

**Long-term compost amendment changes interactions and specialization in the soil bacterial community, activating beneficial N-cycling genes in the soil.**

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**Table S1. Management characteristics of the three cropping systems.**

Cropping system	Conv	Org_C	Org_M
Geographical coordinates	37° 48' 18.5" N; 0° 51' 49.2" W	37° 51' 39.3" N, 0° 54' 03.3" W	37° 49' 30.2" N, 0° 52' 28.4" W
Crop (2017-2018)	Brassica oleracea var. sabellica		
Harvest	Manual on 20-25 February 2018. Crop residues were incorporated into the soil.		
Crops (previous years)	Apium graveolens / Cucumils melo (2016/2017) Lactuca sativa / Brassica oleracea var. Italica (2015/2016) Apium graveolens / Cucumils melo (2014/2015) Brassica oleracea var. Italica / Capsicum annum (2013/2014) Foeniculum vulgare/ Cucurbita moschata (2012/2013)		
Organic amendments (amount per year)	15,000 kg ha <sup>-1</sup> sheep manure	10,000 kg ha <sup>-1</sup> sheep compost; compost tea*	15,000 kg ha <sup>-1</sup> sheep
Fertilizers (amount per year)	15 kg ha <sup>-1</sup> ENTEC solub 21 (ammonium sulfate with inhibition of nitrification); 10 L ha <sup>-1</sup> phosphoric acid; 15 kg ha <sup>-1</sup> calcium nitrate; 10L ha <sup>-1</sup> nitric acid	10 L ha-1 EcoZen NPK 2-2-7 (aminoacids); 10 L ha-1 Sunfol veg agri 12% (aminoacids)	
Pesticides	Linuron; Indoxacarb 30%; Cypermethrin; Lambda cihalotrin 10%; Imidacloprid 20%; Spinosad; Azadirachtin 3.2%; Emamectin 0.85%; Clortalonil 50%; Difenoconazol 25%; Azoxystrobin 2.5%; Propamocarb 52%; Ciflufenamid  No application of chemical pesticides		

Conv, Conventional system; Org\_C, Organic cultivation with sheep manure compost and compost tea; Org\_M, Organic cultivation with sheep manure. \*The compost tea was made on each farm by steeping mature compost in water for 24h.

**Table S2. Abundance of phyla in the different modules (expressed in percent)**

Phylum	C1	C2	C3	C4	C5	C6	C7	C8	C9	C10	C11	C12	C13		
Acidobacteria	7.7	1.25			4.35		22.22	5.88				9.09	3.89		
Actinobacteria	17.95	20	38.46	35	30.43	30	11.11	11.76	41.67	42.85	29.41	9.09	15.58		
Bacteriodes	7.69	6.25	7.69	10	8.70	5	11.11	11.76				18.18	24.67		
BRC1	2.56														
Chloroflexi	7.69	1.25	3.85					11.76			11.76		3.89		
Firmicutes	10.26	16.25				5	11.11				35.29	9.09	3.89		
Proteobacteria	43.59	37.5	30.77	25	56.52	50	22.22	41.18	41.67	28.57	35.29	45.45	33.77		
TM7	2.56	2.5								14.29					
Cyanobacteria		1.25								14.28					
Elusimicrobia		1.25	3.85												
Gemmatimonadetes		7.5						5.88					1.30		
Nitrospirae		1.25											1.30		
Plantcomycetes		2.5		15			11.11	5.88	8.33						
Verrucomicrobia		1.25	3.85			5			8.33		5.88		7.79		
Armatimonadetes			3.85										1.29		
NKB19			3.85										1.30		
OP11			3.85												
Kazan-3B-28				5											
FBP						5									
Chlorobi							11.11						1.30		
WS3								5.88							
Thermi											5.88				
TM6												9.09			
Total nodes	39	80	26	20	24	20	9	17	12	7	17	11	77		
Phylum	OC1	OC2	OC3	OC4	OC5	OC6	OC7	OC8	OC9	OC10	OC11	OC12	OC13	OC14	OC15
Acidobacteria	2.13		4.25	10.53		3.7			6.25	25		33.33		14.28	
Actinobacteria	27.66	36.11	14.89	10.53	25	33.30	33.33	27.27	8.75	25	16.67	16.67	30	14.28	50
Bacteriodes	6.38	16.67	6.38	15.79		3.70			5				20	7.14	
BRC1							11.11								
Chloroflexi	10.64					7.41			2.5				10		
Firmicutes	6.38	11.11	8.51	5.26	12.5	14.81		9.09	7.5						
Proteobacteria	40.42	25	42.55	36.84	56.25	22.22	33.33	54.54	35	25	83.33	33.33	30	64.29	25
TM7	2.12	2.78	2.13												
Cyanobacteria				5.26		3.70			1.25						12.5
Elusimicrobia									3.75						
Gemmatimonadetes		2.78	2.13				11.11	9.09	8.75	12.5					
Nitrospirae							11.11		1.25						
Planctomycetes		2.78	8.51		6.25				8.75				10		12.5
Verrucomicrobia	2.13	2.78	2.13	10.53					6.25	12.5					
Armatimonadetes			2.13						3.75						
NKB19			2.13												
Chlorobi			4.25			3.70									
Thermi	2.13														
BHI80-139				5.26											
OD1						3.70									
GN02						3.70									
OP3									1.25						
Total nodes	47	36	47	19	16	27	9	11	80	8	6	6	10	14	8
Phylum	OM1	OM2	OM3	OM4	OM5	OM6	OM7	OM8	OM9	OM10	OM11	OM12			
Acidobacteria			3.45	11.54		8.51			3.70	28.57	10.34	6.67			
Actinobacteria	36.36	13.79	10.34	7.69	42.10	23.40	25	35.29	11.11		13.79	13.33			
Bacteriodes	6.06		27.59			6.39	9.38	5.88	3.70		6.90	6.67			
BRC1						2.13									
Chloroflexi		6.90	3.45			2.13	12.5		11.11	14.29	3.45				
Firmicutes		20.69			5.26	4.25	12.5		7.41	14.29	3.45	13.33			

