Effects of polymer modifiers on the bacterial communities in cadmium-contaminated alkaline soil

MengJie An, Changzhou Wei , Kaiyong Wang*, Hua Fan & Xiaoli Wang
Agriculture College, Shihezi University, Shihezi, Xinjiang, 832003, China. *email: wky20@163.com

Introduction

The Cd in the soils can be absorbed by plants, and then enter human bodies through food chain. Therefore, remediation of the Cd-contaminated agricultural soils is one of the important ways to reduce human exposure to dietary Cd.

In recent years, studies have shown that chemical modifiers directly or indirectly change the forms and bioavailability of heavy metals without affecting soil structure, which is a low-cost and high-efficiency method to treat heavy metal contamination (Liang et al., 2019). However, most of the polymer materials used in the researches are solid, so we made up liquid polymer modifiers according to the material characteristics and apply them to soils through drip irrigation, aiming to provide help for the remediation of Cd-contaminated dripirrigated farmlands.

The interaction and stability of soil bacteria can be used to reflect the availability of heavy metals in the soil (Qin et al., 2019) and assess the in-situ remediation of soils contaminated by heavy metals (Wang et al., 2020). Moreover, plants produce a variety of small/high molecular organic and inorganic compounds to enrich rhizosphere nutrients, which in turn stimulate the growth of soil microbial communities (Borymski et al., 2018).

Systematic study on the characteristics of rhizosphere bacterial community is one of the important ways to understand what a role polymer modifiers play in the remediation of Cd contaminated cotton fields. The purposes of this study are: (1) to investigate the change of bacterial diversity in Cd contaminated cotton field brought by polymer modifiers, and to clarify the effect of key bacterial populations on soil Cd availability; (2) to reduce Cd uptake by cotton through girdling, and to compare the effects of Cd uptake by cotton and Cd fixation by polymer modifiers on soil bacterial diversity, so as to further clarify the mechanism of the remediation of Cd contaminated soil by polymer modifiers; and (3) to make clear the relationships among soil enzymes, bacterial diversity, root Cd, and soil Cd in the remediation of Cd contaminated farmland soil by polymer modifiers.

Materials and methods

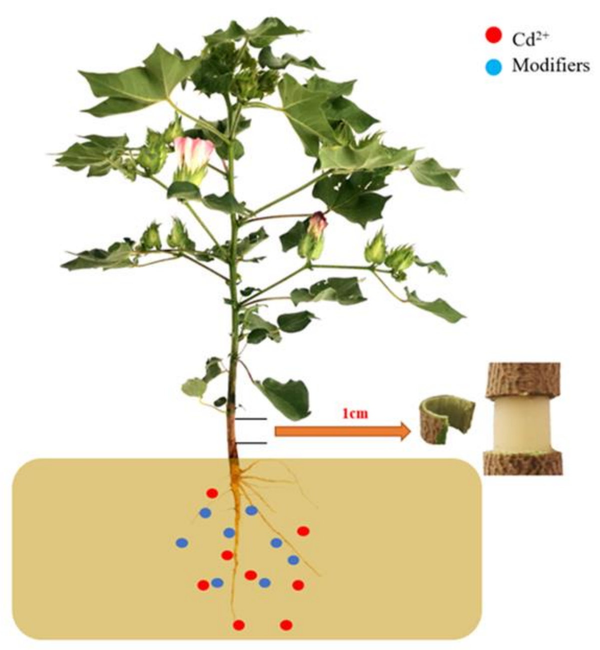

Fig 1. Schematic diagram of girdling in cotton

Table 1. Basic properties of modifiers used

Modifiers	Properties
Polyacrylate compound modifier	A compound modifier composed of polypropylene and iron sulfate. A colorless liquid that features in surface adsorption and co-precipitation for metals
Organic polymer compound modifier	A compound modifier mainly composed of polyacrylamide and manganese sulfate. A colorless liquid that features in surface adsorption, surface complexation, etc.

