

# Supplementary Materials: The Impacts of Different Green Manure on Soil Microbial Communities and Crop Health

Hongwu Yang, Jiaojiao Niu, Jiemeng Tao, Yabing Gu, Chao Zhang, Siyuan She, Wu Chen, Hongqi Yang and Huaqun Yin

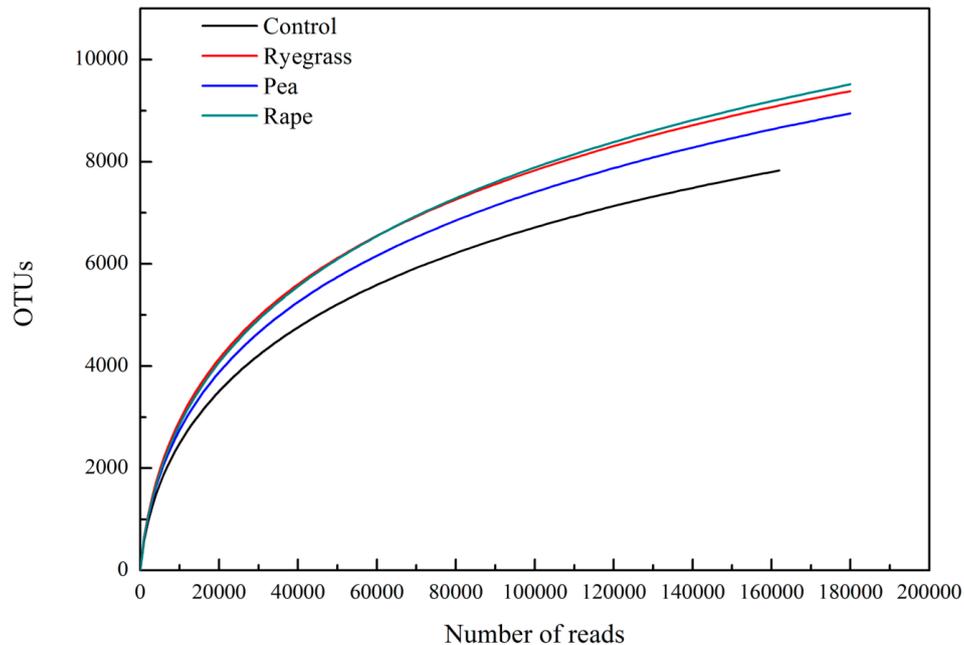


Figure S1. Rarefaction curves of 16r RNA gene sequencing data

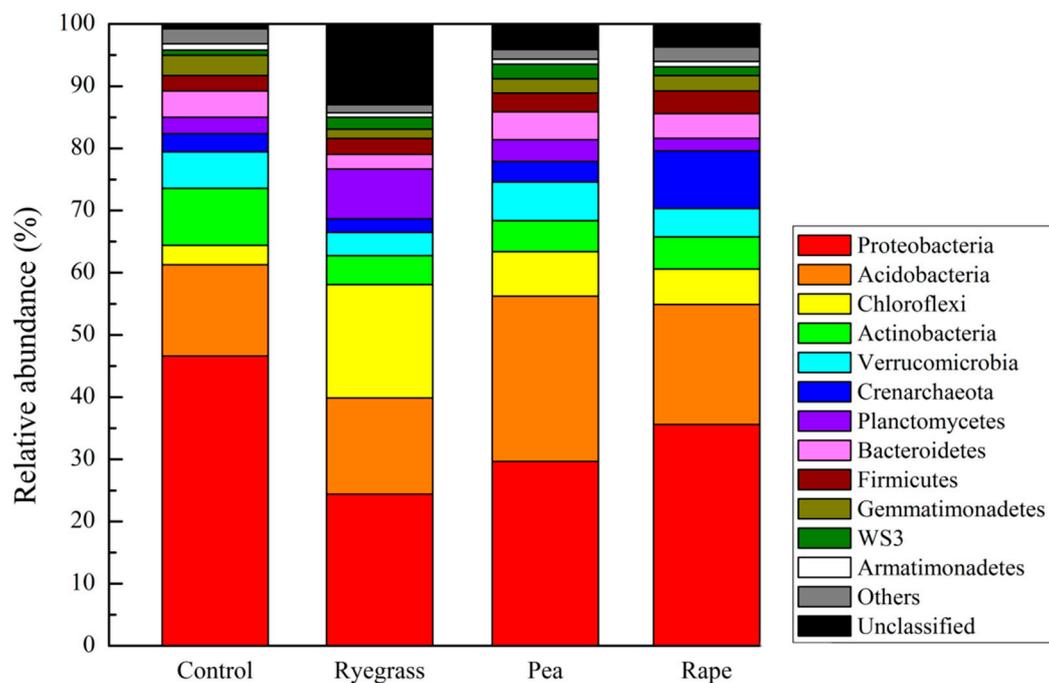


Figure S2. Composition and structure of soil microbial communities in each group

Table S1. Dissimilarity test of 16S rRNA gene sequencing data among four groups. Only p values are showed.

