



Research Article

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Comparison of nitrification inhibitors for mitigating cadmium accumulation in pakchoi and their associated microbial mechanisms

Wenxin DU, Qingyang ZHU[✉], Xiangting JING, Weijie HU, Yao ZHUANG, Yijie JIANG, Chongwei JIN[✉]

State Key Laboratory of Plant Environmental Resilience, Zhejiang University, Hangzhou 310058, China

Abstract: The use of nitrification inhibitors has been suggested as a strategy to decrease cadmium (Cd) accumulation in crops. However, the most efficient nitrification inhibitor for mitigating crop Cd accumulation remains to be elucidated, and whether and how changes in soil microbial structure are involved in this process also remains unclear. To address these questions, this study applied three commercial nitrification inhibitors, namely, dicyandiamide (DCD), 3,4-dimethylpyrazole phosphate (DMPP), and nitrapyrin (NP), to pakchoi. The results showed that both DCD and DMPP (but not NP) could efficiently decrease Cd concentrations in pakchoi in urea- and ammonium-fertilized soils. In addition, among the three tested nitrification inhibitors, DMPP was the most efficient in decreasing the Cd concentration in pakchoi. The nitrification inhibitors decreased pakchoi Cd concentrations by suppressing acidification-induced Cd availability and reshaping the soil microbial structure; the most effective nitrification inhibitor was DMPP. Ammonia oxidation generates the most protons during nitrification and is inhibited by nitrification inhibitors. Changes in environmental factors and predatory bacterial abundance caused by the nitrification inhibitors changed the soil microbial structure and increased the potential participants in plant Cd accumulation. In summary, our study identified DMPP as the most efficient nitrification inhibitor for mitigating crop Cd contamination and observed that the soil microbial structural changes caused by the nitrification inhibitors contributed to decreasing Cd concentration in pakchoi.

Key words: Cadmium (Cd); Nitrification inhibitor; Soil microbial structure; Safe crop production

1 Introduction

Cadmium (Cd) is an environmentally toxic substance that poses a significant risk to human health because of its notable biological toxicity (Satarug et al., 2010; Clemens et al., 2013; Li et al., 2021; Souza-Arroyo et al., 2022). Humans accumulate Cd through food intake, with Cd-contaminated food representing a worldwide problem (Schaefer et al., 2020). The consumption of crop foods produced in contaminated soil is a major route of Cd uptake by humans (Ryan et al., 1982; Clemens et al., 2013; Zulfiqar et al., 2022). Therefore, lowering Cd accumulation in soil and crops is crucial for protecting humans from Cd ingestion. However,

consistent relationships have not been observed between soil and plant Cd concentrations because soil properties, soil Cd contents, plant genetics, and nutrient management all affect plant Cd concentration (Smolders, 2001; Nazar et al., 2012; Schaefer et al., 2020). Many nutrients are associated with the availability of Cd in soil and the absorption capacity of Cd (Dheri et al., 2007; Sarwar et al., 2010; Lux et al., 2011; Liu et al., 2023), including nitrogen (N), which has the largest mineral nutrient demand among plants. Therefore, adjusting nutrient management is considered an effective, inexpensive, and time-saving strategy for minimizing Cd accumulation in plants (Sarwar et al., 2010; Zhu et al., 2023).

N management is one of the most common agronomic practices. In China, urea and ammonium account for over 95% of the total N fertilizer applied in crop production (Zhang and Zhang, 2008). Under most conditions, urea in the soil is quickly converted to ammonia by urease, and ammonia is finally converted to nitrate (NO₃⁻) by nitrification, which produces protons (H⁺) (Shi et al., 2019). This process leads to soil

✉ Qingyang ZHU, 21914114@zju.edu.cn

Chongwei JIN, jincw@zju.edu.cn

Qingyang ZHU, <https://orcid.org/0000-0002-3590-1330>

Chongwei JIN, <https://orcid.org/0000-0003-0896-8596>

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acidification, which increases the availability of Cd in the soil (Kirkham, 2006; Yu et al., 2016; Li et al., 2023). In addition, several lines of evidence have shown that the uptake of NO_3^- by root cells is accompanied by the promotion of Cd^{2+} uptake, which results from the induction of the iron-regulated transporter 1 (*IRT1*) and the requirement for an anion–cation balance (Luo et al., 2012; Mao et al., 2014; Guan et al., 2015). Therefore, inhibiting nitrification may effectively lower Cd uptake by crops in the case of urea or ammonium fertilization.

Nitrification inhibitors are widely used to suppress nitrification, and a few types, such as dicyandiamide (DCD), have been shown to decrease plant Cd accumulation (Xie et al., 2009; You et al., 2020). Although several commercial nitrification inhibitors have been used for N management in agricultural production, there are significant differences among them in terms of their nitrification inhibition efficiency (Wang et al., 2017; Zhou et al., 2020). Moreover, little information is available on which inhibitor is the most effective chemical agent for mitigating Cd accumulation in crops. In addition, nitrification inhibitors have been shown to strongly affect the microbial community in soils (Di and Cameron, 2004; Carneiro et al., 2010; O'Callaghan et al., 2010; Kleineidam et al., 2011); however, whether and how nitrification inhibitor-mediated changes in the microbial community play a role in mitigating plant Cd accumulation remains unknown. Soil microorganisms have been shown to alter the availability and uptake of Cd by plants through various pathways (Dong et al., 2007; Shahid et al., 2019). Therefore, the most efficient nitrification inhibitors for mitigating Cd accumulation in crops must be screened from among the main commercial inhibitors, and how nitrification inhibitor-mediated changes in the microbial community affect Cd accumulation in crops must be determined.

Brassica rapa subsp. *chinensis* (pakchoi) is a vegetable widely cultivated and consumed in East and Southeast Asia. In this study, we conducted a pot experiment using pakchoi to compare the Cd-mitigation effectiveness of three commonly used commercial nitrification inhibitors (Zhou et al., 2020): DCD (CAS: 461-58-5), 3,4-dimethylpyrazole phosphate (DMPP; CAS: 202842-98-6), and nitrapyrin (NP; CAS: 1929-82-4). 16S ribosomal RNA (rRNA) sequencing was performed to investigate the relationship between nitrification inhibitor-mediated changes in the microbial community and Cd accumulation in pakchoi.

