

Figure S1. Venn diagram of soil fungal (A) and bacterial OTUs (B) in rhizospheric (R) or bulk (B) soil substrate samples of *Mimosa acutistipula* growing in a *canga* ecosystem (*canga*) or a rehabilitating mineland (RM) in Serra dos Carajás, eastern Amazon.

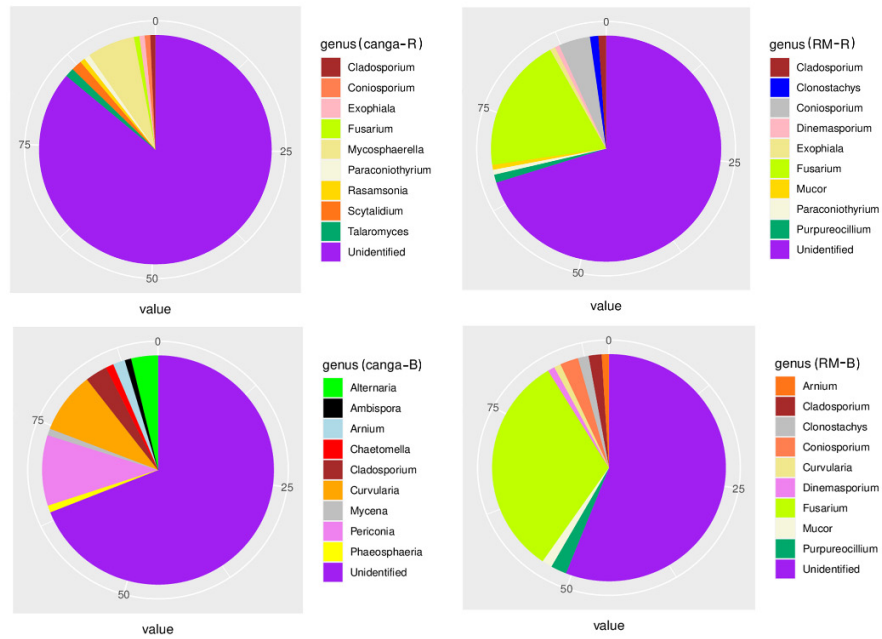


Figure S2. Relative abundance at the genus level of major fungal 18S rRNA sequences obtained from *Mimosa acutistipula* growing in a *canga* ecosystem (*canga*) or a rehabilitating mineland (RM) in Serra dos Carajás, eastern Amazon.