Proteobacteria	45.45	44.83	41.38	38.46	36.84	27.66	34.38	17.65	48.15	14.29	37.93	46.67
TM7			3.45					5.88				
Cyanobacteria	3.03					4.25		5.88				
Elusimicrobia	3.03		3.45			2.13						
Gemmatimonadetes	3.03			19.23		6.38	3.13				6.90	6.67
Nitrospirae				3.85				5.88				
Planctomycetes	3.03	10.34	3.45	7.69	10.53	4.25		5.88	3.70		3.45	
Verrucomicrobia		3.45	3.45	3.84		2.13	3.13	5.88	3.70		10.34	
Armatimonadetes						2.12		5.88				
NKB19								5.88				
Chlorobi					5.26					14.29		
Thermi									3.70			
OP11									3.70			
WS3						2.13						
WPS-2										14.29		
Fibrobacteres				3.85								
OD1											3.45	
Tenericutes												6.67
OP3						2.13						
Total nodes	33	29	29	26	19	47	32	17	27	7	29	15

(C) Conv, Conventional system; (OC) Org\_C, Organic cultivation with sheep manure compost and compost tea; (OM) Org\_M, Organic cultivation with sheep manure.

**Table S3. Subnetworks of the eight most abundant OTUs and their first neighbor nodes in the three cropping systems**

OTU	Cropping System Nodes			Cropping System Edges			Phyla
	Conv	Org_C	Org_M	Conv	Org_C	Org_M	
436	3	7	4	2 np – 1 pp	1 np – 6 pp	1 np – 3 pp	Proteobacteria
605	7	-	-	1 np – 6 pp	-	-	Proteobacteria
110	2	9	4	1 np – 1 pp	5 np – 4 pp	1 np – 3 pp	Actinobacteria
003	1	3	13	1 pp	1 np – 2 pp	13 pp	Acidobacteria
324	8	1	6	8 np	1 pp	6 pp	Gemmatimonadetes
438	1	6	4	1 np	2 np – 4 pp	3 pp	Proteobacteria
486	8	8	4	6 np – 2 pp	4 np – 4 pp	1 np – 3 pp	Proteobacteria
174	5	-	3	3 np – 2 pp	-	3 pp	Bacterioidetes
426	-	12	-	-	4 np – 8 pp	-	Proteobacteria
172	-	-	3	-	-	3 pp	Bacterioidetes

np, negative edges; pp, positive edges; - none detected; Conv, Conventional system; Org\_C, Organic cultivation with sheep manure compost and compost tea; Org\_M, Organic cultivation with sheep manure

**Table S4. Classification of generalists in the three cropping systems**

Cropping system	OTU ID	Generalist	Phylum	Class	Order	Family	Genus
Conv	OTU108	Module Hub	Actinobacteria	Actinobacteria	Actinomycetales	Nocardiodaceae	<i>Nocardioideis</i>
Conv	OTU153	Module Hub	Actinobacteria	Rubrobacteria	Rubrobacterales	Rubrobacteraceae	<i>Rubrobacter</i>
Conv	OTU422	Module Hub	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Unclassified	<i>Unclassified</i>
Conv	OTU483	Module Hub	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	<i>Methylothera</i>
Conv	OTU085	Connector	Actinobacteria	Actinobacteria	Actinomycetales	Micrococcaceae	Unclassified
Conv	OTU442	Connector	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	<i>Sphingopyxis</i>
Org_C	OTU065 *	Module Hub	Actinobacteria	Actinobacteria	Actinomycetales	Microbacteriaceae	<i>Agromyces</i>
Org_C	OTU161	Module Hub	Actinobacteria	Thermoleophilia	Solirubrobacterales	Solirubrobacteraceae	Unclassified
Org_C	OTU239	Module Hub	Chloroflexi	Chloroflexi	Herpetosiphonales	Unclassified	Unclassified
Org_C	OTU339 *	Module Hub	NKB19	Unclassified	Unclassified	Unclassified	Unclassified
Org_C	OTU345 *	Module Hub	Planctomycetes	BD7-11	Unclassified	Unclassified	Unclassified
Org_C	OTU599 *	Module Hub	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	<i>Arenimonas</i>
Org_C	OTU461	Connector	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	<i>Ramlibacter</i>
Org_C	OTU508	Connector	Proteobacteria	Deltaproteobacteria	Desulfuromonadales	Geobacteraceae	<i>Geobacter</i>
Org_M	OTU024	Module Hub	Actinobacteria	Acidimicrobiia	Acidimicrobiales	AKIW874	<i>Unclassified</i>
Org_M	OTU271	Module Hub	Firmicutes	Bacilli	Bacillales	Bacillaceae	<i>Bacillus</i>
Org_M	OTU485	Module Hub	Proteobacteria	Betaproteobacteria	MKC10	Unclassified	Unclassified
Org_M	OTU512	Module Hub	Proteobacteria	Deltaproteobacteria	Unclassified	Unclassified	Unclassified
Org_M	OTU537 *	Module Hub	Proteobacteria	Deltaproteobacteria	Spirobacillales	Unclassified	Unclassified
Org_M	OTU630 *	Module Hub	Verrucomicrobia	Pedosphaerae	Pedosphaerales	OPB35	Unclassified