2 Materials and methods

2.1 Soil properties and plant cultivation

The experimental soil was collected from Jiangan District, Hangzhou, China (120°12'E, 30°16'N), and the following basic properties were determined according to the method described by Bao (2000): clay, 6.2%; silt, 28.8%; sand, 65.0%; electrical conductivity (EC), 0.7 mS/cm; cation-exchange capacity (CEC), 7.9 cmol/kg; organic C, 11.5 g/kg; $\text{NH}_4^+\text{-N}$, 2.5 mg/kg; $\text{NO}_3^-\text{-N}$, 13.4 mg/kg; total Cd, 0.4 mg/kg; and pH 7.20. The air-dried soil was ground and passed through a 2-mm sieve, part of which was mixed with CdCl_2 at 2.5 mg Cd/kg soil. The soil underwent an aging period of one year and was then used to fill pots at 450 g/pot. The experiments were conducted in a greenhouse. Pakchoi plants were germinated on TS-1 substrate (Klasmann-Deilmann, Germany). After 7 d, seedlings with uniform growth were selected and transplanted (one per pot). The soil in each pot was watered to 60% of the field water-holding capacity (FWHC; 22% water content, mass fraction), and water was subsequently added to compensate for evaporation and transpiration. The pots were divided into three groups based on the form of N fertilizer applied, i.e., $\text{CO}(\text{NH}_2)_2$, $(\text{NH}_4)_2\text{SO}_4$, or $\text{Ca}(\text{NO}_3)_2$. They were then further divided into four subgroups (control, DCD, DMPP, and NP) based on whether a nitrification inhibitor was added and the type of nitrification inhibitor that was applied for 12 treatments. At the true leaf and vigorous growth stages (Days 14 and 28, respectively), 0.2 g N/kg N fertilizer with a pre-mixed nitrification inhibitor was applied to the appropriate pots. The recommended nitrification inhibitor use rate was taken from previous studies and suggestions provided by Wolt (2000), Zerulla et al. (2001), and Kelliher et al. (2008). DCD was added at 10% of the N application rate, i.e., 0.02 g/kg, and DMPP and NP were added at 2% and 1%, respectively. On Day 35, the edible parts of the pakchoi were harvested and weighed, and soil samples were collected for further analysis.

2.2 Determination of plant cadmium concentration and soil properties

The edible parts of the pakchoi were dried at 65 °C for 48 h and were then digested (Zhu et al., 2020). The Cd concentration was measured by 4200 microwave plasma-atomic emission spectrometer (MP-AES)

(Agilent Technologies, USA). Soil $\text{NH}_4^+\text{-N}$ and diethylenetriamine pentaacetate (DTPA)-extractable Cd (DTPA-Cd) concentrations were determined according to standard procedures (Bao, 2000). $\text{NH}_4^+\text{-N}$ was determined by the indophenol blue colorimetric method, and the absorbance was measured at 625 nm by SpectraMax i3x (Melville Devices, USA). DTPA-Cd was measured using the 4200 MP-AES. Soil $\text{NO}_3^-\text{-N}$ was determined by dual-wavelength spectrophotometry at 220 and 275 nm according to the procedure of the National Standard of China (GB/T 32737-2016), and soil pH was measured by pH electrode placed in a mixture of 1 g of fresh soil and 10 mL of deionized water.

Data analyses were performed using Excel 2019, IBM SPSS 21.0, and Origin 2018. Both one-way analysis of variance (ANOVA) and two-way ANOVA were used to determine statistical significance ($P < 0.05$), and Duncan's test was used for multiple comparisons.

2.3 DNA extraction and sequencing analysis

Total genomic DNA was extracted and purified from 0.5 g of each individual soil sample by the Mag-Bind Soil DNA Kit (Omega Bio-Tek, USA) following the manufacturer's protocol. DNA quality was checked using electrophoresis in 1% (0.01 g/mL) agarose gel (GUHE Info Technology Co., Ltd., Hangzhou, China).

The primers 515F (5'-GTGCCAGCMGCCGCG GTAA-3') and 806R (5'-GGACTACHVGGGTWTCT AAT-3') were used to amplify the V4 region of bacterial 16S rRNA genes. Polymerase chain reaction (PCR) amplicons were purified, quantified, and sequenced on an Illumina NovaSeq 6000 platform (San Diego, USA). Barcodes were used to assign raw sequencing reads to the respective samples and were identified as valid sequences. Low-quality sequences were filtered (Gill et al., 2006; Chen and Jiang, 2014), and then operational taxonomic units (OTUs) were selected using Vsearch (v2.15.0), including dereplication, cluster, and chimera detection processes (Rognes et al., 2016). The OTU taxonomic classification was performed by searching the representative sequence set against the SILVA138 database using QIIME 2 (v2020.6) (Quast et al., 2013; Bolyen et al., 2019). OTUs containing less than 0.001% of the total sequences across all samples were discarded.

The OTU-level diversity indices, including the Shannon diversity index, Simpson index, Chao1 richness estimator, goods coverage, and rarefaction curves,

were calculated using QIIME 2 to compare the richness and evenness of the microbial communities in the different treatments. A β -diversity analysis was performed using Bray–Curtis distance matrices and was visualized via a constrained principal coordinate analysis (CPCoA) using the R (v.3.2.0) package “amplicon.” A permutational multivariate analysis of variance (PERMANOVA) was performed using the R package “vegan” to investigate variations in microbial community structures across samples. A principal component analysis (PCA) was performed based on genus-level compositional profiles.

Linear discriminant analysis (LDA) effect size (LEfSe) was used to identify microbial taxa with different abundance levels (LDA score > 3 ; $P < 0.05$) (Segata et al., 2011), and upset plots (R package UpSet) were used to visualize the results. A Pearson's correlation analysis (R package stats) was used to explore the relationships between the identified microbial taxa and soil properties, pakchoi yield, and Cd concentration. The ecological functions of different treatments were predicted using the Functional Annotation of Prokaryotic Taxa (FAPROTAX) database (Louca et al., 2016). Structural equation modeling (SEM; IBM SPSS Amos) was performed to evaluate the potential direct or indirect effects of the following factors: nitrification rate (proportion of $\text{NO}_3^-\text{-N}$ in the total $\text{NH}_4^+\text{-N}$ and $\text{NO}_3^-\text{-N}$) (Lin et al., 2004), soil pH, soil available Cd (DTPA-Cd concentration), soil microbial diversity (non-metric multidimensional scaling (NMDS) using Bray–Curtis distance matrices; NMDS2), and pakchoi Cd accumulation.

3 Results

3.1 Effects of different nitrification inhibitors on the yield and Cd concentration of edible parts

In uncontaminated soil, the application of DCD, DMPP, or NP had little effect on the yield of edible pakchoi under all three N fertilizer treatments (Figs. 1a–1c; Table S1). Cd contamination of the soil significantly inhibited the yield of the edible parts in the ammonium and nitrate treatments and had little effect on the urea treatment. Applying DCD and DMPP (but not NP) completely abolished the decreased yield from Cd contamination during the ammonium treatment. However, none of the tested nitrification inhibitors affected the yield of the edible parts of pakchoi under the nitrate

