Coupling Effects of Goat Manure and Water Management on Immobilization of Cadmium and Improvement of Bacterial Community

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Abstract

The objective of this study was to expound possible effect of fertilization and water management in the remediation process of hazardous substance using sepiolite(SP). Meanwhile, Illumina high-throughput sequencing was performed to investigate how the composition of the rhizosphere bacterial community responded to a series of soil remediation process. The results showed that application of SP increased pH, decreased DOM under different water condition, but goat manure (GM) increased pH and DOM at the same time. Under water-saturated condition (FWHC), the application of GM increased the content of available Cd (DTPA-Cd) by 42.0-68.9%, 13.1%-30.3% of unamended and SP-amended soil, respectively. Under normal water condition (NWHC), the application of GM increased DTPA-Cd by 0.7%-5.8%, 73.7%-115.5% of unamended and SP-amended soil, respectively. Consequently, coupling effect of FWHC and GM decreased Cd content in shoots of pak choi. We also found that the application of GM increased the abundance of soil microbial communities. Abundance of proteobacteria reached a peak when applied GM in SP-amended soil under FWHC. RDA analysis showed that soil microbes such as bacteroidetes, patescibacteria, and proteobacteria were correlated positively with pH, DOM, and DTPA-Cd. Acidobacteria was correlated positively with DTPA-Cd, and negatively with pH and DOM. The relationship of soil physicochemical properties and the bacterial community variation indicated that GM and SP mixed additives may indirectly affect the soil microbial community by changing soil physicochemical properties and available Cd content.

1. Introduction

Cadmium (Cd) pollution in agriculture systems caused by mining, smelting industries or agricultural activities is considered one of the most severe environmental problem, because Cd is a highly toxic, persistent pollutant, and easily transferred through the soil-plant-food chain (Rizwan et al., 2016; Khan et al., 2017a). In recent years, passivation remediation of heavy metal has aroused great interests for cost effective, easy accessibility, environmentally friendly, and not affecting agricultural production (Wei et al., 2011; Tang et al., 2016). The application of a series of passivator reduces Cd-induced phytotoxicity and improves land capability during crop growing process.

Cd solubility and bioavailability is affected by many factors, such as pH (Yang et al., 2020), soil organic matters (Yang et al., 2020) and redox potential (Eh) (Sarwar et al., 2010). The increase of pH increased the surface negative charge of soil colloid, motivate Cd sedimentation and adsorption (Sun et al., 2013; Liang et al., 2016; Li and Xu, 2017). As we already know, acid-adjusting soil conditioner decreased available heavy metal of acid contaminated soil (generally refer to soil pH below 6.5) (Liu et al., 2018; Liu et al., 2019).

Soil Eh affects Cd bioavailability as a result of the change in redox status and the change in electron acceptors. Cd often exists as soluble salt and cationic form, e.g., Cd^{2+} , under aerobic oxidizing conditions, but exists as precipitated species such as CdS and CdCO_3 , under low redox potential, anaerobic situations (Sebastian and Prasad, 2014). On the other hand, changes in redox potential affect soil

organic matter and mineral constituents (Gallego et al., 2012). Furthermore, soil redox conditions regulate the microbial community characteristics and functions (Edwardson and Hollibaugh, 2018; Okegbe et al., 2014). For example, wet and dry rotations shift bacteria community composition and the dominant phyla in paddy soils (Somenahally et al., 2011). A 4-week drought treatment caused significant decline in abundance of denitrifiers and 16 rRNA (Kim et al., 2008).

Soil organic matter (SOM) affects the bioavailability of heavy metals in soil, especially in soils used for vegetable cultivation, where extensive organic fertilization is applied (Li et al., 2016). Organic matters (OMs) increased agricultural production through the improvement of soil structure and fertility status, but the release of large amounts of dissolved organic matter (DOM) might affect the adsorption/immobilization capacity of clay minerals in soils (Marschner and Kalbitz, 2003). OMs inhabited heavy metals through absorption, complexation, and precipitation (Ren et al., 2016). Chen et al. (2021) found that the relationship between SOM and the accumulation of Cd in wheat and summer maize demonstrated a significant negative correlation. However, the release of small molecular organic acids may induce the mobilization of metal ion through the formation of DOM-Cd chelate (Salati et al., 2010).

