uncultured_bacterium | Inf | -0.00513 | -0.00718 | 0.024808 |
| g__D_5 | Chujaibacter | Inf | -0.02051 | -0.02359 | 0.02537 |
| g__D_5 | Segetibacter | Inf | -0.01026 | -0.01026 | 0.02537 |
| p__D_1 | Acidobacteria | Inf | 0.082051 | 0.164103 | 0.055556 |
| c__D_2 | Acidobacteriia | Inf | 0.082051 | 0.164103 | 0.055556 |
| c__D_2 | Ktedonobacteria | Inf | -0.07692 | -0.05026 | 0.057008 |
| g__D_5 | Rhizobacter | Inf | -0.00513 | -0.00513 | 0.070701 |
| **Rhizobium vs Control** | | | | | |
| s__D_6 | uncultured_bacterium | 0.736966 | 0.030769 | 0.049231 | 0.015651 |
| g | Ambiguous_taxa | 1.321928 | 0.015385 | 0.020513 | 0.089686 |
| s | Ambiguous_taxa | 1.321928 | 0.015385 | 0.020513 | 0.089686 |
| s__D_6 | uncultured_Conexibacteraceae_bacterium | Inf | -0.04103 | -0.02462 | 0.105998 |
| p__D_1 | Chloroflexi | -0.58496 | -0.03077 | -0.01641 | 0.141238 |
| | | | | | |

| tax_rank | tax_name | log2_median_ratio | median_diff | mean_diff | wilcox_p_value |
|---|---|---|---|---|---|
| **AMF+Rhizobium** | | | | | |
| s__D_6 | uncultured_bacterium | Inf | -0.03077 | -0.02359 | 0.025921 |
| c__D_2 | Ktedonobacteria | -0.58496 | -0.02564 | -0.02974 | 0.058553 |
| p__D_1 | Chloroflexi | -0.46949 | -0.02564 | -0.02667 | 0.059327 |
| s__D_6 | uncultured_bacterium | 1.321928 | 0.015385 | 0.013333 | 0.088683 |
| s__D_6 | uncultured_bacterium | 0.415037 | 0.015385 | 0.033846 | 0.093693 |
| f__D_4 | Burkholderiaceae | 0.485427 | 0.020513 | 0.027692 | 0.095238 |
| **Dryland Site 2** | | | | | |
| **AMF vs Control** | | | | | |
| p__D_1 | Bacteroidetes | -1.28951 | -0.06667 | -0.0759 | 0.021177 |
| c__D_2 | Bacteroidia | -1.28951 | -0.06667 | -0.0759 | 0.021177 |
| o__D_3 | Chitinophagales | -1.28951 | -0.06667 | -0.0759 | 0.021177 |
| f__D_4 | Chitinophagaceae | -1.28951 | -0.06667 | -0.0759 | 0.021177 |
| g__D_5 | uncultured | -1.28951 | -0.06667 | -0.07692 | 0.021177 |
| o__D_3 | Propionibacteriales | 0.440573 | 0.051282 | 0.051282 | 0.074913 |
| f__D_4 | Propionibacteriaceae | Inf | 0.051282 | 0.030769 | 0.156337 |
| **Rhizobium vs Control** | | | | | |
| p__D_1 | Actinobacteria | 0.55849 | 0.133333 | 0.154872 | 0.007937 |
| c__D_2 | Actinobacteria | 0.55849 | 0.133333 | 0.154872 | 0.007937 |
| o__D_3 | Micrococcales | 0.584963 | 0.025641 | 0.036923 | 0.011412 |
| f__D_4 | Micrococcaceae | 0.584963 | 0.025641 | 0.043077 | 0.011667 |
| g__D_5 | Pseudarthrobacter | 0.584963 | 0.025641 | 0.043077 | 0.011667 |
| s__D_6 | Pseudarthrobacter_polychromogenes | 0.584963 | 0.025641 | 0.043077 | 0.011667 |
| o__D_3 | Propionibacteriales | 0.550197 | 0.066667 | 0.094359 | 0.055556 |
| **AMF+Rhizobium** | | | | | |
| o__D_3 | Elsterales | 1.307431499 | 0.06323187 | 0.071085769 | **0.036145** |
| f__D_4 | uncultured | 1.307431499 | 0.06323187 | 0.071085769 | **0.036145** |
| g__D_5 | uncultured_bacterium | 1.307431499 | 0.06323187 | 0.071085769 | **0.036145** |
| s__D_6 | uncultured_bacterium | 1.307431499 | 0.06323187 | 0.071085769 | **0.036145** |
| p__D_1 | Bacteroidetes | -0.494478566 | -0.02973174 | -0.041845041 | 0.055556 |
| c__D_2 | Bacteroidia | -0.494478566 | -0.02973174 | -0.041845041 | 0.055556 |
| o__D_3 | Chitinophagales | -0.494478566 | -0.02973174 | -0.041845041 | 0.055556 |
| f__D_4 | Chitinophagaceae | -0.494478566 | -0.02973174 | -0.041845041 | 0.055556 |

