

Front. Agr. Sci. Eng.  
<https://doi.org/10.15302/J-FASE-2024570>  
Verso: Front. Agr. Sci. Eng.  
Recto: Xinzhan SUN et al. Soil health and microbial network under different wheat yields  
RESEARCH ARTICLE

# Soil health and microbial network analysis in a wheat-maize cropping system under different wheat yields

Xinzhan SUN<sup>1</sup>, Tengteng LI<sup>1</sup>, Jiangzhou ZHANG<sup>2,1</sup> (✉)

1. State Key Laboratory of Nutrient Use and Management, Key Laboratory of Plant–Soil Interactions (Ministry of Education), College of Resources and Environmental Sciences, National Academy of Agriculture Green Development, China Agricultural University, Beijing 100193, China.

2. Key Laboratory of Agricultural Ecological Security and Green Development at Universities of Inner Mongolia Autonomous, Inner Mongolia Key Laboratory of Soil Quality and Nutrient Resources, College of Resources and Environmental Sciences, Inner Mongolia Agricultural University, Hohhot 010018, China.

Received 2024.4.25;

Accepted 2024.8.8.

Correspondence: [zjzky2010@163.com](mailto:zjzky2010@163.com)

© The Author(s) 2024. Published by Higher Education Press. This is an open access article under the CC BY license (<http://creativecommons.org/licenses/by/4.0>)

## SUPPLEMENTARY MATERIALS

**Table S1** The relative abundance of soil dominant bacterial and fungal phyla in four wheat yield categories at soil depths of 0–15 and 15–30 cm

Soil depth (cm)	Microbial taxa	Phylum	Relative abundance (%)			
			Y1	Y2	Y3	Y4
0–15	Bacteria	Proteobacteria	31.2±1.4a	29.7±1.2a	32.0±1.4a	30.0±1.0a
		Acidobacteria	21.0±1.7a	20.6±2.4a	22.5±0.3a	22.2±0.9a
		Actinobacteria	15.4±3.3a	12.8±1.8a	12.6±1.3a	14.8±0.4a
		Chloroflexi	6.5±1.0a	8.1±0.4a	7.5±0.8a	6.8±0.3a
		Firmicutes	4.1±0.4a	5.3±0.8a	4.9±1.2a	4.5±0.3a
		Planctomycetes	6.1±1.9a	7.9±0.9a	6.9±0.8a	6.8±0.7a
	Fungi	Ascomycota	79.3±0.1a	74.2±4.6a	77.9±3.2a	85.3±4.6a
		Basidiomycota	0.8±0.3a	2.3±0.3a	2.2±0.2a	1.4±0.9a
		Zygomycota	16.0±1.3a	18.0±4.7a	14.9±4.4a	11.3±2.7a
15–30	Bacteria	Proteobacteria	29.4±1.1ab	30.2±1ab	<b>32.0±0.8a</b>	26.6±1.1b
		Acidobacteria	18.3±0.7a	19.2±1.0a	18.7±0.3a	21.8±1.6a
		Actinobacteria	<b>15.4±2.2a</b>	9.9±0.8b	11.3±1.1ab	12.4±1.4ab
		Chloroflexi	8.0±0.3ab	<b>9.9±0.6a</b>	7.5±0.6ab	7.4±0.7b
		Firmicutes	3.7±0.1c	5.7±0.8bc	6.6±0.4ab	<b>8.1±0.8a</b>
		Planctomycetes	7.2±1.3a	7.8±0.9a	7.4±0.8a	6.0±0.5a
	Fungi	Ascomycota	69.3±3.9a	77.9±4.6a	81.8±3.5a	80.3±3.3a
		Basidiomycota	1.1±0.7a	2.5±1.6a	1.2±0.1a	0.5±0.3a
		Zygomycota	<b>23.5±0.8a</b>	13.5±0.6b	13.9±3.2b	14.1±2.7b

Note: Different lowercase letters indicate significant differences between yield categories within rows at  $P < 0.05$ . Y1, Y2, Y3, and Y4 indicate the yields of 3.75, 6.00, 8.25, and 10.1 t·ha<sup>-1</sup>, respectively.