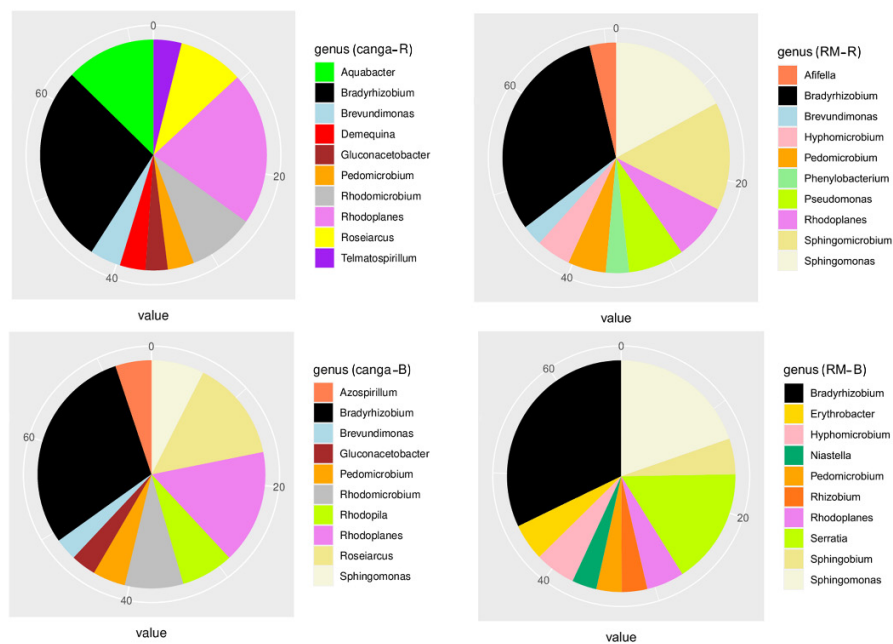


Figure S3. Relative abundance at the genus level of bacterial 16S rRNA sequences obtained from *Mimosa acutistipula* growing in a *canga* ecosystem (*canga*) or a rehabilitating mineland (RM) in Serra dos Carajás, eastern Amazon.

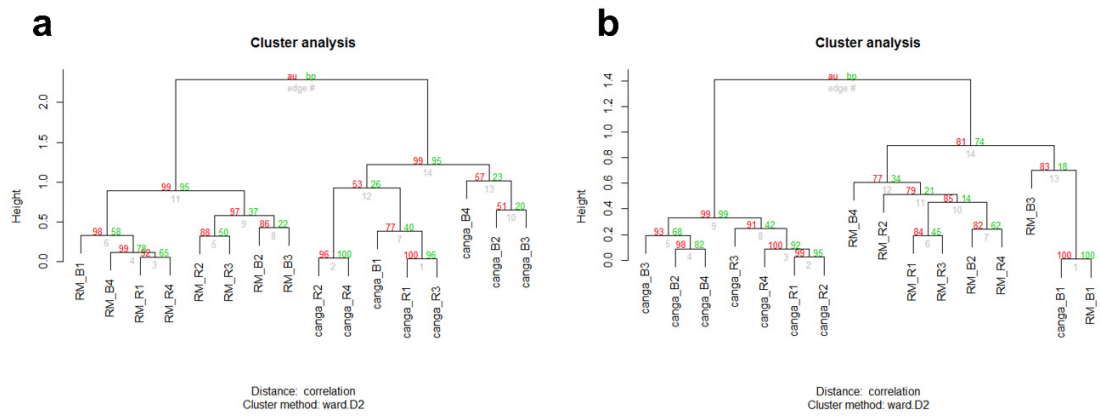


Figure S4. Clustering of fungal 18S rRNA (a) and bacterial 16S rRNA (b) sequences in rhizospheric (R) or bulk (B) soil samples of *Mimosa acutistipula* (M) growing in a *canga* ecosystem (*canga*) or a rehabilitating mineland (RM) in Serra dos Carajás, eastern Amazon.

Table S1. Physical and chemical characteristics of soil substrates associated with *Mimosa acutistipula* growing in a *canga* or rehabilitating mineland (RM).

	RM	<i>Canga</i>
Clay ^a	486,7 ± 37.2	287,5 ± 103
Silt ^a	158,3 ± 40.8	87,5 ± 75
Sand ^a	355 ± 68.9	625 ± 177
pH H ₂ O	6,1 ± 0.3	4,7 ± 0.6
pH CaCl ₂	5,3 ± 0.2	4,2 ± 0.3
Available P ^b	19,5 ± 15.9	1 ± 0.9
Total N ^c	0,1 ± 0.06	0,4 ± 0.3
Organic matter ^d	1,4 ± 0.6	7,7 ± 0.9
Na ^b	4,7 ± 0.6	11,4 ± 6.2
K ^b	22,6 ± 6.8	22,7 ± 6.8
B ^b	0,1 ± 0.03	0,2 ± 0.08
Cu ^b	0,6 ± 0.3	1,8 ± 0.5
Fe ^b	11,3 ± 6.3	372 ± 92
Mn ^b	59,7 ± 9.4	2,8 ± 1.5
Zn ^b	2,1 ± 1.6	1,4 ± 0.9

^a g kg⁻¹

^b mg dm⁻³

^c %

^d dag kg⁻¹

Table S2. Fungal 18S rRNA sequences obtained in rhizospheric and bulk soil samples from *Mimosa acutistipula* growing in a *canga* (*canga*) or a rehabilitating mineland (RM).