Table S14- Fungal taxonomic difference between inoculated microbial communities and the control obtained from heat tree analysis, using the median abundance and non-parametric Wilcoxon Rank Sum test (Foster et al., 2017).

| tax_rank | tax_name | log2_median_ratio | median_diff | mean_diff | wilcox_p_value |
|---|---|---|---|---|---|
| **Dryland Site 1** | | | | | |
| **AMF vs Control** | | | | | |
| o_o | unidentified | 0.963163 | 0.036323 | 0.043266 | 0.007937 |
| f_f | unidentified | 0.963163 | 0.036323 | 0.043266 | 0.007937 |
| g_g | unidentified | 0.963163 | 0.036323 | 0.043266 | 0.007937 |
| s | unidentified | 0.963163 | 0.036323 | 0.043266 | 0.007937 |
| o_o | Dothideales | Inf | 0.001286 | 0.001093 | 0.031141 |
| f_f | Dothideales_fam_Incertae_sedis | Inf | 0.001286 | 0.001093 | 0.031141 |
| g_g | Selenophoma | Inf | 0.001286 | 0.001093 | 0.031141 |
| s | Selenophoma_mahoniae | Inf | 0.001286 | 0.001093 | 0.031141 |
| o_o | Pleosporales | 0.810339 | 0.016715 | 0.018515 | 0.031746 |
| s | Keissleriella_poagena | Inf | 0.005143 | 0.003729 | 0.034454 |
| f_f | Lentitheciaceae | 3 | 0.00675 | 0.006493 | 0.036145 |
| g_g | Keissleriella | 3 | 0.00675 | 0.006493 | 0.036145 |
| g_g | Parastagonospora | 2 | 0.002893 | 0.002893 | 0.036145 |
| c_c | Sordariomycetes | 0.598915 | 0.113468 | 0.106332 | 0.055556 |
| **Rhizobium vs Control** | | | | | |
| o_o | Pleosporales | 0.779401 | 0.015429 | 0.033044 | 0.015873 |
| f_f | Phaeosphaeriaceae | 1.681824 | 0.017036 | 0.018579 | 0.015971 |
| s | Keissleriella_poagena | Inf | 0.007393 | 0.007457 | 0.020008 |
| s | Coniochaeta_discospora | Inf | 0.001607 | 0.001543 | 0.024808 |
| g_g | Chrysanthotrichum | 1.577976 | 0.044037 | 0.03298 | 0.031746 |
| s | Chrysanthotrichum_peruvianum | 1.577976 | 0.044037 | 0.03298 | 0.031746 |
| f_f | Lentitheciaceae | 3.906891 | 0.0135 | 0.010158 | 0.036145 |
| g_g | Keissleriella | 3.906891 | 0.0135 | 0.010158 | 0.036145 |
| g_g | Parastagonospora | 2 | 0.003857 | 0.00405 | 0.046533 |
| c_c | Dothideomycetes | 0.63941 | 0.018644 | 0.034523 | 0.055556 |
| **AMF+Rhizobium** | | | | | |
| o_o | Pleosporales | 0.779401 | 0.015429 | 0.033044 | 0.015873 |
| f_f | Phaeosphaeriaceae | 1.681824 | 0.017036 | 0.018579 | 0.015971 |
| s | Keissleriella_poagena | Inf | 0.007393 | 0.007457 | 0.020008 |
| s | Coniochaeta_discospora | Inf | 0.001607 | 0.001543 | 0.024808 |

