Supplementary material to: Kamgan Nkuekam et al. S Afr J Sci. 2018;114(5/6), Art. #2017-0288, 7 pages.

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Table 1: Sampling sites and GPS coordinate information

Sampling site	Paired samples	GPS coordinates	Elevation
1	A1, G1	25° 51' 336'' S / 29° 22' 918'' E	1501 m
2	A2, G2	25° 37' 178'' S / 29° 26' 318'' E	1566 m
3	A3, G3	25° 43' 327'' S / 29° 31' 058'' E	1569 m
4	A4, G4	25° 22' 409'' S / 29° 47' 793'' E	1509 m
5	A5, G5	25° 19' 736'' S / 29° 52' 538'' E	1491 m
6	A6, G6	24° 52' 880'' S / 30° 19' 108'' E	1010 m
7	A7, G7	24° 46' 667'' S / 30° 32' 610'' E	1144 m
8	A8, G8	25° 26' 729'' S / 30° 55' 721'' E	791 m
9	A9, G9	25° 26' 301'' S / 30° 27' 337'' E	1197 m
10	A10, G10	25° 25' 427'' S / 30° 20' 767'' E	1288 m
11	A11, G11	25° 56' 025'' S / 30° 35' 350'' E	1113 m
12	A12, G12	25° 50' 009'' S / 30° 27' 361'' E	1199 m
13	A13, G13	25° 45' 299'' S / 30° 14' 123'' E	1682 m
14	A14, G14	26° 10' 630'' S / 29° 39' 649'' E	1723 m
15	A15, G15	26° 12' 584'' S / 29° 18' 224'' E	1623 m

Samples prefixed with A were obtained from agricultural soils while those prefixed with G were from grassland soils.

Table 2: Mapping file information for bacteria 16s amplicons

Sample ID	Barcode Sequence	Linker Primer Sequence	Barcode Name	Project Name
A1	TCCGGCCG	GTGYCAGCMGCCGCGGTAA	illCus515bar1	042816TMnew515F
A2	TCCGGTAA	GTGYCAGCMGCCGCGGTAA	illCus515bar2	042816TMnew515F
A3	TCCGTCGG	GTGYCAGCMGCCGCGGTAA	illCus515bar3	042816TMnew515F
A4	TCCGTCTT	GTGYCAGCMGCCGCGGTAA	illCus515bar4	042816TMnew515F
A5	TCCGTGCG	GTGYCAGCMGCCGCGGTAA	illCus515bar5	042816TMnew515F
A6	TCCGTGCT	GTGYCAGCMGCCGCGGTAA	illCus515bar6	042816TMnew515F
A7	TCCGTTCC	GTGYCAGCMGCCGCGGTAA	illCus515bar7	042816TMnew515F
A8	TCCGTTTT	GTGYCAGCMGCCGCGGTAA	illCus515bar8	042816TMnew515F
A9	TCCTAATA	GTGYCAGCMGCCGCGGTAA	illCus515bar9	042816TMnew515F
A10	TCCTCCCT	GTGYCAGCMGCCGCGGTAA	illCus515bar10	042816TMnew515F
A11	TCCTCGTA	GTGYCAGCMGCCGCGGTAA	illCus515bar11	042816TMnew515F
A12	TCCTCGTG	GTGYCAGCMGCCGCGGTAA	illCus515bar12	042816TMnew515F
A13	TCCTGGCA	GTGYCAGCMGCCGCGGTAA	illCus515bar13	042816TMnew515F
A14	TCCTGTAC	GTGYCAGCMGCCGCGGTAA	illCus515bar14	042816TMnew515F
A15	TCCTTCCA	GTGYCAGCMGCCGCGGTAA	illCus515bar15	042816TMnew515F
G1	TCCTTCTT	GTGYCAGCMGCCGCGGTAA	illCus515bar16	042816TMnew515F
G2	TCCTTGGT	GTGYCAGCMGCCGCGGTAA	illCus515bar17	042816TMnew515F
G3	TCGAAAGG	GTGYCAGCMGCCGCGGTAA	illCus515bar18	042816TMnew515F
G4	TCGAACCT	GTGYCAGCMGCCGCGGTAA	illCus515bar19	042816TMnew515F
G5	TCGAAGAG	GTGYCAGCMGCCGCGGTAA	illCus515bar20	042816TMnew515F
G6	TCGAATCC	GTGYCAGCMGCCGCGGTAA	illCus515bar21	042816TMnew515F
G7	TCGACAAC	GTGYCAGCMGCCGCGGTAA	illCus515bar22	042816TMnew515F
G8	TCGACCGG	GTGYCAGCMGCCGCGGTAA	illCus515bar23	042816TMnew515F
G9	TCGACCTA	GTGYCAGCMGCCGCGGTAA	illCus515bar24	042816TMnew515F
G10	TCGACGAA	GTGYCAGCMGCCGCGGTAA	illCus515bar25	042816TMnew515F
G11	TCGACGAC	GTGYCAGCMGCCGCGGTAA	illCus515bar26	042816TMnew515F
G12	TCGAGCCG	GTGYCAGCMGCCGCGGTAA	illCus515bar27	042816TMnew515F
G13	TCGAGCGA	GTGYCAGCMGCCGCGGTAA	illCus515bar28	042816TMnew515F
G14	TCGAGCTG	GTGYCAGCMGCCGCGGTAA	illCus515bar29	042816TMnew515F
G15	TGGTAACC	GTGYCAGCMGCCGCGGTAA	illCus515bar30	042816TMnew515F

