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Horizontal Gene Transfer Mitigates the Effect of Cadmium on Key Mercury-Methylating Microorganisms in Paddy Soils

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Report outline

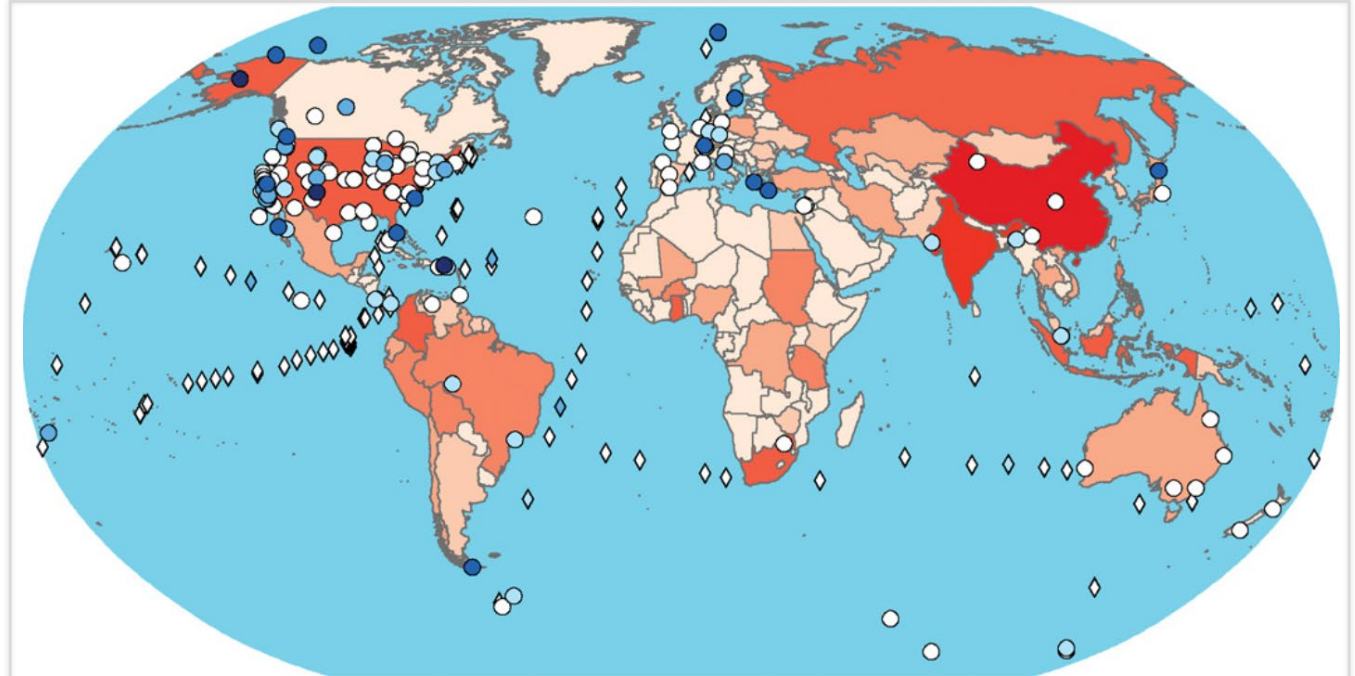
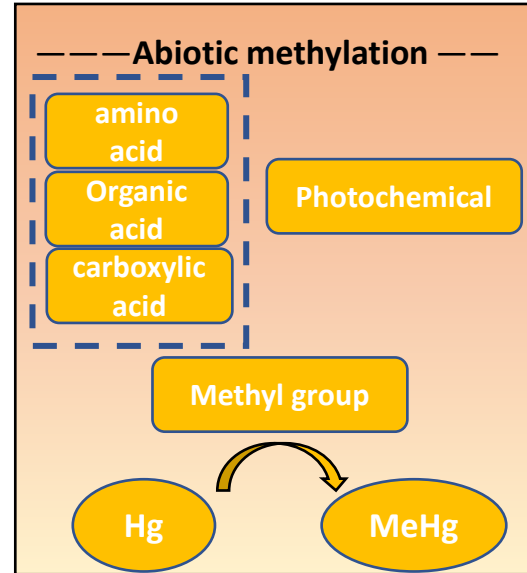
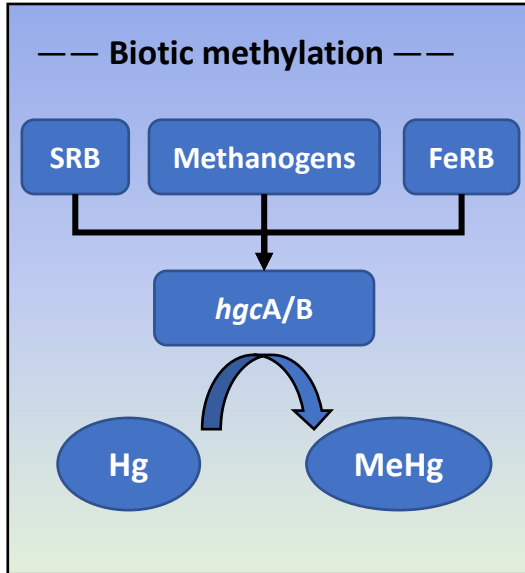
1 *Background*

2 *Methods*

3 *Results and discussion*

4 *Conclusions*

Background



(Podar et al., 2015)

- Mercury methylation: Biotic methylation & Abiotic methylation
- Main pathway: Biotic methylation