	Ryegrass	Pea	Rape
Pea	< 0.001		
Rape	< 0.001	< 0.01	
Control	< 0.001	< 0.001	< 0.01

Table S2(a). Mantel test of sequencing data with environmental attributes at the phylum level.

	water	pH	Ca	Fe	Co	Zn	N	C
Acidobacteria	0.298	<b>0.006</b>	<b>0.001</b>	<b>0.013</b>	<b>0.064</b>	<b>0.02</b>	0.549	0.99
Actinobacteria	0.131	0.319	<b>0.006</b>	0.463	0.835	0.56	<b>0.06</b>	0.394
Chloroflexi	0.251	0.654	0.335	0.121	0.29	0.101	<b>0.004</b>	0.228
Crenarchaeota	0.255	<b>0.023</b>	0.275	<b>0.029</b>	<b>0.039</b>	<b>0.03</b>	0.875	0.852
Cyanobacteria	0.215	0.971	<b>0.077</b>	0.606	0.784	0.641	0.802	<b>0.018</b>
Euryarchaeota	0.152	0.45	0.488	0.654	0.592	0.514	<b>0.098</b>	0.243
Firmicutes	0.128	0.217	0.209	<b>0.095</b>	0.266	0.187	0.535	0.824
Gemmatimonadetes	0.345	<b>0.017</b>	<b>0.002</b>	<b>0.017</b>	<b>0.085</b>	<b>0.023</b>	0.489	0.706
Nitrospira	<b>0.089</b>	<b>0.085</b>	0.594	0.476	0.615	0.712	0.275	0.597
Planctomycetes	0.192	0.54	0.222	0.181	0.167	0.156	0.244	0.372
Proteobacteria	0.171	0.194	<b>0.033</b>	0.24	0.386	0.224	0.159	0.697
WS3	<b>0.099</b>	0.242	0.253	0.33	0.119	0.738	0.403	0.952

Table S2(b). Mantel test of sequencing data with environmental attributes at the genus level.

	water	pH	Ca	Fe	Co	Zn	N
Dokdonella	0.247	0.243	<b>0.05</b>	<b>0.075</b>	0.25	<b>0.083</b>	0.479
Gemmatimonas	0.359	<b>0.016</b>	<b>0.005</b>	<b>0.016</b>	<b>0.086</b>	<b>0.022</b>	0.437
Gp16	0.243	0.237	0.303	0.127	<b>0.058</b>	<b>0.042</b>	0.649
Gp4	0.406	<b>0.072</b>	<b>0.009</b>	0.474	0.198	0.343	0.814
Gp6	0.382	<b>0.001</b>	<b>0.002</b>	<b>0.044</b>	0.122	<b>0.098</b>	0.788
Rhodanobacter	0.518	0.252	<b>0.022</b>	0.335	0.7	0.283	<b>0.083</b>
Spartobacteria_genera_incertae_sedis	0.736	0.219	0.567	<b>0.038</b>	0.491	<b>0.066</b>	0.821
Sphingomonas	0.597	0.555	0.203	0.442	0.887	0.207	<b>0.036</b>
Sphingosinicella	0.441	0.132	<b>0.003</b>	0.364	0.683	0.286	<b>0.031</b>
Subdivision3_genera_incertae_sedis	0.658	0.471	<b>0.081</b>	0.808	0.509	0.715	<b>0.081</b>
WS3_genera_incertae_sedis	<b>0.09</b>	0.264	0.252	0.345	0.136	0.754	0.404

\*Significant impacts ( $p < 0.05$ ) are indicated in bold.

Table S3(a). Pearson correlations between abundances of microbial phyla and tobacco disease rate, soil Ca, total organic N and C content, respectively.