Table 3: Mapping file information for fungal ITS amplicons

Sample ID	Barcode Sequence	Linker Primer Sequence	Barcode Name	Project Name
A1	ATCGATGC	CTTGGTCATTTAGAGGAAGTAA	ITS1F.Bt1	082416TMits
A2	ATCGCCAA	CTTGGTCATTTAGAGGAAGTAA	ITS1F.Bt2	082416TMits
A3	ATCGCCTT	CTTGGTCATTTAGAGGAAGTAA	ITS1F.Bt3	082416TMits
A4	ATCGCGAT	CTTGGTCATTTAGAGGAAGTAA	ITS1F.Bt4	082416TMits
A5	ATCGCGTA	CTTGGTCATTTAGAGGAAGTAA	ITS1F.Bt5	082416TMits
A6	ATCGGCAT	CTTGGTCATTTAGAGGAAGTAA	ITS1F.Bt6	082416TMits
A7	ATCGGCTA	CTTGGTCATTTAGAGGAAGTAA	ITS1F.Bt7	082416TMits
A8	ATCGTACG	CTTGGTCATTTAGAGGAAGTAA	ITS1F.Bt8	082416TMits
A9	ATCGTAGC	CTTGGTCATTTAGAGGAAGTAA	ITS1F.Bt9	082416TMits
A10	ATCGTTCC	CTTGGTCATTTAGAGGAAGTAA	ITS1F.Bt10	082416TMits
A11	ATCGTTGG	CTTGGTCATTTAGAGGAAGTAA	ITS1F.Bt11	082416TMits
A12	ATGCAACC	CTTGGTCATTTAGAGGAAGTAA	ITS1F.Bt12	082416TMits
A13	ATGCAAGG	CTTGGTCATTTAGAGGAAGTAA	ITS1F.Bt13	082416TMits
A14	ATGCATCG	CTTGGTCATTTAGAGGAAGTAA	ITS1F.Bt14	082416TMits
A15	ATGCATGC	CTTGGTCATTTAGAGGAAGTAA	ITS1F.Bt15	082416TMits
G1	ATGCCGAT	CTTGGTCATTTAGAGGAAGTAA	ITS1F.Bt16	082416TMits
G2	ATGCCGTA	CTTGGTCATTTAGAGGAAGTAA	ITS1F.Bt17	082416TMits
G3	ATGCGCAT	CTTGGTCATTTAGAGGAAGTAA	ITS1F.Bt18	082416TMits
G4	ATGCGCTA	CTTGGTCATTTAGAGGAAGTAA	ITS1F.Bt19	082416TMits
G5	ATGCGGAA	CTTGGTCATTTAGAGGAAGTAA	ITS1F.Bt20	082416TMits
G6	ATGCGGTT	CTTGGTCATTTAGAGGAAGTAA	ITS1F.Bt21	082416TMits
G7	ATGCTACG	CTTGGTCATTTAGAGGAAGTAA	ITS1F.Bt22	082416TMits
G8	ATGCTAGC	CTTGGTCATTTAGAGGAAGTAA	ITS1F.Bt23	082416TMits
G9	ATGCTTCC	CTTGGTCATTTAGAGGAAGTAA	ITS1F.Bt24	082416TMits
G10	ATGCTTGG	CTTGGTCATTTAGAGGAAGTAA	ITS1F.Bt25	082416TMits
G11	ATGGAACG	CTTGGTCATTTAGAGGAAGTAA	ITS1F.Bt26	082416TMits
G12	ATGGAAGC	CTTGGTCATTTAGAGGAAGTAA	ITS1F.Bt27	082416TMits
G13	ATGGATCC	CTTGGTCATTTAGAGGAAGTAA	ITS1F.Bt28	082416TMits
G14	ATGGATGG	CTTGGTCATTTAGAGGAAGTAA	ITS1F.Bt29	082416TMits
G15	ATGGCCAT	CTTGGTCATTTAGAGGAAGTAA	ITS1F.Bt30	082416TMits