On the other aspects, biotic factors, *i.e.*, heavy metal contamination significantly changed the diversity and structure of microorganisms, thus, soil microbial community are preferred indicators for soil biochemical characteristics and reflecting the severity of Cd pollution (Sanchez-Hernandez et al., 2018; Ullah et al., 2019). Free-state Cd can be either immobilized by microbial adsorption or be reduced by chemically aided microbes (Meng et al., 2018). For example, Liu et al. (2018) found that the arbuscular mycorrhizal fungi reduce Cd accumulation in plants through the regulating effect on Cd speciation. Many recent studies found that agronomic measures, such as irrigation regime, cultivation practices, and soil amendments affected soil microbe and Cd bioavailability (Wang et al., 2017). Soil microbial communities are crucial in determining the amount of organic matter in soils (Kögel-Knabner et al., 2010; Li et al., 2017), and a decrease in organic matter often results an increase in soil available Cd, vice versa, fertilizing organic matter often causes decrease in soil available Cd (Brams and Anthony, 1983). Majewska et al. (2007) suggested that microbial activity increased soil citric acid, acetic acid, catechol siderophores and Fe-chelators, and contributed to soil Cd mobilization.

Our precious findings indicate that natural sepiolite decreased available Cd as a consequence of the improve of soil pH by 1.0-2.0 (Li and Xu, 2015; Liu et al., 2019). However, during crop growing process, watering and fertilization were essential factors that affect soil environment, growth of crop, and further the efficacy and stability of external materials. As a consequence, field management is likely to influence the immobilizing effect of sepiolite for polluted arable land. In our study, we study the effects of water management and goat manure on the stability of passivator and soil microbial community structure in unamended and sepiolite-amended soil.

2. Materials And Methods

2.1 Physicochemical properties of soil and amendments

Natural Cd-contaminated soil was collected from the cropland in Chenzhou, Hunan, China (112°43'48"N, 25°43'48"E). The basic characteristics of soil are showed in Table 1. Natural sepiolite (particle diameter $\leq 74\text{ }\mu\text{m}$), containing a small amount of dolomite and talc and other impurities, was purchased from Huakai Ltd. (Yixian, Hebei, China). Goat manure (GM) was purchased from a local market in Tianjin, China. The basic physicochemical properties of organic manure are listed in Table 2.

Table 1
Basic Characteristics of soil

Properties	pH	OM (g·kg ⁻¹)	Total N (mg·kg ⁻¹)	Available P (mg·kg ⁻¹)	Available K (mg·kg ⁻¹)	CEC (cmol·kg ⁻¹)	Total Cd (mg·kg ⁻¹)
Value	6.21	34.6	42.9	9.3	182.7	25.3	2.5

Table 2
Selected characteristics of goat manure

Properties	pH	OM(%)	Total N(%)	Total P(%)	Total K(%)	Total S(%)	Total Cd(mg·kg ⁻¹)
Value	10.1	92.1	2.54	0.56	1.09	0.56	0.74

2.2 Pot experiment

The study was conducted in 2019 in a greenhouse of Agri-Environmental Protection Institute, Tianjin, China. The soil samples were air-dried, homogenized and passed through a 4 mm sieve. For each pot (23 cm in diameter, 17cm in height), 2.0 kg Cd polluted soil was thoroughly mixed with basal fertilizers and the desired amendments. There were total sixteen treatment scenarios, including sepiolite(SP) performed as the passivator, goat manure (GM) performed as the fertilizer. and two different water management conditions (Table 3), involving a normal water condition (60% of field water holding capacity, NWHC) and a water-saturated condition (100% of field water holding capacity, FWHC). There were three replicates of each treatment following randomized complete block design.