| tax_rank | tax_name | log2_median_ratio | median_diff | mean_diff | wilcox_p_value |
|---|---|---|---|---|---|
| g_g | Chrysanthotrichum | 1.577976 | 0.044037 | 0.03298 | 0.031746 |
| s | Chrysanthotrichum_peruvianum | 1.577976 | 0.044037 | 0.03298 | 0.031746 |
| f_f | Lentitheciaceae | 3.906891 | 0.0135 | 0.010158 | 0.036145 |
| g_g | Keissleriella | 3.906891 | 0.0135 | 0.010158 | 0.036145 |
| g_g | Parastagonospora | 2 | 0.003857 | 0.00405 | 0.046533 |
| c_c | Dothideomycetes | 0.63941 | 0.018644 | 0.034523 | 0.055556 |
| **Dryland Site 2** | | | | | |
| **AMF vs Control** | | | | | |
| s | Exophiala_radicis | Inf | -0.00064 | -0.00154 | 0.018119 |
| s | Naganishia_diffluens | Inf | -0.00161 | -0.00231 | 0.044171 |
| g_g | Myrothecium | Inf | -0.00064 | -0.00058 | 0.072006 |
| **Rhizobium vs Control** | | | | | |
| f__ | Bulleribasidiaceae | Inf | -0.00032 | -0.00039 | 0.024251 |
| g_g | Dioszegia | Inf | -0.00032 | -0.00039 | 0.024251 |
| s | unidentified | Inf | -0.00032 | -0.00039 | 0.024251 |
| g__ | Articulospora | Inf | 0.000321 | 0.0009 | 0.024808 |
| s | Articulospora_proliferata | Inf | 0.000321 | 0.0009 | 0.024808 |
| c_c | Rhizophlyctidomycetes | Inf | -0.00161 | -0.00154 | 0.072006 |
| **AMF+Rhizobium** | | | | | |
| c_c | Sordariomycetes | 0.164795 | 0.04018 | 0.071167 | 0.007937 |
| s | Exophiala_lacus | Inf | 0.001286 | 0.000964 | 0.024808 |
| s | Mortierella_sarnyensis | 0.658963 | 0.007072 | 0.010929 | 0.027803 |
| f_f | Phaeosphaeriaceae | -1.37137 | -0.05561 | -0.03967 | 0.031746 |
| o_o | Tremellales | Inf | -0.00064 | -0.0009 | 0.039318 |
| s | Mortierella_fimbricystis | Inf | 0.00225 | 0.002314 | 0.044909 |
| c_c | Dothideomycetes | -0.7929 | -0.06075 | -0.06519 | 0.055556 |
| o_o | Pleosporales | -0.73571 | -0.04918 | -0.05773 | 0.055556 |

Table S15- Influence of the microbial inoculants on the relative abundance of potential gene category involved in plant nutrient uptake at two dryland sites. The functional profiles of bacterial communities were predicted based on the 16S rRNA genes of retrieved bacterial taxa using Tax4Fun2 according to the KEGG Ortholog groups (KOs).

