Soil microbial indicators within rotations and tillage systems

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Supplementary Material

Table S1. Summary of field practices from Monmouth, Illinois from 1997-2016; dates are ranges that vary slightly year to year.

Field event type	Dates
Tilled wheat plots	Late Sept - early Oct
Planted wheat crop	Late Sept - early Oct
Fall wheat fertilization	Late Oct - early Nov
Fall tillage of corn and soybean plots†	Mid Nov
Spring wheat fertilization	Late March - early Apr
Secondary tillage in corn and soybean plots‡	Mid April - early May
Spring corn fertilization	Mid April - mid May
Corn planting	Mid April - mid May
Soybean planting	Early - mid May
Harvest of wheat	Late June - late July
Harvest of corn	Late Sept - early Oct
Harvest of soybean	Late Sept - early Oct

†Chisel tillage used a disk-ripper 14" deep in plots designated as tilled; no till received zero tillage

‡Secondary tillage used a field cultivator in plots designated as tilled; no-till received zero tillage

Table S2. Principal component analysis of soil variables (17) for 0-10 cm soil depth with eigenvalues and cumulative proportion of the data set variability explained by the five principal components (PC) extracted with eigenvalues >1. Component correlation scores (eigenvectors) with loadings greater than |0.5| are bolded. Probability values for the analysis of variance (ANOVA) and degrees of freedom (df) available for the effects of rotation|phase (Rotation), tillage (Tillage), and their interaction are shown for each extracted PCs.

		PC1	PC2	PC3	PC4	PC5
Eigenvalue		4.8	4.07	1.87	1.32	1.2
Cum. Proportion		0.28	0.52	0.63	0.71	0.78
Soil variable		**Component Correlation Scores**				
pH		**0.76**	**-0.6**	-0.06	0.02	0.09
CEC		-0.11	**0.95**	-0.04	-0.08	-0.11
SOM		-0.23	**0.59**	**-0.61**	-0.01	0.21
NO_3^-		0.27	0.16	**0.66**	-0.4	-0.17
NH_4^+		-0.38	0.15	-0.26	**0.65**	0.08
P		0.31	0.41	0.25	0.39	0.35
S		-0.32	0.12	0.13	**-0.55**	**0.55**
K		**-0.55**	0.25	0.34	0.04	0.23
Na		**0.55**	**0.71**	-0.14	-0.07	-0.16
Ca		**0.87**	0.35	-0.06	0.12	-0.14
Mg		-0.05	0.28	0.39	0.1	**-0.58**
Al		**-0.74**	0.08	**0.49**	0.29	-0.06
Fe		**-0.49**	**0.77**	0.2	0.1	0.01
B		**0.7**	0.09	0.28	0.15	0.33
Zn		0.44	**0.71**	0.18	-0.06	0.29
Cu		**0.77**	0.45	-0.17	-0.02	-0.11
Mn		**0.56**	-0.37	0.43	0.36	0.2
Factor	**df**	**Probability values**				
Rotation	3	*0.0061*	*0.0175*	*0.0638*	*0.0005*	*0.0574*
Tillage	1	*0.0012*	*0.0006*	*<.0001*	0.5677	*0.0367*
Rotation x Tillage	3	0.8511	0.8368	0.223	0.7103	0.6221

Table S3. List of bacterial principal components (PC) comprised by indicator species that contributed at least 5% of the variability in the data and with eigenvalue of at least 1.