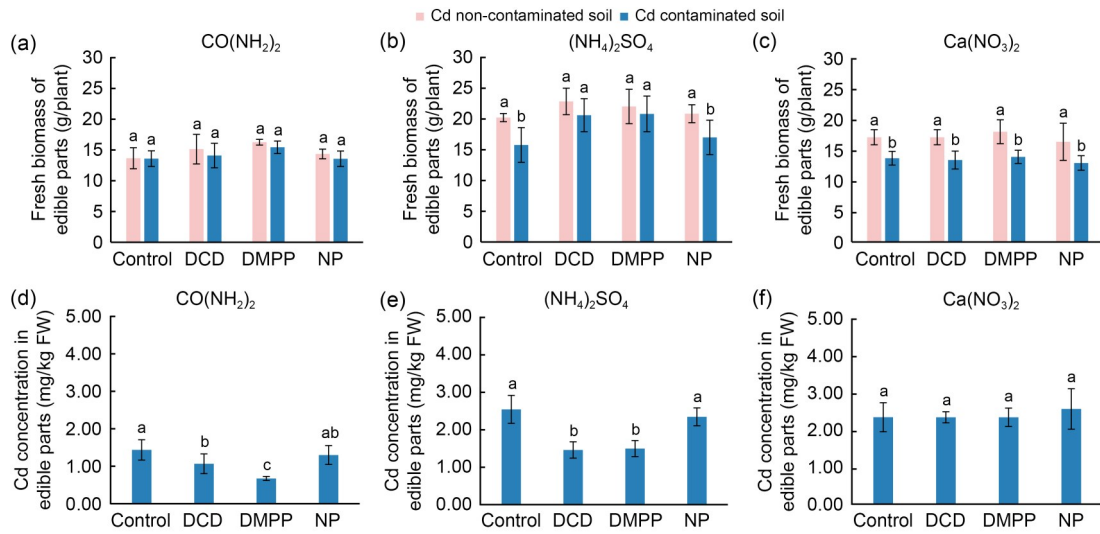


Fig. 1 Effects of the nitrification inhibitors on the yield (a–c) and cadmium (Cd) concentration (d–f) of the edible parts of pakchoi (fresh weight (FW)). $\text{CO}(\text{NH}_2)_2$, $(\text{NH}_4)_2\text{SO}_4$, and $\text{Ca}(\text{NO}_3)_2$ were used as the N fertilizers. Nitrification inhibitors were not applied to the control treatment. Data are expressed as mean \pm standard deviation (SD) ($n=5$). Different letters represent significant differences (Duncan's test; $P < 0.05$). DCD: dicyandiamide; DMPP: 3,4-dimethylpyrazole phosphate; NP: nitrapyrin.

treatment. Compared with the effect on yield, the application of DCD or DMPP lowered the Cd concentration in the edible parts of pakchoi in the urea treatment (Fig. 1d and S1; Table S1). This effect was particularly significant for the application of DMPP, which decreased the Cd concentration by approximately 60% compared with the control (without nitrification inhibitor application). In the ammonium treatment, DCD and DMPP applications similarly decreased the Cd concentration in the edible parts at a rate of approximately 40% (Fig. 1e; Table S1). NP application had little effect on the Cd concentration in the edible parts in both the urea and ammonium treatments. In addition, the tested nitrification inhibitors did not affect the Cd concentration in the edible parts in the nitrate treatment (Fig. 1f; Table S1). The above results suggest that the effects of nitrification inhibitors on the growth and Cd concentration of pakchoi depend on the type of nitrification inhibitor and the form of N fertilizer. Since urea is the most commonly used N fertilizer in agricultural production, DMPP could be considered the most efficient nitrification inhibitor for mitigating Cd accumulation in pakchoi.

3.2 Effects of different nitrification inhibitors on the soil properties

In the soil fertilized with urea, applying the three tested nitrification inhibitors significantly increased the

NH_4^+ -N concentration in the soil at harvest compared with that of the control treatment (Fig. 2; Table S1), with DMPP showing the most significant effect. Compared with the effect on NH_4^+ -N concentration, the three tested nitrification inhibitors significantly decreased the NO_3^- -N concentration in the soil, with DMPP showing the most significant effect. The effects of all three tested nitrification inhibitors on the NH_4^+ -N and NO_3^- -N concentrations in soil fertilized with ammonium were similar to those in soil fertilized with urea. None of the tested nitrification inhibitors affected the NH_4^+ -N and NO_3^- -N concentration in soil fertilized with nitrate. Consequently, DMPP had the lowest nitrification rates (ratio of NO_3^- -N to total mineral N), with urea and ammonium fertilizers at only 5.61% and 4.04%, respectively. The above results suggest that the effects of nitrification inhibitors depend on the type of nitrification inhibitor and the form of N fertilizer, and that DMPP could be the most efficient nitrification inhibitor when urea or ammonium are used as fertilizers.

DCD and DMPP significantly elevated the soil pH in the urea and ammonium fertilizer treatments (Figs. 3a and 3b; Table S1), with DMPP showing greater effectiveness. As expected, the three nitrification inhibitors had little effect on the pH of soil fertilized with nitrate (Fig. 3c). DCD and DMPP (but not NP) decreased DTPA-Cd in soil fertilized with urea or ammonium compared with the control (Figs. 3d and 3e). The greatest decrease was observed with DMPP and urea

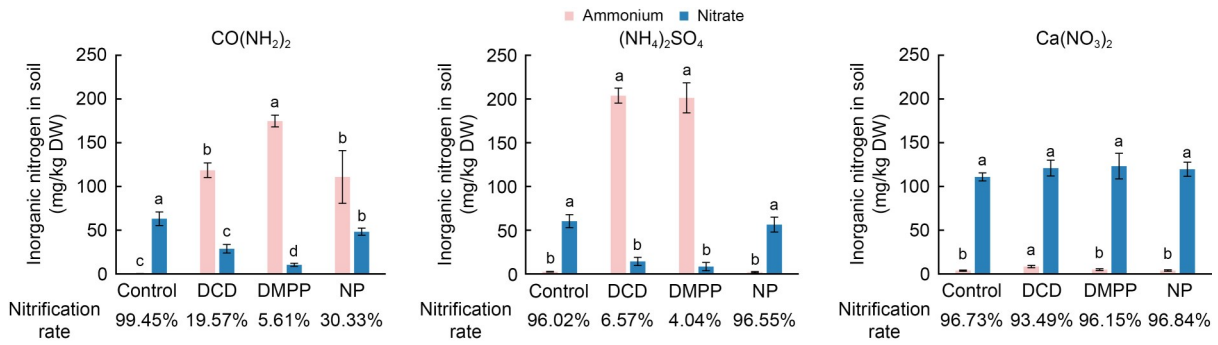


Fig. 2 Effects of the nitrification inhibitors on the concentrations of NH₄⁺-N and NO₃⁻-N in the soil. CO(NH₂)₂, (NH₄)₂SO₄, and Ca(NO₃)₂ were used as the N fertilizers. Nitrification inhibitors were not applied to the control treatment. Data are expressed as mean±standard deviation (SD) (*n*=5). Different letters represent significant differences among the ammonium or nitrate group (Duncan's test; *P*<0.05). DCD: dicyandiamide; DMPP: 3,4-dimethylpyrazole phosphate; NP: nitrapyrin; DW: dry weight.