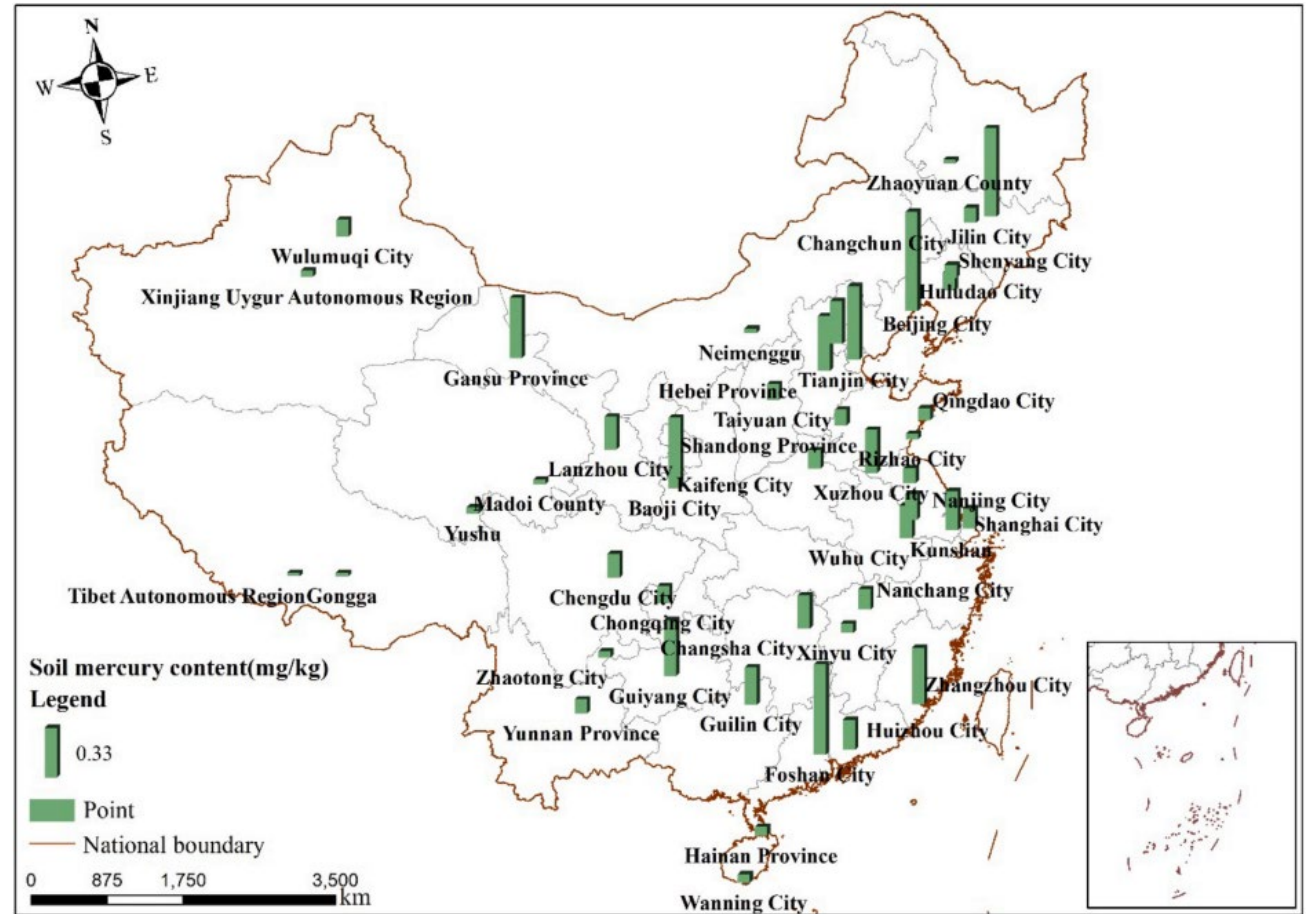
Microbial diversity in mercury methylation

Key microorganisms involved in mercury methylation in paddy soil?

Background

Region	Province	Avg. of agricultural soil	Avg. of urban soil	Average ^a	Background ^b	
North	Beijing	0.200	0.172	0.185	0.074	
	Tianjin	0.278	0.250	0.275	0.090	
	Hebei	0.169		0.134	0.094	
	Shanxi	0.170	0.208	0.176	0.128	
	Inner Mongolia			0.073	0.053	
Northeast	Liaoning	0.144	1.254	0.675	0.108	
	Jilin	0.047	0.367	0.361	0.099	
	Heilongjiang	0.078	0.179	0.090	0.086	
East	Shanghai	0.196	0.391	0.231	0.138	
	Jiangsu	0.182	0.131	0.092	0.126	
	Zhejiang	0.207	0.853	0.265	0.070	
	Anhui	1.328	0.288	1.322	0.097	
	Fujian	0.376	0.350	0.368	0.074	
	Jiangxi	0.175	0.400	0.178	0.108	
	Shandong	0.128	0.239	0.159	0.084	
	South central	Henan	0.067	1.138	0.895	0.074
		Hubei	0.513	0.148	0.167	0.172
Hunan		1.019	4.667	1.019	0.126	
Guangdong		0.313	0.299	0.362	0.056	
Guangxi				1.462	0.267	
Hainan		0.144		0.144	0.027	
Southwest	Chongqing	0.285		0.323	0.133	
	Sichuan	1.121	0.357	0.762	0.079	
	Guizhou	0.323		0.322	0.659	
	Yunnan	0.761		0.761	0.218	
	Tibet	1.507		1.507	0.081	
Northwest	Shaanxi	0.193		0.193	0.094	
	Gansu	0.779	3.561	2.365	0.116	
	Ningxia				0.112	
	Xinjiang	0.120		2.459	0.120	
China			0.674			

(Wang et al., 2015)