| Potential gene category | Microbial Inoculants (M) | | | | Dryland Site (S) | | Significance P value | | |
|---|---|---|---|---|---|---|---|---|---|
| | Control | AMF | Rhizobium | AMF+ Rhizobium | Site 1 | Site 2 | M | S | M*S |
| Carbon fixation | 0.010655 | 0.011127 | 0.010986 | 0.011175 | 0.00995b | 0.0120a | ns‡ | ** | ns |
| Nitrogen metabolism | 0.003088 | 0.00293 | 0.002929 | 0.002996 | 0.00248b | 0.0035a | ns | ** | ns |
| *Complete nitrification* | 0.000532 | 0.000351 | 0.000457 | 0.000485 | 0.000204 | 0.00071 | ns | ** | ns |
| *Nitrification* | 0.001896 | 0.001955 | 0.00188 | 0.001892 | 0.00179b | 0.002023a | ns | * | ns |
| *Assimilatory nitrate reduction* | 0.000651 | 0.000602 | 0.000583 | 0.000609 | 0.00047b | 0.0008a | ns | ** | ns |
| *Nitrogen fixation* | 9.10E-06 | 0.000023 | 9.70E-06 | 0.00001 | 1.35E-05 | 1.2E-05 | ns | ns | ns |
| Phosphorus | 0.013068 | 0.012239 | 0.012631 | 0.012698 | 0.012576 | 0.01274 | ns | ns | ns |
| *P transport* | 0.005302 | 0.005144 | 0.00524 | 0.005137 | 0.005135 | 0.00528 | ns | ns | ns |
| *P solubilization* | 0.005705 | 0.005145 | 0.005413 | 0.005594 | 0.005396 | 0.00553 | ns | ns | ns |
| *P starvation regulation* | 0.002061 | 0.00195 | 0.001978 | 0.001967 | 0.002045 | 0.00193 | ns | ns | ns |

* Significant P≤0.05.

**Significant P≤0.001.

† Means followed by different lowercase letter within a column are significantly different at $P \leq 0.05$.

‡ Not significant

Table S16- The relative abundance of potential fungal traits in dryland condition. The ecological functional profiles of fungal communities were predicted based on the FungalTraits database.

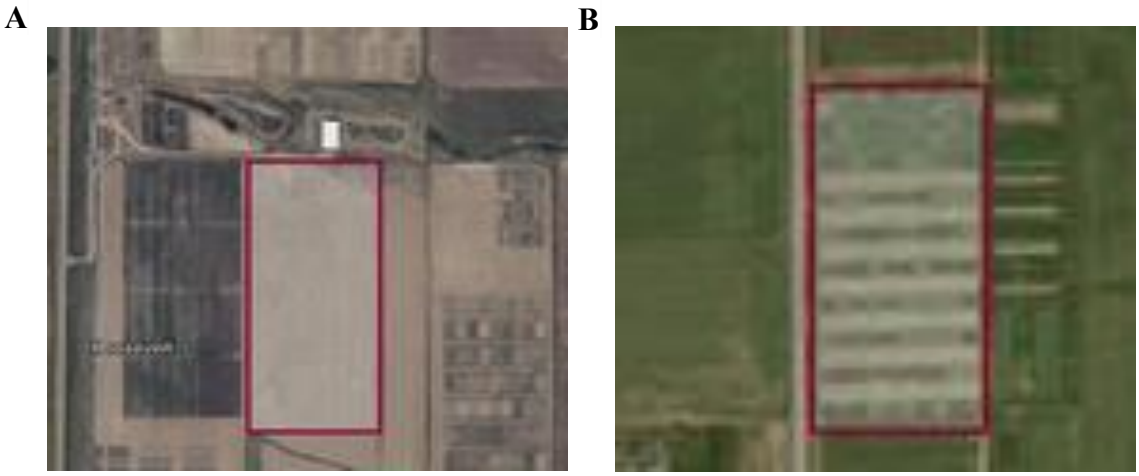
| Ecological fungal traits | Microbial Inoculants (M) | | | | Dryland Site (S) | | Significance P value | | |
|---|---|---|---|---|---|---|---|---|---|
| | Control | AMF | Rhizobium | AMF+ Rhizobium | Site 1 | Site 2 | M | S | M*S |
| Saprotrophs | 1850.5 | 1765.5 | 1803.2 | 1721.4 | 2086a | 1484.3b | ns‡ | ** | ns |
| Arbuscular_mycorrhizal | 4.8 | 0.7 | 3.7 | 2.2 | -4.0E-15b | 5.7a | ns | ** | ns |
| Animal/insect_parasite | 30.7 | 31.3 | 20.4 | 23 | 10.8b | 41.9a | ns | * | ns |
| Mycoparasite | 172.1 | 210.6 | 172.1 | 183.7 | 246.65a | 122.6b | ns | ** | ns |
| Plant_pathogen | 361.7 | 288.3 | 384.7 | 372.7 | 250.45b | 453.3a | ns | ** | ns |
| Others | 474.5 | 523.2 | 499.5 | 619.6 | 416.25b | 642.2a | ns | ** | ns |