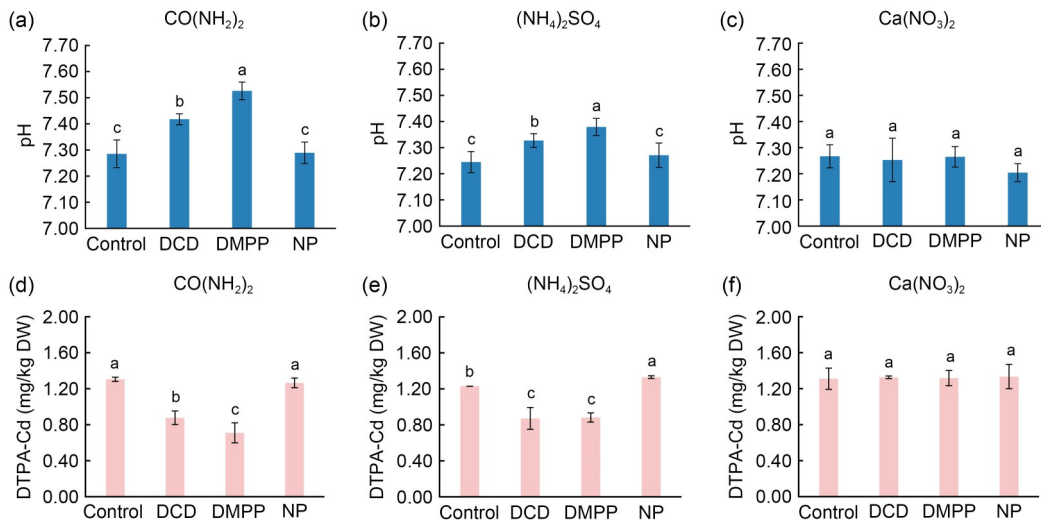


Fig. 3 Effects of the nitrification inhibitors on the pH (a–c) and concentrations of available cadmium (Cd) (d–f) in the soil. CO(NH₂)₂, (NH₄)₂SO₄, and Ca(NO₃)₂ were used as the N fertilizers. Nitrification inhibitors were not applied to the control treatment. Data are expressed as mean±standard deviation (SD) (*n*=5). Different letters represent significant differences (Duncan's test; *P*<0.05). DTPA Cd: diethylenetriamine pentaacetate (DTPA)-extractable Cd; DCD: dicyandiamide; DMPP: 3,4-dimethylpyrazole phosphate; NP: nitrapyrin; DW: dry weight.

at approximately 46% compared with that in the control. However, the nitrification inhibitors did not affect DTPA-Cd in the soil fertilized with nitrate (Fig. 3f). These results suggest that DCD and DMPP can efficiently mitigate acidification and Cd availability in soil fertilized with urea or ammonium; DMPP had a greater effect on soil fertilized with urea.

3.3 Effects of different nitrification inhibitors on the soil microbial structure

We first analyzed the effects of different nitrification inhibitors on the microbial structure in Cd-contaminated soils at the phylum level. The dominant phyla (average relative abundance greater than 1%) in

all treatments accounted for >95% of the total abundance (Fig. 4a). DCD and DMPP (but not NP) significantly decreased the abundance of Actinobacteriota in soil fertilized with urea compared to that of the control. All three nitrification inhibitors decreased the abundance of Patescibacteria in soils fertilized with urea or ammonium, with the greatest decrease observed for DMPP in ammonium-fertilized soil. The abundance of Proteobacteria, the most abundant phylum (32.34%), varied significantly between the different nitrification inhibitors, with DMPP presenting the lowest abundance in soils fertilized with urea or ammonium.

CPCoA based on Bray–Curtis distance matrices was performed to visualize the differences in soil

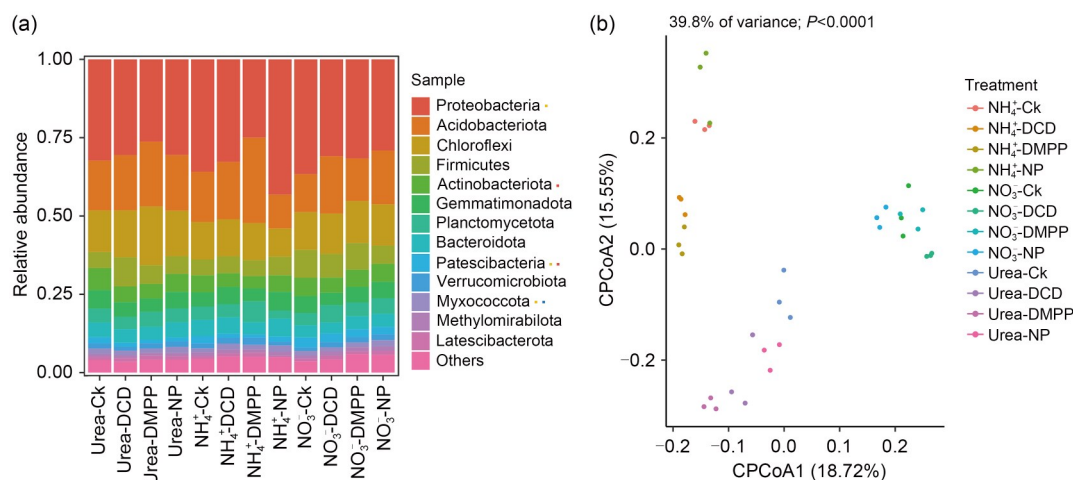


Fig. 4 Effects of different nitrification inhibitors on the soil microbial structure. (a) Phylum-level relative abundance in soil treated with different nitrification inhibitors and different fertilizers. Abundance represents the average ($n=3$). Red, yellow, and blue dots represent significant differences (one-way analysis of variance (ANOVA); Duncan's test; $P<0.05$) in soil fertilized with urea, ammonium, and nitrate, respectively. (b) A constrained principal coordinate analysis (CPCoA) plot was used to characterize the differences in soil β -diversity between different treatments (39.8% of variance; $P<0.0001$, $n=36$; based on the Bray-Curtis distance). Ck: control check; DCD: dicyandiamide; DMPP: 3,4-dimethylpyrazole phosphate; NP: nitrapyrin (Note: for interpretation of the references to color in this figure legend, the reader is referred to the web version of this article).

microbial structures. The results revealed that approximately 39.8% of the overall variance in soil microbial structure was attributed to the nitrification inhibitor type and N fertilizer form (Fig. 4b). CPCoA2 explained 15.55% of the variation in the microbial structure, with the nitrification inhibitor type representing a significant source of variation. Variance in microbial structures among the different nitrification inhibitors was observed in soils fertilized with urea or ammonium, but not with nitrate. This finding was further verified by PERMANOVA (Table S2). These results suggest that the effect of nitrification inhibitors on soil microbial structure is related to the type of nitrification inhibitor and the form of N fertilizer. Considering the above results and the effect of the nitrification inhibitors on the nitrification rate, a higher inhibitory effect on nitrification could lead to greater variation in microbial structure.

3.4 Significant microbial taxa and functional groups in the different nitrification inhibitor treatments

Since nitrification and microbial structure in the soil were significantly affected by nitrification inhibitors, we performed an LEfSe analysis to identify microbial taxa with significant differences in relative abundance between each nitrification inhibitor-treated soil sample and its corresponding control (Figs. 5 and S2).