Phylum	Tobacco disease rate		Ca		Total N		Total C	
	r	p	r	p	r	p	r	p
Proteobacteria	<b>0.703</b>	<b>0.000</b>	<b>-0.501</b>	<b>0.002</b>	<b>-0.631</b>	<b>0</b>	-0.089	0.613
Acidobacteria	<b>-0.351</b>	<b>0.036</b>	<b>0.407</b>	<b>0.015</b>	0.068	0.699	0.001	0.998
Chloroflexi	<b>-0.598</b>	<b>0.000</b>	0.272	0.115	<b>0.712</b>	<b>0</b>	0.15	0.391
Actinobacteria	<b>0.690</b>	<b>0.000</b>	<b>-0.499</b>	<b>0.002</b>	<b>-0.467</b>	<b>0.005</b>	-0.001	0.994
Verrucomicrobia	0.261	0.123	<b>-0.404</b>	<b>0.016</b>	-0.324	0.058	-0.057	0.745
Crenarchaeota	-0.045	0.795	0.179	0.304	-0.176	0.312	-0.069	0.695
Planctomycetes	<b>-0.473</b>	<b>0.004</b>	0.251	0.145	<b>0.585</b>	<b>0</b>	-0.027	0.88
Bacteroidetes	0.229	0.179	-0.176	0.311	-0.28	0.103	0.118	0.5
Firmicutes	-0.174	0.311	0.054	0.756	-0.03	0.862	-0.076	0.664
Gemmatimonadetes	<b>0.615</b>	<b>0.000</b>	-0.246	0.155	<b>-0.499</b>	<b>0.002</b>	-0.027	0.876
WS3	<b>-0.471</b>	<b>0.004</b>	0.299	0.081	<b>0.374</b>	<b>0.027</b>	0.023	0.897
Armatimonadetes	0.304	0.072	<b>-0.453</b>	<b>0.006</b>	-0.275	0.11	-0.062	0.723
Nitrospira	<b>0.373</b>	<b>0.025</b>	-0.182	0.296	<b>-0.57</b>	<b>0</b>	-0.145	0.405

Table S3(b). Pearson correlations between abundances of major microbial genera and tobacco disease rate, soil Ca, total organic N and C content, respectively.

Genus	Tobacco disease rate		Ca		Total N		Total C	
	r	p	r	p	r	p	r	p
Gp6	<b>-0.486</b>	<b>0.003</b>	<b>0.572</b>	<b>0</b>	0.166	0.341	-0.007	0.967
Gp4	<b>-0.498</b>	<b>0.002</b>	<b>0.462</b>	<b>0.005</b>	0.257	0.136	0.096	0.584
Spartobacteria_genera_incertae_sedis	-0.063	0.714	-0.191	0.273	0.007	0.966	0.057	0.747
Gp16	<b>-0.505</b>	<b>0.002</b>	<b>0.403</b>	<b>0.016</b>	0.233	0.179	0.052	0.765
Gemmatimonas	<b>0.615</b>	<b>0.000</b>	-0.246	0.155	<b>-0.499</b>	<b>0.002</b>	-0.027	0.876
Sphingomonas	-0.054	0.756	0.155	0.374	-0.136	0.436	0.159	0.36
Sphingosinicella	<b>0.674</b>	<b>0.000</b>	<b>-0.49</b>	<b>0.003</b>	<b>-0.5</b>	<b>0.002</b>	0.083	0.635
WS3_genera_incertae_sedis	<b>-0.471</b>	<b>0.004</b>	0.299	0.081	<b>0.374</b>	<b>0.027</b>	0.023	0.897
Dokdonella	<b>0.521</b>	<b>0.001</b>	<b>-0.517</b>	<b>0.001</b>	<b>-0.395</b>	<b>0.019</b>	-0.112	0.521
Subdivision3_genera_incertae_sedis	<b>0.440</b>	<b>0.007</b>	<b>-0.389</b>	<b>0.021</b>	<b>-0.455</b>	<b>0.006</b>	-0.131	0.454
Rhodanobacter	<b>0.602</b>	<b>0.000</b>	<b>-0.428</b>	<b>0.01</b>	<b>-0.462</b>	<b>0.005</b>	-0.202	0.246
Gp7	-0.071	0.680	-0.022	0.898	0.042	0.813	0.067	0.7
Gp1	<b>0.750</b>	<b>0.000</b>	<b>-0.668</b>	<b>0</b>	<b>-0.536</b>	<b>0.001</b>	-0.106	0.543
Pasteuria	<b>-0.748</b>	<b>0.000</b>	<b>0.564</b>	<b>0</b>	<b>0.631</b>	<b>0</b>	0.078	0.654
Xanthobacteraceae	<b>0.644</b>	<b>0.000</b>	<b>-0.647</b>	<b>0</b>	<b>-0.549</b>	<b>0.001</b>	-0.124	0.477
Singulisphaera	-0.251	0.139	0.105	0.546	<b>0.376</b>	<b>0.026</b>	-0.061	0.727
Gp3	<b>0.852</b>	<b>0.000</b>	<b>-0.627</b>	<b>0</b>	<b>-0.711</b>	<b>0</b>	-0.183	0.294
Zavarzinella	<b>-0.572</b>	<b>0.000</b>	<b>0.354</b>	<b>0.037</b>	<b>0.651</b>	<b>0</b>	-0.003	0.988
Gemmata	<b>-0.541</b>	<b>0.001</b>	0.333	0.051	<b>0.653</b>	<b>0</b>	0.039	0.825
Bellilinea	<b>-0.644</b>	<b>0.000</b>	0.304	0.076	<b>0.725</b>	<b>0</b>	0.188	0.281

\*Significant correlations ( $p < 0.05$ ) are indicated in bold.