* Significant P≤0.05.

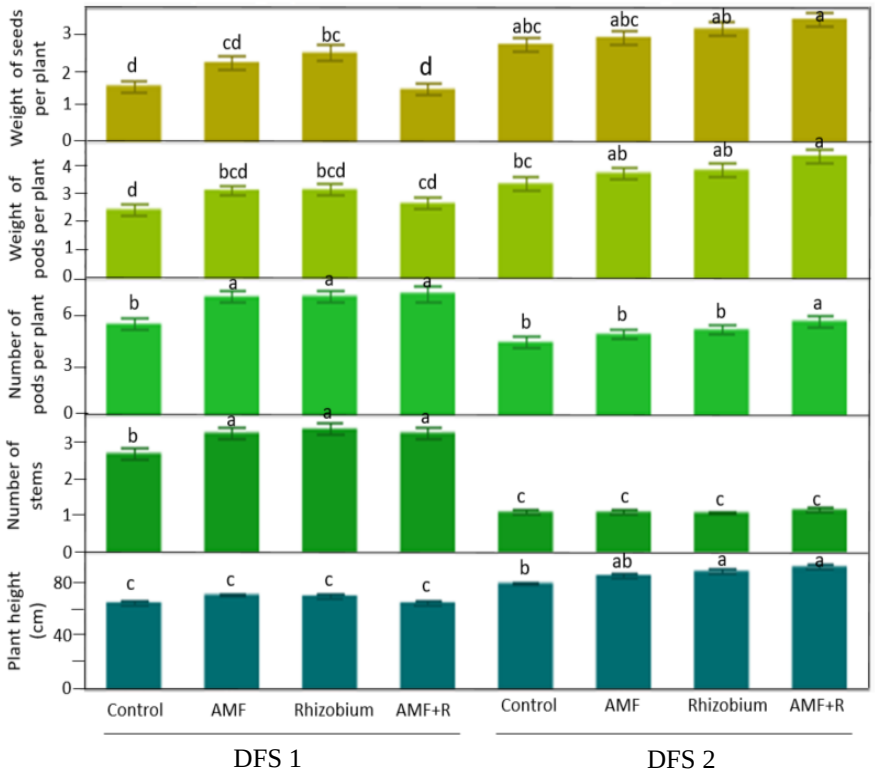
**Significant P≤0.001.

† Means followed by different lowercase letter within a column are significantly different at $P \leq 0.05$ and P≤0.001.

