

Dynamics of Bacterial Communities in a 30-year Fertilized Paddy Field Under Different Organic-Inorganic Fertilization Strategies

Yadong Yang, Peixin Wang, and Zhaohai Zeng *

College of Agronomy and Biotechnology, China Agricultural University/Key Laboratory of Farming System, Ministry of Agriculture of China, Yuanmingyuan West Road 2, Beijing 100193, China; yadong_tracy@cau.edu.cn (Y.Y.); wangpeixin@cau.edu.cn (P.W.)

* Correspondence: zengzhaohai@cau.edu.cn; Tel.: +86-10-6273-1211; Fax: +86-10-6273-2441.

1 **Table S1. Sequencing results and alpha diversity of the bacterial communities in different**
2 **fertilization treatments.**

Treatment	Reads	OTU	ACE index	Chao1 index	Shannon index	inverse Simpson index	Coverage
CK	18728	2331±57a	2760±57ab	2770±77a	6.88±0.04a	450.48±25.30a	0.9691±0.0007a
CF	18728	2284±48a	2743±60ab	2734±59a	6.75±0.05a	330.77±45.25a	0.9685±0.0008a
CFM1	18728	2365±56a	2838±64a	2825±65a	6.87±0.08a	434.34±65.66a	0.9674±0.0007a
CFM2	18728	2125±109a	2603±76b	2614±73a	6.67±0.13a	344.69±63.83a	0.9692±0.0006a

3 Values are mean±SE ($n = 3$). Different letters in the same column indicate significant differences at $p <$
4 0.05. CK, without fertilizer; CF, fertilizers NPK; CFM1, fertilizers NPK plus 30% organic manure; and
5 CFM2, fertilizers NPK plus 60% organic manure.

6 **Table S2. Relative abundance of bacterial phylum in different fertilization treatments**
7 **(mean proportion >1%).**

Phylum	CK (%)	CF (%)	CFM1 (%)	CFM2 (%)
Proteobacteria	27.95±0.90	32.19±5.07	31.41±3.47	26.32±1.89
Chloroflexi	21.17±1.19	18.58±2.51	17.68±2.42	20.74±1.03
Acidobacteria	12.69±0.76	12.17±3.20	14.25±3.26	18.66±2.14
Nitrospirae	11.23±0.29a	9.18±0.60ab	10.78±1.17a	7.35±0.59b
Gemmatimonadetes	3.31±0.10b	5.01±0.58ab	5.13±0.63ab	5.86±0.83a
Actinobacteria	3.06±0.23	5.12±1.00	3.91±0.26	3.55±0.61
Latescibacteria	3.70±0.48	2.93±0.86	2.56±0.41	4.33±0.38
Firmicutes	2.67±0.21	3.58±0.72	2.78±0.76	2.26±0.49
Bacteroidetes	1.41±0.12	1.66±0.16	1.74±0.09	1.25±0.39
Bacteria_unclassified	2.43±0.06a	1.22±0.19b	1.04±0.12b	1.36±0.18b
Planctomycetes	1.63±0.20	1.23±0.46	1.15±0.22	1.29±0.10
Ignavibacteriae	1.06±0.14	1.23±0.09	1.70±0.39	1.23±0.33
Parcubacteria	1.24±0.37	1.08±0.06	1.12±0.10	0.69±0.14

8 Values are mean±SE (*n* = 3). Different letters in the same line indicate significant differences at *p* < 0.05.
9 CK, without fertilizer; CF, fertilizers NPK; CFM1, fertilizers NPK plus 30% organic manure; and CFM2,
10 fertilizers NPK plus 60% organic manure.

11 **Table S3. Pearson's correlation coefficients between soil properties and relative abundance**
12 **of dominant order (mean proportion >1%) of the bacterial communities.**

