

Supplemental material

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Dissecting the role of soybean rhizosphere-enriched bacterial taxa in modulating nitrogen-cycling functions

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Table S1 The accession number, name, type, growth habit, and stem termination of the five varieties in this study (Zheng et al. 2022).

Accession number	Variety	Type	Growth habit	Stem termination
ZDD03460	Deng-feng-chang-yang-hei-dou (DF)	Wild	Semi-sprawl	Indeterminate
ZDD03538	Huo-jia-hong-hei-dou (HJ)	Admixture	Erect	Determinate
ZDD11395	Meng-cheng-bai-jian-ke (MC)	Admixture	Semi-sprawl	Indeterminate
ZDD11396	Chu-xian-da-bai-ke (CX)	Cultivated	Semi-erect	Semi-determinate
ZDD25129	Qu-xian-3-hao (QX)	Cultivated	Erect	Determinate

Table S2 The name, function, and qPCR primers of the genes quantified in this study.

Gene name	Function	Primers	Reference
<i>nifH</i>	Nitrogenase reductase	PolF: TCGGAYCCSAARGCBGACTC PolR: ATSGCCATCATYTCRCCGGA	(Poly et al. 2001)
Archaeal <i>amoA</i>	Ammonia monooxygenase	Arch-amoAF: STAATGGTCTGGCTTAGACG Arch-amoAR: GCGGCCATCCATCTGTATGT	(Francis et al. 2005)
Bacterial <i>amoA</i>	Ammonia monooxygenase	amoA-1F: GGGGTTTCTACTGGTGGT amoA-1R: CCCCTCKGSAAAGCCTTCTTC	(Rotthauwe et al. 1997)
<i>narG</i>	Nitrate reductase	nirG-f: TCGCCSATYCCGGCSATGTC nirG-R: GAGTTGTACCAGTCRGC SGAYTCSG	(Bru et al. 2007)
<i>nirS</i>	Nitrite reductase	Cd3aF: G TSAACG TSAAGGARACSGG R3cd: GASTTCGGRTGSGTCTTGA	(Hallin and Lindgren 1999; Michotey et al. 2000)
<i>nirK</i>	Copper-containing nitrite reductase	F1aCu: ATCATGGT SCTGCCGCG R3Cu: GCCTCGATCAGRTTGTGGTT	(Kandeler et al. 2006)
<i>nosZ</i>	Nitrous-oxide reductase	nosZ 2F: CGCRACGGCAASAAGG TSMSSGT nosZ 2R: CAKRTGCAKSGCRTGGCAGAA	(Henry et al. 2006)