Plant specie	Sample site	Soil source	Sample ID	Total reads	Read after filtering	Number of OTU
<i>Mimosa acutistipula</i>	<i>Canga</i>	Rhizosphere	<i>canga</i> -R1	255991	201572	542
			<i>canga</i> -R2	322665	257605	579
			<i>canga</i> -R3	220560	143587	471
			<i>canga</i> -R4	89712	70495	470
		Bulk	<i>canga</i> -B1	49697	39879	232
			<i>canga</i> -B2	221120	173986	375
			<i>canga</i> -B3	163765	115200	330
			<i>canga</i> -B4	165339	119908	469
	RM	Rhizosphere	RM-R1	254016	210226	737
			RM-R2	313656	132732	436
			RM-R3	20607	126926	493
			RM-R4	248033	175531	722
		Bulk	RM-B1	163765	226122	684
			RM-B2	296340	4503	197
			RM-B3	188122	162984	495
			RM-B4	184655	163293	699

Table S3. Bacterial 16S rRNA sequences obtained in rhizospheric and bulk soil samples from *Mimosa acutistipula* growing in a *canga* (*canga*) or rehabilitating mineland (RM).

Plant specie	Sample site	Soil source	Sample ID	Total reads	Read after filtering	Number of OTU
<i>Mimosa acutistipula</i>	<i>Canga</i>	Rhizosphere	<i>canga</i> -R1	171026	26539	376
			<i>canga</i> -R2	186239	30134	372
			<i>canga</i> -R3	94558	16726	240
			<i>canga</i> -R4	116008	6597	234
		Bulk	<i>canga</i> -B1	147974	22873	295
			<i>canga</i> -B2	220057	27277	220
			<i>canga</i> -B3	195881	23535	418
			<i>canga</i> -B4	119161	12452	287
	RM	Rhizosphere	RM-R1	174851	24177	504
			RM-R2	113964	13648	432
			RM-R3	151960	20845	513
			RM-R4	467029	6892	311
		Bulk	RM-B1	233428	42968	414
			RM-B2	219140	28426	504
			RM-B3	190153	27779	458
			RM-B4	314963	33040	507

Table S4. Most abundant fungal and bacterial taxa identified in soils associated with *Mimosa acutistipula* growing in a *canga* or rehabilitating mineland (RM) in Serra dos Carajás, eastern Amazon.

