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Supplementary materials

Ameliorating acidic soil using bioelectrochemistry systems

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Table S1. Overall Illumina sequencing information from the six samples.

Samples	Effective sequences	Per 13056 sequences			
		Observed species	Chao 1	Phylogenetic diversity	Good's coverage
CS-10^4	14115	3915	16193	269.03	0.773
CS-10^3	13056	4412	18600	300.55	0.740
CS-10^2	27065	4576	20315	309.05	0.727
CS-10	18197	4638	20448	312.37	0.722
CS-Control	15151	3734	15535	260.98	0.787
Raw soil	14069	3759	14714	265.26	0.784

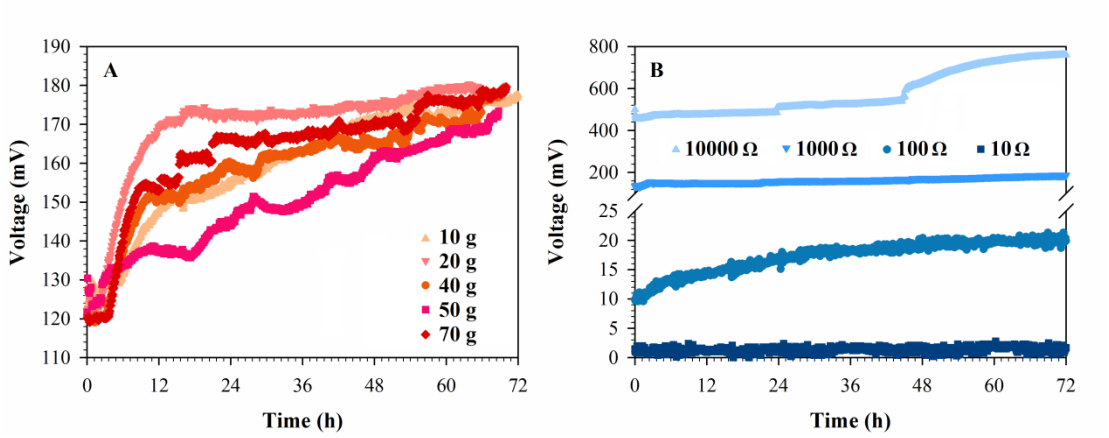

Figure S1. The voltage outputs of MFCs under closed circuit in different soil loads with 1000 Ω external resistance (A) and in different external resistances with 50 g soil load (B).

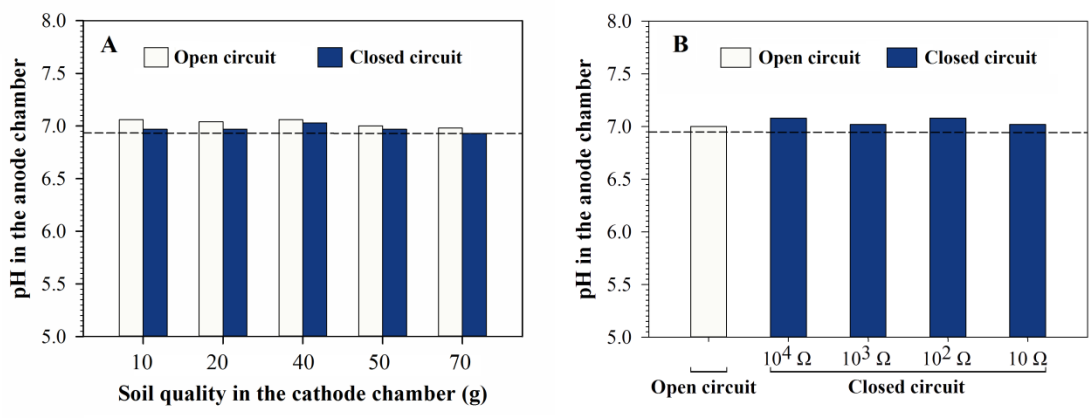

Figure S2. The anodic pH under open circuit and closed circuit with 1000 Ω external resistance in different soil loads (A) and in different external resistances with 50 g soil load (B).

