

1 Table S1. Primers used in this study.

FUNCTION	TARGET GENE	GENE DEFINITION	PRIMER SET	PRIMER SEQUENCE (5' – 3')	ANNEALING TEMPERATURE (°C)	AMPLICON SIZE (BP)	REFERENCE
Nitrification	<i>amoA</i>	ammonia monooxygenase	amoA1F	GGGGTTTCTACTGGTGGT	57	491	[75]
			amoA2R	CCCCTCKGSAAAGCCTTCTTC			
Denitrification	<i>nirK</i>	nitrite reductase	nirK876F nirK1040R	ATYGGCGGVCA YGGCGA GCCTCGATCAGRTRTGTT	58	165	[76]
N ₂ fixation	<i>nifH</i>	nitrogenase reductase	PolF	TGC GAY CCS AAR GCB GAC TC	55	362	[46]
			PolR	ATSGCCATCATYTCRCCGGA			
Carbon fixation	<i>cbbL</i>	cbbL red-like gene	cbbL-RedF	AAGGAYGACGAGAACATC	57	820	[77]
			cbbL-RedR	TCGGTCGGSGTGTAGTTGAA			
Carbon degradation	<i>GH7</i>	cellulose degradation	GH7-F GH7-R	GAGATCAAGCGCYTCTAYGTBCA GTCRAGCCASAGCATGTTGG	56	242	[78]

2

Table S2. *amoA* PCR cycling conditions.

Step	# of cycles	Temperature	Time
Initial denaturation	1	95°C	10 min
Denaturation	40	95°C	15 sec
Annealing		58°C	30 sec
Extension		72°C	45 sec

Table S3. *nirK* PCR cycling conditions.

Step	# of cycles	Temperature	Time
Denaturation	1	95°C	10 min
Denaturation	40	95°C	25 sec
Annealing		60°C	30 sec
Extension		72°C	30 sec

Table S4. *cbbL* PCR cycling conditions.

Step	# of cycles	Temperature	Time
Denaturation	1	95°C	10 min
Denaturation	40	95°C	1 min
Annealing		57°C	2 min
Extension		72°C	2 min

Table S5. *GH7* PCR cycling conditions.

Step	# of cycles	Temperature	Time
Denaturation	1	95°C	10 min
Denaturation	40	95°C	30 sec
Annealing		56°C	30 sec
Extension		72°C	30 sec

Table S6. *nifH* PCR cycling conditions.

Step	# of cycles	Temperature	Time
Denaturation	1	95°C	5 min
Denaturation	40	95°C	30 sec
Annealing		55°C	30 sec
Extension		72°C	30 sec

Table S7. Pearson correlation results of the properties analyzed.

* P-value < 0.05; ** P-value < 0.01.

Table S8. Main soil characteristics. Values are mean \pm standard error (n = 4).

