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Supplementary Material

Different Distribution of Core Microbiota in Upper Soil Layer in Two Places of North China Plain

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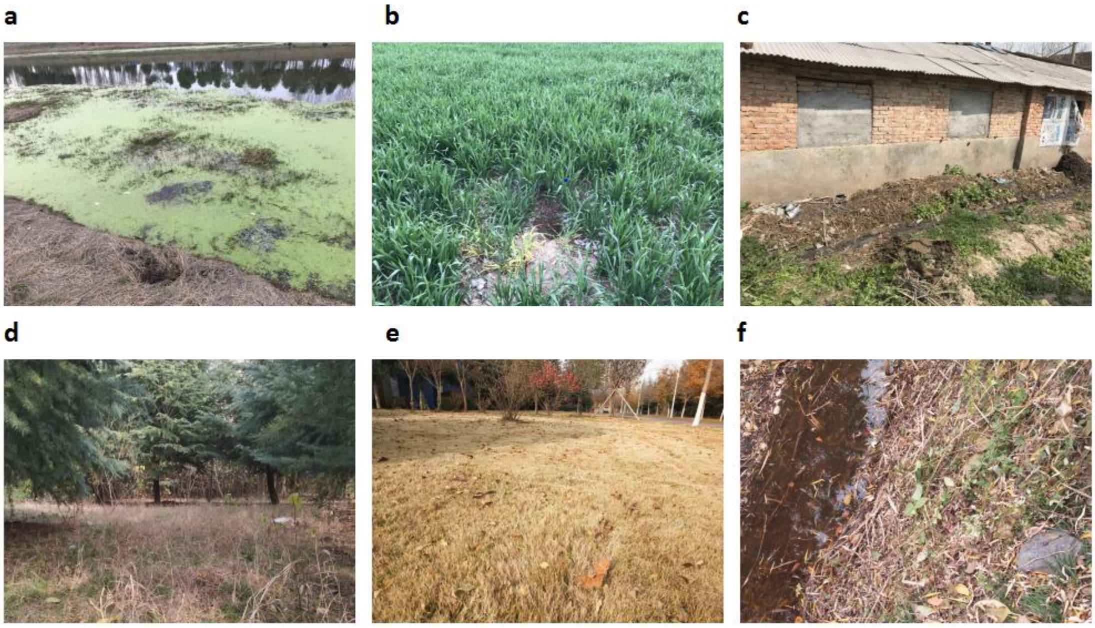

Fig. S1. Representative soil sampling site pictures of the 6 different Vegetation types. (**a**) riverside in Xincai, (**b**) wheat in Xincai, (**c**) pig farm in Xincai, (**d**) pine forest near riverside in Zhengzhou, (**e**) grass in Zhengzhou, and (**f**) riverside in Zhengzhou

Table S1. The read and OTU numbers of each soil sample.

Samples	Read numbers	OTU numbers
HN-S1	59106	1441
HN-S2	131450	1890
HN-S8	23038	1305
HN-S9	24136	1002
HN-S10	24387	1723
HN-S11	36040	1087
HN-S12	78110	1256

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(Table S1) contd.....

Samples	Read numbers	OTU numbers
HN-S13	41465	1579
HN-S14	60973	2029
HN-S15	58942	1940
HN-S18	58666	2400
HN-S19	60449	2305
HN-S21	59523	2047
Total	716285	4838

Table S2. Alpha diversity indices of all the soil samples.

Sample	richness	chao1	shannon_2	simpson	dominance	equitability
HN-S1	1500.0	1503.9	8.00	0.00991	0.990	0.758
HN-S2	1947.0	1949.5	7.37	0.0371	0.963	0.674
HN-S8	1381.0	1383.5	8.37	0.0105	0.989	0.802
HN-S9	1019.0	1021.4	8.46	0.00651	0.993	0.846
HN-S10	1765.0	1766.9	8.94	0.00658	0.993	0.829
HN-S11	1088.0	1090.9	7.20	0.0226	0.977	0.714
HN-S12	1261.0	1264.2	7.17	0.0299	0.970	0.696
HN-S13	1617.0	1619.7	8.70	0.00611	0.994	0.816
HN-S14	2050.0	2052.0	8.68	0.00897	0.991	0.789
HN-S15	1949.0	1950.9	8.86	0.00513	0.995	0.811
HN-S18	2463.0	2464.3	9.47	0.00397	0.996	0.840
HN-S19	2415.0	2416.1	9.56	0.00296	0.997	0.851
HN-S21	2126.0	2127.8	9.14	0.00448	0.996	0.827
HN-S22	1703.0	1704.6	8.84	0.00566	0.994	0.823
HN-S23	1791.0	1792.4	9.05	0.00521	0.995	0.837

Table S3. The dominant phyla in the soil samples.