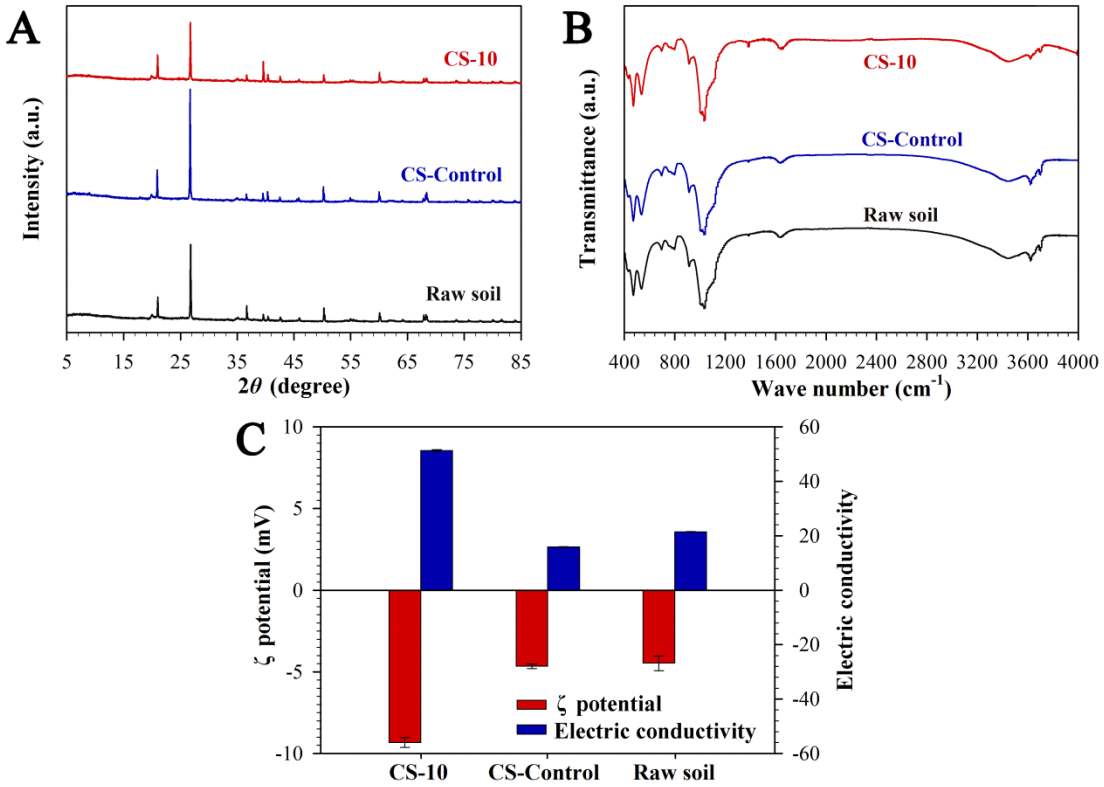

Figure S3. The structure and electrochemical characteristics of the acidic soil before and after BES-amelioration. CS-10 denotes the soil of MFCs loaded with 10 Ω external resistances; CS-Control denotes the soil of MFC under open circuit. All the soil and water in the cathode chamber were transferred to a glass flask. The soil was air-dried, and ground to pass a sieve for analysis of (A) XRD, (B) FTIR and (C) Zeta potential and Electric conductivity. (A) XRD operated at 40 kV and 40 mA with a Cu Kλ radiation (λ = 0.154 nm) at room temperature using X'Pert Pro (PANalytical B.V., Netherlands). (B) FTIR spectra were determined using a KBr pellet technique in the 400-4000 cm^{-1} range by using a spectrometer, with a resolution of 4 cm-1 and 8 accumulations; (C) Zeta potential and Electric conductivity were measured by ZetaPALS (Malvern, UK) and FE30-FiveEasy (METTLER TOLEDO, Switzerland).

To understand the structural characterization of soil samples used in this study, XRD,

FTIR, Zeta potential and electric conductivity were tested. In the soil before or after BES-amelioration, silicon oxide is the best matching result according to XRD result. The value showed higher in the peak of 36.6 °2Th. than that in the peak of 39.5 °2Th. in soil sample after BES-amelioration, while the two peak showed almost equal in the soil sample before BES-amelioration. This difference could be attributed to the existence of Quartz low in the soil after BES-amelioration. There is no obvious difference between soils samples before or after BES-amelioration from the results of the FTIR. The Zeta potential of the soil sample after BES-amelioration showed more negative than that before BES-amelioration, it suggests the soil colloid become more stable after BES-amelioration. The electric conductivity increased after BES-amelioration, which is help for decreasing the internal resistance of bioelectrochemistry systems. All of the test results were provided in the supporting material.