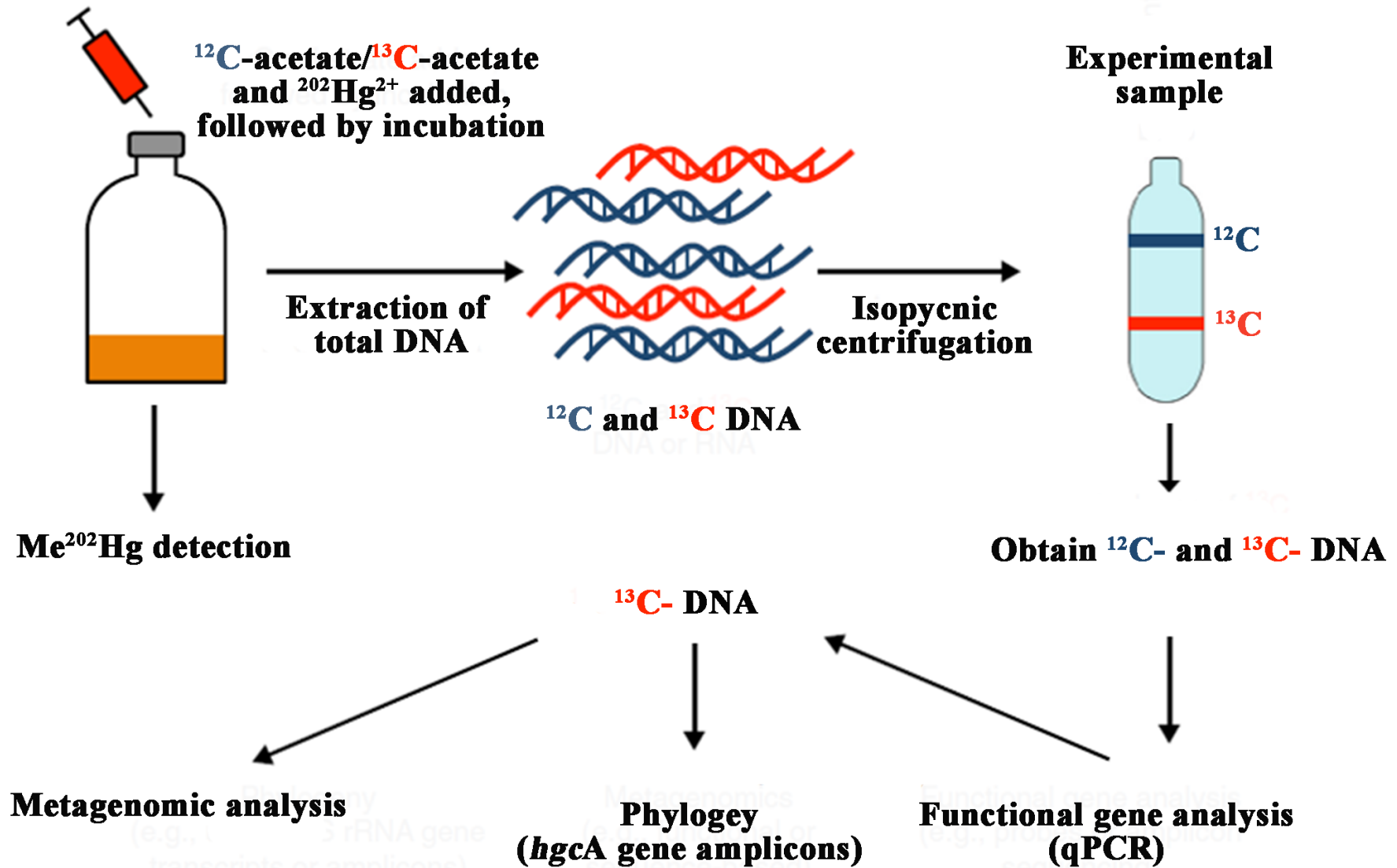


(Liu et al., 2021)

What mechanisms do mercury-methylating microorganisms use to adapt to cadmium pollution?