Table 3
Summary of pot experiment treatments

Water management	Amendment	Amount of sepiolite	Amount of chicken manure			
			0	0.5%	1.0%	2.0%
NWHC	Goat manure	-	CK	G1	G2	G3
	Sepiolite (SP)+Goat manure(GM)	0.5%	SP	SG1	SG2	SG3
FWHC	Goat manure	-	CK	G1	G2	G3
	Sepiolite (SP)+Goat manure(GM)	0.5%	SP	SG1	SG2	SG3

Each pot was equilibrated for a period of four weeks (watered daily with deionized water to maintain at 70% of water-holding capacity). Seeds of pak choi (*Brassica campestris* L., cultivar Siyueman) were sown into each prepared pot on 17 April 2019. Water management was conducted on the 10th day after germination using the weighing method[40]. After 5 weeks of growth under a normal diel light cycle in a semi-closed greenhouse, all plants of the cultivars were harvested on 2 May 2019. All the plant samples were washed with tap water, rinsed 3–4 times with deionized water, and separate into two parts. The roots and shoots were then oven dried (60 °C) until a constant weight was reached. The plant samples were ground using a stainless steel mill and passed through a 0.25 mm sieve. Rhizosphere soil samples were collected following plant harvest. Specifically, for each pot, soil cores were collected from three random sites under the root base at a depth of 0–5 cm using a small shovel. The collected soil samples were immediately divided into two parts: one part was stored at –80 °C for molecular analysis and the other one was air-dried immediately for chemical analysis.

2.3 Sampling and analyses

2.3.1 Basic analysis of soil and plant tissue Cd

Soil pH was measured with a pH meter (PB-10, Sartorius, Germany), and the solid-to-liquid ratio (m:v) = 1:2.5. DOM content was measured using a total organic carbon analyzer (Vario TOC, Elementar Germany element) at a solid-to-water ratio of 1:5. The bioavailability of Cd in soil was determined by diethylenetriaminepentaacetic acid (DTPA). Dried and powered rice plant samples (0.2500 ± 0.0005 g) were digested in 4:1 (v/v) $\text{HNO}_3/\text{HClO}_4$ (10 mL) using a block digester. The concentration of Cd in the digested samples and soil solutions was determined by inductively coupled plasma mass spectrometry (iCAP Q; Thermo Scientific, Waltham, MA, USA).

2.3.2 DNA extraction and PCR amplification

The soil samples were three replicates of the same treatment. The protocol for soil DNA extraction: total DNA from the amendments and control microcosms was extracted at each time point (total 24 DNA extracts) by the CTAB method, and then the purity and concentration of DNA were detected by agarose gel electrophoresis. Then the diluted genomic DNA was used as template, and specific primers with Barcodes were selected according to sequencing regions. Phusion® High-Fidelity PCR Master Mix with GC Buffer (New England Biolabs Company, Ipswich, US) and high-fidelity enzyme were used for PCR amplification to ensure its efficiency and accuracy. The amplification regions in the primers corresponded to the following parameters: The V3-V4 hyper-variable region of the 16S rRNA gene was selected as the bacterial target segments. The library was constructed using the TruSeq DNA PCR-Free Sample Preparation Kit, and the library was quantified by Qubit and Q-PCR. After quantification, the Illumina HiSeq-2500 was used for sequencing the library in Novogene Bioinformatics Technology Ltd (Tianjin, China).