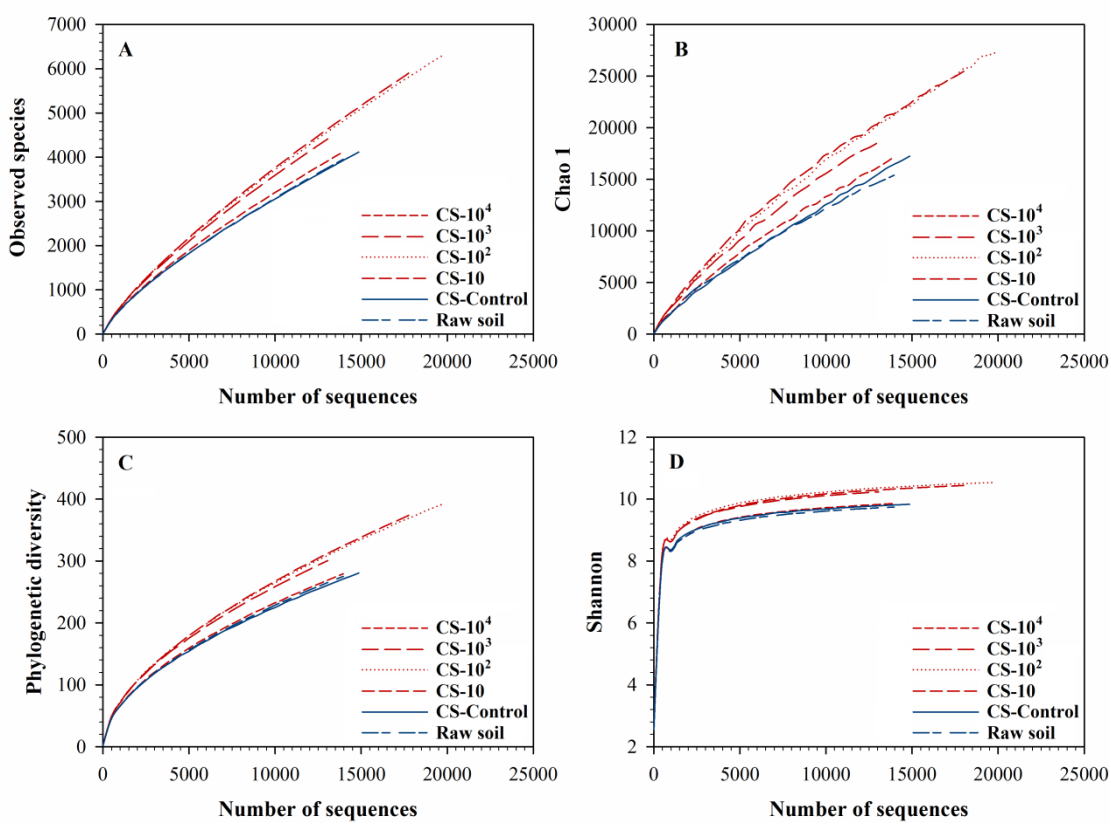

Figure S4. Rarefaction curves of Observed species (A), Chao1 index (B), Phylogenetic diversity index (C) and Shannon index (D) for soil bacterial communities from bioelectrochemical systems. CS-10, CS-10^2, CS-10^3 and CS-10^4 denotes the cathodic soil of MFC loading 10, 100, 1000 and 10000 Ω external resistance, respectively; CS-Control denotes cathodic soil of MFC under open circuit.

