

The impacts of a biochar application on selected soil properties and bacterial communities in an Albic Clayic Luvisol

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Electronic Supplementary Material (ESM)

Table S1. The correlation and significance between the bacterial communities and the soil properties using the Mantel test

Soil properties	Surface (0–10 cm)		Second depth (10–20 cm)		Total	
	<i>r</i>	<i>P</i>	<i>r</i>	<i>P</i>	<i>r</i>	<i>P</i>
TC	0.387	0.004	0.650	0.001	0.519	0.002
TN	0.059	0.334	0.043	0.235	0.051	0.185
TP	0.025	0.331	0.262	0.058	0.174	0.217
TK	0.153	0.165	0.169	0.133	0.161	0.149
AN	0.251	0.067	0.277	0.035	0.264	0.045
AP	0.068	0.348	0.168	0.153	0.148	0.181
AK	0.238	0.082	0.351	0.051	0.294	0.055
Moisture	0.416	0.010	0.318	0.023	0.366	0.014
BD	0.452	0.003	0.626	0.001	0.539	0.001
pH	0.512	0.001	0.538	0.001	0.525	0.001

Total – the comprehensive data for the correlation and significance analysis without considering the soil depth; TC – the soil's total carbon; TN – the total nitrogen; TP – the total phosphorus; TK – the total potassium; AN – the available nitrogen; AP – the available phosphorus; AK – the available potassium; BD – the bulk density; *r* – a simple correlation coefficient.