	Average Distribution	HN-S1	HN-S2	HN-S8	HN-S9	HN-S10	HN-S11	HN-S12	HN-S13	HN-S14	HN-S15	HN-S18	HN-S19	HN-S21
Proteobacteria	38.34%	46.30%	44.43%	47.26%	37.45%	47.84%	43.48%	44.93%	19.10%	25.66%	31.01%	36.29%	38.19%	36.43%
Actinobacteria	20.56%	18.31%	10.22%	9.55%	26.01%	12.98%	20.69%	10.79%	38.35%	43.99%	37.70%	14.97%	13.54%	10.12%
Acidobacteria	15.18%	9.34%	16.23%	8.61%	10.62%	7.04%	13.48%	21.00%	21.55%	9.32%	15.68%	18.87%	22.54%	23.04%
Above_phylum	12.65%	6.87%	4.23%	24.04%	12.71%	19.31%	5.09%	5.26%	13.05%	14.21%	9.41%	15.39%	15.85%	18.99%
Bacteroidetes	4.57%	8.67%	15.09%	2.72%	3.95%	5.76%	3.60%	2.86%	1.31%	1.75%	1.85%	4.06%	4.45%	3.38%
Gemmatimonadetes	1.47%	0.66%	0.87%	1.50%	0.57%	1.02%	8.93%	4.08%	0.78%	0.18%	0.40%	0.11%	0.07%	0.02%
Firmicutes	1.45%	5.17%	1.71%	0.20%	3.60%	0.67%	1.31%	0.26%	0.17%	2.45%	0.31%	1.18%	0.67%	1.11%
Verrucomicrobia	1.25%	2.79%	1.19%	0.60%	1.87%	0.80%	0.78%	0.76%	2.72%	0.33%	0.65%	1.36%	1.11%	1.32%
Thaumarchaeota	1.11%	0.13%	0.17%	1.84%	0.61%	0.30%	0.23%	0.13%	1.26%	0.93%	1.24%	4.71%	0.87%	1.96%
Candidatus_Saccharibacteria	0.73%	0.72%	1.79%	0.18%	0.24%	1.13%	0.37%	2.36%	0.38%	0.20%	0.81%	0.24%	0.33%	0.73%
candidate_division_WPS-2	0.68%	0.05%	2.44%	0.02%	0.00%	0.02%	1.05%	5.20%	0.06%	0.00%	0.00%	0.00%	0.00%	0.00%
Nitrospirae	0.59%	0.58%	0.11%	1.69%	0.56%	1.44%	0.52%	0.22%	0.25%	0.56%	0.34%	0.46%	0.59%	0.29%
Chloroflexi	0.48%	0.19%	0.18%	0.66%	0.49%	1.21%	0.25%	0.37%	0.15%	0.17%	0.11%	0.69%	0.76%	1.07%
Latescibacteria	0.38%	0.06%	0.08%	0.62%	0.32%	0.29%	0.01%	0.00%	0.09%	0.14%	0.14%	1.19%	0.70%	1.27%
Armatimonadetes	0.23%	0.04%	0.06%	0.12%	0.42%	0.04%	0.14%	0.97%	0.24%	0.04%	0.27%	0.33%	0.16%	0.11%
Chlamydiae	0.09%	0.01%	0.61%	0.02%	0.00%	0.01%	0.01%	0.48%	0.01%	0.00%	0.00%	0.01%	0.00%	0.00%
Euryarchaeota	0.07%	0.03%	0.01%	0.08%	0.04%	0.08%	0.00%	0.01%	0.48%	0.06%	0.02%	0.03%	0.03%	0.04%
candidate_division_WPS-1	0.06%	0.00%	0.39%	0.00%	0.00%	0.01%	0.01%	0.21%	0.04%	0.00%	0.02%	0.05%	0.04%	0.06%
Planctomycetes	0.05%	0.06%	0.08%	0.00%	0.36%	0.01%	0.01%	0.04%	0.01%	0.00%	0.01%	0.02%	0.03%	0.01%
Parcubacteria	0.03%	0.00%	0.08%	0.20%	0.04%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Deinococcus-Thermus	0.01%	0.00%	0.00%	0.02%	0.12%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
BRC1	0.01%	0.00%	0.02%	0.02%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.02%	0.02%	0.04%
Unclassified	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.06%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
Ignavibacteriae	0.00%	0.03%	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%

(Table S3) contd.....

