Supplementary Materials

Formula S1

$$AWCD = \sum(C_i - R_i)/n;$$

Where C_i is the absorbance value of each carbon source well, R_i is the absorbance value of each blank control well, n is the number of carbon source wells. In the test, the value is 31.

Formula S2

$$\text{Simpson}_{MF}\ \text{index(D)} = 1 - \sum P_i^i;$$

Where C_i is the absorbance value of each carbon source well, R_i is the absorbance value of each blank control well. $P_i = (C_i - R_i)/\sum(C_i - R_i)$.

Formula S3

$$\text{Shannon}_{MF}\ \text{index (H)} = -\sum P_i \times \ln(P_i);$$

Where C_i is the absorbance value of each carbon source well, R_i is the absorbance value of each blank control well. $P_i = (C_i - R_i)/\sum(C_i - R_i)$.

Formula S4

$$\text{McIntosh index (U)} = \sqrt{\sum \left(C_i - R_i\right)^2};$$

Where C_i is the absorbance value of each carbon source well, R_i is the absorbance value of each blank control well.

Formula S5

$$H_{shannon} = -\sum_{i=1}^{S_{obs}} \frac{n_i}{N} \ln \frac{n_i}{N};$$

Where Sobs = number of observed OTUs; n_i = number of OTUs containing i sequences; N = number of all sequences.

Formula S6

$$D_{simpson} = 1 - \frac{\sum_{i=1}^{S_{obs}} n_i\left(n_i - 1\right)}{N(N-1)};$$

Where Sobs = number of observed OTUs; n_i = number of OTUs containing i sequences; N = number of all sequences.

Formula S7-S11

$$S_{ACE}=\begin{cases} S_{abund}+\dfrac{s_{rare}}{C_{ACE}}+\dfrac{n_1}{C_{ACE}}, for\ \hat{\gamma}^2{}_{ACE}<0.80 \\ S_{abund}+\dfrac{s_{rare}}{C_{ACE}}+\dfrac{n_1}{C_{ACE}}, for\ \hat{\gamma}^2{}_{ACE}\geq 0.80 \end{cases};$$

$$C_{ACE}=\frac{n_1}{N_{rare}},\ N_{rare}=\sum_{i=1}^{abund} in_i;$$

$$\hat{\gamma}^2{}_{ACE}=max\left[\frac{S_{rare}\sum_{i=1}^{abund} i(i-1)n_i}{C_{ACE}Nrare(Nrare-1)}-1,0\right];$$

$$\hat{\gamma}^2{}_{ACE}=max\left[\hat{\gamma}^2{}_{ACE}\left\{1+\frac{N_{rare}\left(1-C_{ACE}\right)\sum_{i=1}^{abund} i(i-1)n_i}{N_{rare}\left(N_{rare}-C_{ACE}\right)}\right\},0\right];$$

Where n_i is the number of OTU with i sequences, Srare is the number of OTU with or less that "abund" sequences, Sabund is the number of OTU more than "abund" sequences, abund is the threshold of dominate OTU and default to be 10.

Formula S12

$$S_{chao1}=S_{obs}+\frac{n_1\left(n_1-1\right)}{2\left(n_2+1\right)};$$

Where Schao1 = estimated number of OTUs; Sobs = observed number of OTUs; n_1 = number of OTUs with only one sequence (e.g., "singletons"); n_2 = number of OTUs with only two sequences (e.g., "doublctprs ").

Table S1. Main technical specifications of the biochar under study.

Stationary Carbon ($g \cdot kg^{-1}$)	TN ($g \cdot kg^{-1}$)	Av.P/TP ($g \cdot kg^{-1}$)	Olsenk/TK ($g \cdot kg^{-1}$)	Bulk ($g \cdot kg^{-1}$)	Gross porosity ($m^2 \cdot g^{-1}$)	pH	EC ($mS \cdot cm^{-1}$)	Specific surface area ($g \cdot cm^{-1}$)	CEC (Cmol· Kg^{-1})
650	0	10.2	55.65	0.19	67.03	10.24	4.68	9	60.8

Table S2. PCR primer of bacteria.

Target gene	Primer	Sequence (5′–3′)
Bacterial 16s rRNA gene	338F	ACTCCTACGGGAGGCAGCAG
	806R	GGACTACHVGGGTWTCTAAT

Table S3. PCR reaction system and amplification program of bacteria.