Table 4: Most abundant bacterial and fungal taxa detected in agricultural soils and natural grassland soils

Bacteria			Fungi		
Taxa	**Agriculture**	**Grassland**	**Taxa**	**Agriculture**	**Grassland**
Phylum					
Acidobacteria	3827 (8.5%)^{a}	7312 (16.2%)^{b}	Ascomycota	132667 (71.6%)^{a}	117544 (63.4%)^{a}
Actinobacteria	17362 (38.6%)^{a}	14762 (32.8%)^{a}	Unclassified	30976 (16.7%)^{a}	40845 (22%)^{a}
Proteobacteria	10698 (23.8%)^{a}	10860 (24.1%)^{a}			
Unclassify	5663 (12.6%)^{a}	5015 (11.14%)^{a}			
Class					
Actinobacteria	7792 (17.3%)^{a}	5578 (12.4%)^{b}	Dothideomycetes	35090 (18.9%)^{a}	23341 (12.6%)^{a}
Alphaproteobacteria	6529 (14.5%)^{a}	7058 (15.7%)^{a}	Sordariomycetes	69324 (37.4%)^{a}	53875 (29.1%)^{a}
Thermoleophillia	8980 (19.9%)^{a}	8232 (18.3%)^{a}	Unclassified	55050 (29.7%)^{a}	60219 (32.5%)^{a}
Unclassify	7959 (17.7%)^{a}	8157 (18.1%)^{a}			
Order					
Actinomycetales	7671 (17%)^{a}	5311 (11.8%)^{b}	Hypocreales	48264 (26%)^{a}	30384 (16.1%)^{a}
Solirubrobacterales	4567 (10.2%)^{a}	5419 (12%)^{a}	Pleosporales	31655 (17.1%)^{a}	18601 (10%)^{a}
Rhizobiales	4472 (9.9%)^{a}	5500 (12.2%)^{a}	Unclassified	60338 (32.6%)^{a}	69239 (37.4%)^{a}
Unclassify	10547 (23%)^{a}	15699 (34.9%)^{b}			
Family					
Unclassify	19918 (44%)^{a}	24613 (54.7%)^{b}	Nectriaceae	32175 (17.4%)^{a}	16175 (8.7%)^{b}
			Unclassified	99867 (53.9%)^{a}	105824 (57.1%)^{a}

The values for each taxa represent the number and proportion (in brackets) of reads in the habitat sampled.