	Average Distribution	HN-S1	HN-S2	HN-S8	HN-S9	HN-S10	HN-S11	HN-S12	HN-S13	HN-S14	HN-S15	HN-S18	HN-S19	HN-S21
SR1	0.00%	0.00%	0.00%	0.02%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.00%
Microgenomates	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Spirochaetes	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Hydrogenedentes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.01%	0.00%
Synergistetes	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Diapherotrites	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Pacearchaeota	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%

Table S4. The dominant genera in the soil samples.

	Average Distribution	HN-S1	HN-S2	HN-S8	HN-S9	HN-S10	HN-S11	HN-S12	HN-S13	HN-S14	HN-S15	HN-S18	HN-S19	HN-S21
Above_genus	56.59%	47.25%	73.22%	66.30%	52.87%	55.81%	41.95%	53.92%	53.84%	51.89%	56.22%	58.51%	60.69%	63.26%
Gaiella	3.66%	2.49%	1.33%	0.26%	5.68%	1.32%	10.31%	1.95%	4.13%	9.49%	7.04%	1.43%	1.13%	1.04%
Sphingomonas	3.60%	5.56%	2.31%	1.07%	1.65%	6.51%	5.13%	15.15%	1.07%	0.64%	1.41%	2.51%	2.28%	1.47%
Gp6	3.52%	1.23%	1.24%	1.53%	2.40%	2.12%	0.13%	0.23%	8.27%	2.77%	5.02%	5.62%	7.67%	7.55%
Nocardioides	2.10%	3.55%	1.13%	0.62%	5.01%	1.51%	0.27%	0.52%	4.37%	4.17%	4.23%	0.78%	0.74%	0.35%
Arthrobacter	2.00%	0.93%	0.16%	5.68%	2.35%	1.55%	0.73%	0.30%	3.06%	6.88%	1.89%	1.09%	0.97%	0.41%
Gp4	1.81%	0.33%	0.21%	0.07%	0.32%	0.39%	0.03%	0.06%	3.75%	1.47%	3.15%	4.93%	4.51%	4.35%
Gp16	1.65%	1.89%	0.38%	0.27%	3.64%	1.33%	0.21%	0.11%	3.15%	1.29%	1.52%	2.02%	2.43%	3.27%
Gemmatimonas	1.47%	0.66%	0.87%	1.50%	0.57%	1.02%	8.93%	4.08%	0.78%	0.18%	0.40%	0.11%	0.07%	0.02%
Rhodanobacter	1.31%	3.47%	0.45%	0.18%	0.04%	0.69%	9.58%	2.36%	0.03%	0.04%	0.16%	0.01%	0.01%	0.01%
Nitrososphaera	0.95%	0.13%	0.16%	0.09%	0.61%	0.28%	0.21%	0.12%	1.26%	0.90%	1.18%	4.63%	0.82%	1.91%
Gp3	0.90%	0.88%	2.65%	0.75%	0.42%	0.54%	1.68%	1.83%	0.48%	0.39%	0.80%	0.42%	0.52%	0.29%
Pseudomonas	0.80%	1.71%	0.15%	0.61%	2.74%	0.58%	2.24%	0.12%	0.03%	0.02%	0.11%	0.42%	1.33%	0.36%
Streptomyces	0.69%	0.33%	0.28%	0.12%	0.82%	0.37%	0.14%	0.81%	1.60%	2.63%	1.22%	0.23%	0.30%	0.20%
Gp7	0.68%	0.17%	0.02%	2.00%	0.73%	0.49%	0.74%	0.04%	1.14%	0.63%	2.01%	0.34%	0.32%	0.21%
Gp1	0.60%	0.25%	0.23%	0.06%	0.43%	0.17%	2.66%	3.66%	0.10%	0.02%	0.04%	0.02%	0.05%	0.08%
Nitrospira	0.59%	0.58%	0.11%	1.69%	0.56%	1.44%	0.52%	0.22%	0.25%	0.56%	0.34%	0.46%	0.59%	0.29%
Subdivision3_genera incertae_sedis	0.56%	1.32%	0.42%	0.30%	1.07%	0.18%	0.50%	0.40%	1.14%	0.11%	0.19%	0.62%	0.38%	0.66%
Clostridium_sensu stricto	0.55%	4.14%	1.27%	0.02%	1.26%	0.03%	0.14%	0.06%	0.05%	0.02%	0.01%	0.06%	0.00%	0.05%
Ensifer	0.50%	0.44%	0.14%	0.10%	1.46%	1.35%	0.07%	0.06%	0.28%	0.61%	0.33%	0.52%	0.73%	0.34%
Other identified genera	15.47%	22.69%	13.27%	16.79%	15.36%	22.32%	13.83%	14.01%	11.22%	15.32%	12.73%	15.28%	14.45%	13.89%