2.3.3 Analysis of Illumina Miseq sequencing

The Trimmomatic software (version 0.33) was used to filter the raw Illumina HiSeq sequencing data (Bolger et al., 2014), then Cutadapt (version 1.9.1)(Martin et al., 2011) was used to identified and removed primer sequences. A total of 1,918,529 pairs of Raw Reads were obtained by sequencing 8 samples. A total of 1,486,094 Clean Reads were generated after splicing and filtering the double-ended Reads. Each sample generated at least 181,647 Clean Reads, with an average of 185,762 Clean Reads. USEARCH (version 10.0)(Edgar, 2013) was used to cluster the Effective Tags of all samples, and the samples were clustered into operational taxonomic units (OTUs) based on a default identity of 97%. According to the algorithm principle, the highest-frequency sequences in the OTUs were screened as the representative sequences of the respective OTUs. All treatments were replicated three times in the experiment. The means and standard deviations (SD) were calculated by Microsoft Office Excel 2013. Analysis of variance was carried out with SAS 9.1. Significantly different means between treatments were separated by the least significant difference (LSD) method at the 0.05 level.

3. Results And Discussion

3.1 Effects of amendments on fresh weight

Table 4 showed the fresh weight of pak choi under different treatments. The application of sepiolite increased the fresh weight of pak choi by 38.1%, 20.8% under FWHC, NWHC, respectively. Because sepiolite alleviated Cd toxicity on pak choi. Liang et al.(2017) reported that sepiolite increase the total antioxidant capacity and nonprotein thiols contents, and reduce the MDA content of rice root to alleviate the stress of Cd in rice. In unamended soil, the application of goat manure increased fresh weight of pak choi by 34.9%-88.4% under FWHC. In SP-amended soil, the application of goat manure slightly decreased fresh weight of pak choi at different application rate under NWHC treatment, whilst significantly increased fresh weight of pak choi when applied at a concentration of 2.0%. The results indicated that the coupling effect of water management and organic fertilizer reduce the toxicity of Cd on plant growth. Our

results are in the agreement with previous studied reported by Lahori et al. (2017) found that the combined application of tobacco biochar and mineral additives increased soil pH and dry biomass production of Chinese cabbage.

Table 4
Fresh weight of pak choi

Water Management	Treatments				
		CK	G1	G2	G3
FWHC	Unamended	23.51±1.84 e	31.71±2.19 c	44.30±3.35 a	28.19±0.83 d
	SP-Amended	32.46±2.31 c	28.72±1.25 d	28.75±1.20 d	40.58±4.27 b
NWHC	Unamended	19.35±0.21 fg	21.51±1.81 ef	17.59±1.67 gh	16.44±0.88 h
	SP-Amended	23.38±1.31 e	20.12±0.06 fg	16.59±1.33 h	21.45±0.28 ef

3.2 Effects of amendments on soil pH and DOM

Figure 1 showed the effect of goat manure on soil pH and DOM of unamended and SP-amended soil under NWHC and FWHC. The application of goat manure and sepiolite alone increased soil pH by 0.30-0.63, 1.0-1.1 respectively. Fard et al. (2011) found a negative relationship between pH and Cd sorption capacity of biosolids and a similar pattern is seen here. Soil pH was relatively low under NWHC treatment. As a consequence, available Cd extracted by DTPA remained at a low level under FWHC compared with NWHC treatment. The application of sepiolite decreased DOM by 31.5%-32.6%. Because, clay minerals, especially secondary mineral, tend to adsorbed organic matter to form stratified structure through ligand exchange, complexation, cationic bridge, hydrogen bond, and Van der Waals forces. Thus, the clay mineral increased thermal and chemical stability of organic matters and resulted in the rearrangement of organic microstructures (Kleber et al., 2007, Chasse et al., 2015). The application of goat manure increased DOM by 1.14-4.75, 1.16-2.9 under NWHC, FWHC treatment. Goat manure increased the content of humic acid and fulvic acid, because they are main components of DOM in soil. In SP-amended soil, soil DOM increased with the increase of goat manure, however, the changes of water contents had no effect on soil DOM.