PC	Eigenvalue	Proportion (%)	Loadings	Phylum	Class	Order	Family	Genus	Species
			-0.76	Acidobacteria	Acidobacteriia	Acidobacteriales	Acidobacteriaceae (Subgroup 1)		
			-0.76	Acidobacteria	Acidobacteriia	Solibacterales	Solibacteraceae (Subgroup 3)	*Candidatus*	*solibacter*
			0.63	Acidobacteria	Acidobacteriia	Solibacterales	Solibacteraceae (Subgroup 3)	*Paludibaculum*	uncultured bacterium
			0.78	Acidobacteria	Blastocatellia (Subgroup 4)	Pyrinomonadales	Pyrinomonadaceae	*RB41*	uncultured bacterium 16H1
			0.80	Acidobacteria	Holophagae	Subgroup 7			
			0.60	Acidobacteria	Subgroup 25	uncultured bacterium	uncultured bacterium	uncultured bacterium	uncultured bacterium
			0.77	Actinobacteria	Acidimicrobiia	Actinomarinales	uncultured	uncultured soil bacterium	uncultured soil bacterium
			-0.50	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae		
			0.69	Actinobacteria	MB-A2-108	Actinomycetales	uncultured Actinomycetales bacterium	uncultured Actinomycetales bacterium	uncultured Actinomycetales bacterium
			0.58	Actinobacteria	MB-A2-108	Actinobacterium	uncultured actinobacterium	uncultured actinobacterium	uncultured actinobacterium
1	12.76	36%	0.57	Chloroflexi	Anaerolineae	RBG-13-54-9	UASB_TL14	UASB_TL14	UASB_TL14
			0.75	Chloroflexi	Dehalococcoidia	S085	uncultured bacterium	uncultured bacterium	uncultured bacterium
			-0.83	Chloroflexi	Ktedonobacteria	Ktedonobacterales	JG30-KF-AS9	uncultured bacterium	uncultured bacterium
			0.66	Planctomycetes	OM190	uncultured bacterium	uncultured bacterium	uncultured bacterium	uncultured bacterium
			-0.87	Planctomycetes	Phycisphaerae	Tepidisphaerales	WD2101 soil group	uncultured Planctomycetales bacterium	uncultured Planctomycetales bacterium
			0.55	Planctomycetes	Phycisphaerae	mle1-8	uncultured bacterium	uncultured bacterium	uncultured bacterium
			-0.88	Proteobacteria	Alphaproteobacteria	Micropepsales	Micropepsaceae	uncultured	
			0.80	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiales Incertae Sedis	*Nordella*	
			0.67	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	TRA3-20		
			-0.70	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	*Chujaibacter*	
			-0.57	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Rhodanobacteraceae	*Rhodanobacter*	
			0.54	Rokubacteria	NC10	Rokubacteriales	uncultured Firmicutes bacterium	uncultured Firmicutes bacterium bacterium	uncultured Firmicutes bacterium bacterium
			-0.83	Verrucomicrobia	Verrucomicrobiae	Pedosphaerales	Pedosphaeraceae	Ellin516	Ellin516
			-0.73	Bacteroidetes	Bacteroidia	Chitinophagales			
2	3.12	9%	-0.60	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Nitrosomonadaceae	*MND1*	uncultured Nitrosomonadales bacterium
			-0.64	Actinobacteria	Thermoleophilia	Gaiellales	Gaiellaceae	*Gaiella*	
3	2.64	8%	0.60	Bacteroidetes	Bacteroidia	Sphingobacteriales	AKYH767	metagenome	metagenome
			0.63	Proteobacteria	Gammaproteobacteria	R7C24	metagenome	metagenome	metagenome
4	2.17	6%	0.49	Proteobacteria	Deltaproteobacteria	Myxococcales	Archangiaceae		
5	2.06	6%	-0.63	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	*Luteimonas*	

Table S4. List of fungal principal components (PC) comprised by indicator species that contributed at least 5% of the variability in the data and with eigenvalue of at least 1.

PC	Eigenvalue	Proportion (%)	Loadings	Phylum	Class	Order	Family	Genus	Species
1	3.06	8%	0.55	Ascomycota	Sordariomycetes	Hypocreales	Nectriaceae	*Fusarium*	*sporotrichioides*
			0.53	Ascomycota	Dothideomycetes	Capnodiales	Mycosphaerellaceae		
2	2.58	7%	0.58	Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae	*Gibellulopsis*	*piscis*
			0.71	Ascomycota	Sordariomycetes	Glomerellales	Plectosphaerellaceae	*Plectosphaerella*	
			0.58	Ascomycota	Sordariomycetes	Coniochaetales	Coniochaetaceae		
3	2.51	7%	0.73	Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae	*Schizothecium*	
			0.56	Ascomycota	Sordariomycetes	Sordariales	Lasiosphaeriaceae	*Schizothecium*	*carpinicola*
4	2.12	6%	0.51	Ascomycota	Sordariomycetes	Hypocreales	Bionectriaceae	*Clonostachys*	*rosea*
5	2.08	6%	0.49	None selected					

Table S5. List of archaeal principal components (PC) comprised by indicator species that contributed at least 5% of the variability in the data and with eigenvalue of at least 1.