PCR Reaction System (20 μL)	Addition (μL)	Amplification System
5×FastPfu Buffer	4	Denaturation at 95 °C for 3 min
2.5mM dNTPs	2	Degeneration at 95 °C for 30 s
Forward Primer (5 μM)	0.8	Annealing at 55 °C for 30 s
Reverse Primer (5 μM)	0.8	Extension at 72 °C for 45 s
FastPfu Polymerase	0.4	25 recycling
BSA	0.2	Extension at 72 °C for 10 min
Template DNA	10 ng	
Add ddH_2O to	20	Stored at 10 °C

Table S4. Mean values (± standard error) of diversity of soil microbial functional after biochar and PGPR treatments. Average well colour development (*AWCD*), Simpson index of soil microbial functional diversity ($Simpson_{MF}$), Shannon index of soil microbial functional diversity ($Shannon_{MF}$). Four treatments were set up as no biochar and no PGPR (M0B0, referred to as the control), 5×10^{10} CFU·mL^{-1} PGPR-only (MB0), 20 t·hm^{-2} biochar-only (B20), and co-application of 20 t·hm^{-2} biochar and 5×10^{10} CFU·mL^{-1} PGPR (MB20). Lowercase letters represent the significant differences between samples.

Treatments	*AWCD*	$Simpson_{MF}$	$Shannon_{MF}$	Mclntosh
M0B0	0.47 ± 0.72	0.93 ± 0.01	2.89 ± 0.10	3.88 ± 0.43
MB0	0.81 ± 0.14	0.95 ± 0.00	3.10 ± 0.04	5.58 ± 0.83
B20	0.69 ± 0.15	0.94 ± 0.01	3.00 ± 0.12	4.89 ± 0.89
MB20	0.35 ± 0.13	0.90 ± 0.04	2.57 ± 0.32	2.95 ± 0.83

Table S5. Carbon sources with contribution rates for principal component 1 (PC1) and principal component 2 (PC2) in soils treated by biochar-only, PGPR only, co-application of biochar and PGPR, and the control.

Carbon Type	Order	Carbon Source	PC1	PC2
Carbohydrate	C6	D-cellose	0.29389	-0.03607
	C7	a-D-lactose	0.18621	0.12491
	C8	β-menthyl-D-glycoside	0.30031	0.10047
	C9	D-xylose	0.02948	-0.30854
	C10	L-erthritol	0.08143	-0.14113
	C11	D-mannitol	0.0083	-0.1521
	C12	N-acetyl-D-gluosamine	0.06726	0.01534
	C14	Glucose-1-phosphate	0.19044	0.21387
	C15	D,L-a-glycerol	0.29738	-0.0746
	C16	D-glactonicacid γ lactone	0.19152	0.16068
Amino acid	C24	L-arginine	-0.09396	0.23244
	C25	L-asparagine	0.17174	0.18846
	C26	L-phenylalanine	-0.06745	0.27655
	C27	L-serine	0.19585	-0.09948
	C28	L-threonine	0.02905	0.18409
	C29	Glycyl-L-glutamate	0.25994	0.12178
Carboxylic acid	C1	Methyl pyruvate	0.24289	-0.03185
	C20	r-hydroxybutyric acid	0.06854	-0.31644
	C21	Itaconic acid	-0.15388	-0.18206
	C22	a-ketobutyric acid	0.18461	-0.27264
	C23	D-malic acid	0.25991	-0.05554
Multipoymer	C13	D-glucosaminicacid	0.19044	0.21387
	C17	D-galactose	0.31627	-0.04389
	C2	Tween 40	0.22514	0.20464
	C3	Tween 80	0.02919	0.01761
	C4	a-cyclodextrin	-0.21634	0.11106
	C5	Glycogenin	-0.16606	0.10758

Carbon Type	Order	Carbon Source	PC1	PC2
Phenoliacids	C18	2-hydroxy-benzoic acid	0.0788	-0.25581
	C19	4-hydroxy-benzoic acid	-0.02845	-0.05524
Amines	C30	Phenylethylamine	-0.03042	-0.31867
	C31	Putrescine	0.20406	0.04748

Table S6. Pearson's correlation coefficients of relative abundance and community composition of dominant bacteria and impact factors based on Mantel tests.