Conv, Conventional cropping system; Org\_C, Organic cropping system with compost and compost tea, Org\_M, Organic cropping system with manure. " " indicates that the node was shared by Org\_C such as specialist; " " indicates that the node was shared by Org\_M such as specialist; and "\*" indicates that the node was shared by Conv such as specialist.

**Table S5. Predicted functions of the bacterial communities found in the three cropping systems (relative abundances)**

Metabolic pathway	Conv	Org_C	Org_M	Anova	Kruskal-Wallis
Amino acid metabolism	0.23±0.00 ab	0.24±0.00 a	0.19±0.01 b	-	**
Amino acid related enzymes	1.23±0.04 a	1.22±0.03 a	1.08±0.07 b***	**	-
Bacterial toxins	0.06±0.00 ab	0.07±0.01 a	0.04±0.01 b	-	**
Biosynthesis and biodegradation of secondary metabolites	0.07±0.00 ab	0.08±0.01 a	0.06±0.01 b	-	**
Carbon fixation photosynthetic organism	0.41±0.02 ab	0.44±0.01 a	0.34±0.03 b	-	**
Carbon fixation in prokaryotes	0.98±0.03 b	1.18±0.03 a***	0.62±0.01 c***	***	-
Nitrogen metabolism	0.69±0.03 a	0.73±0.02 a	0.50±0.04 b***	***	-
Lipid metabolism	0.10±0.00 ab	0.12±0.01 a	0.08±0.00 b	-	**
Nucleotide metabolism	0.03±0.00 a	0.03±0.00 a	0.02±0.00 b	-	**
Penicillin and cephalosporin biosynthesis	0.07±0.00 a	0.07±0.00 a	0.05±0.00 b	-	**
Phosphotransferase system PTS	0.08±0.00 ab	0.09±0.00 a	0.06±0.00 b	-	**
Signal transduction mechanism	0.42±0.02 ab	0.45±0.02 a	0.32±0.01 b	-	**
Tetracycline biosynthesis	0.13±0.01 ab	0.13±0.00 a	0.12±0.00 b	-	**
Toluene degradation	0.20±0.01 ab	0.23±0.01 a	0.13±0.01 b	-	**
Sulfur metabolism	0.34±0.01 ab	0.37±0.02 a	0.26±0.01 b		**
Benzoate degradation	0.55±0.03 b	0.70±0.02 a***	0.59±0.03 b	***	-
DNA replication proteins	0.76±0.01 b	0.80±0.01 a***	0.48±0.01 c***	***	-
Phenylalanine, tyrosine and tryptophan biosynthesis	0.58±0.01 ab	0.71±0.01 a	0.52±0.00 b	-	**

(mean±sd; n=5 values are expressed with an e-value of 1x10<sup>-2</sup>). The mean value followed asterisks in each cropping system (\*, \*\*, \*\*\*) represents significant differences with respect to the conventional cropping system (Conv) by Dunnett's test (\*P < 0.05; \*\*P < 0.01, \*\*\*P < 0.001, respectively). The mean value followed by different letters represent significant differences between systems by Tukey's test or Dunn's Kruskal-Wallis Multiple Comparison test. Conv, Conventional cropping system; Org\_C, Organic cropping system with compost and compost tea; Org\_M, Organic cropping system with manure.

**Table S6. Mantel analysis of the relationships between the overall bacterial community and soil properties and N cycling genes.**

	Network Topology					
	Conv		Org_C		Org_M	
	r <sub>M</sub>	P	r <sub>M</sub>	P	r <sub>M</sub>	P
Soil properties	0.09133	**	0.06448	**	0.07088	**
Functionality (N cycling genes)	0.2121	**	-0.001593	0.518	-0.01519	0.728

Significant P values are indicated as \*P < 0.05; \*\*P < 0.01, \*\*\*P < 0.001, respectively. Conv, Conventional cropping system; Org\_C, Organic cropping system with compost and compost tea; Org\_M, Organic cropping system with manure; r<sub>M</sub> Mantel statistic r.