**Table S2** Classification of the top 10 bacterial taxa based on abundance at each taxonomic level

Treatment	ID	Degree	Phylum	Class	Order	Family	Genus
Y4	OTU2323	49	Actinobacteria	Actinobacteria	Propionibacteriales	<i>Nocardioideaceae</i>	<i>Nocardioides</i>
	OTU5015	48	Firmicutes	Bacilli	Bacillales	<i>Bacillaceae</i>	<i>Bacillus</i>
	OTU935	47	Actinobacteria	Actinobacteria	Micrococcales	<i>Micrococcaceae</i>	<i>Pseudarthrobacter</i>
	OTU1560	46	Nitrospirae	Nitrospira			
	OTU4447	46	Proteobacteria	Alphaproteobacteria	Rhizobiales	<i>Hyphomicrobiaceae</i>	<i>Pedomicrobium</i>
	OTU1429	44	Acidobacteria	Acidobacteria			
	OTU5647	44	Acidobacteria	Acidobacteria	Blastocatellales		
	OTU5736	44	Proteobacteria	Alphaproteobacteria	Sphingomonadales	<i>Erythrobacteraceae</i>	<i>Altererythrobacter</i>
	OTU841	44	Proteobacteria	Alphaproteobacteria	Rhizobiales	<i>Xanthobacteraceae</i>	<i>Variibacter</i>
	OTU2479	43	Proteobacteria	Deltaproteobacteria	Desulfurellales	<i>Desulfurellaceae</i>	
Y3	OTU2281	25	Tectomicrobia				
	OTU2399	25	Acidobacteria	Acidobacteria			
	OTU5388	25	Actinobacteria	Actinobacteria	Micrococcales	<i>Microbacteriaceae</i>	<i>Agromyces</i>
	OTU2098	24	Actinobacteria	Actinobacteria	Streptosporangiales	<i>Streptosporangiaceae</i>	<i>Nonomuraea</i>
	OTU3845	24	Proteobacteria	Deltaproteobacteria	Desulfurellales	<i>Desulfurellaceae</i>	
	OTU4742	24	Actinobacteria	Actinobacteria	Gaiellales		
	OTU4001	23	Acidobacteria	Acidobacteria			
OTU5634	23	Proteobacteria	Gammaproteobacteria	Xanthomonadales			

	OTU5702	23	Nitrospirae	Nitrospira			
	OTU854	23	Proteobacteria	Gammaproteobacteria	Xanthomonadales	<i>Xanthomonadales_Incertae_Sedis</i>	<i>Acidibacter</i>
Y2	OTU2091	37	Acidobacteria	Acidobacteria			
	OTU1719	36	Proteobacteria	Alphaproteobacteria	Rhizobiales	<i>Bradyrhizobiaceae</i>	<i>Bradyrhizobium</i>
	OTU6326	35	Proteobacteria	Betaproteobacteria	TRA3-20		
	OTU886	35	Proteobacteria	Alphaproteobacteria	Rhizobiales	<i>Hyphomicrobiaceae</i>	<i>Devosia</i>
	OTU6946	34	Chloroflexi	KD4-96			
	OTU5632	33	Actinobacteria	Actinobacteria	Acidimicrobiales		
	OTU2193	32	Acidobacteria	Acidobacteria			
	OTU2479	32	Proteobacteria	Deltaproteobacteria	Desulfurellales	<i>Desulfurellaceae</i>	
	OTU541	32	Proteobacteria	Alphaproteobacteria	Rhizobiales	<i>Phyllobacteriaceae</i>	
	OTU1429	31	Acidobacteria	Acidobacteria			
Y1	OTU4744	27	Actinobacteria	Actinobacteria	Micrococcales	<i>Microbacteriaceae</i>	<i>Microbacterium</i>
	OTU6361	27	Actinobacteria	Actinobacteria	Propionibacteriales	<i>Nocardioideaceae</i>	<i>Marmoricola</i>
	OTU2326	25	Actinobacteria	Actinobacteria	Solirubrobacterales	<i>Solirubrobacteraceae</i>	<i>Solirubrobacter</i>
	OTU2236	24	Planctomycetes	Planctomycetacia	Planctomycetales	<i>Planctomycetaceae</i>	<i>Pir4_lineage</i>
	OTU2479	24	Proteobacteria	Deltaproteobacteria	Desulfurellales	<i>Desulfurellaceae</i>	
	OTU7125	24	Proteobacteria	Betaproteobacteria	Burkholderiales	<i>Comamonadaceae</i>	
	OTU3881	23	Actinobacteria	Actinobacteria	Solirubrobacterales		
	OTU3969	23	Proteobacteria	Deltaproteobacteria	Desulfurellales	<i>Desulfurellaceae</i>	

OTU1560	22	Nitrospirae	Nitrospira
OTU2350	22	Nitrospirae	Nitrospira

---

Note: Y1, Y2, Y3, and Y4 indicate the yields of 3.75, 6.00, 8.25, and 10.1 t·ha<sup>-1</sup>, respectively.