Values in the same row followed by different superscript letters are significantly different according to paired Student's t-*tests* (p*<0.05).*

Table 5: Mean values of the soil chemical parameters

Agriculture									Natural grassland									
Samples	**pH**	**P**	**Mg**	**Na**	**Ca**	**K**	**C**	**NH_4**	**NO_3**	**Samples**	**pH**	**P**	**Mg**	**Na**	**Ca**	**K**	**C**	**NH_4**	**NO_{33}**
A1	5.39	23.4825	111.9353	21.1915	542.8173	55.33	1.1022	11.28	8.24	**G1**	7.6	0.393	206.5353	23.7415	1419.217	89.58	2.18436	9.59	1.13
A2	5.74	3.56025	95.77525	0.0285	349.5173	111.5	0.88176	10.82	1.83	**G2**	7.09	2.046	131.5353	1.2595	512.5173	86.48	0.86172	8.38	1
A3	5.31	24.5775	89.57525	0	266.0173	68.83	1.18236	17.81	1.79	**G3**	6.4	1.89825	118.0353	0	585.6173	69.75	1.42284	13.16	2.25
A4	5.22	7.605	224.6353	1.8605	742.6173	155.8	1.7034	17.77	16.86	**G4**	6.91	0.6015	518.3353	7.8215	2066.217	140.4	1.64328	14.1	0.2
A5	6.23	20.2125	362.0353	5.0015	1749.217	573.6	2.58516	17.7	13.3	**G5**	7.19	1.09725	257.3353	2.3345	1926.217	139.3	1.36272	11.07	0.34
A6	7.34	18.015	303.6353	4.2915	836.5173	222.5	0.76152	7.64	13.28	**G6**	8.18	0.41025	430.5353	9.7015	5785.217	514.8	1.3026	12.76	0.88
A7	5.14	40.935	267.4353	8.8215	857.8173	567	0.94188	45.88	37.24	**G7**	7.75	22.2225	544.7353	14.5715	2529.217	656.3	1.28256	10.66	1.36
A8	5.91	41.115	72.80525	4.7815	326.3173	281.2	0.86172	12.91	5.5	**G8**	6.57	11.2575	142.6353	2.9455	503.4173	173.3	0.6012	10.63	0.32
A9	6.91	12.39	908.6353	25.8815	2314.217	307.1	0.9018	14.88	13.25	**G9**	8.09	0.59925	221.3353	9.9915	4178.217	169.9	1.44288	9.48	0.62
A10	5.48	5.03625	90.04525	24.7915	236.5173	47.83	0.74148	9.69	13.83	**G10**	6.4	0.90675	375.1353	10.8115	1165.217	79.38	2.3046	9.8	7.42
A11	5.99	31.125	147.4353	4.1015	559.7173	239.8	1.26252	7.92	8.34	**G11**	7.36	4.0395	162.1353	8.9315	953.5173	172.2	0.78156	8.47	3.28
A12	7.6	30.555	100.5353	12.8115	1432.217	113	0.92184	10.18	12.75	**G12**	6.16	6.69825	116.9353	0.6135	297.6173	67.11	1.002	8.87	0.3
A13	4.88	4.2015	321.9353	9.7015	368.4173	105.3	3.04608	12.42	22.2	**G13**	5.86	2.985	457.3353	4.1615	815.2173	103.7	1.88376	10.25	14.7
A14	7.92	22.5075	216.8353	4.3115	797.5173	315.2	1.04208	8.85	7.29	**G14**	6.49	3.117	197.7353	0.5935	782.0173	431.1	2.22444	10.98	1.46
A15	5.82	38.2425	55.49525	0	332.2173	128.5	0.84168	11.27	0.98	**G15**	6.91	5.8485	143.5353	4.8615	673.9173	181.3	2.34468	15.48	1.22
Mean†	6.06^a	21.6^a	224.6^a	8.5^a	780.8^a	219.5^a	1.3^a	14.5^a	11.8^a	**Mean**	6.99^b	4.3^b	268.3^a	6.8^a	1612.9^b	205^a	1.5^a	10.9^a	2.4^a
SD	0.95	13.13	214.31	8.82	606.8	167.91	0.68	9.34	9.23	**SD**	0.7	5.8	153.6	6.5	1540.9	180.05	0.57	2.099	3.85

†*The values represent the average concentration (mg/kg) for soil chemical parameters; corresponding mean values (agricultural vs grassland soils) in the same row followed by different superscript letters are significantly different according to paired Student's* t-*tests* ($p<0.05$).