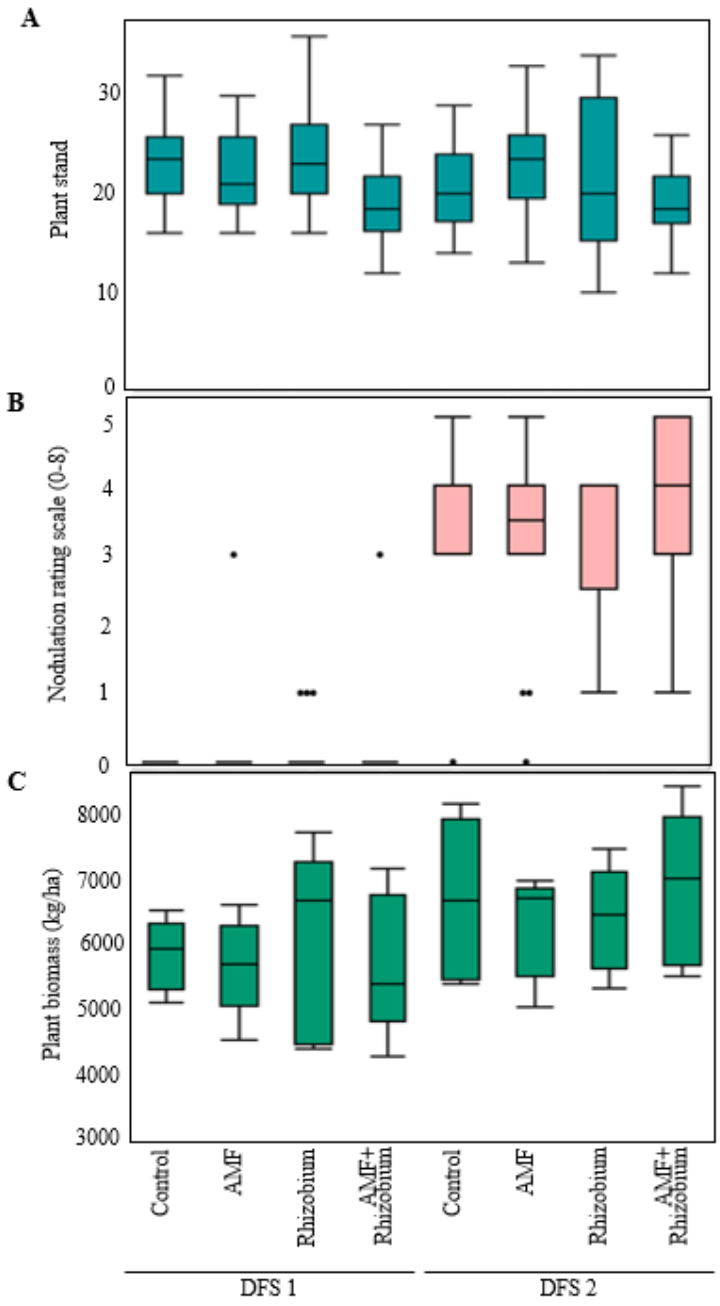
‡ Not significant




**Supplementary Figure 1.** The field sites at (**A**) DFS 1(Froid) and (**B**) DFS 2 (Sidney) were managed under no-till practices. Each site was set up in 20,000 sq.ft. with four treatments: Control, AMF, Rhizobium, and dual AMF and rhizobial inoculants in a randomized complete block design (RCBD) with 5 replications.