Identification source		Identified Phyla (RA %)	Identified Genera (RA %)
FUNGI	<i>Rhizosphere</i>	Ascomycota (98.10); Basidiomycota (1.04); Mucoromycota (0.55); Unidentified (0.31)	Unidentified (85.4); <i>Mycosphaerella</i> (6.61); <i>Scytalidium</i> (1.49); <i>Talaromyces</i> (1.24); <i>Paraconiothyrium</i> (0.82); <i>Coniosporium</i> (0.78); <i>Fusarium</i> (0.75); <i>Exophiala</i> (0.71); <i>Cladosporium</i> (0.69); <i>Rasamsonia</i> (0.67)
	<i>Canga</i>		
	<i>Bulk</i>	Ascomycota (95.80); Basidiomycota (2.17); Glomeromycota (1.34); Chytridiomycota (0.41); Unidentified (0.28)	Unidentified (63.6); <i>Periconia</i> (9.19); <i>Curvularia</i> (7.97); <i>Alternaria</i> (3.46); <i>Cladosporium</i> (2.84); <i>Arnium</i> (1.56); <i>Chaetomella</i> (1.01); <i>Phaeosphaeria</i> (0.89); <i>Mycena</i> (0.86); <i>Ambispora</i> (0.81)
	RM		
BACTERIA	<i>Rhizosphere</i>	Ascomycota (93.1), Basidiomycota (4.83); Glomeromycota (1.25); unidentified (0.40); Mucoromycota (0.31); Mortierellomycota (0.11)	Unidentified (65.6); <i>Fusarium</i> (18.0); <i>Coniosporium</i> (4.16); <i>Clonostachys</i> (1.1); <i>Purpureocillium</i> (1.08); <i>Cladosporium</i> (1.0); <i>Exophiala</i> (0.69); <i>Mucor</i> (0.66); <i>Paraconiothyrium</i> (0.64); <i>Dinemasporium</i> (0.59); <i>Thielavia</i> (0.53)
	<i>Canga</i>		
	<i>Bulk</i>	Ascomycota (94.2); Basidiomycota (2.3); Mucoromycota (1.51); Glomeromycota (1.25); unidentified (0.74)	Unidentified (50.7); <i>Fusarium</i> (28.7); <i>Coniosporium</i> (2.32); <i>Purpureocillium</i> (1.99); <i>Cladosporium</i> (1.61); <i>Clonostachys</i> (1.31); <i>Mucor</i> (1.25); <i>Arnium</i> (0.9); <i>Dinemasporium</i> (0.88); <i>Curvularia</i> (0.83); <i>Myceliophthora</i> (0.71)
	RM		
BACTERIA	<i>Rhizosphere</i>	Acidobacteria (56.2); Proteobacteria (33.2); Actinobacteria (8.63); candidate_division_WPS-1 (1.97)	<i>Bradyrhizobium</i> (20.3); <i>Rhodoplanes</i> (15.6); <i>Aquabacter</i> (9.24); <i>Rhodomicrobium</i> (6.82); <i>Roseiarcus</i> (6.69); <i>Brevundimonas</i> (3.18); <i>Telmatosporillum</i> (2.89); <i>Pedomicrobium</i> (2.72); <i>Demequina</i> (2.65); <i>Gluconacetobacter</i> (2.27);
	<i>Canga</i>		
	<i>Bulk</i>	Acidobacteria (71.8); Proteobacteria (24.0); Actinobacteria (3.49); candidate_division_WPS-1 (0.71)	<i>Bradyrhizobium</i> (22.4); <i>Rhodoplanes</i> (12.2); <i>Roseiarcus</i> (10.8); <i>Rhodomicrobium</i> (6.27); <i>Sphingomonas</i> (5.64); <i>Rhodopila</i> (5.58); <i>Azospirillum</i> (3.85); <i>Pedomicrobium</i> (3.49); <i>Gluconacetobacter</i> (2.68); <i>Brevundimonas</i> (2.35)
	RM		
BACTERIA	<i>Rhizosphere</i>	Proteobacteria (54.3); Acidobacteria (28.8); Actinobacteria (14.7); Bacteroidetes (1.22); Firmicutes (0.98)	<i>Bradyrhizobium</i> (20.7); <i>Sphingomonas</i> (16.5); <i>Sphingomicrobium</i> (5.24); <i>Pseudomonas</i> (5.18); <i>Rhodoplanes</i> (4.84); <i>Pedomicrobium</i> (4.59); <i>Hyphomicrobium</i> (2.51); <i>Aftifella</i> (2.4); <i>Phenylobacterium</i> (2.15); <i>Brevundimonas</i> (2.07)
	<i>Canga</i>		
	<i>Bulk</i>	Proteobacteria (56.6); Acidobacteria (33.6); Actinobacteria (8.59); Bacteroidetes (0.85); Candidate_division_WPS-1 (0.36)	<i>Bradyrhizobium</i> (21.3); <i>Sphingomonas</i> (13.1); <i>Serratia</i> (10.8); <i>Hyphomicrobium</i> (3.81); <i>Rhodoplanes</i> (3.52); <i>Erythrobacter</i> (3.41); <i>Sphingobium</i> (3.3); <i>Rhizobium</i> (2.4); <i>Pedomicrobium</i> (2.37); <i>Niastella</i> (2.31); <i>Actinotalea</i> (1.96)
	RM		