Text S1 Determination of soil N, P, K and enzyme activities

Soil nutrient contents were analyzed as follows: total nitrogen (TN) was measured using an elemental analyzer; total phosphorus (TP) was determined by the molybdenum-antimony colorimetric method at 880 nm; total potassium (TK) was measured using flame atomic absorption spectrometry (FAAS); and available potassium (AK) was extracted with ammonium acetate and quantified using FAAS.

Soil enzyme activities were assessed using commercial kits from Shanghai Keruisi Biotech Co., Ltd. Sucrase activity (SC) was determined by the colorimetric method based on the hydrolysis of substrate (incubation at 37 °C for 24 h, detection at 540 nm). Dehydrogenase activity (DHA) was evaluated by measuring the reduction of iodonitrotetrazolium chloride (INT) to INT-formazan (incubation at 37 °C for 24 h, detection at 485 nm).

Text S2 Soil microbial community analysis

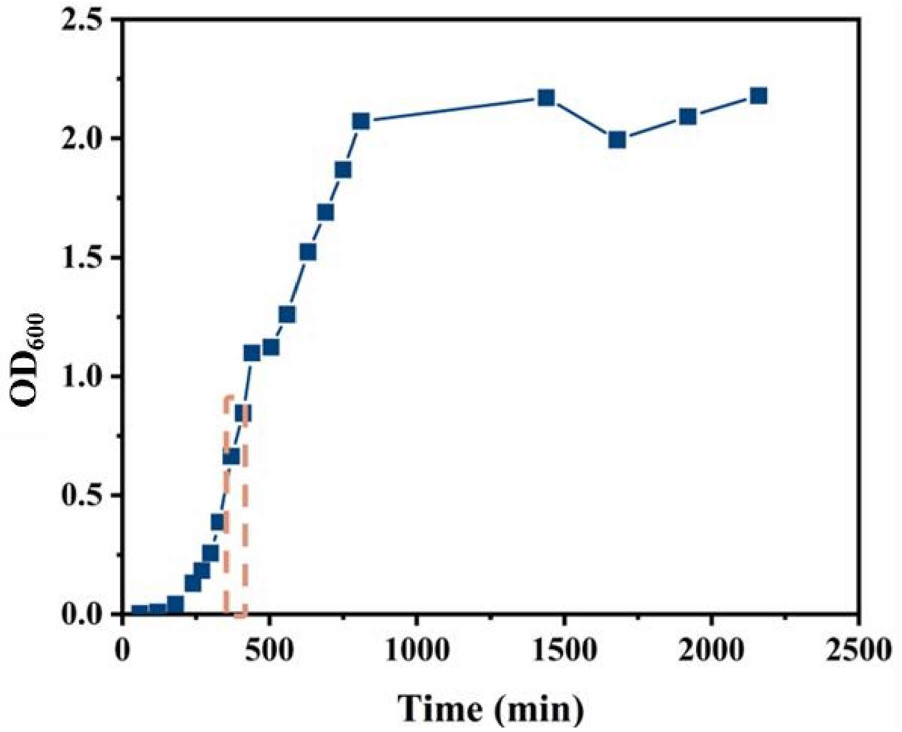
Soil samples were sent to Shanghai Meiji Biotechnology Co., Ltd. for testing, which included analysis of bacterial and fungal communities. High-throughput sequencing was employed to analyze the diversity of microbial communities and their composition. The sequenced raw sequences were trimmed under Linux using QIIME2 software to remove PCR primers as well as lower-quality sequences. For this experiment, 97% similarity was chosen for clustering and bioinformatics analysis of OTUs, and the comparative databases chosen for bacteria and fungi were Silva and Unite databases, respectively, with a truncation length of 373 bp for bacteria and 244 bp for fungi Diversity analysis as well as species taxonomic annotation were performed using QIIME2 software.

