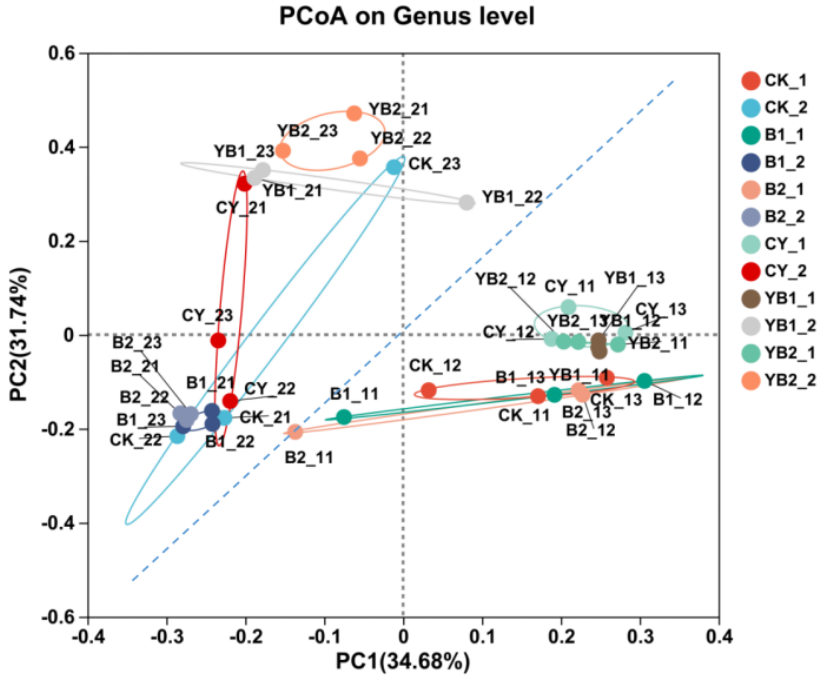

Figure S1. Comparison of bacterial 16S rRNA communities at genus level in the different treatments at different times using principal coordinates analysis (PCoA).

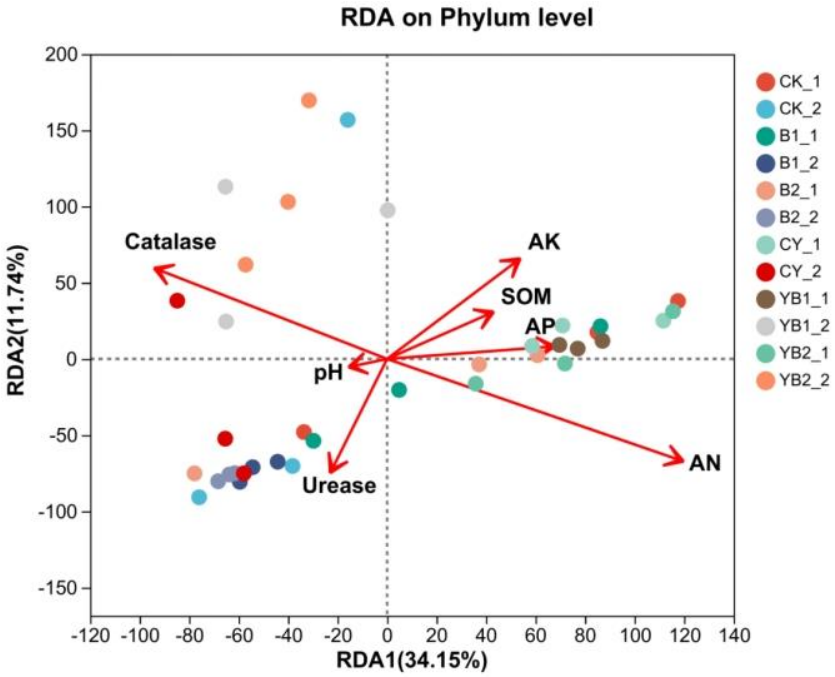

Figure S2. Redundancy analysis (RDA) for seven primary soil bacterial communities (Proteobacteria, Actinobacteria, Acidobacteria, Patescibacteria, Bacteroidetes, Firmicutes, Gemmatimonadetes) from all samples associated with environmental variables (pH, SOM, available P, available N, available K, catalase and urease).

Table S1. General physical and chemical properties of soil for each group.

