



Figure S1: Root ingrowth core surrounded by 1000 μ m mesh bag



Figure S2: Root ingrowth core after 14 days of incubation

Table S1: Analysis of Variance (ANOVA) comparing 1000 micron mesh (roots and hyphae access n=9) and 30 micron (only hyphae access, n=9).

Treatment	15N uptake		
	F.value	P.value	Df
Mesh Sizes	0.22	0.648	1
Soil Amendment	0.77	0.483	2
Plant Community x Soil Amendment	0.12	0.891	2

Significance is indicated at $p < 0.05$ (*); $p < 0.01$ (**) and $p < 0.001$ (***)

Table S2: Test for homogeneity of variances for ANOVA: Results of Fligner-Killeen test for homogeneity of variance. The substrate amendments were grouped within the plant community types resulting in n=9 per plant community and n=3 for each substrate type grouped under the plant community. Non-significance indicates the homogeneity of variances.

Variable	Df	Chi.square.value	p.value
Root:Shoot 13C	5	2.76	0.735
Microbial Biomass (13C)	5	1.29	0.936
Shoot (15N)	5	3.38	0.642
Carbon Cost (Total Community)	5	3.73	0.590
Carbon Cost (AMF)	5	3.48	0.627
Carbon Cost (Fungi)	5	4.52	0.478
Carbon Cost (Bacteria)	5	3.13	0.680

Significance is indicated at $p < 0.05$ (*); $p < 0.01$ (**) and $p < 0.001$ (***)

Table S3: Alpha diversity indices across plant community: Comparison of alpha diversity indices for bacterial and fungal communities grouped by AM (n = 9) and NM (n = 8) plant communities

Microbial.Group	Diversity.Indice	Mean (SEM)		ANOVA		
		AM.Mean	NM.Mean	Df	F.Value	p.value
Bacteria	Observed.OTU	2198.1 (53.60)	2174.4 (35.70)	1	0.13	0.725
Bacteria	Shannon.Evenness	7.2 (0.10)	7.1 (0.03)	1	0.42	0.526
Fungi	Observed.OTU	455.0 (63.63)	352.67 (48.81)	1	1.69	0.215
Fungi	Shannon.Evenness	5.92 (0.14)	5.67 (0.16)	1	1.25	0.283

Significance is indicated at $p < 0.05$ (*); $p < 0.01$ (**) and $p < 0.001$ (***)

Table S4: Alpha Diversity indices across soil amendments: Comparison of alpha diversity indices for bacterial and fungal communities grouped by litter type across both plant communities. Plant root litter (n =5) , Microbial Necromass (n=5) ; Inorganic-N (n=6)

Microbial.Group	Diversity.Indice	Mean (SEM)			ANOVA		
		Plant.Root.Litter	Microbial.Necromass	Inorganic.N	Df	F.Value	p.value
Bacteria	Observed.OTU	2179 (30)	2195 (62)	2187 (83)	2	0.02	0.981
Bacteria	Shannon.Evenness	7.12 (0.07)	7.13 (0.05)	7.14 (0.02)	2	0.05	0.948
Fungi	Observed.OTU	535 (43)	353 (52)	319 (71)	2	3.81	0.049 (*)
Fungi	Shannon.Evenness	6.13 (0.08)	5.73 (0.11)	5.54 (0.23)	2	3.16	0.076

Significance is indicated at $p < 0.05$ (*); $p < 0.01$ (**) and $p < 0.001$ (***)

Table S5: Bacterial Response to Plant Community: Mean (SEM) relative abundance of each bacterial group for each plant community type irrespective of soil amendment. F value and significance represents one way anova results to determine responsiveness to plant community context. Replicates: AM community n = 9 and NM community n = 8.

Taxa	Mean (SEM)		ANOVA	
	Rel.Abundance.in.AM	Rel.Abundance.in.NM	F.value	p.value
<i>Acidobacteria</i>	0.241 (0.010)	0.307 (0.021)	8.21	0.012 (*)
<i>Actinobacteria</i>	0.076 (0.003)	0.064 (0.003)	6.24	0.025 (*)
<i>Bacteroidetes</i>	0.117 (0.005)	0.107 (0.011)	0.79	0.389
<i>Choloroflexi</i>	0.027 (0.001)	0.027 (0.002)	0.02	0.903
<i>Gemmamonadetes</i>	0.022 (0.002)	0.018 (0.002)	2.73	0.120
<i>Nitrospirae</i>	0.016 (0.002)	0.017 (0.002)	0.32	0.578
<i>Proteobacteria</i>	0.358 (0.011)	0.312 (0.012)	8.38	0.011 (*)
<i>Verrucomicrobia</i>	0.103 (0.007)	0.106 (0.006)	0.11	0.741
Others	0.038 (0.002)	0.041 (0.001)	1.42	0.253
<i>Alphaproteobacteria</i>	0.139 (0.005)	0.124 (0.006)	3.62	0.076
<i>Betaproteobacteria</i>	0.076 (0.003)	0.063 (0.003)	8.36	0.011 (*)
<i>Deltaproteobacteria</i>	0.073 (0.005)	0.066 (0.002)	2.09	0.168
<i>Gammaproteobacteria</i>	0.070 (0.004)	0.059 (0.004)	3.89	0.067