A total of 135 microbial taxa with significant differences in relative abundance (70% of the total relative abundance) were identified, and more taxa were significantly depleted in the nitrification inhibitor-treated soil than were significantly enriched. Additionally, soils with greater nitrification inhibition (urea-DCD, urea-DMPP, NH₄⁺-DCD, and NH₄⁺-DMPP) had more significant microbial taxa. Urea-DMPP and NH₄⁺-DMPP led to the most significant microbial taxa ($n=59$ and $n=57$, respectively). Furthermore, significantly depleted taxa in the nitrification inhibitor-treated soil exhibited a greater overlap across different pairwise comparisons, particularly in the nitrification inhibitor-treated soil with significantly suppressed nitrification. In contrast, enriched taxa in the nitrification inhibitor-treated soil showed less overlap across the pairwise comparisons.

The Pearson's correlation analysis identified microbial taxa with significant differences in relative abundance that was significantly correlated with at least one of the soil properties: pH, DTPA-Cd, NH₄⁺-N, NO₃⁻-N, pakchoi yield, and Cd concentration. Among the 99 screened microbial taxa, 57 were significantly correlated with Cd concentration in pakchoi (Fig. 6), suggesting that these microbial taxa may affect Cd uptake by pakchoi. At the phylum level, Acidobacteriota (17% of the total relative abundance, including Blastocatellia 3%) was significantly enriched in urea-DMPP

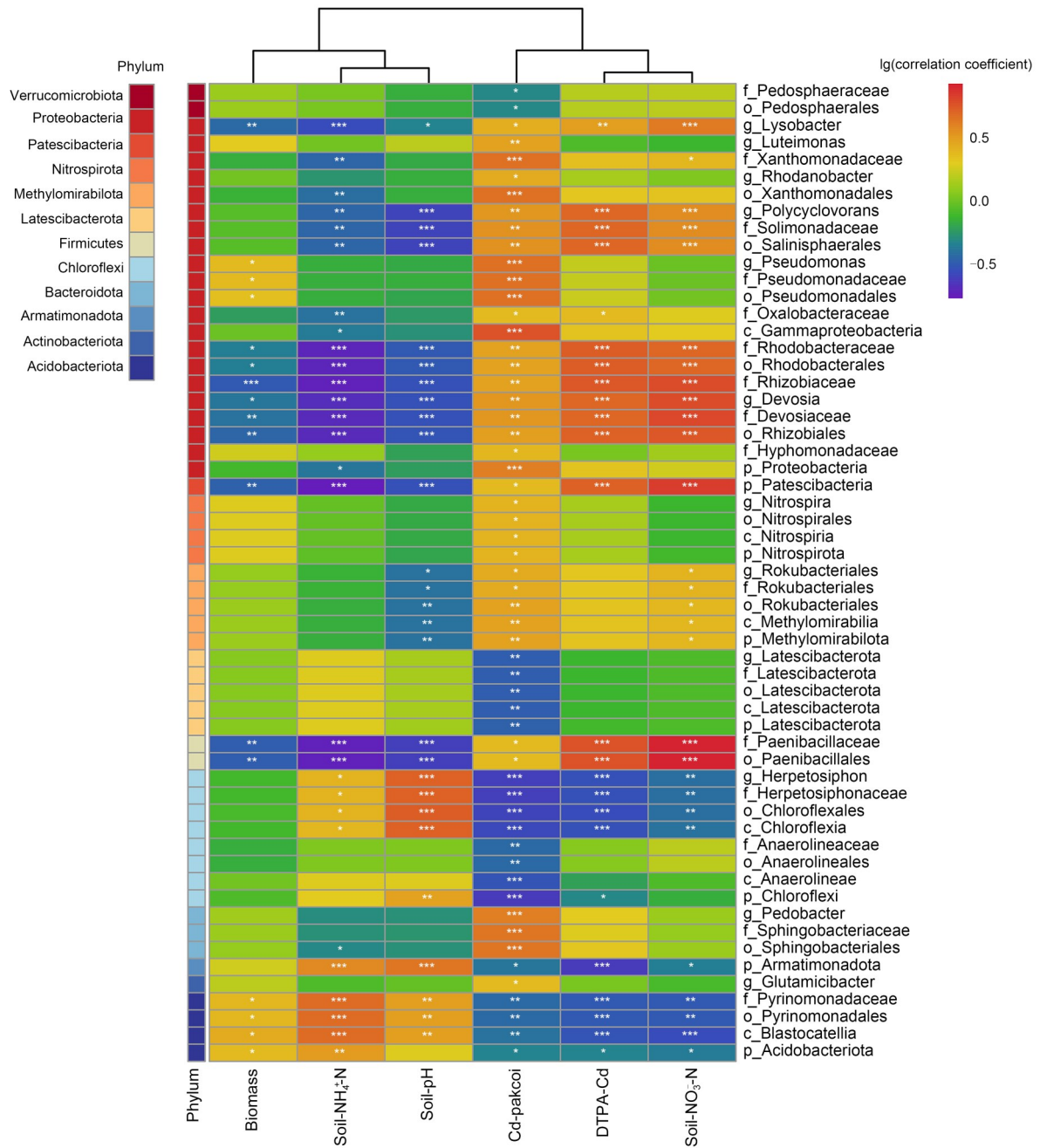


Fig. 6 Pearson's correlation heatmap of significant abundance of microbial taxa and soil properties, pakchoi yield, and pakchoi cadmium (Cd) concentration. The color scale indicates the strength and direction of the correlation, with warmer colors indicating a positive correlation and cooler colors indicating a negative correlation. The *P*-values for each correlation are indicated by asterisks (* *P*<0.05, ** *P*<0.01, and *** *P*<0.001). Strong correlations had absolute lg(correlation coefficient) values greater than 0.5. DTPA: diethylenetriamine pentaacetate; p: phylum; c: class; o: order; f: family; g: genus (Note: for interpretation of the references to color in this figure legend, the reader is referred to the web version of this article).

and NH₄⁺-DMPP soils compared with their respective controls. Additionally, Chloroflexi (13%, including Anaerolineae 7% and Chloroflexia 3%) was significantly enriched in the urea-DMPP soil. The application of N inhibitors (DCD, DMPP, and NP) to soils

fertilized with urea or ammonium resulted in the depletion of Patescibacteria (2% relative abundance). Moreover, Proteobacteria (32%) was significantly depleted in the urea-DMPP, NH₄⁺-DCD, and NH₄⁺-DMPP soils, and Gammaproteobacteria (17%) was significantly

depleted in the NH_4^+ -DCD and NH_4^+ -DMPP soils. Proteobacteria and Chloroflexi had a strong linear correlation with the Cd concentration in pakchoi ($|\text{rho}|>0.5$). Acidobacteriota and Patescibacteria showed significant correlations with soil pH, soil DTPA-Cd, soil NH_4^+ -N, soil NO_3^- -N, pakchoi yield, and Cd concentration.