**Table S3** Classification of the top 10 fungal taxa based on abundance at each taxonomic level

Treatment	ID	Degree	Phylum	Class	Order	Family	Genus
Y4	OTU865	26	Ascomycota	Sordariomycetes	Sordariales	<i>Chaetomiaceae</i>	<i>Chaetomium</i>
	OTU2003	21	Ascomycota	Sordariomycetes	Sordariales	<i>Lasiosphaeriaceae</i>	<i>Podospora</i>
	OTU2036	21	Ascomycota	Sordariomycetes	Sordariales	<i>Lasiosphaeriaceae</i>	<i>Podospora</i>
	OTU1229	19	Ascomycota	Sordariomycetes	Sordariales	<i>Chaetomiaceae</i>	<i>Humicola</i>
	OTU1367	19	Ascomycota	Sordariomycetes	Hypocreales	<i>Nectriaceae</i>	<i>Fusarium</i>
	OTU2860	19	Ascomycota	Sordariomycetes	Hypocreales	<i>norank_Hypocreales</i>	<i>Stachybotrys</i>
	OTU1110	18	Ascomycota	Sordariomycetes	Microascales	<i>Microascaceae</i>	<i>Pseudallescheria</i>
	OTU2171	18	Ascomycota	Sordariomycetes	Hypocreales	<i>norank_Hypocreales</i>	
	OTU23	18	Ascomycota	Sordariomycetes	Microascales	<i>Microascaceae</i>	
OTU735	18	Ascomycota	Sordariomycetes	norank_Sordariomycetes	<i>Plectosphaerellaceae</i>	<i>Lectera</i>	
Y3	OTU1577	22	Zygomycota	norank_Zygomycota	Mortierellales	<i>Mortierellaceae</i>	<i>Mortierella</i>
	OTU2860	22	Ascomycota	Sordariomycetes	Hypocreales	<i>norank_Hypocreales</i>	<i>Stachybotrys</i>
	OTU1232	19	Ascomycota	Sordariomycetes	Sordariales	<i>Lasiosphaeriaceae</i>	<i>Schizothecium</i>
	OTU1738	19	Basidiomycota	Agaricomycetes	Agaricales	<i>Psathyrellaceae</i>	<i>Coprinellus</i>
	OTU1913	19	Ascomycota	Sordariomycetes	Hypocreales	<i>norank_Hypocreales</i>	<i>Acremonium</i>
	OTU2849	19	Ascomycota	Dothideomycetes	Pleosporales	<i>Cucurbitariaceae</i>	<i>Pyrenochaetopsis</i>
	OTU440	19	Ascomycota	Sordariomycetes	Hypocreales	<i>Clavicipitaceae</i>	<i>Metarhizium</i>
	OTU865	19	Ascomycota	Sordariomycetes	Sordariales	<i>Chaetomiaceae</i>	<i>Chaetomium</i>

	OTU1229	18	Ascomycota	Sordariomycetes	Sordariales	<i>Chaetomiaceae</i>	<i>Humicola</i>
	OTU144	18	Ascomycota	Sordariomycetes	norank_Sordariomycetes	<i>Plectosphaerellaceae</i>	<i>Gibellulopsis</i>
Y2	OTU1344	21	Ascomycota	Sordariomycetes	Hypocreales	<i>Nectriaceae</i>	<i>Fusarium</i>
	OTU1691	18	Ascomycota	Dothideomycetes	Pleosporales	<i>Cucurbitariaceae</i>	<i>Pyrenochaetopsis</i>
	OTU2476	18					
	OTU2849	17	Ascomycota	Dothideomycetes	Pleosporales	<i>Cucurbitariaceae</i>	<i>Pyrenochaetopsis</i>
	OTU350	17	Ascomycota	Sordariomycetes	Hypocreales		
	OTU1367	16	Ascomycota	Sordariomycetes	Hypocreales	<i>Nectriaceae</i>	<i>Fusarium</i>
	OTU1582	16	Ascomycota	Sordariomycetes	Sordariales	<i>Chaetomiaceae</i>	<i>Chaetomium</i>
	OTU2520	16	Ascomycota	Sordariomycetes	Coniochaetales	<i>Coniochaetaceae</i>	<i>Lecythophora</i>
	OTU2690	16	Ascomycota	Dothideomycetes	Pleosporales	<i>Pleosporaceae</i>	<i>Bipolaris</i>
	OTU2691	16	Ascomycota	Eurotiomycetes	Eurotiales	<i>Trichocomaceae</i>	<i>Talaromyces</i>
Y1	OTU2680	27	Ascomycota	Sordariomycetes	Sordariales	<i>Lasiosphaeriaceae</i>	
	OTU272	24	Ascomycota	Dothideomycetes	Pleosporales	<i>Cucurbitariaceae</i>	<i>Pyrenochaetopsis</i>
	OTU20	22	Zygomycota	norank_Zygomycota	Mortierellales	<i>Mortierellaceae</i>	<i>Mortierella</i>
	OTU2800	22	Ascomycota	Sordariomycetes	Hypocreales	<i>Nectriaceae</i>	<i>Nectria</i>
	OTU2928	22	Ascomycota	Sordariomycetes	Hypocreales	<i>Nectriaceae</i>	<i>Fusarium</i>
	OTU440	22	Ascomycota	Sordariomycetes	Hypocreales	<i>Clavicipitaceae</i>	<i>Metarhizium</i>
	OTU126	21	Ascomycota	Sordariomycetes	Hypocreales	<i>Nectriaceae</i>	<i>Gibberella</i>
	OTU2041	21	Zygomycota	norank_Zygomycota	Mortierellales	<i>Mortierellaceae</i>	<i>Mortierella</i>

OTU1601 20

OTU1692 20 Zygomycota norank\_Zygomycota Mortierellales *Mortierellaceae* *Mortierella*

---

Note: Y1, Y2, Y3, and Y4 indicate the yields of 3.75, 6.00, 8.25, and 10.1 t·ha<sup>-1</sup>, respectively.