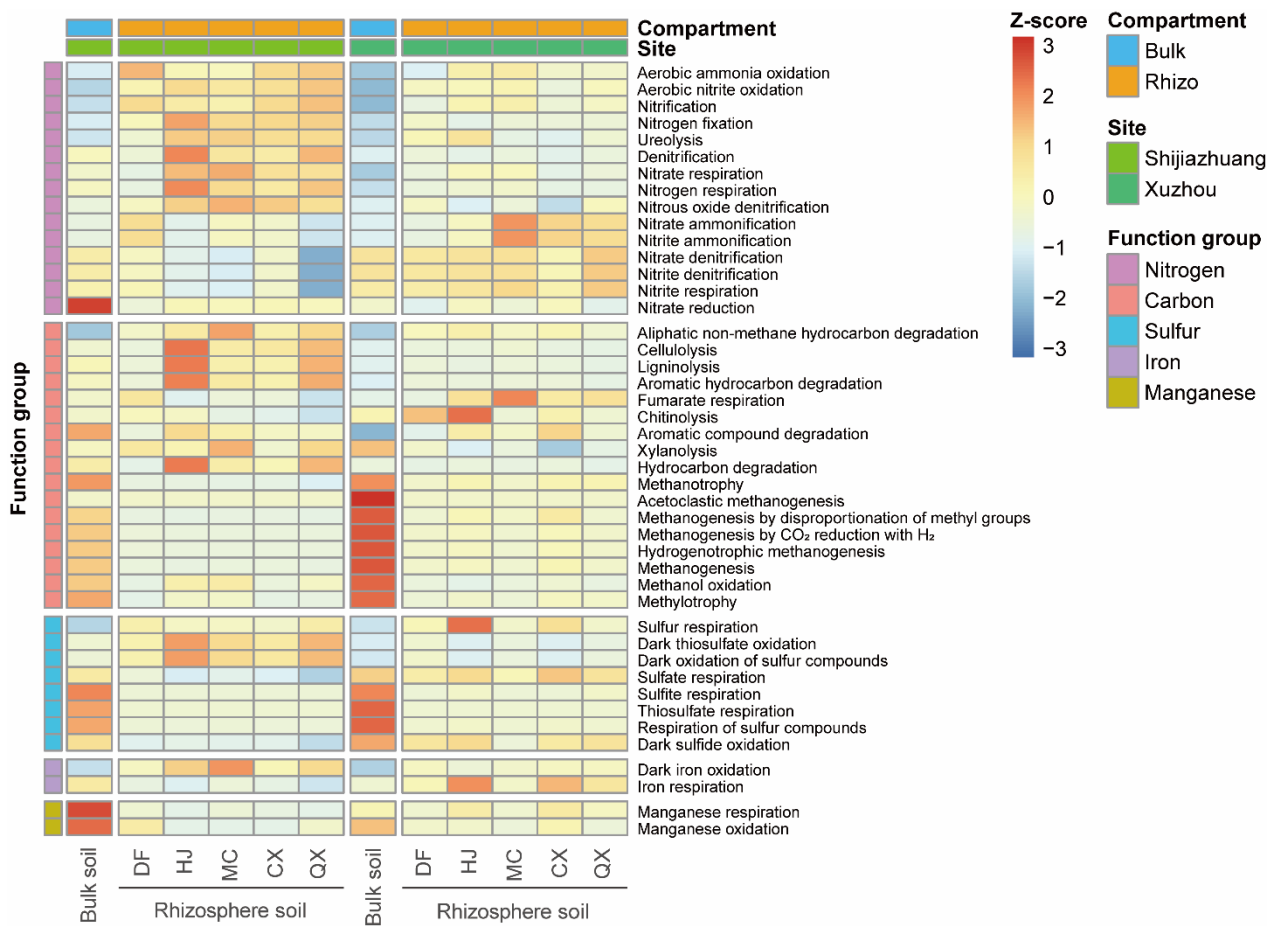


Fig. S1 The ecological function of the bacterial communities in bulk soil and the rhizosphere of five varieties in Shijiazhuang and Xuzhou as predicted by FAPROTAX.

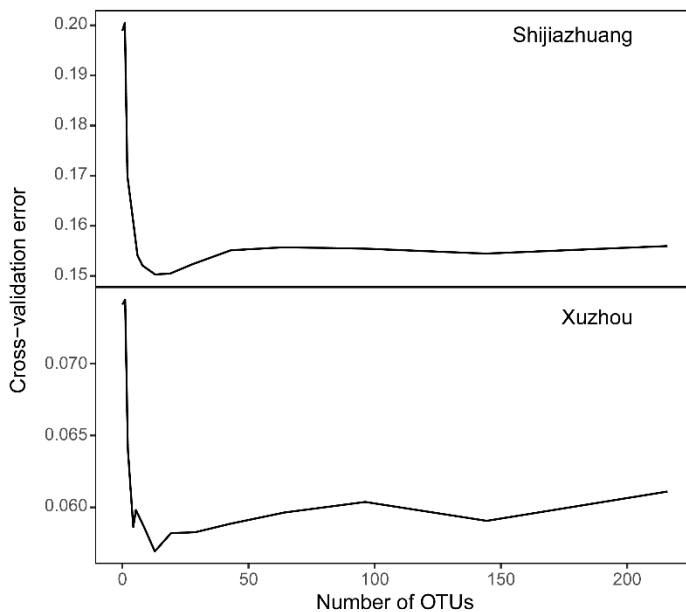


Fig. S2 The average ten-fold cross-validation error (N = 5) of the number of OTUs in the randomforest model in Shijiazhuang and Xuzhou.

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