At the genus level, *Devosia* and *Pedobacter* were significantly depleted in the NH_4^+ -DCD and NH_4^+ -DMPP soils compared with their corresponding controls. In contrast, *Lysobacter* was significantly depleted in all nitrification inhibitor treatments in soils with urea fertilization, in the DCD-treated soils with ammonium fertilization, and in the NP-treated soils with nitrate fertilization. *Herpetosiphon* was significantly enriched in all nitrification inhibitor treatments in soil fertilized with urea. *Pedobacter* and *Herpetosiphon* showed a strong linear correlation with the Cd concentration in pakchoi ($|\text{rho}|>0.5$). *Devosia* and *Lysobacter* were significantly correlated with soil pH, soil DTPA-Cd, soil NH_4^+ -N, soil NO_3^- -N, pakchoi yield, and Cd concentration.

FAPROTAX was used to assess the functional diversity of the microbial communities under different treatments (Fig. 7). Of the 1498 analyzed OTUs, 305 (20.4%) were assigned to 41 functional groups. PERMANOVA revealed that different nitrification inhibitors, N fertilization, and their interactions significantly influenced the functional microbial groups, reporting 61.95% of the variation (Table S3). Functional groups with significant differences under different nitrification inhibitors were screened in soil fertilized with urea, ammonium, or nitrate. The proportion of microorganisms involved in photoautotrophy and chitinolysis after DMPP or DCD application was significantly lower than that in the control soil fertilized with urea. In soil with ammonium fertilization, low-abundance OTUs with cellulolysis function were detected in the DCD, DMPP, and NP treatments compared with the control soil with ammonium fertilization. Meanwhile, DCD and DMPP decreased the abundance of OTUs associated with ureolysis and methylotrophy, and increased dark hydrogen oxidation. The highest

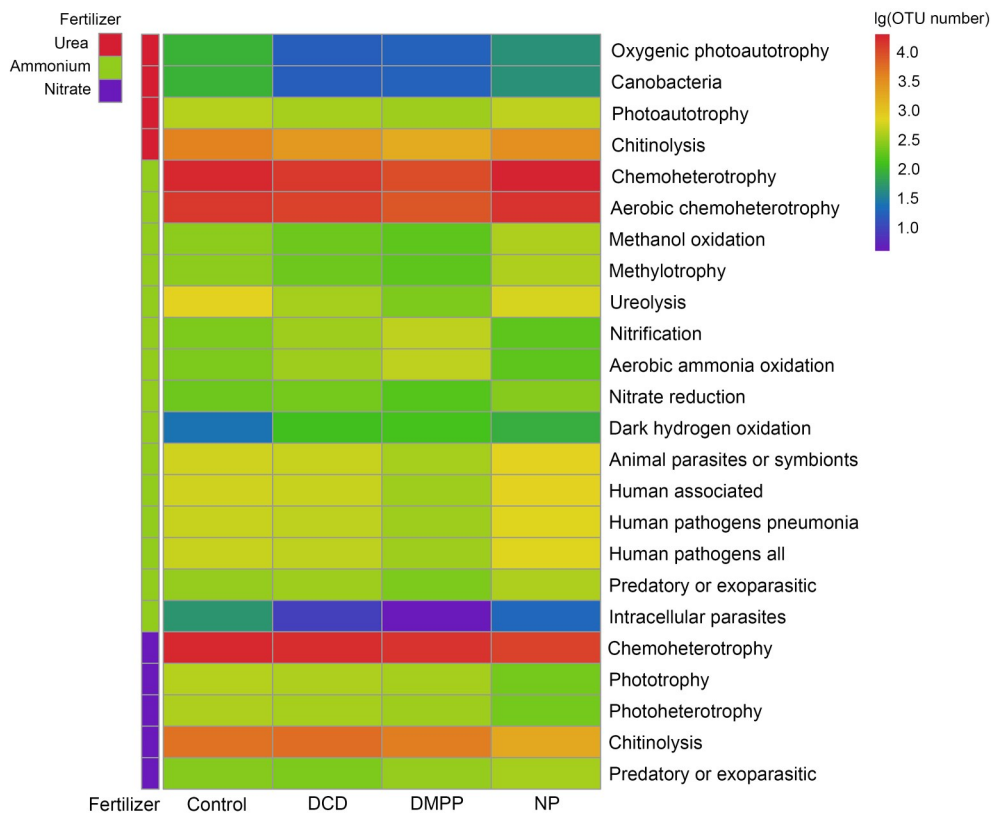


Fig. 7 Functional Annotation of Prokaryotic Taxa (FAPROTAX) heatmap showing significant functional microbial groups (one-way analysis of variance (ANOVA); Duncan's test; $P<0.05$, $n=3$) and their operational taxonomic unit (OTU) numbers under different nitrification inhibitor treatments. DCD: dicyandiamide; DMPP: 3,4-dimethylpyrazole phosphate; NP: nitrapyrin.

abundance of OTUs with aerobic ammonia oxidation and nitrification was detected in the DMPP treatment. In contrast, OTUs involved in chemoheterotrophy were not as abundant in the control, DCD, and NP treatments. Additionally, DMPP significantly decreased the number of microorganisms, such as human pathogens, animal parasites, and symbionts. NP decreased chemoheterotrophy, phototrophy, and chitinolysis; however, it increased predatory or exoparasitic microorganisms in nitrate-fertilized soil.

The LEfSe and FAPROTAX analyses showed that the abundance of ammonia-oxidizing microorganisms increased after the DMPP treatment in soil with ammonia fertilization. To further understand the variations in abundance, we summarized the genus-level relative abundances of ammonia-oxidizing archaea (AOA), ammonia-oxidizing bacteria (AOB), and nitrite-oxidizing bacteria (NOB) in the treatments that had significant inhibitory effects on nitrification (Fig. 8). The abundance of *Nitrosomonas* was significantly lower in the DCD and DMPP treatments than in the control soil with urea and ammonia fertilization. However, the DMPP treatment decreased the abundance of *Nitrospira* in urea- and ammonia-fertilized soil. In contrast, *Nitrosococcus* was more abundant in the DCD and DMPP treatments than in the control soil fertilized with ammonia. In soil fertilized with ammonia, DMPP application significantly increased the abundance of *Nitrososphaeraceae*, *Candidatus_Nitrosotenuis*, and

Candidatus_Nitrososphaera; *Nitrososphaeraceae* increased in soil with DCD application. In addition, the relative abundance of *Nitrospira* (NOB) was significantly decreased in the ammonia-fertilized soil with DMPP application compared with the control, consistent with the LEfSe analysis. Furthermore, the Pearson's correlation analysis showed that the abundance of *Nitrospira* was significantly and positively correlated with the Cd concentration in pakchoi.