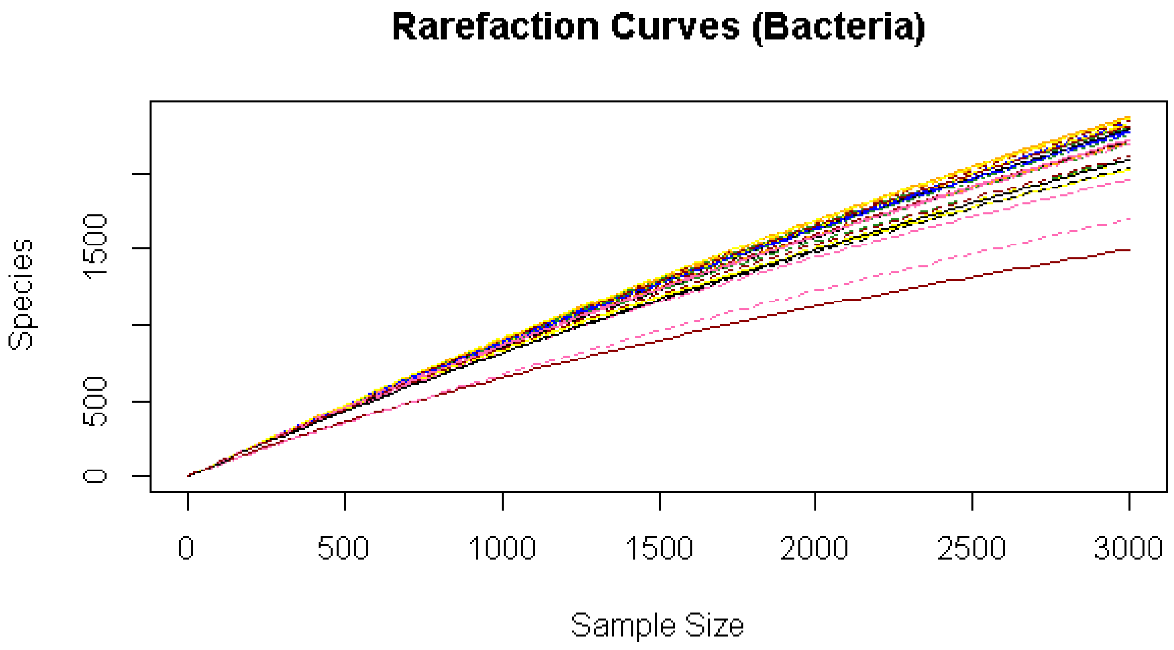

Figure 1: Rarefaction curve for each bacterial sample.