3.3 Effects of amendments on Cd contents of pak choi

Figure 2 showed the effect of goat manure in unamended and SP-amended soil under NWHC and FWHC treatment. Compared to NWHC treatment, Cd content in shoot and root decreased by 43.9%, 28.0% under FWHC, respectively. When applied sepiolite alone, Cd content of shoot and root decreased by 37.3%-75.3%, 36.5%-62.9%, respectively. When applied at the concentration of 0.5%, coupling effect of goat manure and NWHC reduced the accumulation of Cd in shoot of pak choi compared with the goat

manure and FWHC treatment. When applied at the concentration of 1.0% and 2.0%, coupling effect of goat manure and FWHC reduced the accumulation of Cd in shoot of pak choi compared with the goat manure and NWHC treatment. Whether in the unamended or SP-amended soil, coupling effect of organic manure and water management have the same tendency.

3.4 Effects of amendments on available Cd

Figure 3 showed the effect of goat manure and water management on available Cd extracted by DTPA. Under NWHC, the application of sepiolite decreased DTPA-Cd by 74.5%. Sun et al. (2016) found that the addition of sepiolite was effective in immobilizing Cd in pot and field applied research, because sepiolite decreased the content of Cd extracted by TCLP. Under FWHC, the application of sepiolite increased DTPA-Cd by 79.2%, and the application of goat manure increased DTPA-Cd by 42.0%-68.9%.

3.5 Microbial community abundance and structural diversity

3.5.1 Soil bacteria alpha diversity

A total of 1,486,094 high-quality sequences and 1598 OTUs for the bacterial 16S gene from all 24 samples were obtained. The Good's average coverage of all the samples exceeded 99.9%, indicating that the bacterial OTUs for each soil sample were well captured by this sequencing method. Generally, the Shannon and Simpson indexes can be used to evaluate soil bacterial community diversity, and the ACE and Chao1 indexes can be used to evaluate soil bacterial community richness (Shi et al., 2019). The larger the Chao1 index and ACE index, the higher the abundance of the microbial community. The greater the Shannon index, the higher the diversity of microbial community while the larger the Simpson index, the lower the diversity of microbial community.

The soil microbial alpha diversity is shown in Table 5. Compared with the control, the abundance-based coverage estimators (ACE) index, Chao1 index and Shannon index were significantly increased under the G, SP, and SG treatments, whereas the Simpson index had no significant difference between treatments. The results showed that the G, SP, and SG treatments increased the diversity and richness of soil bacteria, especially the simultaneous application of goat manure and sepiolite (SG). Previous studies showed that lime mixed with organic manure can further enhance specific bacterial communities (Ai et al., 2015; Martínez García et al., 2018). In addition, the bacterial diversity is high in neutral soils and low in acidic soils (Fierer and Jackson, 2006; Lauber et al., 2009). Chodak et al. (2013) reported that heavy metals had a negative impact on soil bacterial diversity. Thus, the increase in pH and the inhibition of the heavy metal activity may contribute to the improvements in the richness and diversity of bacterial communities in this study. The soils collected under the G, SP, and SG treatment had a much higher pH (Fig. 1) and a lower Cd bioavailability than CK, which may have caused the significant differences in microbial diversity.

Table 5
α-diversity indices

Treatments	ACE	Chao1	Shannon	Simpson
FCK	1477	1491	7.96	0.9872
FG	1533	1535	8.32	0.9905
FSP	1555	1558	8.34	0.9887
FSG	1498	1503	8.21	0.9889
NCK	1479	1486	8.38	0.9917
NG	1585	1588	8.66	0.9925
NSP	1576	1576	8.78	0.9922
NSG	1539	1544	8.66	0.9919

3.5.2 Composition of the microbiota

Bacteria are the most important decomposers in soil. The microbiota compositions at phylum, for the 8 soil samples were analyzed. Fig. 4A showed the bacterial composition of the soil under the different treatments and its frequency of bacterial phyla. The soil bacteria in the experimental field were mainly from 10 phyla. Ten types of bacteria accounted for more than 90% of the total bacterial count. Proteobacteria, Actinobacteria, Bacteroidetes, Gemmatimonadetes, Acidobacteria in soil were the dominant community of soil microbes in the current experiment, accounting for 38.46%, 25.75%, 9.47%, 11.05%, 7.10%, respectively. These phyla have also been reported as the dominant groups in heavy metal contaminated soils (Liu et al., 2019; Tipayno et al., 2018).