Supplementary Table

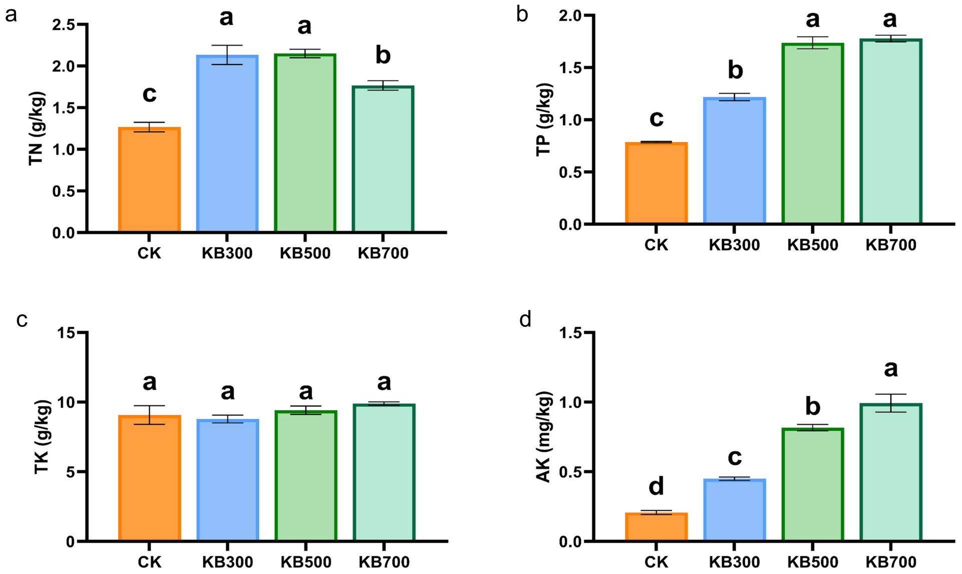
Table S1 Elemental composition of biochars

Biochar	Elemental content（%）				Atomic ratio			
	N	C	H	O	H/C	O/C	（O+N）/C	C/N
KB300	3.31 ± 0.06d	59.58 ± 0.56b	5.57 ± 0.11a	13.52 ± 0.13a	0.09 ± 0.00b	0.23 ± 0.00d	0.28 ± 0.00e	18.02 ± 0.18e
KB500	3.24 ± 0.06d	56.06 ± 0.73c	2.41 ± 0.02d	7.48 ± 0.26cd	0.04 ± 0.00g	0.13 ± 0.00f	0.19 ± 0.00f	17.29 ± 0.07f
KB700	2.72 ± 0.02f	55.92 ± 0.30c	1.58 ± 0.03g	6.28 ± 0.17ef	0.03 ± 0.00j	0.11 ± 0.00g	0.16 ± 0.00g	20.56 ± 0.24d

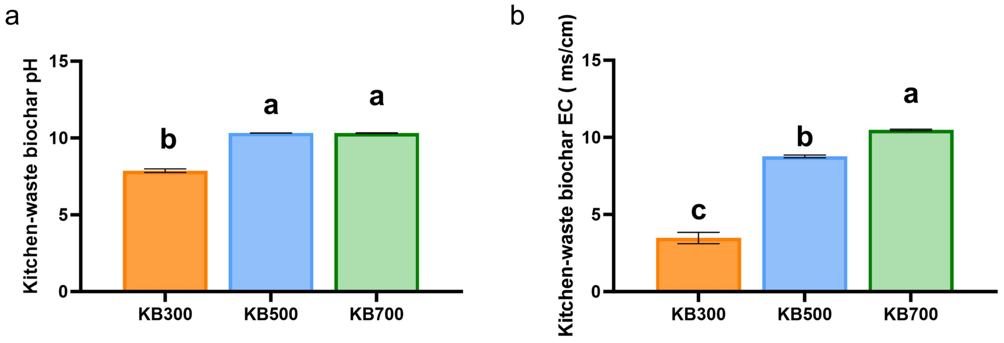
Supplementary Figures



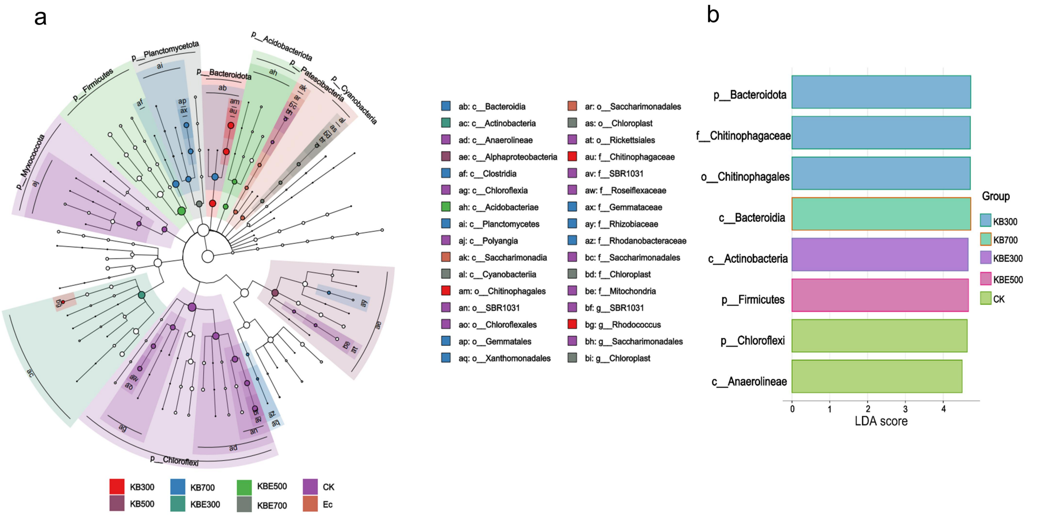
Supplementary Fig. S1 Growth curve of *Escherichia coli*.



