

Supplementary materials

Table S1. Relative abundances (%) of the dominant bacterial phylum of soil with different biochar amendment.

Phylum	C0	C1	C2	C3
Proteobacteria	40.27 ± 3.22 a	39.06 ± 1.03 a	40.22 ± 1.33 a	40.38 ± 0.89 a
Chloroflexi	13.77 ± 1.48 a	15.35 ± 0.91 a	13.78 ± 0.28 a	14.26 ± 0.36 a
Acidobacteria	13.12 ± 1.52 a	12.02 ± 1.97 ab	12.05 ± 1.87 ab	10.52 ± 0.21 b
Bacteroidetes	8.60 ± 1.31 a	9.00 ± 1.60 a	9.42 ± 0.78 a	9.47 ± 0.46 a
Actinobacteria	6.16 ± 2.00 a	5.62 ± 1.40 a	4.07 ± 0.17 a	5.06 ± 1.38 a
Gemmatimonadetes	3.72 ± 0.55 a	3.96 ± 0.40 a	3.66 ± 0.58 a	3.81 ± 0.13 a
Nitrospirae	2.21 ± 0.43 c	2.79 ± 0.25 bc	3.61 ± 0.38 ab	3.76 ± 0.33 a
Ignavibacteriae	3.40 ± 0.64 a	2.86 ± 0.82 a	2.77 ± 0.81 a	2.59 ± 0.76 a
Parcubacteria	1.61 ± 0.13 a	1.41 ± 0.53 a	1.77 ± 0.44 a	1.80 ± 0.18 a
Verrucomicrobia	1.13 ± 0.19 b	1.54 ± 0.29ab	1.89 ± 0.19 a	1.67 ± 0.23 ab

Note: Values (\pm standard error) are means of three replicates. Different letters represent significant difference among treatments ($p < 0.05$).

Table S2. Significant differences in taxa at the genus level.

Genus	C0	C1	C2	C3	p
Thiobacillus	2.386	1.787	1.243	2.141	0.050
Bryobacter	1.730	1.314	1.076	1.012	0.015
Anaerolinea	1.211	1.043	0.771	0.833	0.039
uncultured_bacterium_c_KD4-96	1.291	1.279	0.856	0.747	0.047
Candidatus_Solibacter	1.045	0.845	0.591	0.518	0.001
uncultured_Acidobacteria_bacterium	0.721	0.417	0.372	0.228	0.012
Bdellovibrio	0.319	0.236	0.102	0.170	0.027
uncultured_bacterium_c_Chitinivibrionia	0.240	0.170	0.139	0.150	0.015
Gemmatimonas	0.607	0.314	0.174	0.128	0.002
Roseomonas	0.137	0.114	0.051	0.082	0.027
uncultured_bacterium_c_Candidatus_Pacebacteria	0.103	0.069	0.036	0.044	0.023
uncultured_bacterium_f_Sh765B-TzT-35	0.036	0.021	0.019	0.022	0.037
Desulfobacca	0.070	0.024	0.025	0.017	0.003
uncultured_bacterium_c_Gammaproteobacteria	0.080	0.055	0.015	0.011	0.029
Ignavibacterium	0.022	0.008	0.000	0.007	0.029
Turneriella	0.025	0.007	0.009	0.007	0.038
Angustibacter	0.023	0.005	0.002	0.005	0.002
Aurantimonas	0.017	0.013	0.007	0.005	0.014
Blastocatella	0.023	0.001	0.005	0.003	0.042
CL500-29_marine_group	0.205	0.261	0.166	0.181	0.025
uncultured_bacterium_c_Candidatus_Beckwithbacteria	0.081	0.266	0.191	0.175	0.022
H16	0.520	0.698	1.015	0.895	0.019
Nitrospira	0.418	0.526	0.779	0.606	0.004
Geobacter	0.340	0.405	0.645	0.382	0.006
Leptospirillum	0.001	0.259	0.439	0.348	0.015
uncultured_bacterium_o_Rhizobiales	0.075	0.134	0.212	0.184	0.017
Reyranella	0.148	0.224	0.241	0.168	0.039
uncultured_bacterium_f_OM1_clade	0.020	0.061	0.144	0.144	0.026
uncultured_bacterium_c_Subgroup_2	0.000	0.034	0.148	0.119	0.001
uncultured_bacterium_c_MD2898-B26	0.033	0.067	0.185	0.113	0.044
uncultured_bacterium_f_Gracilibacteraceae	0.019	0.065	0.118	0.050	0.014
uncultured_bacterium_p_TM6_[Dependentiae]	0.006	0.011	0.051	0.009	0.007
I-8	0.003	0.009	0.016	0.007	0.008
uncultured_bacterium_f_Nitrospiraceae	1.504	1.759	2.148	2.611	0.016
Candidatus_Tenderia	0.049	0.693	0.680	1.127	0.014
uncultured_bacterium_c_S085	0.038	0.461	0.995	1.043	0.000
uncultured_bacterium_f_Thiotrichaceae	0.019	0.211	0.258	0.383	0.001
Gillisia	0.053	0.168	0.156	0.346	0.023
uncultured_bacterium_f_Desulfobacteraceae	0.082	0.080	0.083	0.211	0.050
uncultured_bacterium_p_WS6	0.058	0.070	0.120	0.137	0.015
uncultured_bacterium_c_Subgroup_22	0.068	0.065	0.087	0.114	0.034
uncultured_bacterium_c_Subgroup_18	0.106	0.086	0.089	0.109	0.036

Desulfuromonas	0.001	0.003	0.037	0.061	0.001
uncultured_bacterium_f_B122	0.005	0.041	0.026	0.055	0.048
uncultured_bacterium_o_AKYG1722	0.016	0.037	0.051	0.053	0.021
uncultured_bacterium_f_Methylobacteriaceae	0.001	0.004	0.013	0.028	0.022
Pseudoxanthomonas	0.015	0.014	0.019	0.028	0.022
uncultured_bacterium_c_Subgroup_13	0.007	0.008	0.029	0.016	0.025
Roseimicrobium	0.007	0.005	0.006	0.013	0.046
uncultured_bacterium_f_Geodermatophilaceae	0.012	0.008	0.001	0.013	0.049
uncultured_planctomycete	0.003	0.006	0.011	0.013	0.031

Note: The bold values represent the highest values.