Sample name	pH	SOM ($g \cdot kg^{-1}$)	Available N ($mg \cdot kg^{-1}$)	Available P ($mg \cdot kg^{-1}$)	Available K ($mg \cdot kg^{-1}$)	Urease ($g \cdot kg^{-1}$)	Catalase (0.1 mol/L· $KMnO_4$)/h·g)	TPH ($mg \cdot kg^{-1}$)
CK_1	8.20 ± 0.05 a	18.07 ± 0.03 e	36.33 ± 2.14 abcd	25.02 ± 1.84 g	33.05 ± 1.82 f	1.073 ± 0.060 efg	0.525 ± 0.017 f	/
CK_2	8.25 ± 0.02 a	17.63 ± 0.36 e	37.21 ± 2.57 abcd	31.01 ± 2.67 f	36.17 ± 1.37 f	0.957 ± 0.098 g	0.586 ± 0.027 ef	/
CY_1	7.53 ± 0.04 e	23.22 ± 0.62 d	37.67 ± 3.55 abc	40.15 ± 0.19 cde	46.38 ± 0.51 e	1.200 ± 0.115 def	0.613 ± 0.024 de	19591.00 ± 268.53 a
CY_2	7.77 ± 0.03 d	23.76 ± 0.76 cd	35.34 ± 2.89 bcd	39.87 ± 1.24 de	37.81 ± 3.12 f	1.053 ± 0.134 efg	0.724 ± 0.009 b	14802.31 ± 284.54 b
B1_1	7.62 ± 0.04 e	24.55 ± 0.47 c	38.68 ± 1.55 abc	46.96 ± 1.15 b	56.13 ± 1.95 d	1.567 ± 0.261 b	0.672 ± 0.012 bcd	/
B1_2	8.04 ± 0.06 b	23.62 ± 0.42 cd	34.34 ± 1.49 cd	45.08 ± 4.24 bc	55.80 ± 4.66 dc	1.507 ± 0.073 bc	0.726 ± 0.009 b	/
B2_1	7.93 ± 0.02 c	23.17 ± 0.62 d	40.63 ± 1.68 a	47.16 ± 2.03 b	61.11 ± 2.14 cd	1.327 ± 0.019 cd	0.693 ± 0.010 bc	/
B2_2	8.18 ± 0.02 a	28.24 ± 0.60 b	31.70 ± 0.51 de	37.57 ± 2.42 e	55.46 ± 2.47 d	1.840 ± 0.016 a	0.804 ± 0.029 a	/
YB1_1	7.94 ± 0.01 c	29.06 ± 0.18 b	38.11 ± 0.61 bc	54.74 ± 2.11 a	73.28 ± 0.56 ab	1.320 ± 0.017 d	0.687 ± 0.046 bc	19433.67 ± 106.19 a
YB1_2	7.74 ± 0.01 d	23.61 ± 0.66 d	29.14 ± 2.71 de	43.93 ± 2.25 bcd	66.44 ± 5.13 bc	1.148 ± 0.035 def	0.803 ± 0.050 a	10831.68 ± 237.86 c
YB2_1	7.98 ± 0.03 bc	37.77 ± 0.48 a	39.97 ± 1.69 ab	56.81 ± 0.87 a	78.56 ± 0.42 a	1.227 ± 0.056 de	0.641 ± 0.130 c	19338.67 ± 94.55 a
YB2_2	7.92 ± 0.08 c	29.17 ± 0.75 b	27.91 ± 2.31 e	41.12 ± 2.18 cde	63.91 ± 7.33 c	1.015 ± 0.032 fg	0.861 ± 0.023 a	9102.07 ± 334.99 d

Notes: Data are presented as mean ± SD (n = 3). Different lowercase letters indicate significant differences among groups at $p < 0.05$ according to one-way analysis of variance (ANOVA) followed by Tukey's honestly significant difference (HSD) test.

Table S2. Effects of biochar treatment, sampling time, and their interaction on bacterial alpha diversity indices based on two-way ANOVA.

Alpha diversity index	Treatment effect	Sampling time effect	Treatment × Sampling time interaction
Ace	$p = 0.00198$**	$p = 0.00017$**	$p = 0.00021$**
Chao	$p = 0.00318$**	$p = 0.00016$**	$p = 0.00027$**
Shannon	$p = 0.10273$	$p = 0.00113$**	$p = 0.00118$**
Simpson	$p = 0.19128$	$p = 0.16862$	$p = 0.04034$*
Sobs	$p = 0.03559$*	$p = 0.00247$**	$p = 0.000018$**

Notes: *and ** indicate significance at $p < 0.05$ and $p < 0.01$, respectively.