	M0B0		MB0		B20		MB20	
	r	p	r	p	r	p	r	p
NO_3^-	-0.149	0.835	-0.207	0.889	0.127	0.038	0.250	0.002
NH_4^+	0.135	0.169	0.064	0.307	0.198	0.051	0.153	0.177
Soil TN	-0.248	0.990	-0.241	0.967	0.541	0.002	0.726	0.001
Soil TP	0.147	0.175	0.183	0.099	0.291	0.029	0.082	0.296
Soil TK	0.349	0.017	0.244	0.039	0.037	0.511	-0.221	0.926
pH	-0.195	0.967	-0.128	0.850	0.023	0.362	0.114	0.182
EC	0.005	0.443	-0.177	0.802	0.074	0.308	0.089	0.362
SWC	0.138	0.123	0.083	0.218	0.068	0.233	0.201	0.064

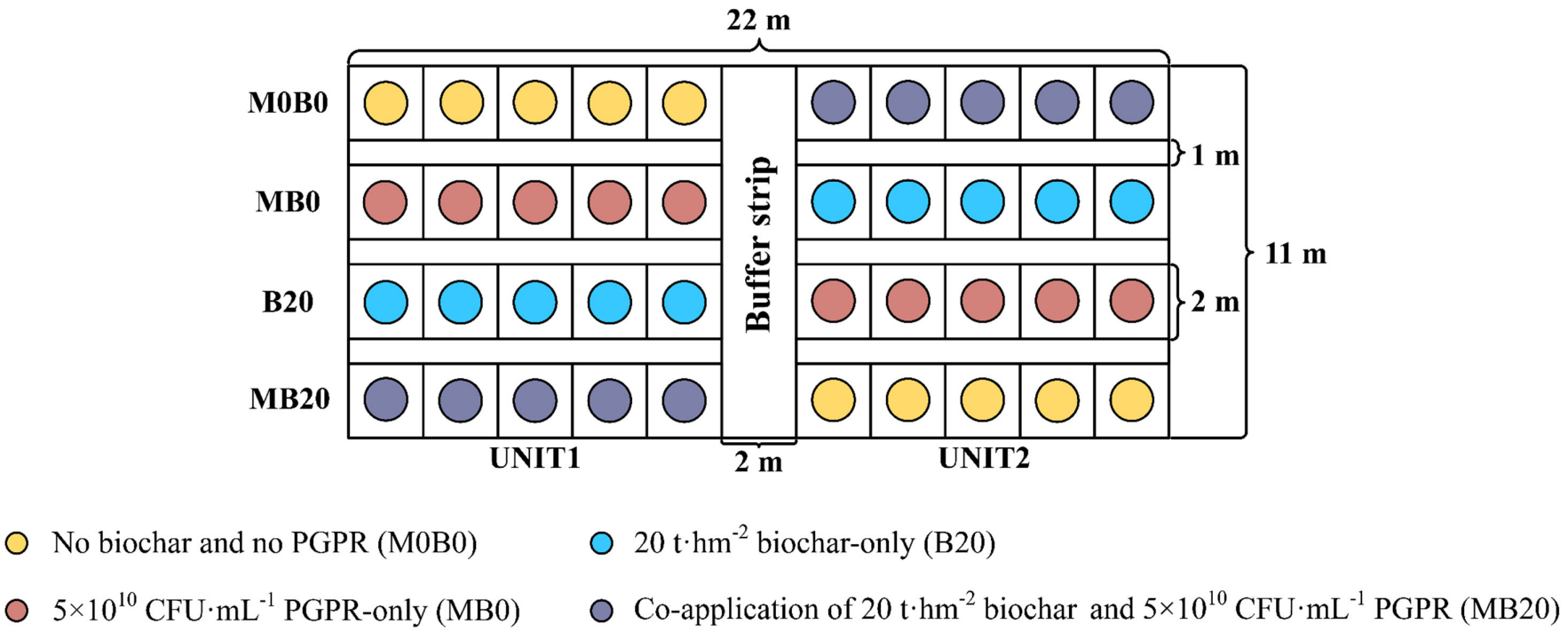

Figure S1. Experimental design in at Changke Forest Center. Two units were divided by a 2-m-width buffer strip. Each experimental unit was further divided into 5 columns. Each column was divided into 2 m × 2 m plots with 1m buffer strips between plots.