Significance is indicated at $p < 0.05$ (*); $p < 0.01$ (**) and $p < 0.001$ (***)

Table S6: Fungal Guild Response to Plant Community: Mean (SEM) relative abundance of each fungal guild for each plant community type irrespective of soil amendment. F value and significance represents one way anova results to determine responsiveness to plant community context. Replicates: AM community n = 7 and NM community n = 9.

Taxa	Mean (SEM)		ANOVA	
	Rel.Abundance.in.AM	Rel.Abundance.in.NM	F.value	Sign
Saprotroph	0.345 (0.023)	0.493 (0.015)	32.310	< 0.001 (***)
AMF	0.370 (0.035)	0.120 (0.009)	58.370	< 0.001 (***)
Ectomycorrhizal	0.013 (0.002)	0.012 (0.002)	0.078	0.784
Endophyte	0.233 (0.023)	0.324 (0.022)	8.26	0.012 (*)
Others	0.040 (0.004)	0.051 (0.010)	0.919	0.354

Significance is indicated at $p < 0.05$ (*); $p < 0.01$ (**) and $p < 0.001$ (***)

Table S7: Bacterial Response to Soil Amendment: Mean (SEM) relative abundance of each bacterial group for each soil amendment type irrespective of plant community. F value and significance represents one way ANOVA results to determine responsiveness to soil amendment. Replicates: Plant Root Litter n = 6 ; Microbial Necromass n = 6 and Inorganic-N n = 5.

Taxa	Mean (SEM)			ANOVA	
	Plant.Root.Litter	Microbial.Necromass	Inorganic.N	F.value	p.value
<i>Acidobacteria</i>	0.299 (0.029)	0.279 (0.018)	0.223 (0.005)	2.718	0.101
<i>Actinobacteria</i>	0.068 (0.003)	0.070 (0.006)	0.068 (0.005)	0.351	0.710
<i>Bacteroidetes</i>	0.096 (0.009)	0.114 (0.008)	0.128 (0.009)	3.244	0.070
<i>Choloroflexi</i>	0.029 (0.002)	0.027 (0.001)	0.026 (0.002)	0.987	0.397
<i>Gemmamonadetes</i>	0.024 (0.002)	0.015 (0.002)	0.021 (0.001)	7.866	0.005 (**)
<i>Nitrospirae</i>	0.021 (0.001)	0.014 (0.001)	0.014 (0.001)	21.880	<0.001 (***)
<i>Proteobacteria</i>	0.325 (0.018)	0.331 (0.019)	0.359 (0.009)	1.102	0.359
<i>Verrucomicrobia</i>	0.089 (0.002)	0.111 (0.008)	0.113 (0.010)	3.296	0.067
Others	0.045 (0.002)	0.037 (0.002)	0.036 (0.003)	5.787	0.015 (*)
<i>Alphaproteobacteria</i>	0.121 (0.005)	0.136 (0.008)	0.140 (0.007)	2.008	0.171
<i>Betaproteobacteria</i>	0.066 (0.004)	0.071 (0.006)	0.072 (0.003)	0.398	0.679
<i>Deltaproteobacteria</i>	0.076 (0.003)	0.059 (0.003)	0.075 (0.004)	7.253	0.007 (**)
<i>Gammaproteobacteria</i>	0.061 (0.006)	0.064 (0.004)	0.072 (0.004)	1.086	0.364

Significance is indicated at p < 0.05 (*); p < 0.01 (**) and p < 0.001 (***)

Table S8: Fungal Guild Response to Soil Amendment: Mean (SEM) relative abundance of each fungal guild for each soil amendment type irrespective of plant community. F value and significance represents one way ANOVA results to determine responsiveness to soil amendment. Replicates: Plant Root Litter n = 5 ; Microbial Necromass n = 5 and Inorganic-N n = 6.

Taxa	Mean (SEM)			ANOVA	
	Plant.Root.Litter	Microbial.Necromass	Inorganic.N	F.value	p.value
Saprotroph	0.465 (0.0422)	0.442 (0.022)	0.387 (0.045)	1.103	0.361
AMF	0.224 (0.067)	0.191 (0.045)	0.265 (0.073)	0.341	0.717
Ectomycorrhizal	0.014 (0.003)	0.011 (0.003)	0.012 (0.003)	0.136	0.874
Endophyte	0.231 (0.020)	0.314 (0.034)	0.304 (0.035)	2.023	0.172
Others	0.067 (0.010)	0.042 (0.005)	0.032 (0.009)	4.534	0.032 (*)

Significance is indicated at $p < 0.05$ (*); $p < 0.01$ (**) and $p < 0.001$ (***)

Table S9: Test for homogeneity of variance assumption: Multivariate homogeneity of group dispersions (variances) using betadisper was tested for fungal and bacterial community for the entire experimental setup. F value and p value reported represents results of analysis of variance (ANOVA) on the betadisper output. Non-significance indicates homogeneity of variances.