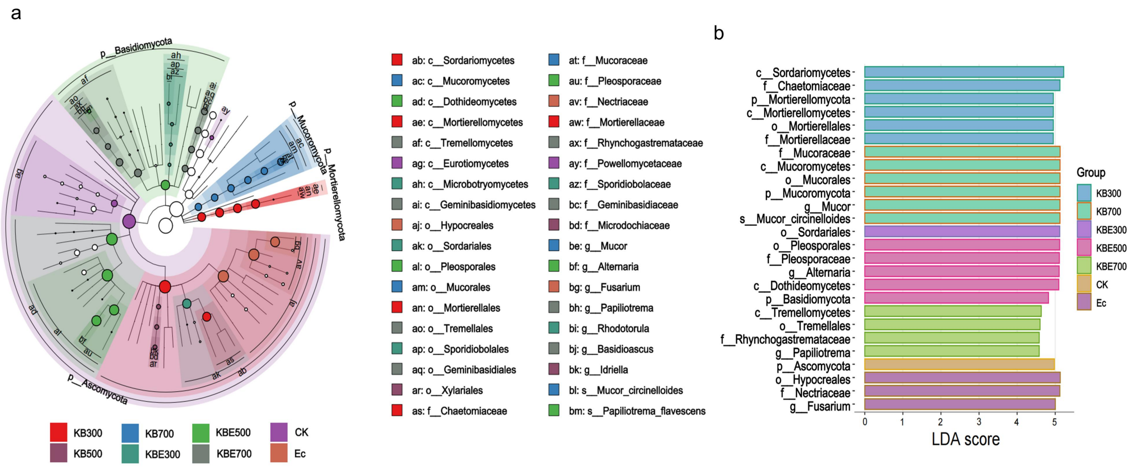
Supplementary Fig. S2 Soil nutrient contents under different treatments. (a) Soil TN content under different treatments; (b) Soil TP content under different treatments; (c) Soil TK content under different treatments; (d) Soil AK content under different treatments.



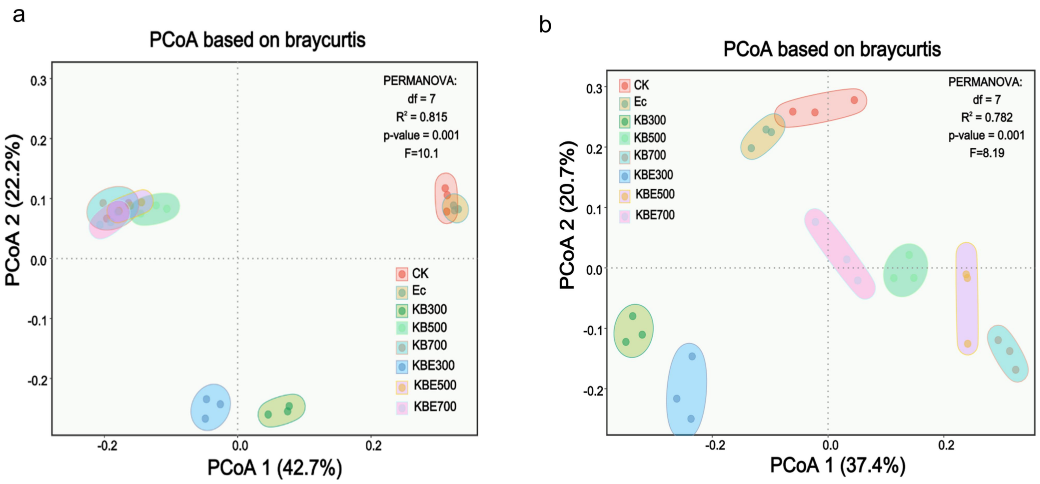
Supplementary Fig. S3 Biochar pH and EC under different pyrolysis temperatures. (a) Biochar pH under different pyrolysis temperatures; (b) Biochar EC under different pyrolysis temperatures.



Supplementary Fig. S4 Phylogenetic distribution and indicator bacteria of soil bacterial communities. (a) Phylogenetic distribution of soil-associated bacterial lineages among different treatments; (b) Indicator bacteria (LDA score ≥ 4) associated with soil bacterial communities among different treatments.



Supplementary Fig. S5 Phylogenetic distribution and indicator fungi of soil fungal communities. (a) Phylogenetic distribution of soil-associated fungal lineages among different treatments; (b) Indicator fungi (LDA score ≥ 4) associated with soil fungal communities among different treatments.



Supplementary Fig. S6 PCoA plots based on Bray-Curtis distance for (a) bacterial and (b) fungal communities.