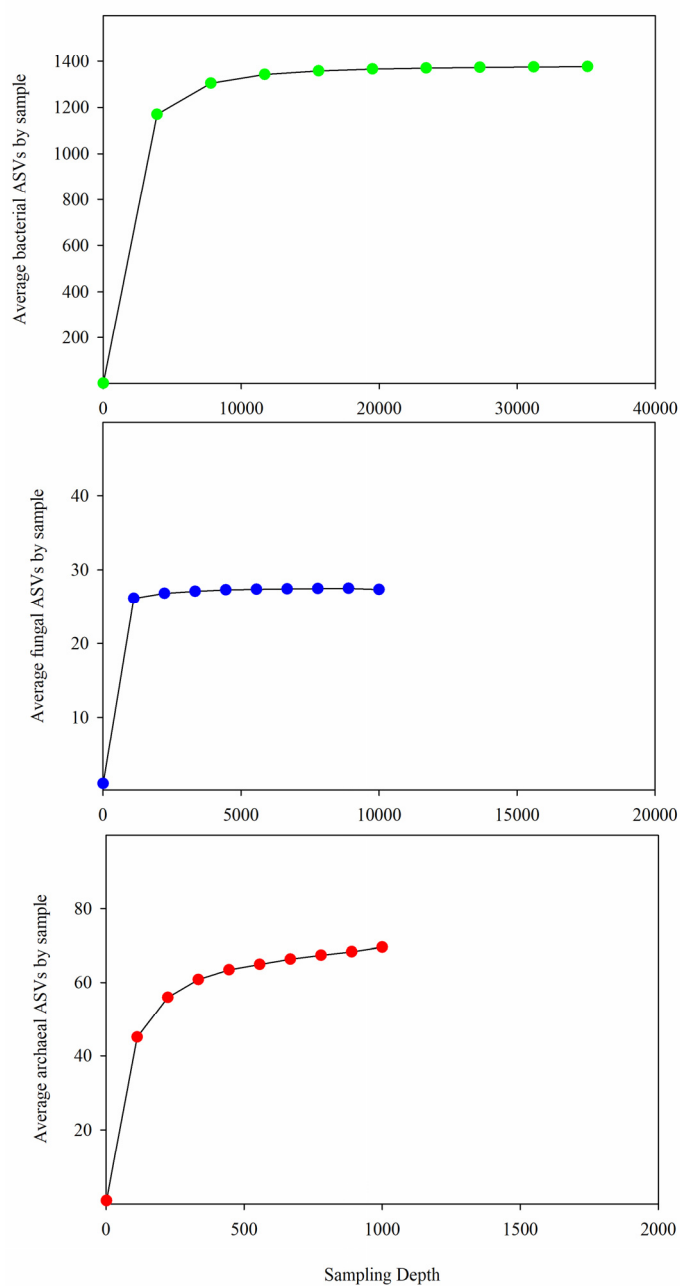| PC	Eigenvalue	Proportion (%)	Loadings	Phylum	Class	Order	Family	Genus	Species
1	2.24	20%	0.54	Thaumarchaeota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	*Candidatus*	*nitrocosmicus*
			0.50	Thaumarchaeota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	uncultured ammonia-oxidizing archaeon	uncultured ammonia-oxidizing archaeon
			-0.56	Thaumarchaeota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	uncultured soil archaeon	uncultured soil archaeon
			0.60	Thaumarchaeota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae		
2	1.69	15%	-0.84	Thaumarchaeota	Nitrososphaeria	Nitrosotaleales	Nitrosotaleaceae	*Candidatus*	*nitrosotalea* uncultured archaeon
			-0.29	Thaumarchaeota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	uncultured compost archaeon	uncultured compost archaeon
			-0.72	Thaumarchaeota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae		
3	1.27	12%	0.72	Nanoarchaeaeota	Woesearchaeia				
4	1.26	11%	0.75	Euryarchaeota	Thermoplasmata	Marine Group II	uncultured archaeon	uncultured archaeon	uncultured archaeon
5	1.08	10%	0.59	Euryarchaeota	Thermoplasmata	uncultured	uncultured archaeon	uncultured archaeon	uncultured archaeon
			-0.57	Thaumarchaeota	Nitrososphaeria	Nitrososphaerales	Nitrososphaeraceae	*Candidatus*	*mitrososphaera*

Figure. S1. Rarefaction curves for the major kingdoms of bacteria (green; top panel), fungi (blue; middle panel), and archaea (red; bottom panel). Points show the average number of observed ASVs for a given sampling depth (x-axis). For each taxa, rarefaction curves plateaued at sampling depths of 35,100, 10,000, and 1000 for bacterial, fungal, and archaeal sequences per sample, respectively.