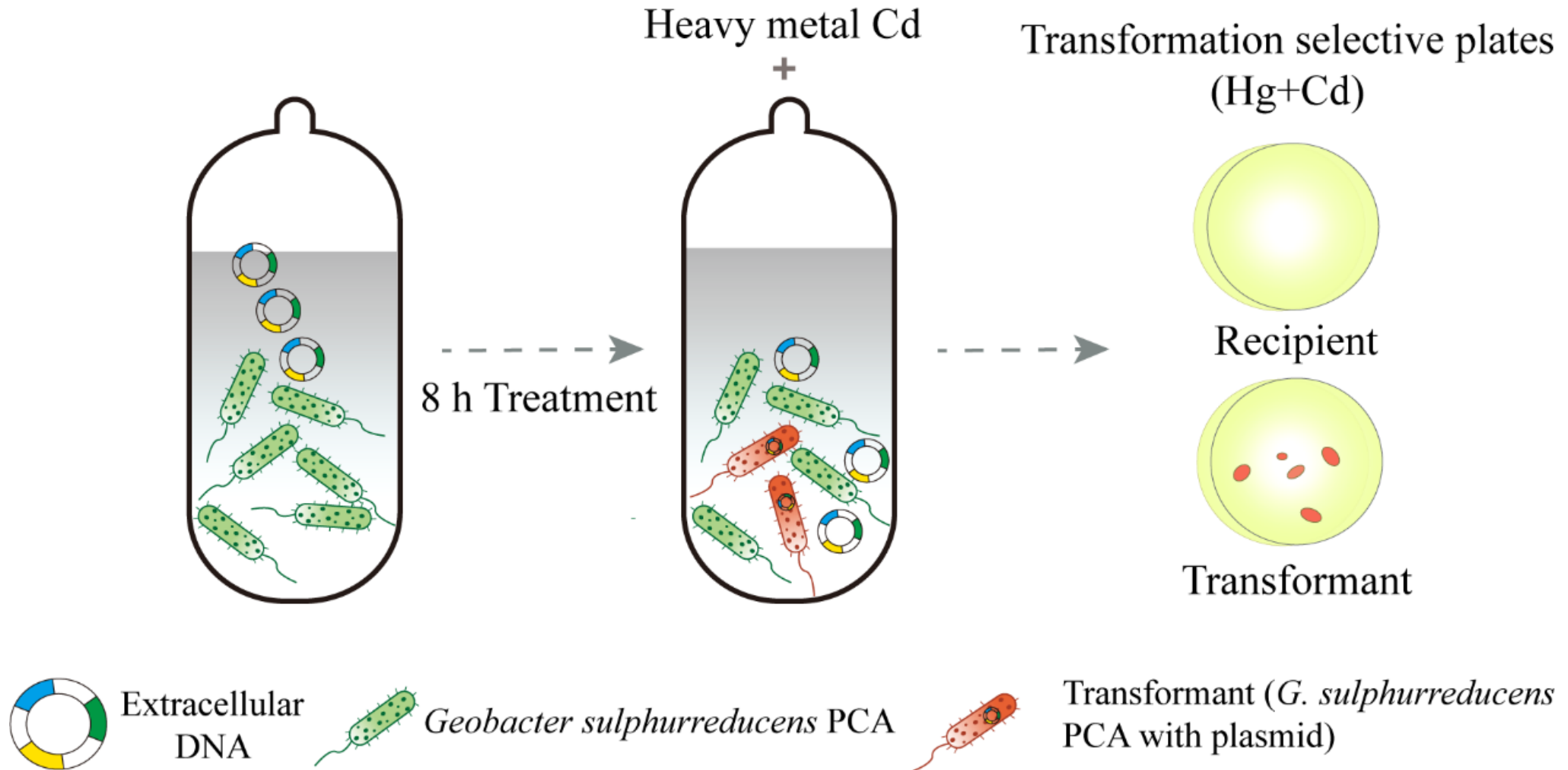
Methods

DNA-SIP: Identification of Mercury-Methylating Microorganisms



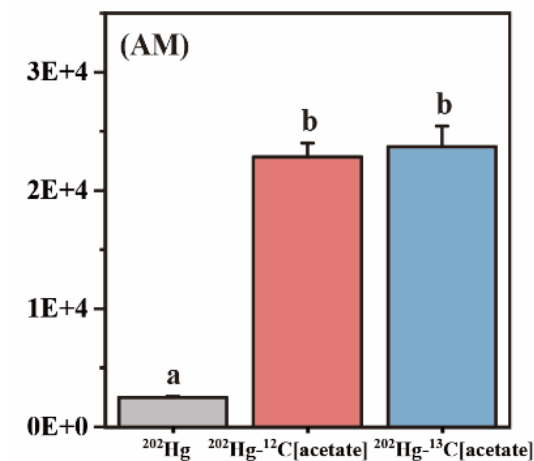
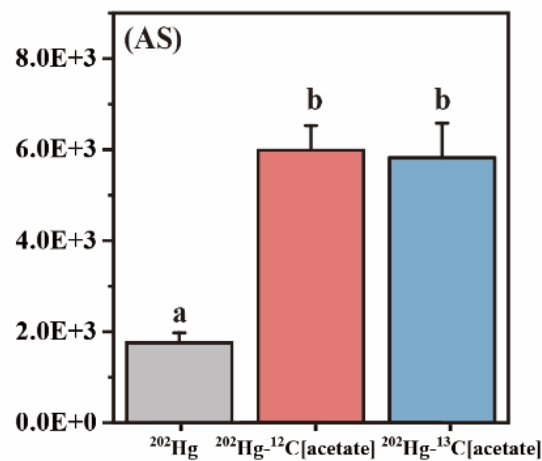
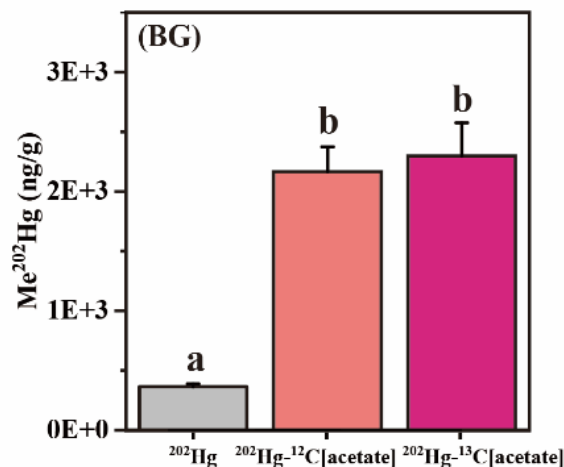
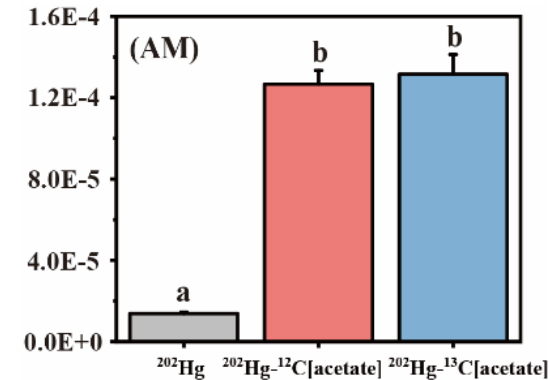
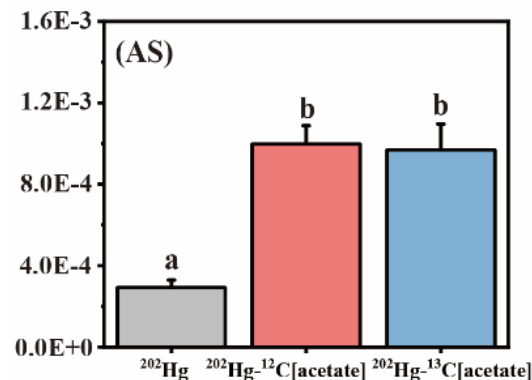
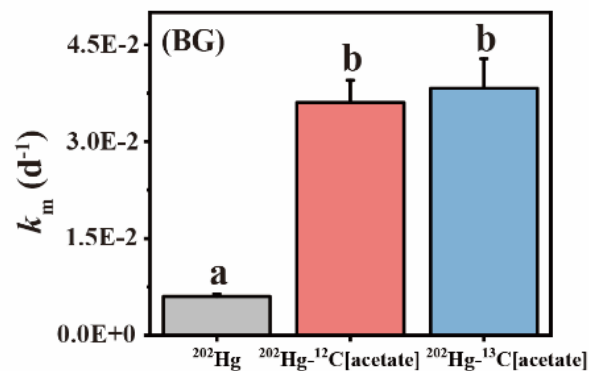
Methods

Transformation experiments: Potential mechanisms of cadmium tolerance in mercury-methylating microorganisms.



Results And Discussion

Identification of key Hg-methylating microorganisms by DNA-SIP



BG: background area

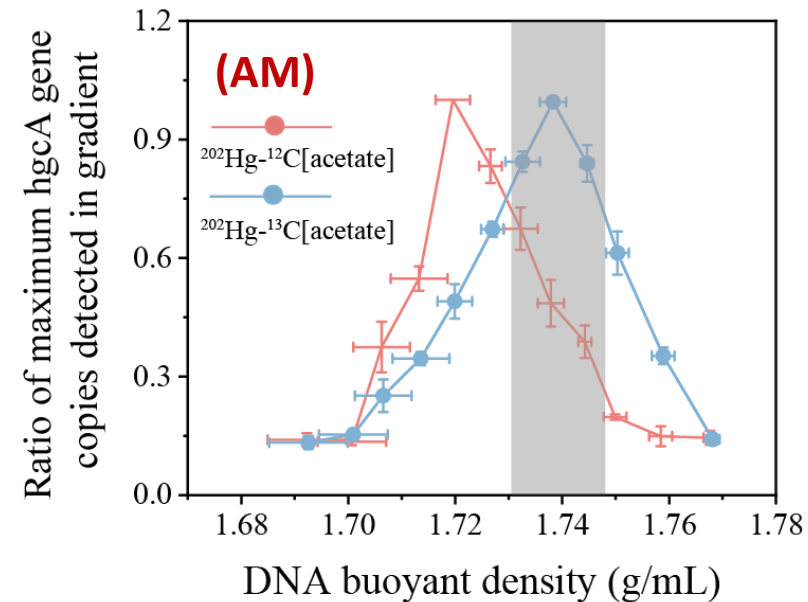
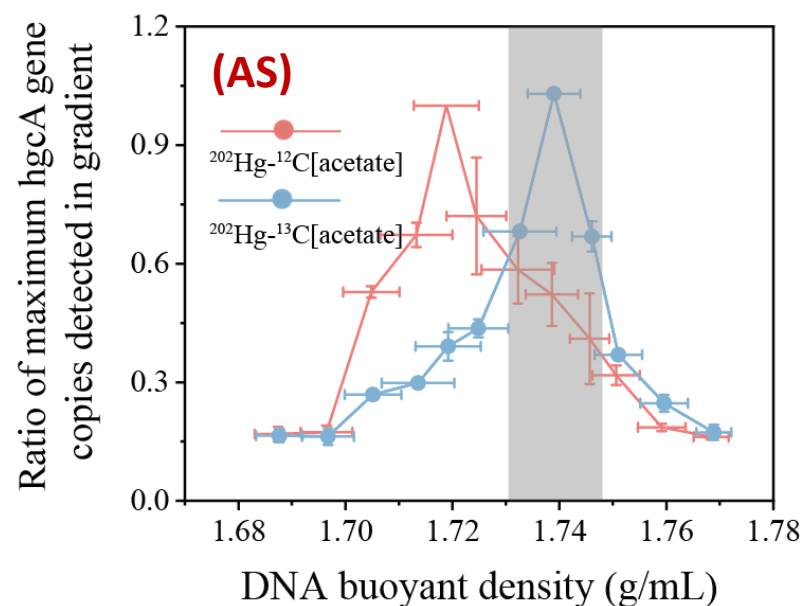
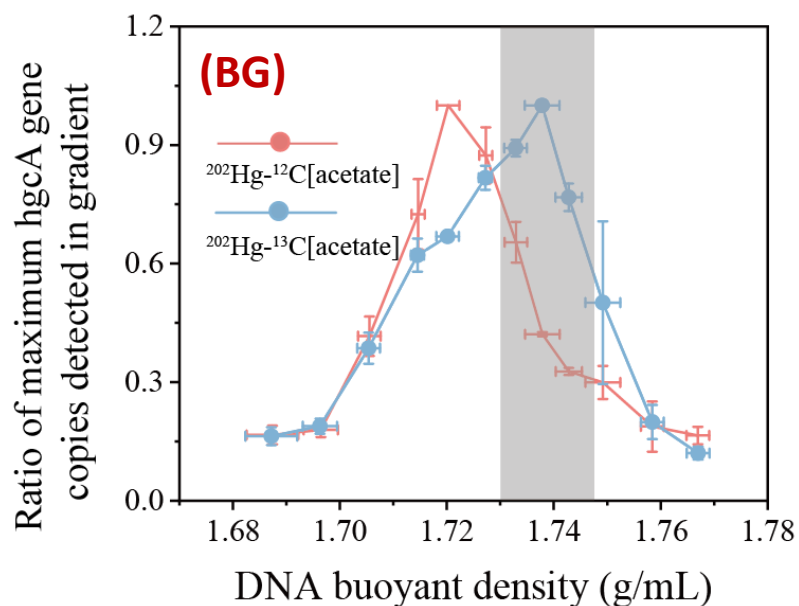
AS: artisanal Hg smelting area