In general, toxic pollutants reduce the relative abundance of microbial communities in normal soils but increase the relative abundance of heavy metal-resistant microbial communities (Xu et al., 2018). According to reports, Proteobacteria has the vast majority of heavy metal resistance genes, followed by Actinobacteria and Bacteroidetes as shown by metagenomic sequencing (Li et al., 2020).

In this study, the abundance of proteobacteria, which accounted for the largest proportion of soil bacteria, significantly increased under the FG, FSG, FSP treatments compared with control. Besides, abundance of proteobacteria reached a peak in the FSG treatment, which probably attribute to the more nutrient-rich environment present and higher soil pH under the goat manure treatment (Wu et al., 2017; Huang et al., 2018).

Actinobacteria was the other highly represented phylum in soil. The frequency of actinobacteria significantly decreased with the application of amendments under FWHC, while slightly increased under NWHC. The reason might be the GM and SP amendment had an immobilization effect on the toxicity of

heavy metals, thereby increasing the abundance of microbial communities that are not resistant to heavy metals. Gemmatimonadetes and Acidobacteria were basically stable between different treatments.

Figure 4B showed unweighted Pair-group Method with Arithmetic Mean (UPGMA) of the control and amended soil. The closer the samples and the shorter the branch length indicates that the species composition of the two samples are more similar. According to the genetic relationship between samples, all the treatment can be divided into three group. FCK and NCK represented the soil microbial environment without artificial disturbance. Under NWHC treatments, NG, NSP, and NSG indicated soil water capacity was another factor that affect the microbial diversity. The single immobilization treatments, for instance NG and NSP, were more closer than simultaneous application of SP and GM (refers to the NSG). There was similar findings among FG, FSP, and FSG treatments.

The similarity of species composition data among samples in control soil and amended soil was investigated by principal component analysis (PCoA). Fig. 4C showed comprehensive impact of water management and organic manure on the diversity of microbial communities based on the weighted Euclidean distance. This explained about 67.5% of the changes in the microbial community composition (first and second dimensions were 49.43% and 18.07%, respectively), indicating that relevant parameters such as soil moisture and organic manure had a significant impact on the microbial community. As shown in the PCoA analysis plots, the control and amended treatment could be easily separated, with CK results gathered together on the left side of the abscissa PC1, well separated from the NG, FG, NSP, FSP, NSG, and FSG treatments. Besides, the microbial communities in the normal water condition and water-saturated condition were independent of each other.

Furthermore, we could intuitively determine the relative dominance microbe through the comparison of absolute values of abundance with a heat map. Generally, one square represented one kind of bacteria (horizontal range) and its corresponding habitat (vertical range). The redder the square, the more dominant of abundance, and the bluer the square, the less prevalent of the abundance (Uddin et al., 2019). The heat map of the microbial genera after different soil treatments is shown in Fig. 4D. The bacterias were clustered according to the similarity of distribution in eight soil samples. Among the control treatments, the top five dominant bacteria genera (high to low dominance) were Armatimonadetes, Cyanobacteria, Gemmatimonadetes, Chloroflexi, Verrucomicrobia. Among the SP-amended treatments, the top five dominant bacteria genera (high to low dominance) were Firmicutes, Nitrospirae, Rokubacteria, GAL15, Elusimicrobia.

3.5.3 Relationships between bacteria community composition and environmental variables

Understanding the role of microbes in the solubility of Cadmium (Cd) is of fundamental importance for remediation of Cd toxicity. The present study aimed to identify the microbes that involved in regulating Cd solubility and to reveal possible mechanisms.