Table 2. Test design

Treatment	Phloem girdling in 2018	Modifier application in 2017 and 2018
CK	No girdling	/
P	No girdling	Polyacrylate polymer (8.48 kg hm^{-2})
O	No girdling	Organic polymer (8.48 kg hm^{-2})
CK-PG	Stem girdling	/
P-PG	Stem girdling	Polyacrylate polymer (8.48 kg hm^{-2})
O-PG	Stem girdling	Organic polymer (8.48 kg hm^{-2})

Conclusion

Polyacrylate and organic polymers transform soil Ex-Cd into other Cd fractions (Carb-Cd, Ox-Cd, OrgeCd, and ReseCd) in Cd-contaminated alkaline soils, which decreases the bioavailability of Cd; they also increase the relative abundances of dominant bacteria and the negative interaction of Gemmatimonadetes with other bacteria and decrease the rhizosphere bacterial diversity, decreasing the complexity of bacterial community networks. This may be related to the increase of soil pH and enzyme activities. Moreover, organic polymer has a good effect in reducing the bioavailability of Cd, and polyacrylate polymer has a good mobility in soil-plant system. As a whole, organic polymer and polyacrylate polymer can not only immobilize soil Cd, but also improve soil microbial community structure, so as to achieve the remediation of Cd-contaminated soil.

Acknowledgements

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Publications

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Results and discussion

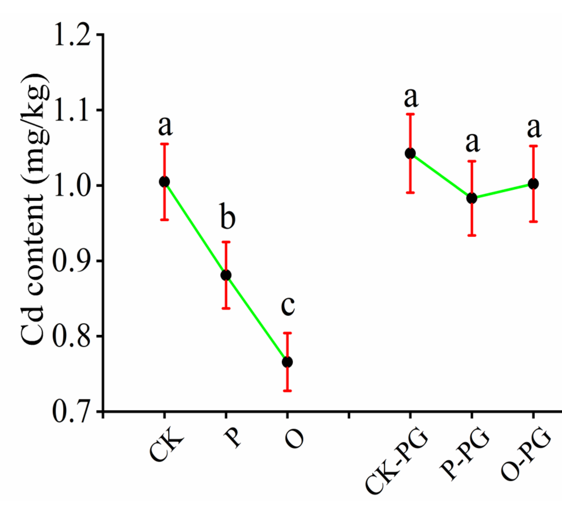


Fig.2 Cd content in root under treatments. Different lowercase letters indicate a significant difference (P<0.05).

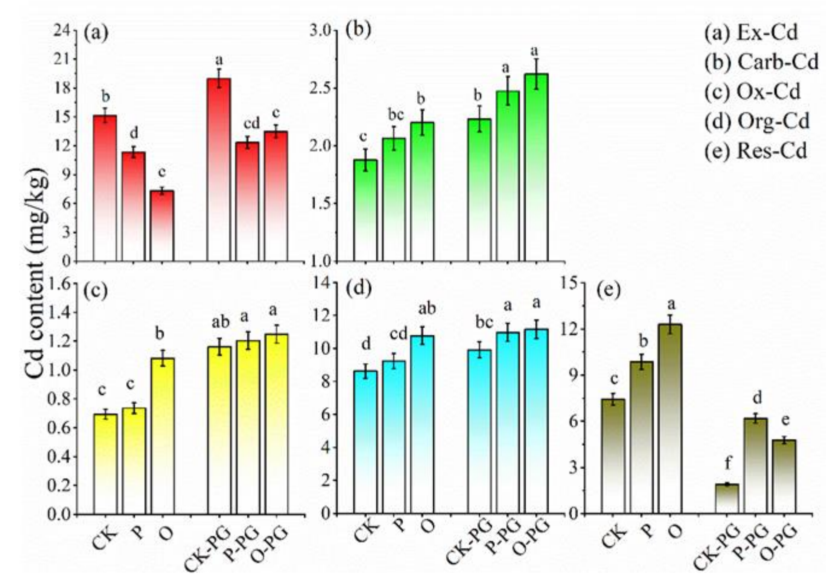


Fig.3 Soil Cd fractionation under treatments. Ex-Cd, Carb-Cd, Ox-Cd, Org-Cd and Res-Cd indicate exchangeable Cd, carbonate-bound Cd, Fe-Mn oxides-bound Cd, Organic Cd and residuals Cd, respectively. Different lowercase letters indicate a significant difference (P<0.05).