2 Table S2. The relative abundance (%) of certain bacterial classes in soil samples

Class	B0-10	B1-10	B2-10	B3-10	B0-20	B1-20	B2-20	B3-20	Phylum
<i>Betaproteobacteria</i>	12.29 ± 1.51	10.79 ± 1.30	12.08 ± 0.71	11.4 ± 1.31	11.07 ± 0.50	9.98 ± 1.44	13.84 ± 4.87	11.93 ± 1.74	<i>Proteobacteria</i>
<i>Alphaproteobacteria</i>	11.23 ± 0.36	11.45 ± 0.80	9.96 ± 0.36	10.81 ± 0.87	10.94 ± 1.10	10.26 ± 0.60	10.42 ± 1.54	8.70 ± 1.30	<i>Proteobacteria</i>
<i>Actinobacteria</i>	8.43 ± 0.33	7.91 ± 0.53	8.57 ± 0.52	8.02 ± 0.90	7.49 ± 0.14	7.38 ± 1.03	8.98 ± 0.21	9.24 ± 1.25	<i>Actinobacteria</i>
<i>Sphingobacteriia</i>	7.59 ± 0.94	6.83 ± 1.22	7.60 ± 1.36	8.00 ± 1.01	8.33 ± 0.54	6.91 ± 1.28	8.30 ± 3.10	8.82 ± 5.30	<i>Bacteroidetes</i>
<i>Gammaproteobacteria</i>	5.45 ± 1.13	5.14 ± 1.31	5.68 ± 1.86	7.60 ± 2.94	5.91 ± 0.65	4.88 ± 0.61	6.63 ± 2.15	9.65 ± 8.48	<i>Proteobacteria</i>
<i>Gemmatimonadetes</i>	6.38 ± 0.10	5.64 ± 1.20	6.38 ± 0.57	5.61 ± 0.96	5.56 ± 0.24	5.77 ± 1.31	5.80 ± 0.66	4.86 ± 1.46	<i>Gemmatimonadetes</i>
<i>Acidobacteria_Gp4</i>	4.95 ± 0.55	5.77 ± 0.75	6.18 ± 0.92	5.16 ± 0.89	6.00 ± 0.83	7.28 ± 1.21	5.01 ± 0.49	4.21 ± 0.96	<i>Acidobacteria</i>
<i>Acidobacteria_Gp1</i>	3.82 ± 0.96	5.33 ± 3.09	5.38 ± 1.31	6.68 ± 3.40	4.26 ± 0.57	6.52 ± 4.28	5.30 ± 2.17	5.36 ± 2.09	<i>Acidobacteria</i>
<i>Deltaproteobacteria</i>	4.58 ± 0.58	5.42 ± 1.88	4.14 ± 0.70	3.56 ± 0.81	5.16 ± 0.68	4.74 ± 0.36	4.28 ± 1.87	4.29 ± 2.52	<i>Proteobacteria</i>
<i>Acidobacteria_Gp3</i>	2.65 ± 0.32	3.40 ± 0.76	3.06 ± 0.43	3.43 ± 0.68	2.87 ± 0.16	3.70 ± 0.69	2.62 ± 0.38	2.41 ± 0.34	<i>Acidobacteria</i>
<i>Planctomycetia</i>	2.01 ± 0.08	2.28 ± 0.15	1.81 ± 0.23	1.86 ± 0.35	2.08 ± 0.21	2.03 ± 0.27	1.82 ± 0.79	2.01 ± 0.83	<i>Planctomycetes</i>
<i>Acidobacteria_Gp6</i>	2.16 ± 0.36	2.24 ± 0.66	1.96 ± 0.31	1.60 ± 0.54	2.17 ± 0.27	2.01 ± 0.47	1.88 ± 1.01	1.58 ± 0.80	<i>Acidobacteria</i>
<i>Nitrospira</i>	1.84 ± 0.56	1.56 ± 0.24	1.91 ± 0.57	2.08 ± 0.32	1.87 ± 0.32	1.76 ± 0.31	1.64 ± 0.83	1.90 ± 1.03	<i>Nitrospirae</i>
<i>Anaerolineae</i>	1.12 ± 0.18	1.38 ± 0.25	1.25 ± 0.30	1.22 ± 0.53	1.37 ± 0.25	1.61 ± 0.26	1.16 ± 0.61	1.15 ± 0.55	<i>Chloroflexi</i>
<i>Acidobacteria_Gp7</i>	1.02 ± 0.34	1.09 ± 0.07	1.46 ± 0.59	0.99 ± 0.4	0.98 ± 0.20	1.14 ± 0.06	1.17 ± 0.65	1.34 ± 1.17	<i>Acidobacteria</i>
<i>Bacilli</i>	0.68 ± 0.11	0.97 ± 0.29	0.82 ± 0.26	1.14 ± 0.23	0.86 ± 0.24	1.16 ± 0.37	0.78 ± 0.20	1.29 ± 0.46	<i>Firmicutes</i>
<i>Cytophagia</i>	1.35 ± 0.70	1.46 ± 1.54	0.56 ± 0.32	0.45 ± 0.10	1.24 ± 0.59	0.99 ± 0.62	0.60 ± 0.50	0.54 ± 0.58	<i>Bacteroidetes</i>
<i>Chloroplast</i>	0.51 ± 0.25	0.41 ± 0.19	0.49 ± 0.06	1.34 ± 0.59	0.48 ± 0.26	0.31 ± 0.08	0.97 ± 0.84	1.40 ± 1.27	<i>Chloroplast</i>
<i>Ktedonobacteria</i>	0.40 ± 0.07	0.46 ± 0.30	0.73 ± 0.60	0.91 ± 0.69	0.43 ± 0.19	0.64 ± 0.56	0.87 ± 0.86	0.92 ± 0.58	<i>Chloroflexi</i>
<i>Chloroflexia</i>	0.59 ± 0.09	0.57 ± 0.07	0.61 ± 0.10	0.50 ± 0.13	0.58 ± 0.05	0.59 ± 0.15	0.50 ± 0.23	0.54 ± 0.28	<i>Chloroflexi</i>
<i>Verrucomicrobiae</i>	0.33 ± 0.11	0.39 ± 0.09	0.61 ± 0.53	0.27 ± 0.19	0.49 ± 0.19	0.48 ± 0.22	0.57 ± 0.47	0.90 ± 1.17	<i>Verrucomicrobia</i>
<i>Acidobacteria_Gp16</i>	0.50 ± 0.08	0.42 ± 0.10	0.46 ± 0.04	0.42 ± 0.10	0.5 ± 0.05	0.42 ± 0.09	0.49 ± 0.14	0.45 ± 0.17	<i>Acidobacteria</i>
<i>Flavobacteriia</i>	1.16 ± 1.31	0.17 ± 0.08	0.22 ± 0.08	0.25 ± 0.05	0.82 ± 0.17	0.20 ± 0.12	0.27 ± 0.20	0.17 ± 0.07	<i>Bacteroidetes</i>
<i>Thermomicrobia</i>	0.43 ± 0.04	0.41 ± 0.05	0.38 ± 0.05	0.47 ± 0.05	0.36 ± 0.05	0.40 ± 0.14	0.37 ± 0.09	0.43 ± 0.15	<i>Chloroflexi</i>
<i>Spartobacteria</i>	0.37 ± 0.08	0.42 ± 0.18	0.49 ± 0.08	0.33 ± 0.06	0.33 ± 0.08	0.44 ± 0.10	0.35 ± 0.18	0.26 ± 0.14	<i>Verrucomicrobia</i>
<i>Opitutae</i>	0.43 ± 0.02	0.42 ± 0.21	0.30 ± 0.10	0.32 ± 0.04	0.43 ± 0.08	0.39 ± 0.11	0.35 ± 0.16	0.31 ± 0.13	<i>Verrucomicrobia</i>
<i>Chthonomonadetes</i>	0.32 ± 0.04	0.36 ± 0.03	0.39 ± 0.05	0.32 ± 0.11	0.39 ± 0.06	0.41 ± 0.04	0.26 ± 0.16	0.23 ± 0.13	<i>Armatimonadetes</i>
<i>Cyanobacteria</i>	0.67 ± 1.09	0.14 ± 0.03	0.18 ± 0.13	0.54 ± 0.46	0.08 ± 0.08	0.18 ± 0.13	0.13 ± 0.11	0.40 ± 0.58	<i>Cyanobacteria</i>
<i>Subdivision3</i>	0.28 ± 0.07	0.38 ± 0.13	0.36 ± 0.11	0.19 ± 0.06	0.28 ± 0.03	0.39 ± 0.05	0.22 ± 0.09	0.16 ± 0.10	<i>Verrucomicrobia</i>
<i>Acidobacteria_Gp10</i>	0.18 ± 0.09	0.20 ± 0.10	0.23 ± 0.10	0.17 ± 0.06	0.22 ± 0.07	0.19 ± 0.10	0.26 ± 0.14	0.36 ± 0.37	<i>Acidobacteria</i>
<i>No_Rank</i>	15.15 ± 0.59	15.13 ± 1.00	14.48 ± 1.10	13.19 ± 2.47	14.91 ± 0.84	15.24 ± 1.41	12.72 ± 4.47	12.65 ± 5.76	–

-10 and -20 represent soil samples collected from 0–10 and 10–20 cm soil layer; B0, B1, B2 and B3 represent 0, 10, 20 and 30 t/ha doses of biochar addition, respectively; values are means ± standard error