		BA+FU	BA	F50	F100	ANOVA
pH		9,03 \pm 0,02	9,00 \pm 0,04	9,02 \pm 0,04	9,02 \pm 0,02	ns
Total organic C	g kg ⁻¹	10,6 \pm 0,3	10,96 \pm 0,49	10,52 \pm 0,46	10,17 \pm 1,62	ns
Total N	g kg ⁻²	1,00 \pm 0,05	1,07 \pm 0,03	1,02 \pm 0,04	0,99 \pm 0,00	ns
Cation exchange capacity	cmol kg ⁻¹	14,9 \pm 0,40	15,07 \pm 0,43	14,95 \pm 0,41	14,99 \pm 0,33	ns
Exchangeable Ca	cmol kg ⁻¹	10,3 \pm 0,30	10,19 \pm 0,27	10,09 \pm 0,24	10,25 \pm 0,28	ns
Exchangeable Mg	cmol kg ⁻¹	2,44 \pm 0,05	2,41 \pm 0,06	2,39 \pm 0,06	2,41 \pm 0,06	ns
Exchangeable K	cmol kg ⁻¹	1,45 \pm 0,05	1,75 \pm 0,15	1,79 \pm 0,15	1,58 \pm 0,06	ns
Exchangeable Na	cmol kg ⁻¹	0,71 \pm 0,00	0,72 \pm 0,05	0,68 \pm 0,02	0,75 \pm 0,03	ns
Sum of bases	cmol kg ⁻¹	14,9 \pm 0,40	15,07 \pm 0,43	14,95 \pm 0,41	14,99 \pm 0,33	ns
Carbonate content	%	28,10 \pm 1,49	26,53 \pm 1,63	27,23 \pm 2,80	30,98 \pm 6,30	ns
NH₄⁺	mg kg ⁻¹	1,39 \pm 0,08	1,66 \pm 0,09	1,44 \pm 0,03	1,72 \pm 0,44	ns
NO₃⁻	mg kg ⁻¹	13,28 \pm 4,08	13,79 \pm 1,62	11,07 \pm 6,61	12,93 \pm 6,02	ns
P available	mg kg ⁻¹	60,65 \pm 4,58	60,75 \pm 1,38	57,5 \pm 2,83	51,88 \pm 4,34	ns
Fe bioavailable	mg kg ⁻¹	2,23 \pm 0,19	2,1 \pm 0,09	2,13 \pm 0,13	2,22 \pm 0,07	ns
Cu bioavailable	mg kg ⁻¹	1,75 \pm 0,17	1,76 \pm 0,10	1,74 \pm 0,11	1,58 \pm 0,07	ns
Zn bioavailable	mg kg ⁻¹	5,68 \pm 0,56	5,74 \pm 0,36	5,81 \pm 0,30	5,01 \pm 0,14	ns
Mn bioavailable	mg kg ⁻¹	7,97 \pm 0,17	7,72 \pm 0,21	7,73 \pm 0,49	8,42 \pm 0,13	ns
Mo bioavailable	mg kg ⁻¹	7,13 \pm 3,21	2,63 \pm 1,46	8,67 \pm 3,53	11,18 \pm 2,50	ns
B bioavailable	mg kg ⁻¹	7,59 \pm 0,08	7,7 \pm 0,18	7,73 \pm 0,24	7,78 \pm 0,10	ns

BA+FU (F50 + the application of a formulation of bacteria and non-mycorrhizal fungi), BA (F50 + the application of a formulation of nitrogen-fixing and phosphorus and potassium solubilizing bacteria), F50 (50% of the rate of inorganic fertilizers added in F100), F100 (inorganic fertilizers applied at the rate to cover the nutritional demands of the crop). ns: not significant ($p = 0.05$).

References

- Henry, S., Baudoin, E., López-Gutiérrez, J.C., Martin-Laurent, F., Brauman, A., Philippot, L., 2004. Quantification of denitrifying bacteria in soils by nirK gene targeted real-time PCR. *J. Microbiol. Methods* 59, 327–335. <https://doi.org/10.1016/j.mimet.2004.07.002>
- Poly, F.; Ranjard, L.; Nazaret, S.; Gourbière, F.; Monrozier, L.J. Comparison of nifH Gene Pools in Soils and Soil Microenvironments with Contrasting Properties. *Appl. Environ. Microbiol.* 2001, 67, 2255–2262. <https://doi.org/10.1128/AEM.67.5.2255-2262.2001>.
- Rotthauwe, J.H., Witzel, K.P., Liesack, W., 1997. The ammonia monooxygenase structural gene amoA as a functional marker: molecular fine-scale analysis of natural ammonia-oxidizing populations. *Appl. Environ. Microbiol.* 63, 4704–4712. <https://doi.org/10.1128/aem.63.12.4704-4712.1997>
- Selesi, D., Schmid, M., Hartmann, A., 2005. Diversity of Green-Like and Red-Like Ribulose-1,5-Bisphosphate Carboxylase/Oxygenase Large-Subunit Genes (cbbL) in Differently Managed Agricultural Soils. *Appl. Environ. Microbiol.* 71, 175–184. <https://doi.org/10.1128/AEM.71.1.175-184.2005>
- Tian, X., Yang, T., He, J., Chu, Q., Jia, X., Huang, J., 2017. Fungal community and cellulose-degrading genes in the composting process of Chinese medicinal herbal residues. *Bioresour. Technol.* 241, 374–383. <https://doi.org/10.1016/j.biortech.2017.05.116>