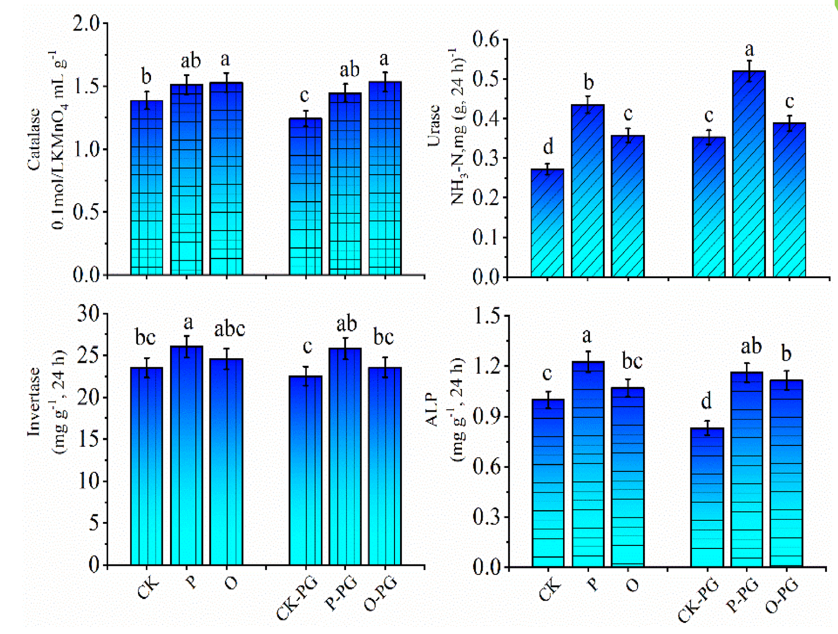


Fig.4 Soil enzyme activity under treatments. Different lowercase letters indicate a significant difference (P<0.05).

Modifiers significantly decreased soil Ex-Cd concentration, which might be due to soil surface complexation, surface adsorption, or co-precipitation (He et al., 2019). When soil Cd concentration was low (CK), organic polymer decreased the Ex-Cd concentration more than polyacrylate polymer; while when soil Cd concentration was high (CK-PG), polyacrylate polymer decreased the Ex-Cd concentration more than the organic polymer, indicating that polyacrylate polymer had a greater effect on the remediation of soils with high Cd concentrations, and the mobility of polyacrylate polymer in the soil-plant system was higher than that of organic polymer.