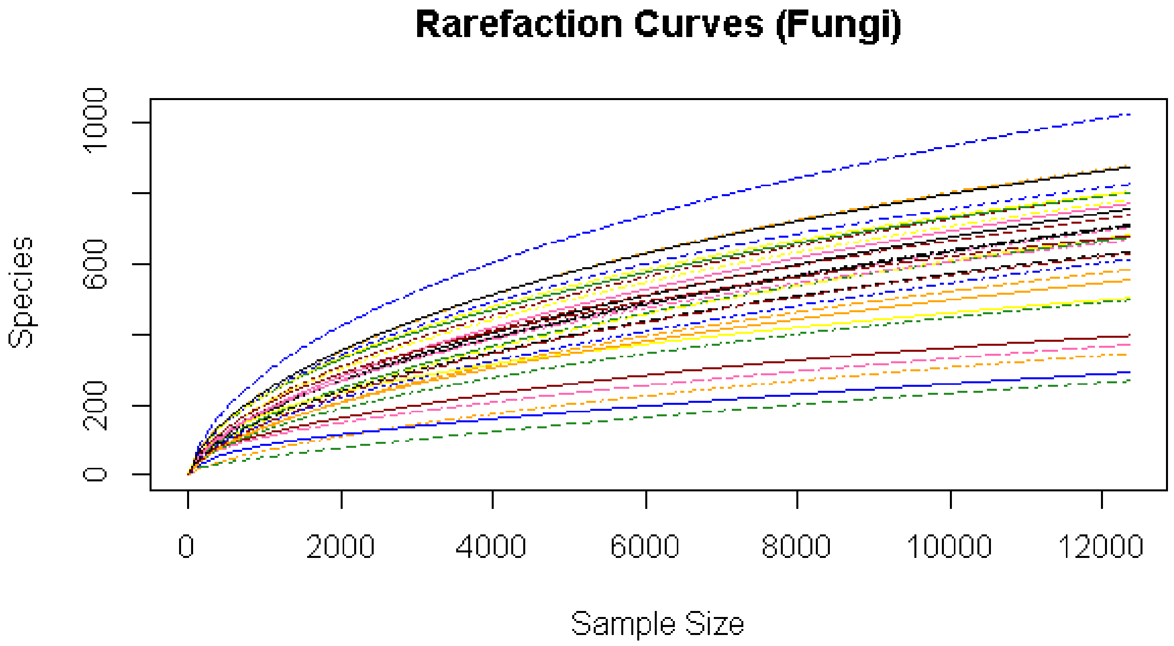

Figure 2: Rarefaction curve for each fungal sample.

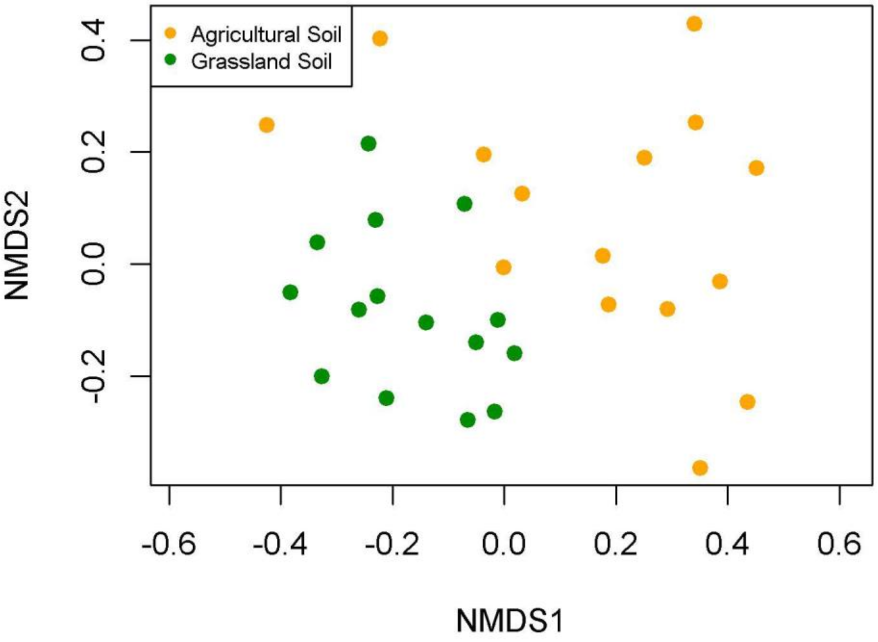

Figure 3: Non-metric multidimensional scaling (NMDS) plot using Bray–Curtis dissimilarity distances. Each point represents the bacterial community of an individual sample. Stress value=0.169.