AM: abandoned Hg mining area

Acetate amendment could promote microbial MeHg production.

Results And Discussion

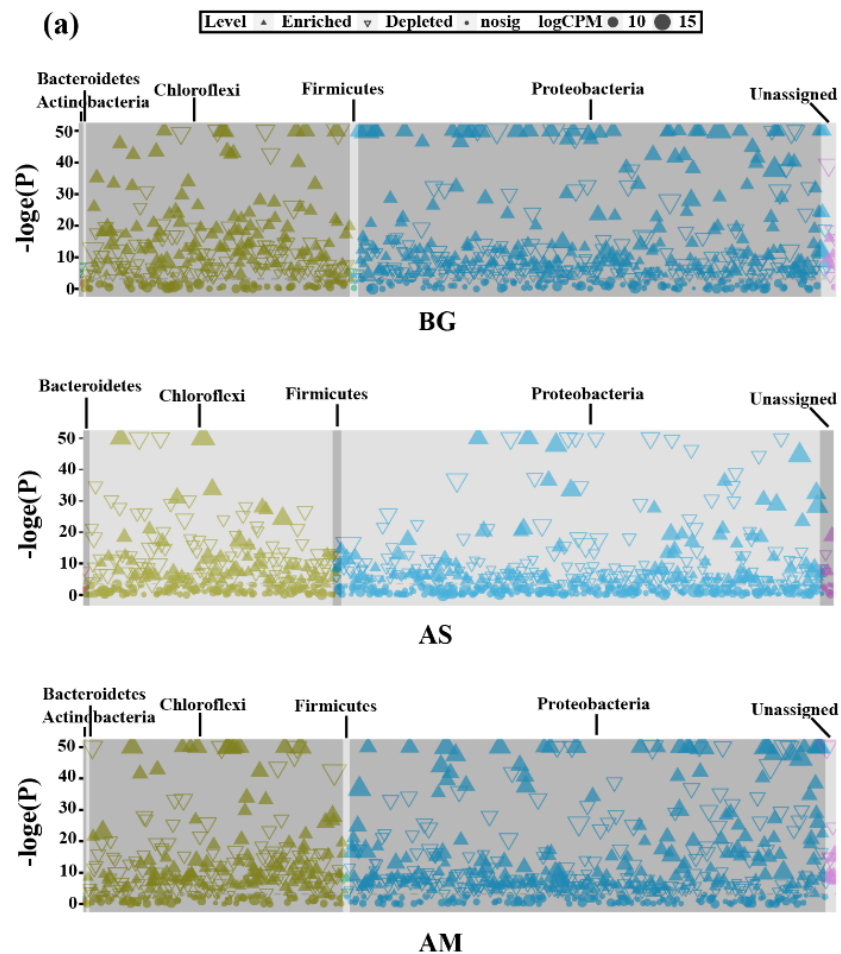
Identification of key Hg-methylating microorganisms by DNA-SIP



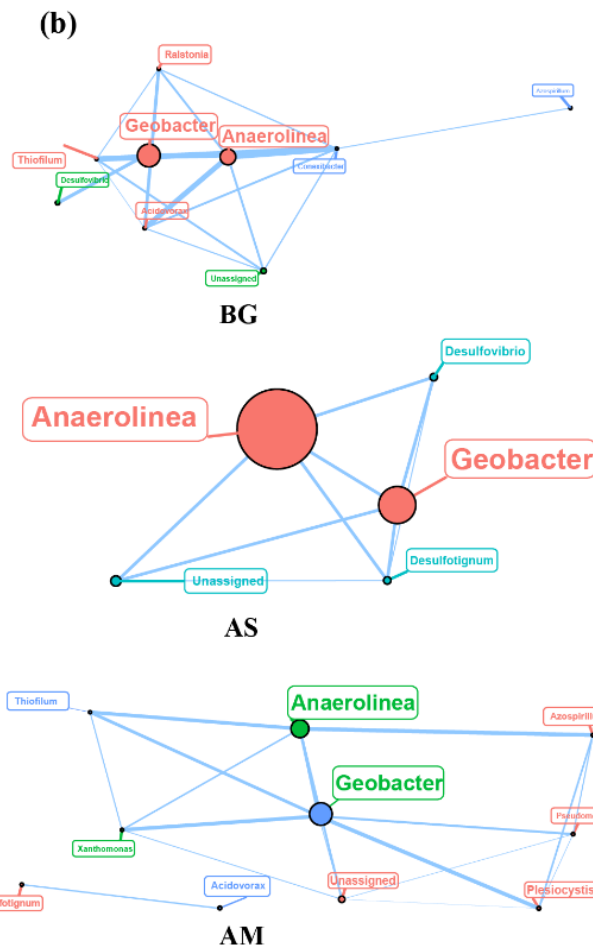
A clear shift in the distribution along the density gradient between the $^{202}\text{Hg-}^{13}\text{C}[\text{acetate}]$ treatment and $^{202}\text{Hg-}^{12}\text{C}[\text{acetate}]$ treatments