Root Cd concentration, soil Cd fractions, and soil enzyme

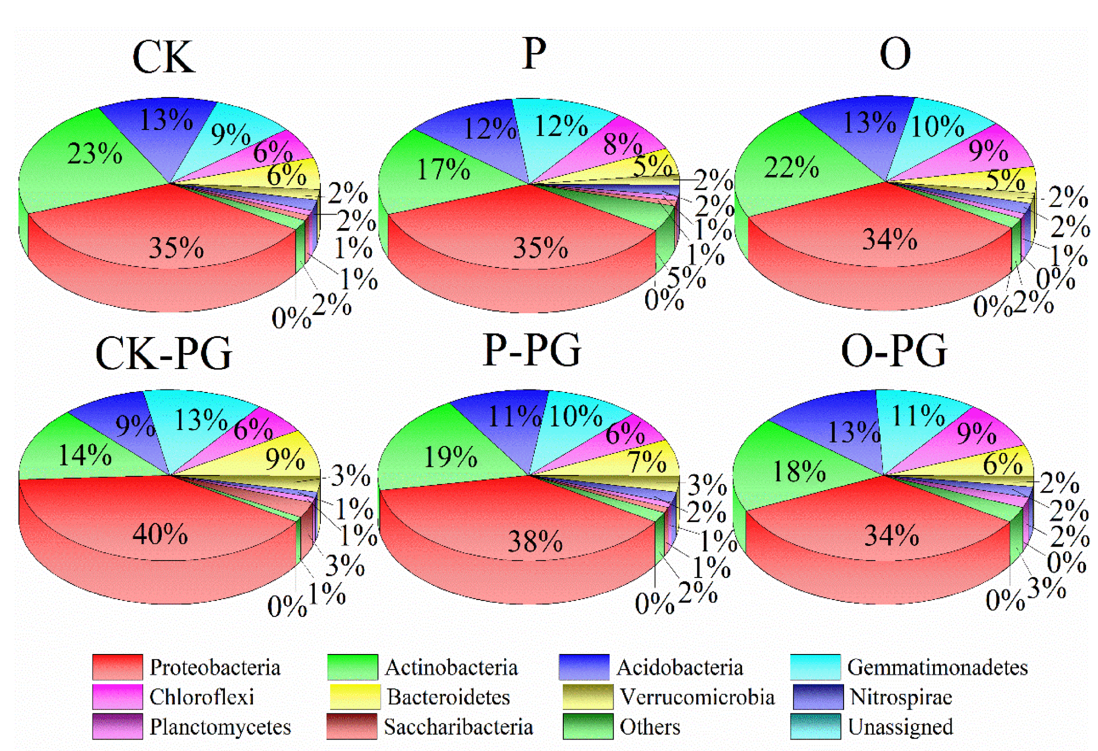


Fig.5 Rhizosphere bacterial communities in different treatments with the relative abundance of the bacterial phyla.