Item	pH	NH ₄ ⁺ -N	NO ₃ ⁻ -N	TN	SOC	C/N ratio
Anaerolineales	0.082	0.098	-0.074	0.118	0.101	-0.155
Acidobacteria_norank	-0.245	-0.356	0.402	0.479	0.521	0.311
Nitrospira_norank	0.489	0.524	-0.437	-0.45	-0.491	-0.323
Myxococcales	-0.208	-0.136	0.114	-0.032	-0.055	-0.049
Gemmatimonadales	-0.664*	-0.482	0.690*	0.638*	0.599*	0.117
Nitrosomonadales	-0.372	0.010	0.452	0.432	0.374	-0.120
Latescibacteria_norank	0.163	-0.092	0.015	0.162	0.196	0.166
43F-1404R	0.061	-0.113	-0.084	-0.313	-0.273	0.165
Rhizobiales	-0.291	-0.270	0.253	0.167	0.198	0.327
Bacillales	0.159	0.104	-0.099	-0.318	-0.373	-0.350
SBR2076_norank	0.740**	0.292	-0.752**	-0.847**	-0.854**	-0.374
Desulfurellales	0.039	0.113	-0.102	-0.005	0.016	0.167
Bacteria_unclassified	0.704*	0.614*	-0.765**	-0.572	-0.560	-0.215
Solibacterales	-0.757**	-0.447	0.615*	0.620*	0.621*	0.308
Rhodospirillales	-0.265	0.049	-0.064	-0.001	0.049	0.318
Chloroflexales	-0.149	-0.321	-0.009	-0.199	-0.167	0.150
Ignavibacteriales	-0.315	0.170	0.330	0.305	0.254	-0.135
KD4-96_norank	0.311	-0.188	-0.183	-0.004	0.036	0.227
Xanthomonadales	-0.235	-0.130	0.089	-0.049	-0.027	0.178
Desulfuromonadales	0.364	0.715**	-0.600*	-0.647*	-0.670*	-0.397
Burkholderiales	-0.103	0.090	-0.064	-0.126	-0.133	-0.014
Blastocatellales	0.028	-0.135	0.076	0.079	0.063	-0.181
NB1-j	-0.171	0.014	0.215	0.539	0.507	0.109
Syntrophobacterales	0.529	0.503	-0.651*	-0.757**	-0.770**	-0.289
Others	0.283	0.309	-0.454	-0.559	-0.555	-0.138

13 * $p < 0.05$; ** $p < 0.01$. Significant correlations ($p < 0.05$) are highlighted in bold.

14 **Table S4. Significance of environmental variables in explaining the differences of bacterial**
15 **community structures obtained from the RDA results.**

Factor	RDA1	RDA2	r^2	Pr(>r)
pH	-0.73334	0.67986	0.6196	0.006**
NO ₃ ⁻ -N	-0.53154	0.84703	0.7329	0.006**
NH ₄ ⁺ -N	0.75086	-0.66046	0.3875	0.102
TN	0.91637	-0.40032	0.8760	0.001**
SOC	0.92242	-0.38619	0.8816	0.001**
C/N ratio	0.86836	-0.49594	0.1370	0.510

16 **** $p < 0.01$. Significant correlations ($p < 0.01$) are highlighted in bold.**