Previous studies have documented that soil microbes are sensitive to environmental changes (Fierer and Jackson, 2006; Paul, 2014; Zheng et al., 2016). but at the same time they are resilient and have the ability

to recover its structure to initial state after the perturbation disappeared (Allison and Martiny, 2008; Sydow et al., 2016). The effect of changed soil physicochemical properties and the available Cd on microbial community composition was performed by RDA (Fig. 5). The results of bacterial community analysis showed that the first two axes of RDA explain 37.24% and 18.53% of the total variation in the data, respectively. The bacterial communities in the soils following the FG, FSG, NG, and NSG treatments were distinct from those in the control, being separated primarily by the first axis, which was positively correlated with pH and DTPA-Cd, negative correlated with DOM.

Figure 5 also showed the relationship between abundant genera and soil physicochemical properties. The results showed that soil microbes such as bacteroidetes, patescibacteria, and proteobacteria were correlated positively with pH, DOM, and DTPA-Cd. Acidobacteria was correlated positively with DTPA-Cd, and negatively with pH and DOM.

The relationship of soil physicochemical properties and the available Cd content to the bacterial community variation and significant correlation indicated that GM or SP mixed additives may indirectly affect the soil microbial community by changing soil physicochemical properties and soil available Cd content (Fig. 5). Soil microbial community of SP treatments were closer than G and SG treatments compared to control.

4. Conclusions

As we already know, the application of SP inhibited transfer of Cd to plants through the increased of soil pH and decreased of available Cd. But, in this study, we found that SP decreased DOM in soil, and SP decreased available Cd under normal water condition, and increased available Cd under water-saturated condition. Besides, the application of GM significantly increased pH and DOM, but increased available Cd under different water condition. But, coupling of GM and water-saturated condition decreased Cd content in edible parts of pak choi. Furthermore, based on the Illumina NovaSeq sequencing platform, we found that the application of GM increased the diversity and richness of soil bacteria, especially the simultaneous application of goat manure and sepiolite (SG). Ten types of bacteria accounted for more than 90% of the total bacterial count. Proteobacteria, Actinobacteria, Bacteroidetes, Gemmatimonadetes, Acidobacteria in soil were the dominant community of soil microbes in the current experiment, accounting for 38.46%, 25.75%, 9.47%, 11.05%, 7.10%, respectively. The abundance of proteobacteria significantly increased under the FG, FSG, FSP treatments compared with control. The PCoA analysis indicated that relevant parameters such as soil moisture and organic manure had a significant impact on the microbial community. Soil microbes such as bacteroidetes, patescibacteria, and proteobacteria were correlated positively with pH, DOM, and DTPA-Cd. Acidobacteria was correlated positively with DTPA-Cd, and negatively with pH and DOM.

Declarations

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Competing Interests

The authors have no relevant financial or non-financial interests to disclose.

Author Contributions

All authors contributed to the study conception and design. Yiyun Liu and Yingming Xu contributed to the conception of the study. Yiyun Liu, Qinging Huang and Qin Xu performed the experiment. Lijie Zhao contributed significantly to data collection. Xuefeng Liang, Lin Wang, and Yuebing Sun helped perform the analysis with constructive discussions. The first draft of the manuscript was written by Yiyun Liu and all authors commented on previous versions of the manuscript. All authors read and approved the final manuscript.

Data Availability

The datasets generated during and analysed during the current study are available from the corresponding author on reasonable request.

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Figures

Figure 1

Effects of goat manure and water management on Soil pH and DOM

Figure 2

Effects of goat manure and water management on Cd content of pak choi

Figure 3

Effect of goat manure and water management on available Cd extracted by DTPA

Figure 4

(A) Bacterial community composition at the phylum level; (B) UPGMA analysis of the control and amended soil; (C) PCA analysis indicating the similarity in bacterial community composition at the phylum level; (D) Hierarchical clustering analysis and heat map at the phylum level

Figure 5

Redundancy analysis (RDA) between environmental factors and bacteria