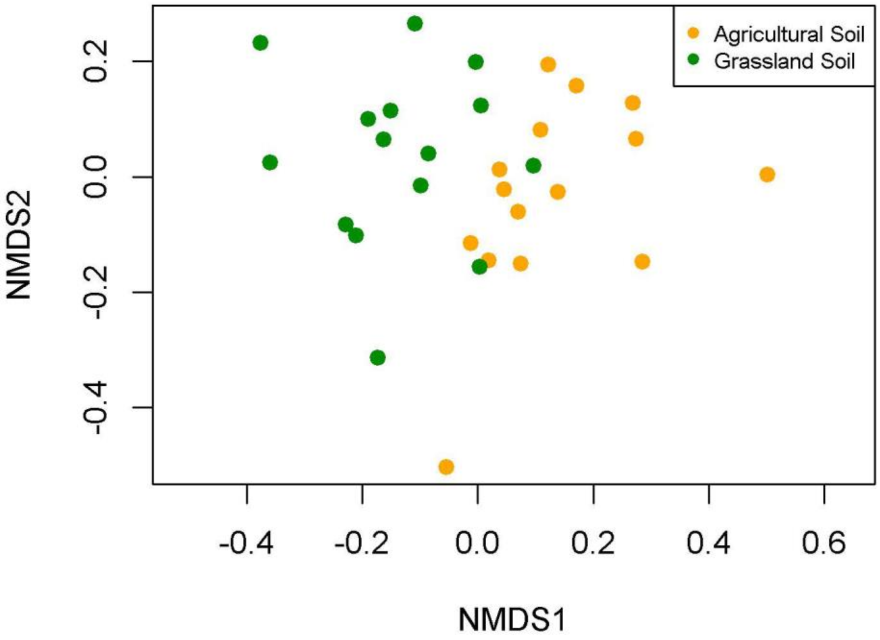

Figure 4: Non-metric multidimensional scaling (NMDS) plot using Bray–Curtis dissimilarity distances. Each point represents the fungal community of an individual sample. Stress value=0.179.

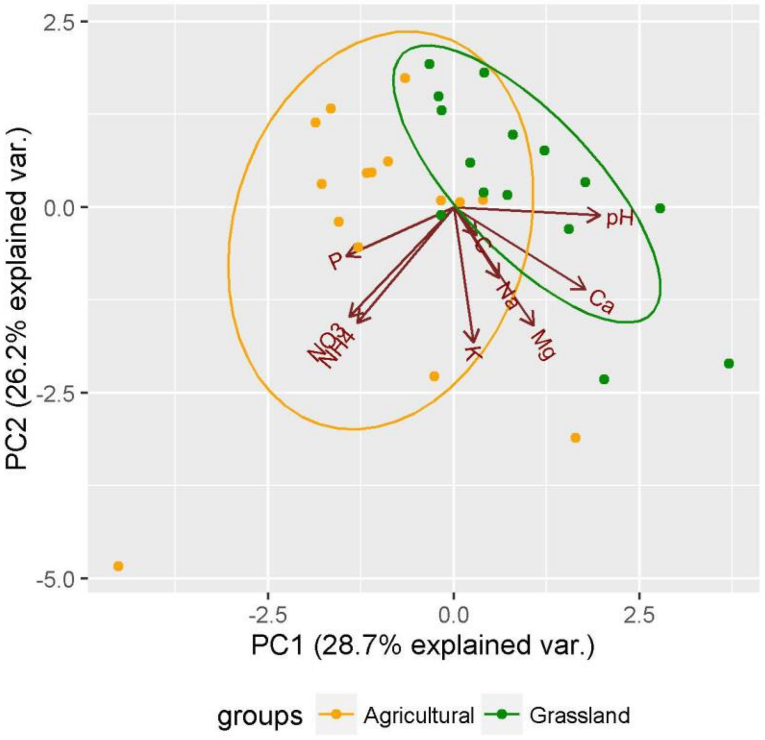

Figure 5: Principal component analysis ordination biplot of soil chemistry parameters for the 15 sampling sites. Each point represents an individual sample from either habitat type. Vectors represent environmental variables.