3.5 Factors contributing to the decrease of Cd in edible parts by the application of nitrification inhibitors

The question then arises of how nitrification inhibitors lower Cd concentration in the edible parts of pakchoi. SEM was used to analyze the relationships, among nitrification rate, pH, DTPA-Cd, soil microbial diversity, and Cd concentration in the edible parts of pakchoi (Fig. 9). The results showed that both pH and microbial diversity were negatively correlated with the nitrification rate. In contrast, soil pH was negatively correlated with soil DTPA-Cd. Therefore, the decrease in available Cd due to DMPP or DCD application in the urea or ammonium treatment should be attributed to an increase in pH resulting from the inhibition of nitrification. As expected, the Cd concentration in the edible parts of pakchoi was positively correlated with that of DTPA-Cd. However, a negative correlation was observed between the β -diversity and Cd concentration

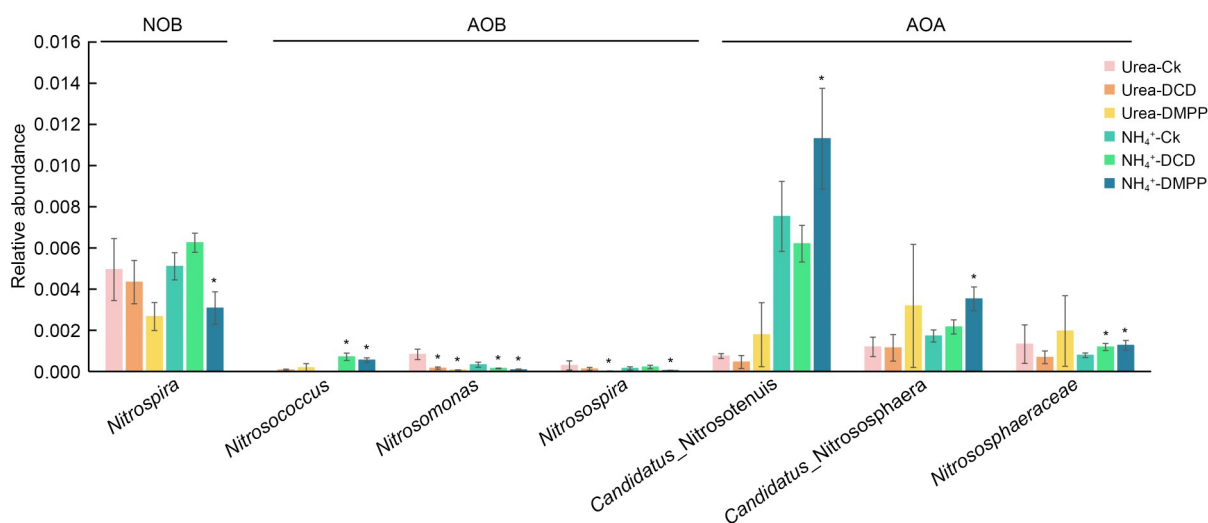


Fig. 8 Relative abundance of ammonia-oxidizing archaea (AOA), ammonia-oxidizing bacteria (AOB), and nitrite-oxidizing bacteria (NOB) in the different treatments. Data are expressed as mean \pm standard deviation (SD) ($n=3$). * Significant difference compared with the control (one-way analysis of variance (ANOVA); Duncan's test; $P<0.05$). Ck: control check; DCD: dicyandiamide; DMPP: 3,4-dimethylpyrazole phosphate; NP: nitrapyrin.

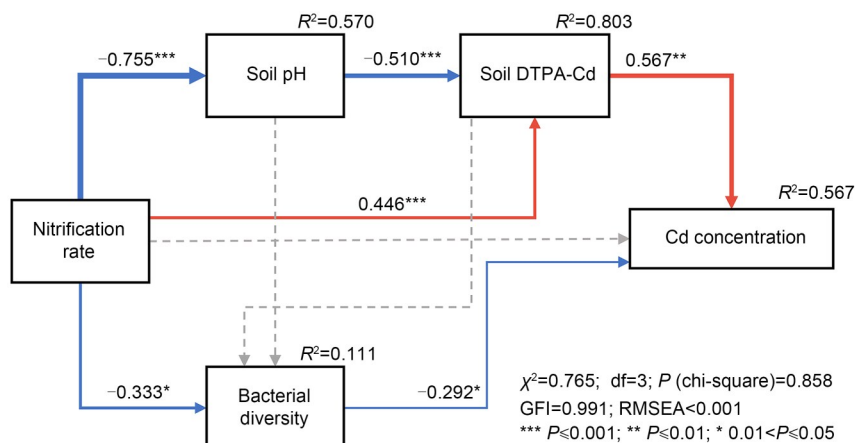


Fig. 9 Structural equation modeling (SEM) illustration of the direct or indirect effects of various factors, including the inhibitory effect of nitrification inhibitors (larger nitrification rates indicate a worse inhibitory effect), soil properties (soil pH and diethylenetriamine pentaacetate (DTPA)-extractable cadmium (DTPA-Cd)), bacterial diversity, and Cd concentration of pakchoi. The red line represents a significant positive correlation, and the blue represents a significant negative correlation. A thicker line indicates a stronger correlation between factors. The dotted lines indicate no significant correlation. df: degree of freedom; GFI: goodness of fit index; RMSEA: root mean square error of approximation (Note: for interpretation of the references to color in this figure legend, the reader is referred to the web version of this article).

of pakchoi. Consequently, the decrease in available Cd and the increase in microbial diversity because of the inhibited nitrification should contribute to the decreased Cd accumulation in the edible parts of pakchoi in the urea or ammonium treatment with DMPP or DCD application.

4 Discussion

4.1 DMPP as a highly efficient nitrification inhibitor for mitigating Cd accumulation in pakchoi

DCD, DMPP, and NP are three commercial nitrification inhibitors that are commonly used in agricultural production. In this study, we observed that DCD and DMPP (but not NP) could efficiently lower the Cd concentration in the edible parts when urea or ammonium was used as the N fertilizer. This was particularly true when applying DMPP with urea fertilization, which decreased the Cd concentration in the edible parts of pakchoi much more than the application of DCD did. Since urea is widely used as an N fertilizer in agricultural production (Witte, 2011; Singh et al., 2023), DMPP can be considered the most efficient nitrification inhibitor for mitigating Cd accumulation in pakchoi. Considering that DCD has a high N content (66.7%) and requires a high input amount to realize an efficient inhibitory effect on nitrification, the

nature of the decomposition of DCD to ammonia in the soil after its application may intensify soil acidification caused by nitrification (Vilmsmeier, 1980), which is not favorable for the mitigation of Cd contamination in crops. NP had little effect on the mitigation of Cd concentration in the edible parts (Fig. 1; Table S1), which may have been due to the unstable nature of NP in soils (Lewis et al., 2016; Papadopoulou et al., 2020).

Nitrification inhibitors may negatively affect plant growth, thereby inhibiting Cd absorption by plant roots (Macadam et al., 2003; Kelliher et al., 2008). However, this should not be the case in this study because the three tested nitrification inhibitors had little effect on Cd concentration in the edible parts of pakchoi when nitrate was used as the N source. SEM (Fig. 9) revealed that the differences in pakchoi Cd concentration between treatments were mainly related to the reduced availability of Cd in the soil due to the inhibition of nitrification. This was expected because nitrification results in soil acidification, increasing Cd availability. A decrease in available soil Cd by increasing soil pH decreases Cd accumulation in crops. For example, Cd concentrations decreased in lettuce, cabbages (Jackson and Alloway, 1991), and rice (Zhu et al., 2016) as the soil pH increased. The SEM results suggested an important role for soil microbial diversity in mitigating Cd concentrations, as discussed below.