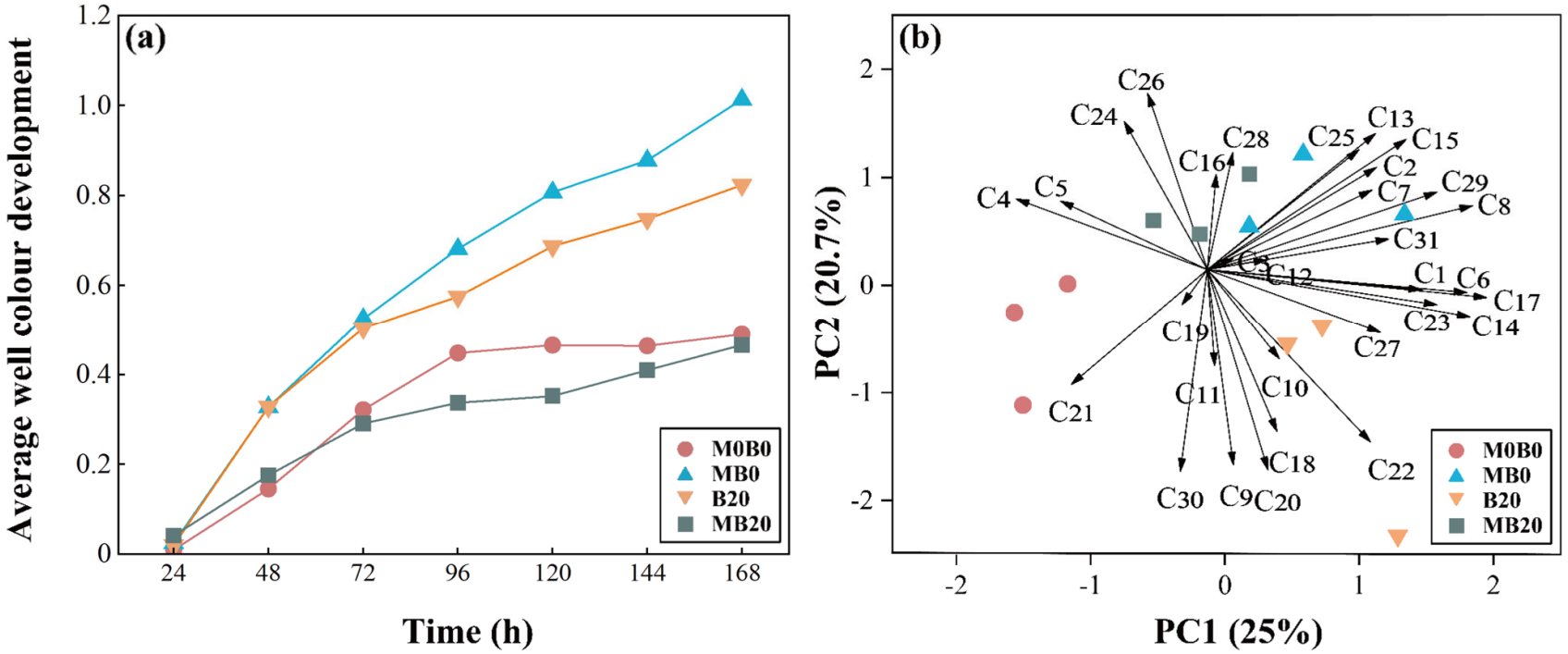

Figure S2. (a) Microbial metabolic activity of carbon sources in soil under M0B0, MB0, B20 and MB20 treatments, average well colour development (AWCD). **(b)** Principal component Analysis (PCA) of selected parameters measured on a grown under no biochar and no PGPR (M0B0), 5×10^{10} CFU·mL^{-1} PGPR-only (MB0), 20 t·hm^{-2} biochar-only (B20), and co-application of 20 t·hm^{-2} biochar and 5×10^{10} CFU·mL^{-1} PGPR (MB20). The parameters are: Methyl pyruvate (C1), Tween 40 (C2)Tween 80 (C3), a-cyclodextrin (C4), Glycogenin (C5), D-cellose (C6), a-D-lactose (C7), β-menthyl-D-glycoside (C8), D-xylose (C9), L-erthritol (C10), D-mannitol (C11), N-acetyl-D-gluosamine (C12), D-glucosaminicacid (C13), Glucose-1-phosphate (C14), D,L-a-glycerol (C15), D-glactonicacid γ lactone (C16), D-galactose (C17), 2-hydroxy-benzoic acid (C18), 4-hydroxy-benzoic acid (C19), r-hydroxybutyric acid (C20), Itaconic acid (C21), a-ketobutyric acid (C22),

D-malic acid (C23), L-arginine (C24), L-asparagine (C25), L-phenylalanine (C26), L-serine (C27), L-threonine (C28), Glycyl-L-glutamate (C29), Phenylethylamine (C30), Putrescine (C31). The carbon sources listed as black arrows in the figure represented the contribution to PC1 & PC2. PC1 accounted for 25.0% of the variance, and PC2 accounted for 20.7%.