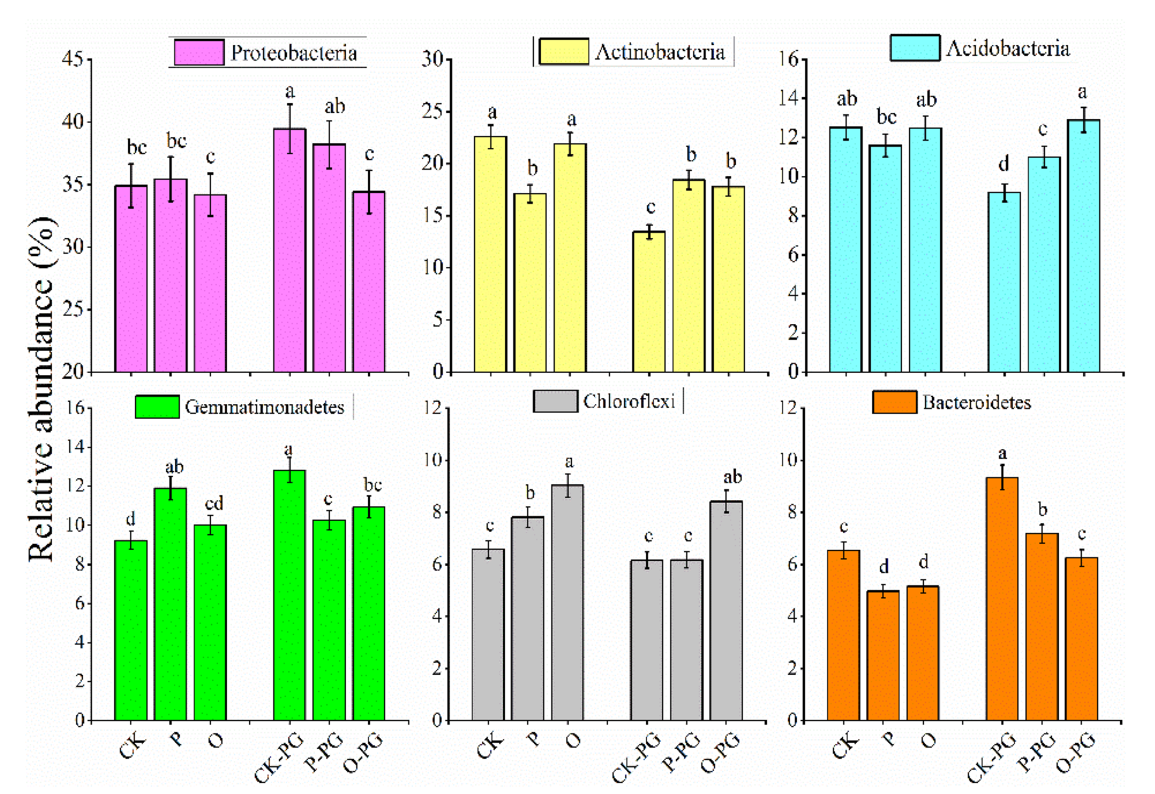
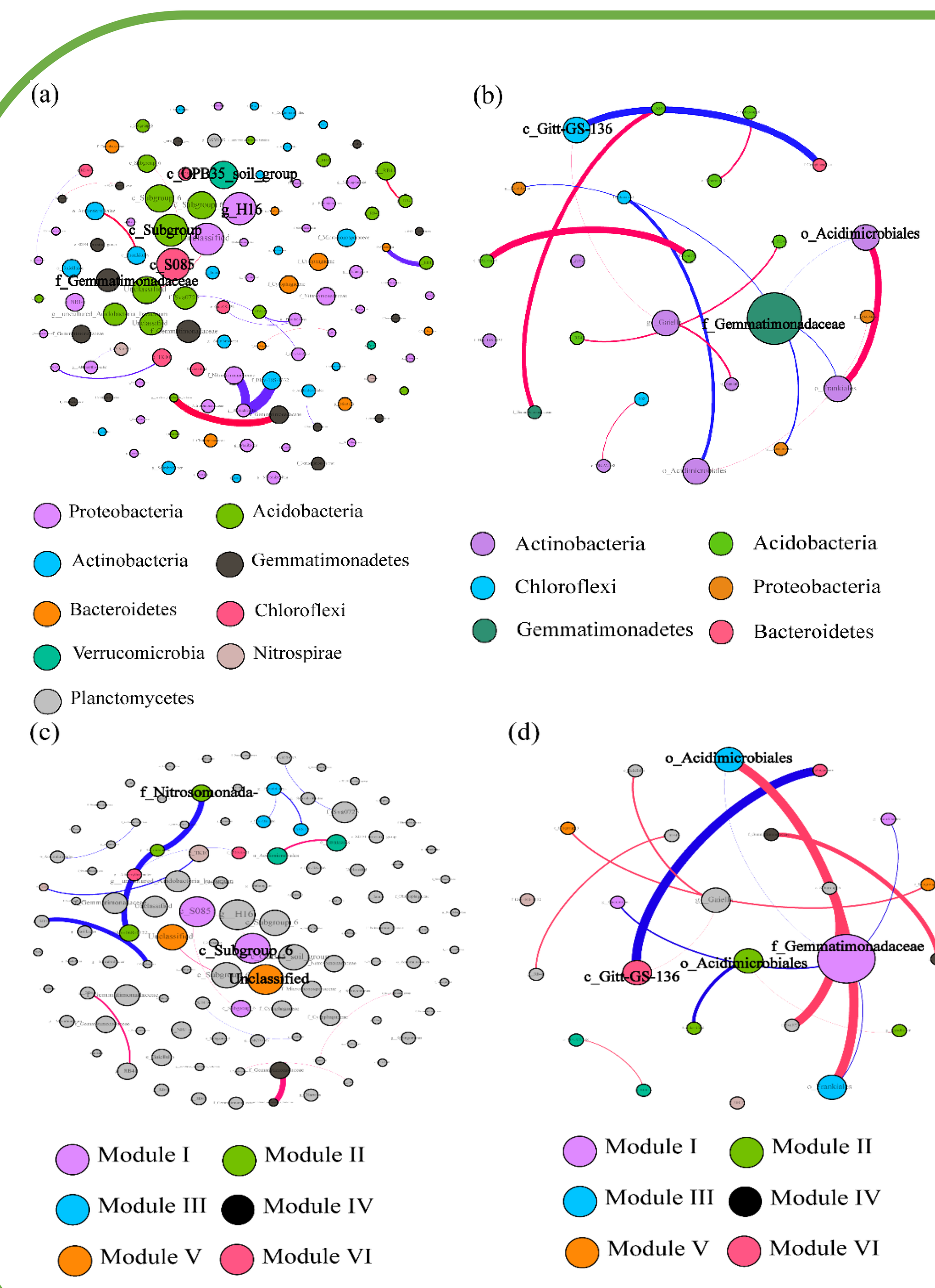


Fig.6 Distributions of dominant phyla which showed differences in the rhizospehre in the treatments. Bars with different lowercase letters indicate significant differences (P < 0.05) within the bacterial phyla, as revealed by one-way analysis of variance (ANOVA) with Duncan's new multiple range method.