Community	Factor	ANOVA		
		d.f	F.value	p.value
Fungi	Plant Community	1	0.9728	0.399
Fungi	Soil Amendment	2	1.9751	0.143
Fungi	Plant Community : Soil Amendment	5	1.5002	0.271
Bacteria	Plant Community	1	0.0340	0.856
Bacteria	Soil Amendment	2	0.4083	0.692
Bacteria	Plant Community : Soil Amendment	5	2.3314	0.099

Significance is indicated at $p < 0.05$ (*); $p < 0.01$ (**) and $p < 0.001$ (***)

Table S10: Permutational Multivariate Analyses of Variance (PERMANOVA) of soil fungal community matrix from ingrowth core soil decomposing various litter types in presence or absence of AMF association.

Community	Exp.Variable	Df	F.value	R.squared	p.value
Fungal community	Plant Community	1	1.87	0.11	0.013 (*)
Fungal community	Soil Amendment	2	1.99	0.23	0.0003 (**)
Fungal community	Plant Community x Soil Ammendment	2	0.90	0.10	0.677

Significance is indicated at $p < 0.05$ (*); $p < 0.01$ (**) and $p < 0.001$ (***)

Table S11: Permutational Multivariate Analyses of Variance (PERMANOVA) of soil bacterial community matrix from ingrowth core soil decomposing various litter types in presence or absence of AMF association.

Community	Exp.Variable	Df	F.value	R.squared	p.value
Bacterial community	Plant Community	1	1.24	0.07	0.019 (*)
Bacterial community	Soil Amendment	2	1.50	0.17	0.0001 (***)
Bacterial community	Plant Community x Soil Ammendment	2	1.08	0.12	0.129

Significance is indicated at $p < 0.05$ (*); $p < 0.01$ (**) and $p < 0.001$ (***)

Table S12: Bacterial amplicon data at  I SRA

SRA.Exp.Accession	SRA.Run.number	Sample.ID	Plant.Community	Soil.Amendment
SRX3647783	SRR6671091	D1	NM	Plant Root Litter
SRX3647784	SRR6671090	D2	NM	Plant Root Litter
SRX3647785	SRR6671089	D3	NM	Plant Root Litter
SRX3647781	SRR6671093	D7	AM	Plant Root Litter
SRX3647782	SRR6671092	D8	AM	Plant Root Litter
SRX3647777	SRR6671097	D9	AM	Plant Root Litter
SRX3647778	SRR6671096	D37	NM	Microbial Necromass
SRX3647795	SRR6671079	D38	NM	Microbial Necromass
SRX3647796	SRR6671078	D39	NM	Microbial Necromass
SRX3647792	SRR6671082	D43	AM	Microbial Necromass
SRX3647789	SRR6671085	D44	AM	Microbial Necromass
SRX3647790	SRR6671084	D45	AM	Microbial Necromass
SRX3647787	SRR6671087	D73	NM	Inorganic N
SRX3647788	SRR6671086	D75	NM	Inorganic N
SRX3647771	SRR6671103	D79	AM	Inorganic N
SRX3647776	SRR6671098	D80	AM	Inorganic N
SRX3647775	SRR6671099	D81	AM	Inorganic N

Table S13: Fungal amplicon data at NCBI SRA

SRA.Exp.Accession	SRA.Run.number	Sample.ID	Plant.Community	Soil.Amendment
SRX4378626	SRR7508173	R1	NM	Plant Root Litter
SRX4378627	SRR7508172	R2	NM	Plant Root Litter
SRX4378624	SRR7508175	R3	NM	Plant Root Litter
SRX4378623	SRR7508176	R8	AM	Plant Root Litter
SRX4378620	SRR7508179	R9	AM	Plant Root Litter
SRX4378621	SRR7508178	R37	NM	Microbial Necromass
SRX4378628	SRR7508171	R38	NM	Microbial Necromass
SRX4378629	SRR7508170	R39	NM	Microbial Necromass
SRX4378643	SRR7508156	R43	AM	Microbial Necromass
SRX4378636	SRR7508163	R45	AM	Microbial Necromass
SRX4378637	SRR7508162	R73	NM	Inorganic-N
SRX4378638	SRR7508161	R74	NM	Inorganic-N
SRX4378639	SRR7508160	R75	NM	Inorganic-N
SRX4378630	SRR7508169	R79	AM	Inorganic-N
SRX4378633	SRR7508166	R80	AM	Inorganic-N
SRR7508167	SRX4378632	R81	AM	Inorganic-N