Results And Discussion

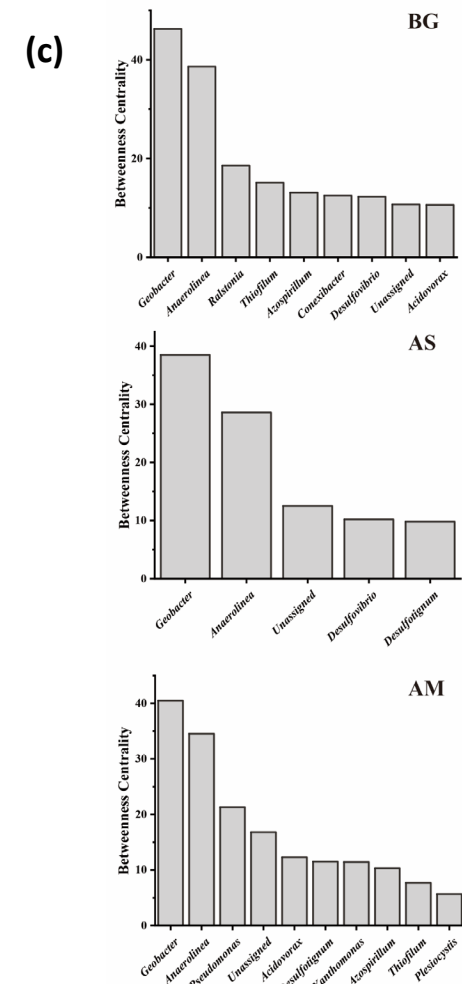
Identification of key Hg-methylating microorganisms by DNA-SIP



Enriched microorganisms



Hg-methylating microbial community

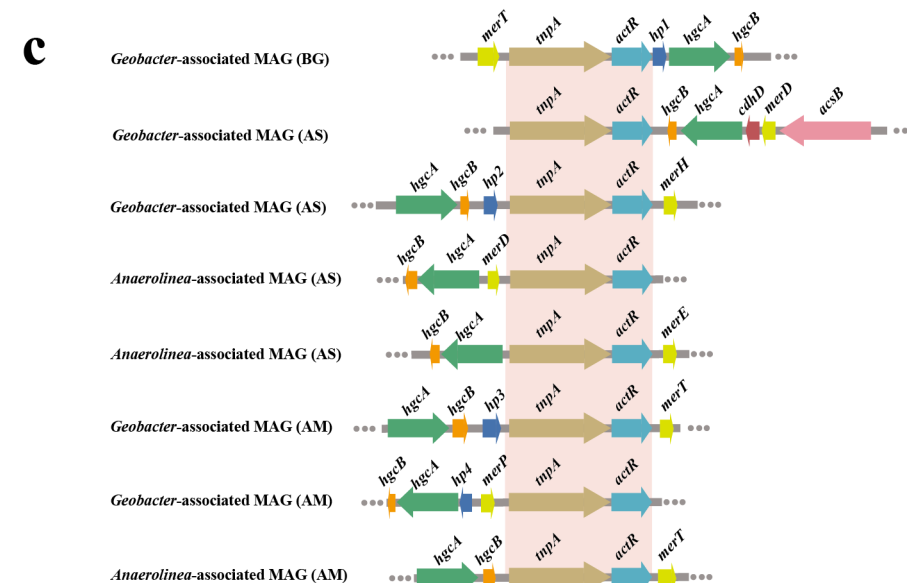
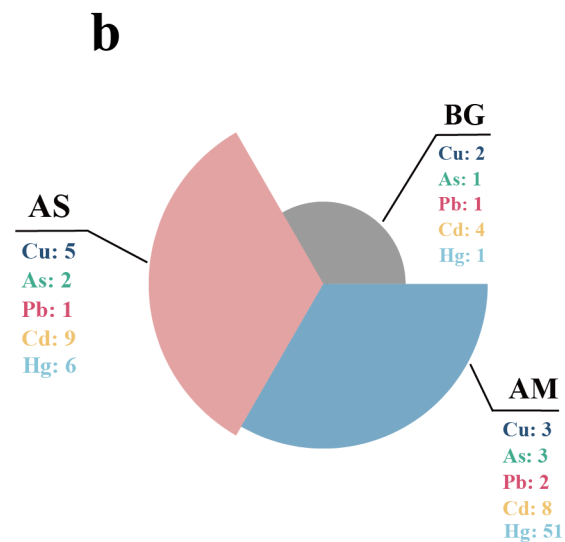
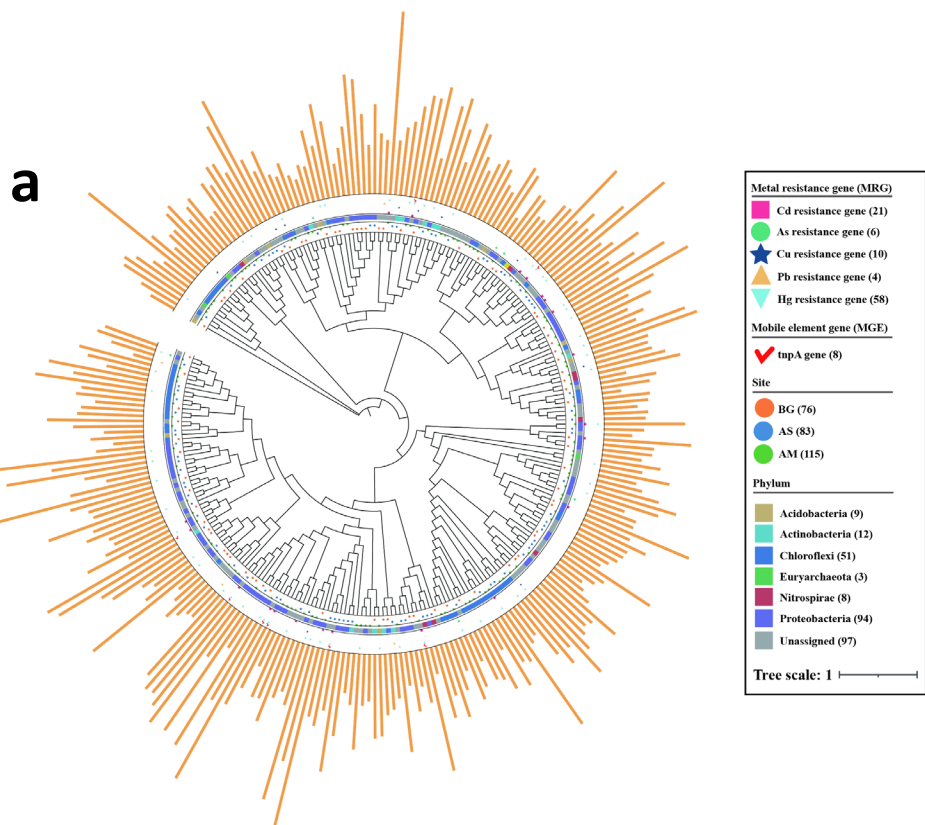