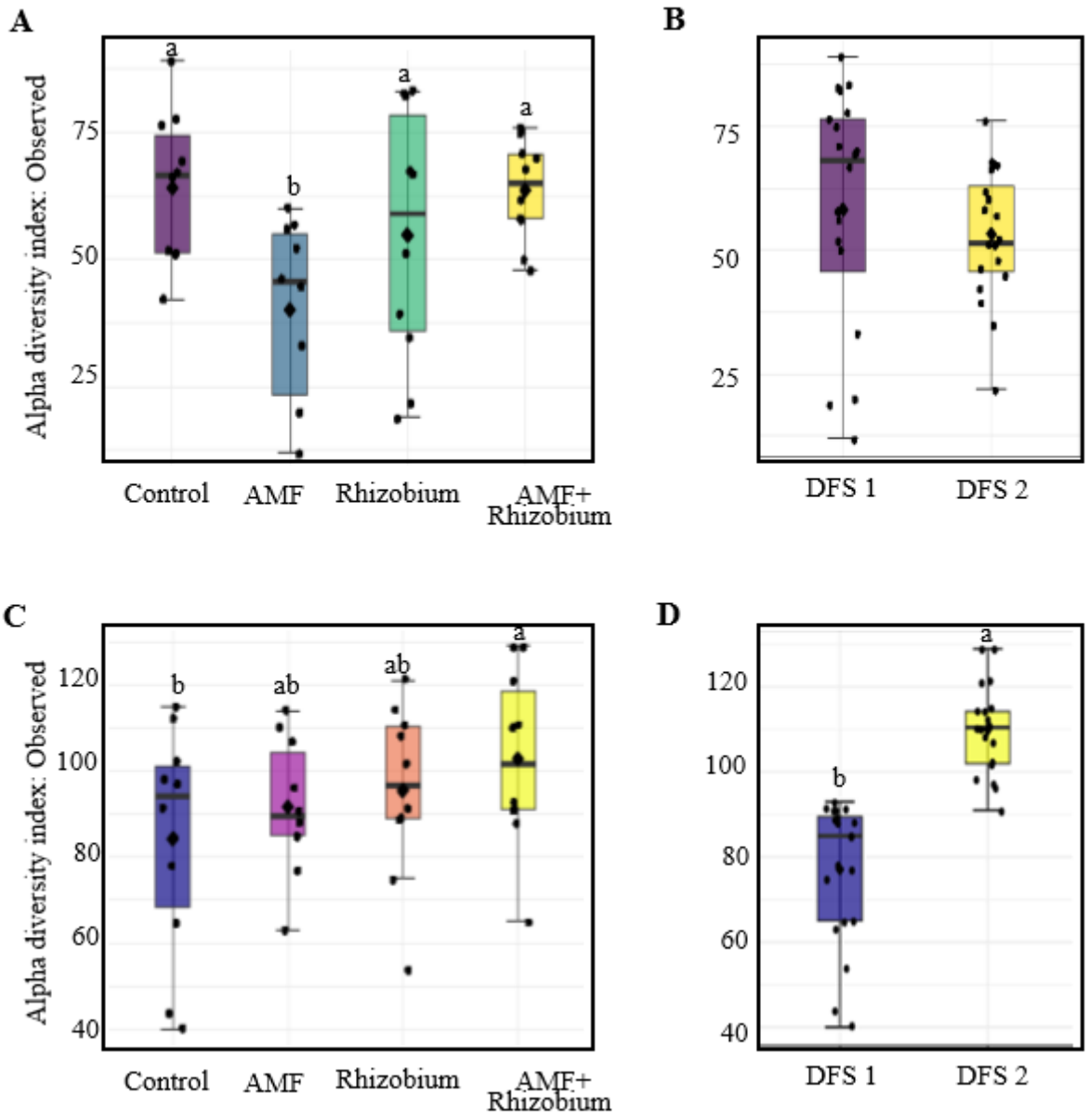



**Supplementary Figure 2.** The yield components across dryland field sites. Two-way ANOVA analysis, means followed by different letters are significantly different according to Tukey's Test HSD at P <0.05 (n=400 plants).




**Supplementary Figure S3.** Boxplots of the (**A**) plant stand, (**B**) nodulation rating scale using Yates et al. (2016), and (**C**) plant biomass across dryland field sites. Two-way ANOVA analysis, means followed by different letters are significantly different according to LSD at P <0.05.

*Yates, R J, R Abaidoo, and J G Howieson. 2016. "Field Experiments with Rhizobia." In . Australian Centre for International Agricultural Research.




**Supplementary Figure S4.** Influence of microbial inoculants on microbial species richness comparison among treatments and between sites on (**A, B**) bacterial, and (**C, D**) fungal communities. Boxplot and LS mean lines with common letter are not significantly different based on LSD tests at 0.05% probability level.