Additionally, the nitrification inhibitory effect of nitrification inhibitors on soil was observed to be

correlated with soil pH. As soil pH increases, the dominance of AOB with lower ammonia affinity increases relative to that of AOA with nitrification (Amoo and Babalola, 2017; Kits et al., 2017; Jung et al., 2022). These AOBs are the main targets of nitrification inhibitors (Shi et al., 2016; Papadopoulou et al., 2020). In addition, nitrification inhibitors exhibited more robust inhibitory effects on nitrification in alkaline soils than in acidic or neutral soils (Cui et al., 2021). The above findings suggest that applying nitrification inhibition may be more effective in inhibiting soil acidification and decreasing Cd solubility in alkaline soils.

4.2 Possible mechanisms: how nitrification inhibitors alter soil microbial community to decrease Cd content in pakchoi

Soil microorganisms play an important role in the biogeochemical cycles of soil ecosystems (Leibold and McPeck, 2006). The application of nitrification inhibitors resulted in significant changes in the soil microbial structure. This phenomenon was particularly evident in urea- and ammonium-fertilized soils treated with DMPP. Meanwhile, the SEM results showed that nitrification inhibitors suppressed the acidification-induced availability of Cd in soil by inhibiting nitrification and reshaping microbial communities to lower the Cd concentration in pakchoi. Specific microbial groups may be associated with the mitigating effects of nitrification inhibitors on Cd accumulation in pakchoi; alterations in nitrifying microorganisms may be the key factors. Among the three tested nitrification inhibitors, DMPP had the greatest inhibitory effect on the abundance of *Nitrosomonas* and *Nitrosospora* (Fig. 8), which are known to have higher maximum rates of ammonia oxidation than AOA (Martens-Habbena et al., 2009; Kits et al., 2017; Jung et al., 2022). This effect may be the main reason for the inhibition of nitrification in the tested soils. Additionally, although AOAs are more abundant than AOBs, they do not dominate the nitrification process (Schauss et al., 2009). Given that the ammonia oxidation process is the main step of nitrification that produces H^+ , a decrease in the ammonia oxidation rate may decrease the available Cd in the soil. Additionally, DMPP has a slight inhibitory effect on NOB (Papadopoulou et al., 2020), which may be coupled with the inhibition of the upstream limiting step (ammonia oxidation), thus leading to a decrease in *Nitrosospora* abundance in the NH_4^+ -DMPP treatment.

This decrease may further lower nitrite oxidation to decrease NO_3^- -N production, which could decrease Cd^{2+} uptake by root cells. This is because the decrease in root cell uptake of NO_3^- lowers Cd^{2+} uptake by inducing the Fe^{2+} transporter *IRT1* and the requirement for anion-cation balance (Luo et al., 2012; Mao et al., 2014; Guan et al., 2015).

We focused on *Herpetosiphon* and *Lysobacter* in the LEfSe analysis because of their significant correlation with Cd concentration in pakchoi and their high abundance (>1%) in soils (Figs. 6 and S3). Both are predatory bacteria that may enhance the effects of nitrification inhibitors on the soil microbial structure (Pasternak et al., 2013; Pérez et al., 2016) and ultimately affect plants' uptake of Cd by preying on other bacteria (Yang et al., 2020). In addition, due to changes in the soil chemistry and biological environment, significant changes occurred in the abundance of many microorganisms that have been reported to promote plant growth or decrease soil Cd availability. For example, Pedosphaeraceae, Anaerolineaceae, *Gemmata*, and *Terrimonas* increased with DMPP or DCD in the urea and NH_4^+ treatments. *Terrimonas* and Pedosphaeraceae exhibited Cd tolerance and plant growth-promoting capabilities (She et al., 2021; Yuan et al., 2022). Similarly, *Gemmata* abundance negatively correlated with heavy metal concentrations in plants, and a few of its species had heavy metal resistance genes (Aghnatiou and Drancourt, 2016; Singh et al., 2020). Anaerolineaceae lowered Cd solubility by coexisting with methane-metabolizing microorganisms (Meng et al., 2019). In contrast, a few microorganisms decreased in the DMPP or DCD treatment. For example, *Devosia* had a high abundance (0.6%) and was significantly positively correlated with the Cd concentration in pakchoi. Previous research has shown a significant positive correlation between *Devosia*, soil heavy metal availability, and plant Cd concentration, suggesting that it may play a role in shaping the soil microbial community (Chen et al., 2018; Wang et al., 2021).

Certain microbial groups may indirectly decrease soil Cd availability by influencing the soil environment. For example, in the NH_4^+ -DMPP and NH_4^+ -DCD treatments, the number of functional groups involved in dark hydrogen oxidation increased significantly (Fig. 7). Hydrogen-oxidizing microorganisms (HOMs) play an important role in the soil-carbon cycle (Piché-Choquette and Constant, 2019) and CO_2 fixation, which may

contribute to the formation of complexes between Cd and organic matter (Dong and Layzell, 2001; Stein et al., 2005). Moreover, HOM is believed to enhance the soil nutrient status and serve as a plant growth-promoting rhizobacteria (PGPR) (Dong et al., 2003), which may decrease the Cd content in pakchoi because of the dilution effect resulting from growth promotion. However, the effect of nitrification inhibitors on the microbial community structure is poorly understood, and the function of microorganisms involved in Cd accumulation remains unclear. Future studies on microbial functions via the isolation of individual bacterial strains and metagenomics may provide a better understanding of how nitrification inhibitors reshape the microbial community structure and subsequently influence crops' uptake of Cd.

5 Conclusions

DCD and DMPP (but not NP) efficiently mitigated Cd concentration in pakchoi grown in soil fertilized with urea or ammonium. DMPP showed a greater effect than DCD. The difference in the rate of decrease in the pakchoi Cd concentrations between different nitrification inhibitor treatments was related to the inhibition of the acidification-induced availability of Cd in the soil. The changes in the soil microbial community caused by nitrification inhibitors played an important role in mitigating the Cd concentration in pakchoi. Many microorganisms were regulated by the changes in soil chemistry and the biological environment and directly or indirectly participated in the mitigation of Cd accumulation in pakchoi in diverse ways.

Data availability statement

All data generated or analyzed during this study are included in this published article. For further detailed information, please refer to us.

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Author contributions

Wenxin DU: investigation, formal analysis, visualization, and writing – original draft. Qingyang ZHU: methodology and writing – review & editing. Xiangting JING, Weijie HU, and Yao ZHUANG: methodology. Yijie JIANG: data curation. Chongwei JIN: conceptualization and writing – original draft.

All authors have read and approved the final manuscript, and therefore, have full access to all the data in the study and take responsibility for the integrity and security of the data.

Compliance with ethics guidelines

Wenxin DU, Qingyang ZHU, Xiangting JING, Weijie HU, Yao ZHUANG, Yijie JIANG, and Chongwei JIN declare that they have no conflict of interest.

This article does not contain any studies with human or animal subjects performed by any of the authors.

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Supplementary information

Tables S1–S3; Figs. S1–S3