betweenness centrality

Geobacter and Anaerolinea were identified as key Hg methylators

Results And Discussion

Identification of key Hg-methylating microorganisms by DNA-SIP



Hg-methylating microorganisms

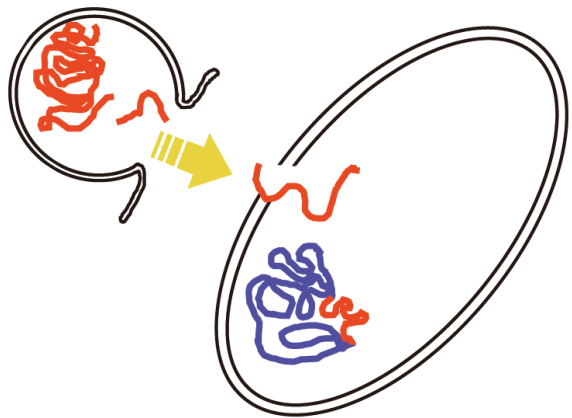
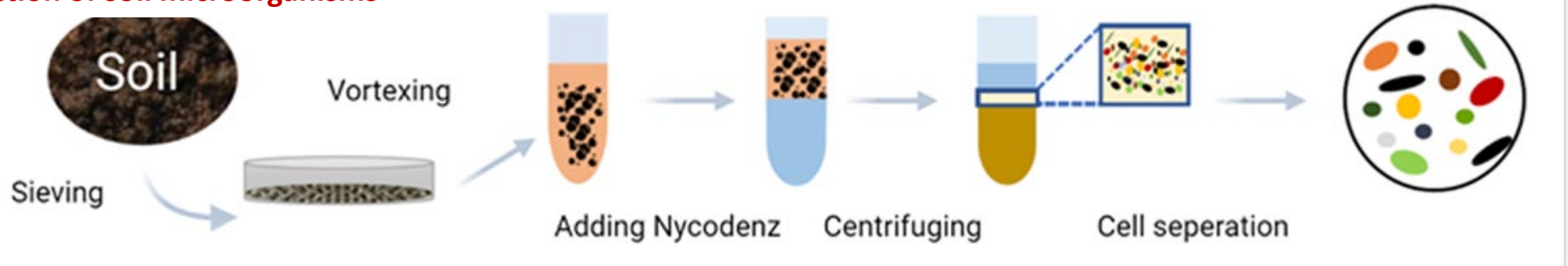
Heavy metal resistance annotation in Hg-methylating microorganisms

These two types of Hg-methylating microorganisms can survive and reproduce in Cd-contaminated soil

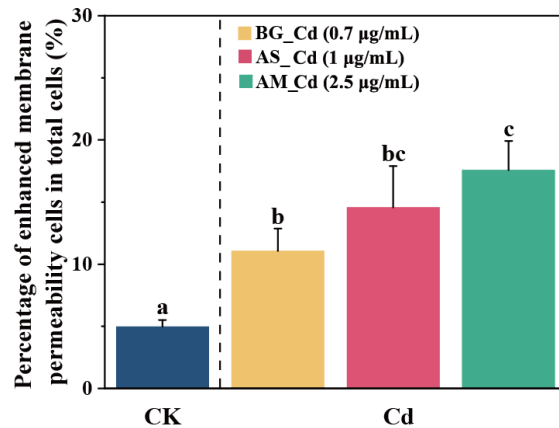
Results And Discussion

Potential mechanisms of Cd tolerance in Hg-methylating microorganisms by Transformation