Our results also showed that Proteobacteria, Actinobacteria, Acidobacteria, Gemmatimonadetes, Chloroflexi, and Bacteroidetes were the dominant bacteria in soil. The modifier decreased the number of soil bacterial species and changed the soil bacterial composition. The analysis of bacterial diversity at the phylum level revealed that polyacrylate polymer increased the relative abundances of Proteobacteria, Gemmatimonadetes, and Chloroflexi, and organic polymer increased the relative abundance of Chloroflexi, which might be due to that modifiers immobilized soil Cd, leading to the decrease of Cd bioavailability; while some species of bacteria are able to live and reproduce in soils with low Cd activity, thus the relative abundances of some bacteria were increased.

Microbial rhizosphere diversity and community composition



To further explore the key species that affect the stability of bacterial network after the application of modifiers, we analyzed the network at phylum level and found that after the application of modifiers, the dominant bacterial species (Proteobacteria, Acidobacteria, Actinobacteria, and Gemmatimonadetes) in the Cd-contaminated rhizosphere soil were changed to Proteobacteria, Acidobacteria, Actinobacteria, and Chloroflexi, indicating that Gemmatimonadetes has a higher tolerance to Cd stress than Chloroflexi. Modifiers reduced soil Cd bioavailability, leading to a decrease in the interference of Cd contamination on bacterial communities, which promoted the development of dominant bacteria and their interactions.

Soil alkaline phosphatase activity plays an important role in bacterial diversity, and root Cd concentration, soil Ex-Cd and Res-Cd concentrations, and catalase activity play important roles in bacterial community structure.

$\chi 2$ = 6.105, P = 0.191, RMR=0.048, GFI=0.920, CFI=0.980

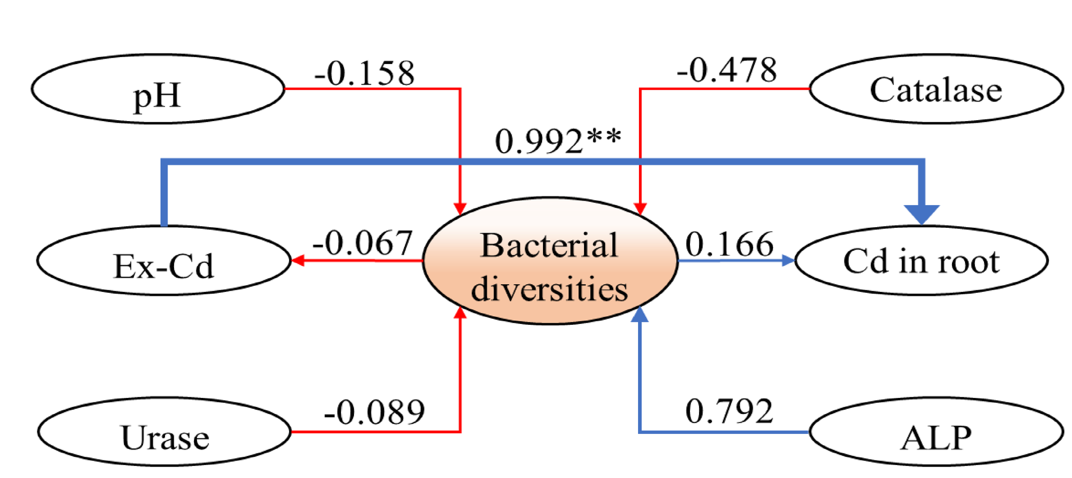


Fig.7 Structural equation modeling (SEM) showing the relationship between soil properties. Blue lines indicate positive relationships, while red lines indicate negative relationships. The bacterial diversities are represented by the Shannon indexes based on the rarified same sequencing depth. The width of arrows indicates the strength of significant standardized path coefficients (P < 0.05). ***P < 0.001; **P < 0.01.

Fig.8 The bacterial co-occurrence networks under the non-amended and polymer-amended treatments based on correlation analysis. A connection stands for a strong (Spearman's ρ>0.6) and significant (P<0.01) correlation. The non-amended (a, c) and polymer-amended (b, d) networks are colored by the bacterial phyla/classes and modules, respectively. The bacterial modules I–VI in the non-amended and polymer-amended networks were the six clusters of closely interconnected nodes. The bacterial keystone taxa (module hubs) and their connected edges in the networks are in bold. For each panel, the size of each node is proportional to the node degrees. A blue edge indicates a negative interaction between two individual nodes, while a red edge indicates a positive interaction.

Relationship between microbial communities and environmental factors