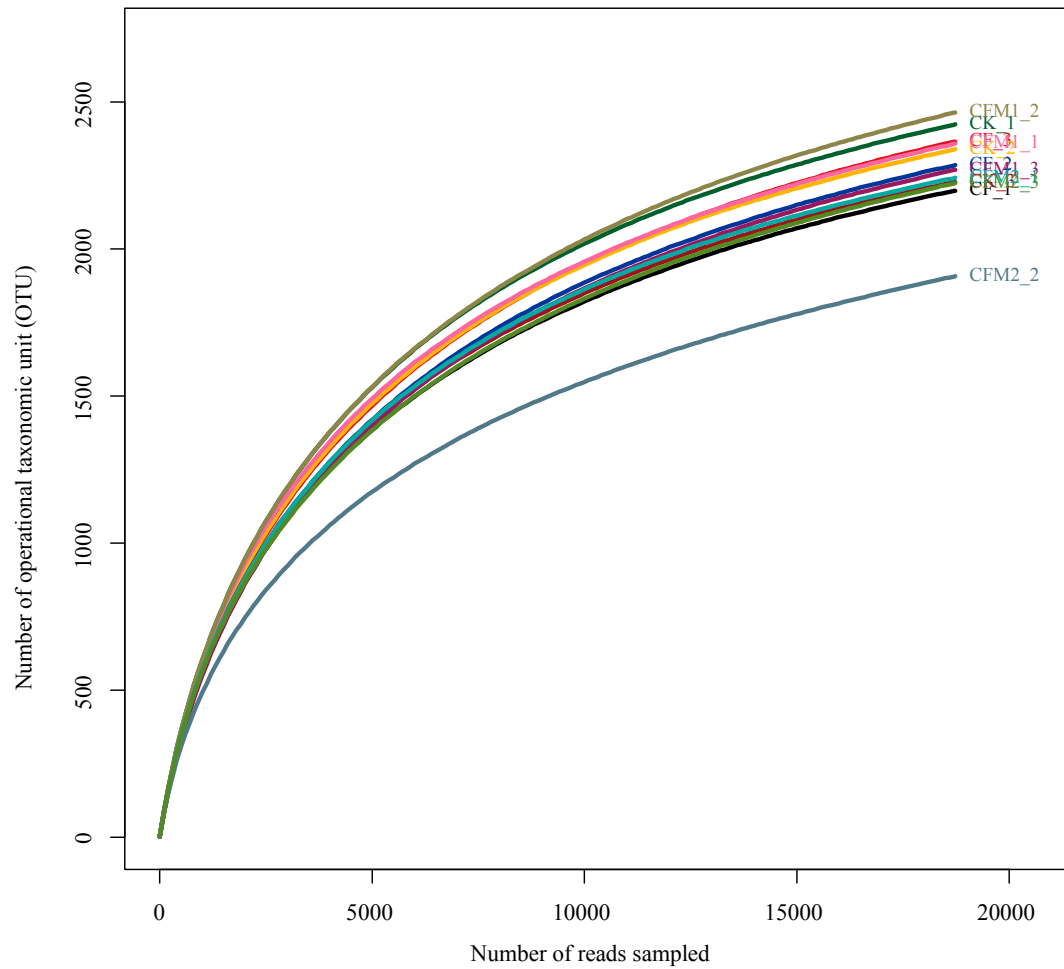


Figure S1. Rarefaction curve of the bacterial communities at 97% similarity.

CK, without fertilizer; CF, fertilizers NPK; CFM1, fertilizers NPK plus 30% organic manure; and CFM2, fertilizers NPK plus 60% organic manure.

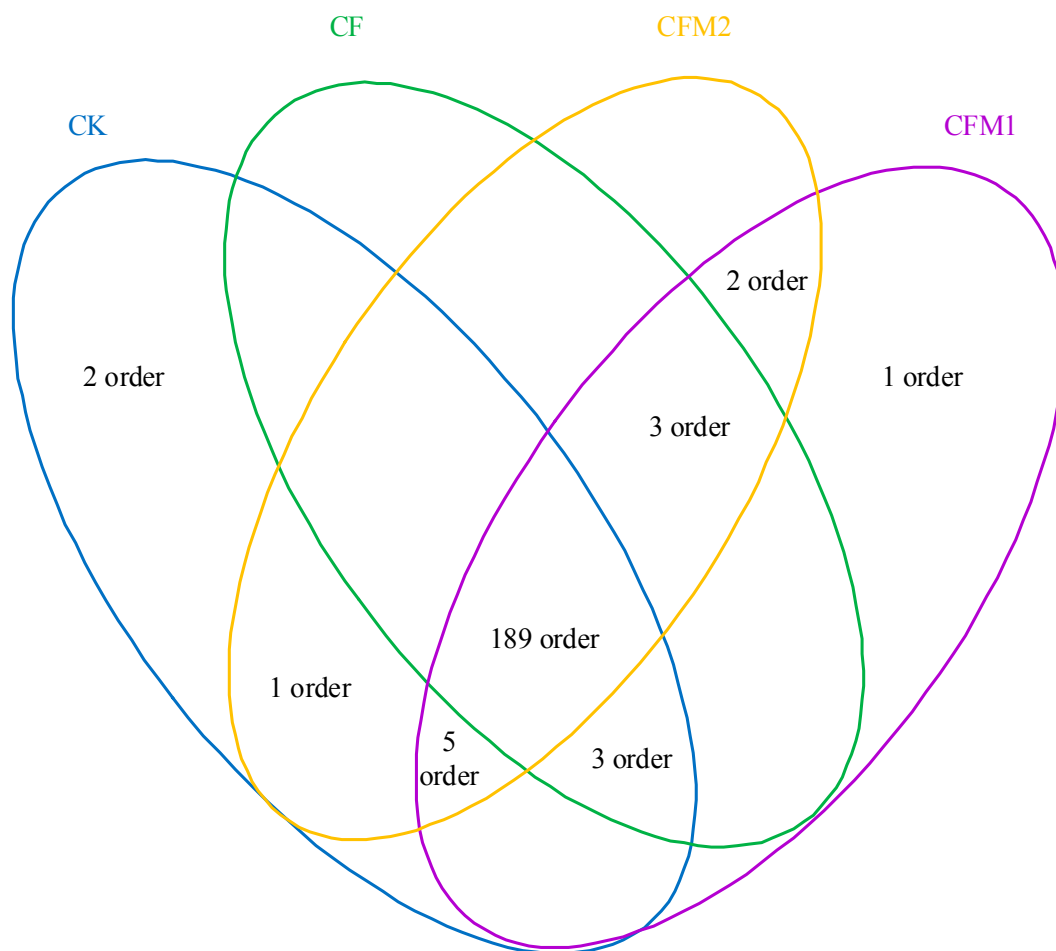


Figure S2. Venn drawing showing the shared bacterial community order in the soils under different fertilization regimes.

Values are total of three replicates. CK, without fertilizer; CF, fertilizers NPK; CFM1, fertilizers NPK plus 30% organic manure; and CFM2, fertilizers NPK plus 60% organic manure.