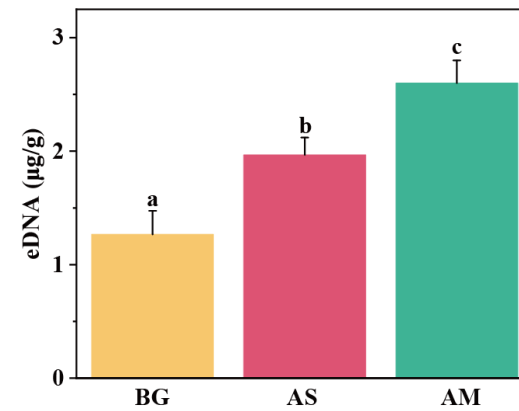
Extraction of soil microorganisms



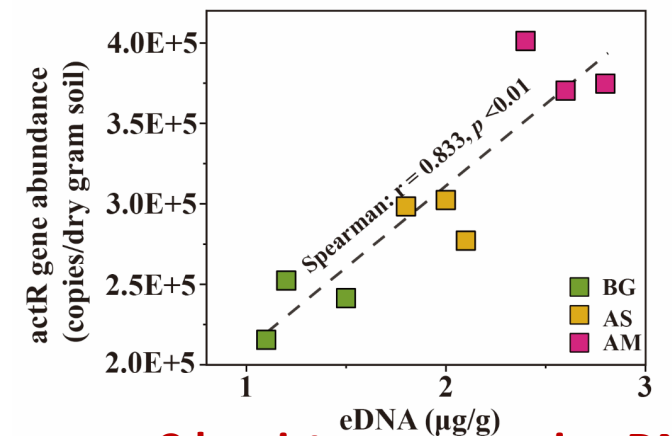
Transformation setup



Membrane permeability



Extracellular DNA

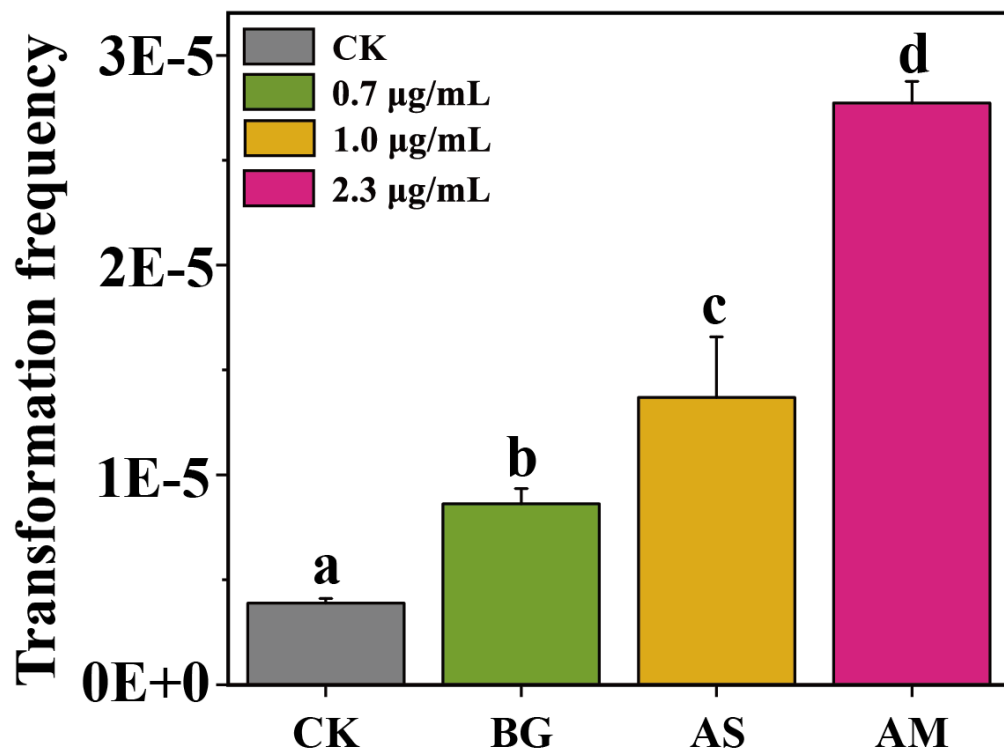


Cd resistance genes in eDNA

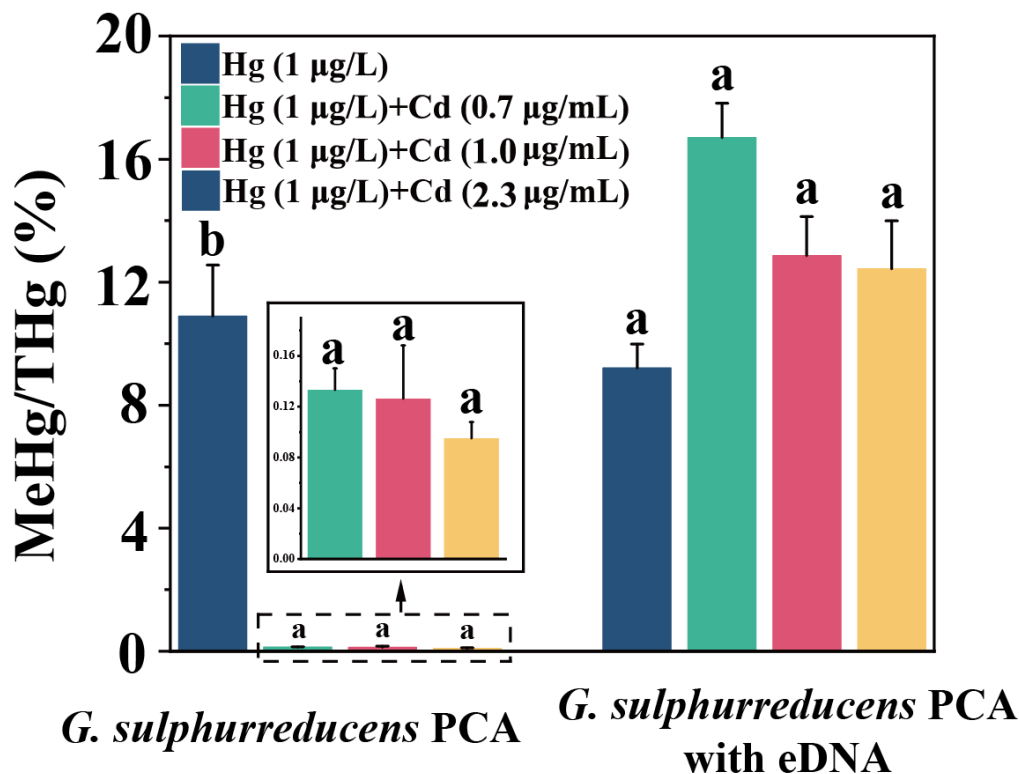
Microorganisms may obtain cadmium resistance genes carried on eDNA through transformation

Results And Discussion

Identification of key Hg-methylating microorganisms by DNA-SIP



Transformation frequency



MeHg production under transformation

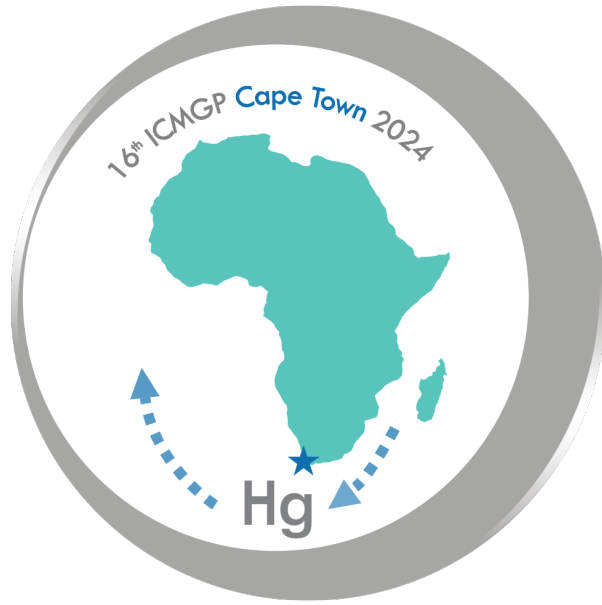
Enhanced cell membrane permeability may facilitate horizontal gene transfer of Cd resistance genes among Hg-methylating microorganisms

Conclusion

① *Geobacter and Anaerolinea are identified as key active Hg-methylating microorganisms in paddy soils.*

② *Hg-methylating microorganisms obtain Cd resistance genes through transformation increases, which also enhances Hg methylation in paddy soils.*

This study provides strong scientific evidence for guiding future research on the potential effects of Cd on Hg methylation, a topic that has been neglected in earlier studies.



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Thanks for your attention!

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