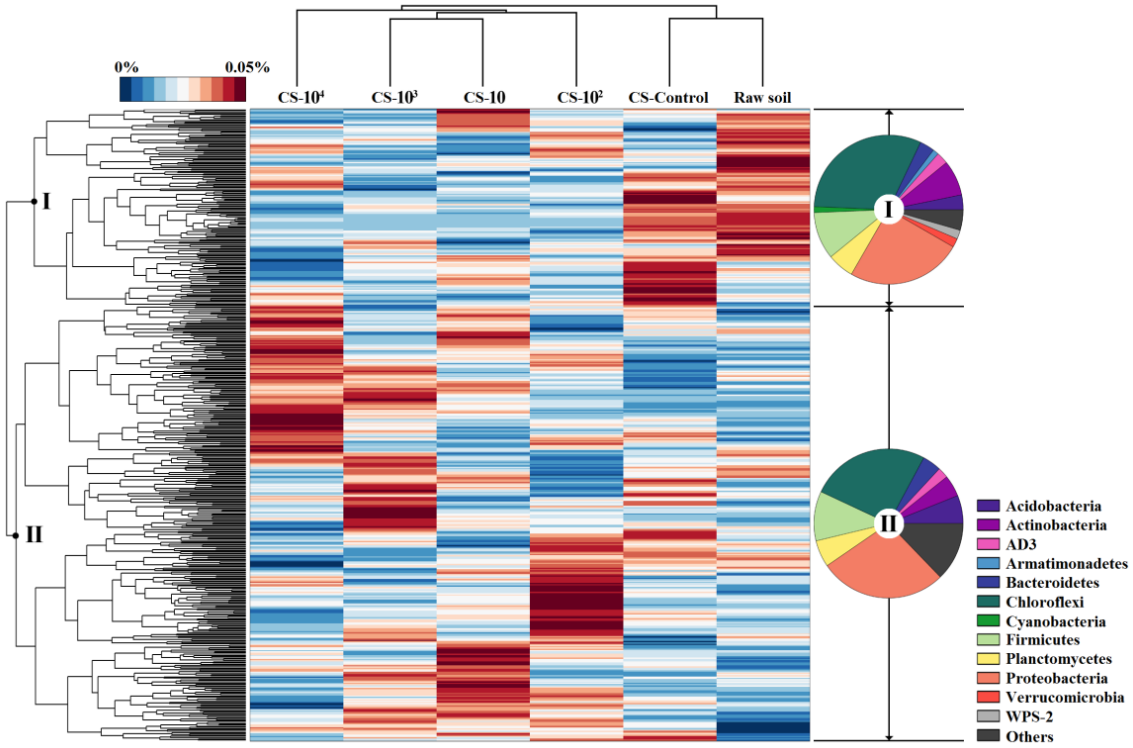

Figure S5. Cluster analysis of bacterial communities of the soil samples. The 500 most abundant OTUs (3% distance) were clustered in two forms: OTUs and samples. The relative abundance of OTUs is reflected by the color of scale. Two OTU groups I and II represented relatively high abundance in acidic soil before and after BES-amelioration, respectively. The two OTU groups were assigned to taxonomies at phylum level.

The most abundant 500 OTUs (3% distance) could be classified into two groups (I and II) based on the cluster analysis of OTUs (Fig. S4). Two OTU groups I and II represented relatively high abundance in soil samples before and after BES-amelioration, respectively. The number of OTU in group II was more than double that in group I. These OTUs were assigned to known taxonomies at phylum level, and 12 main phyla (the relative abundances were more than 1%) were detected.

The clearest difference between two groups was the different distribution of phyla Armatimonadetes, Verrucomicrobia, Cyanobacteria and WPS-2 which only existed in group I. Armatimonadetes, as a novel phylum, was phylogenetic delineated recently [1], and it's function was uncertain. Verrucomicrobia and Cyanobacteria were often found in soil environment, while some Cyanobacteria produce toxins which was dangerous to humans as well as other animals [2]. The disappearance of Cyanobacteria after BES-amelioration may be a good sign for decreasing hazardous composition. Majority of OTUs belonged to Proteobacteria, Firmicutes and Chloroflexi which abound in both two groups. The cluster analysis based on samples also supported weighted principal coordinated analysises where samples after BES-amelioration were separated from that before BES-amelioration.

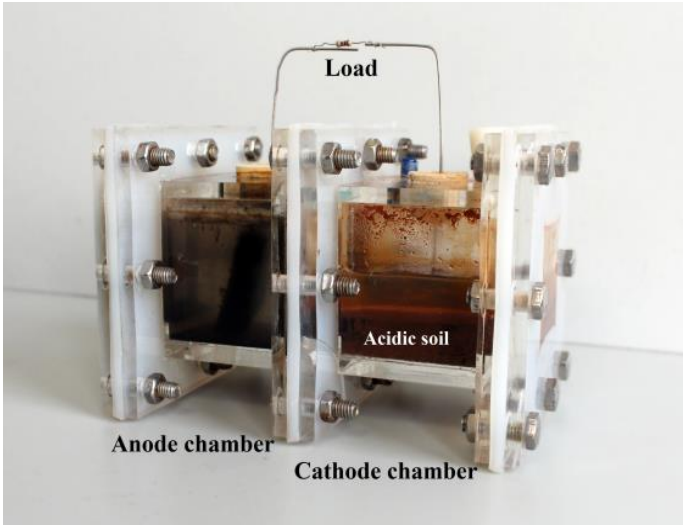

Figure S6. The photo of the bioelectrochemisty system reactor

References:

[1] K. Lee, C. Herbold, P.F. Dunfield, X.C. Morgan, I.R. McDonald, M.B. Stott, Phylogenetic Delineation of the Novel Phylum Armatimonadetes (Former Candidate Division OP10) and Definition of Two Novel Candidate Divisions, Appl. Environ. Microbiol. 79 (2013) 2484-2487.

[2] G.A. Codd, L.F. Morrison, J.S. Metcalf, Cyanobacterial toxins: risk management for health protection, Toxicol. Appl. Pharmacol. 203 (2005) 264-272.