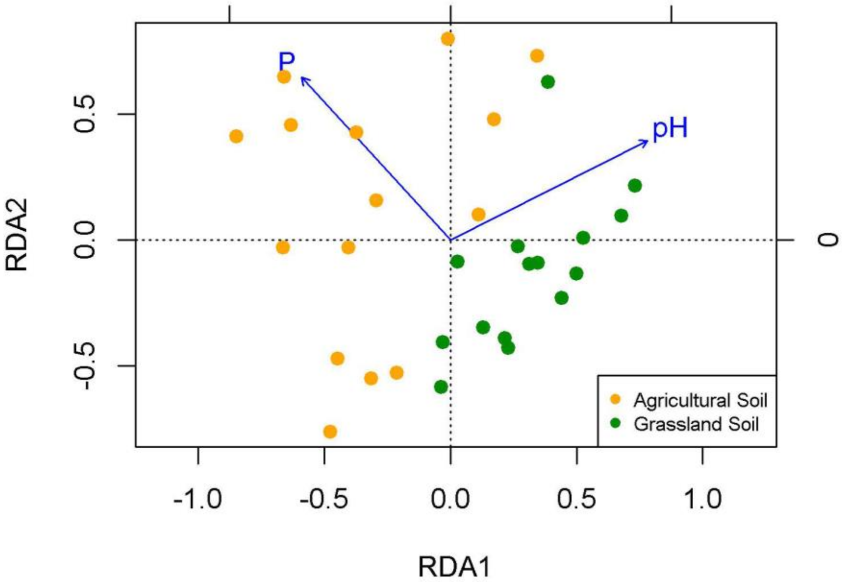

Figure 6: Distance-based redundancy analysis (db-RDA) biplot of bacterial communities and soil chemistry parameters. Only the soil chemistry parameters which significantly (p<0.05 for 999 permutation tests) explained bacterial communities variation are shown.

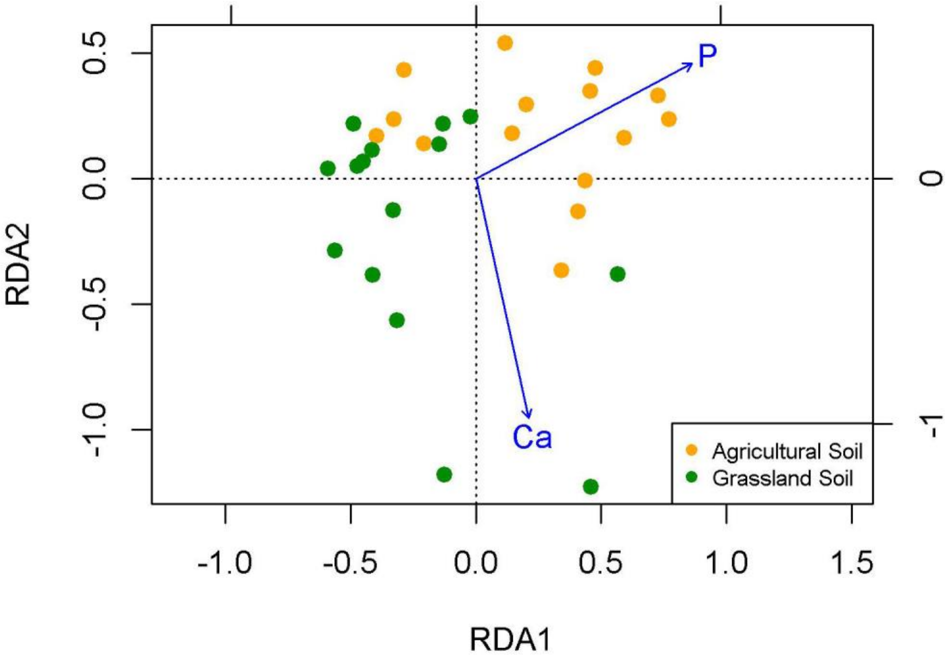

Figure 7: Distance-based redundancy analysis (db-RDA) biplot of fungal communities and soil chemistry parameters. Only the soil chemistry parameters which significantly (*p*<0.05 for 999 permutation tests) explained fungal communities variation are shown.