Supplementary Information

Dissimilatory Nitrate Reduction to Ammonium in the Yellow River Estuary: Rates, Abundance, and Community Diversity

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Supplementary Figures

Legends for Supplementary Figure

Supplementary Figure 1. Venn diagram of OTUs in the four sites of the Yellow River Estuary.

Supplementary Figure 2. Rank abundance curve based on *nrfA* sequencing in the Yellow River Estuary.

Supplementary Figure 3. Functional gene abundance of two dissimilatory nitrate reduction processes (DNRA and Denitrification) in the Yellow River Estuary. Genes include *nirS* (cytochrome cd1 nitrite reductase), *nirK* (copper containing nitrite reductase), *nosZ* (nitrous oxide reductase) and *nrfA* (periplasmic nitrite reductase). Error bars represent standard deviation.

Supplementary Figure 4. Sampling sites in the Yellow River Estuary, Shandong, China. The figure was generated according to the distribution of land, sea and river using Adobe Photoshop CS5 (http://www.52z.com/soft/23642.html).

Supplementary Figure 5. Bioinformatic pipeline of *nrfA* pyrosequencing analysis.

Study site		1(mouth)	2	3	4	5
Bottom water	Depth (m)	1.3	2	4	3	5
	Temperature (℃)	25.0	23.4	21.0	20.8	20.6
	Salinity (‰)	22.1	21.3	7.7	5.1	4.2
	pH	7.94	7.94	8.08	8.03	8.05
	DO (mg/L)	8.92	9.19	10.31	9.90	9.76
	NO ₃ - (μM)	102.86	159.29	229.29	269.29	272.14
	$NH_{4^{+}}(\mu M)$	155.71	118.57	110.71	110.71	118.57
Sediment	Moisture content (%)	20.76	23.62	28.22	22.07	45.11
	Organic carbon (g/kg)	3.60	4.28	5.37	3.95	6.71
	Extractable NH_4^+ (µmol/g)	0.28	0.10	0.40	0.18	0.81

Supplementary Table 1. Environmental parameters of bottom water and sediment in the five sites of the Yellow River Estuary.

Supplementary Table 2. DO saturation in the five sites of the Yellow River Estuary.

Study site	Temperature	DO	DO saturation	
	°C	mg/L	%	
1	25.0	8.92	108	
2	23.4	9.19	107	
3	21.0	10.31	116	
4	20.8	9.90	111	
5	20.6	9.96	112	

Supplementary Table 3. DNRA rate and *nrfA* gene abundance in the five sampling sites of the Yellow River Estuary. ds: dry sediment.

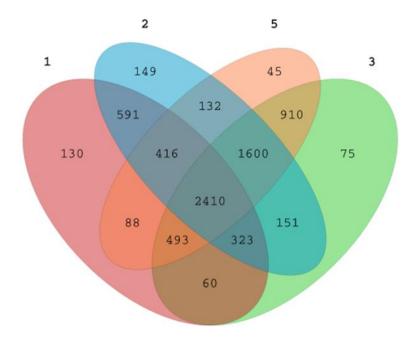
Study site	DNRA rate	nrfA gene
	nmoles N g ⁻¹ h ⁻¹	copies g ⁻¹ ds
1	0.19	$3.19 \times 10^9 \pm 1.38 \times 10^8$
2	0.10	$6.00 \times 10^9 \pm 5.81 \times 10^8$
3	1.52	$2.27\ \times 10^{10} \pm 1.75\ \times 10^{9}$
4	0.21	$8.65 \times 10^9 \ \pm 1.61 \times 10^8$
5	3.29	$1.74 \times 10^{10} \pm 9.27 \times 10^{7}$

Study site	Valid reads	High quality reads	OTUs	Chao 1	ACE	Simpson	Shannon
1	114,138	104,395	4,511	3,680	3680.00	0.9907	9.34
2	169,444	145,453	5,699	4,512	5256.75	0.9906	9.04
3	205,444	174,960	6,022	5,068	6316.29	0.9895	9.12
5	205,114	165,790	6,093	5,240	6444.56	0.9926	9.36

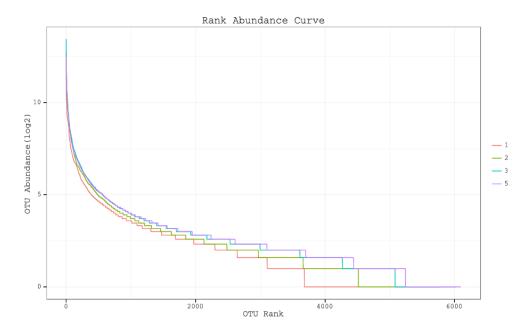
Supplementary Table 4. Number of *nrfA* sequences, richness and diversity in the Yellow River Estuary.

Supplementary Table 5. OTUs classification at different levels.

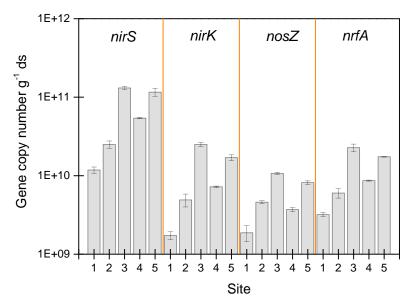
Supplementary Table 5. 01 03 classification at different levels.							
Study site	Phylum	Class	Order	Family	Genus	Species	
1	21	47	55	77	106	121	
2	25	55	68	86	114	128	
3	25	58	65	78	102	116	
5	23	54	61	72	95	107	



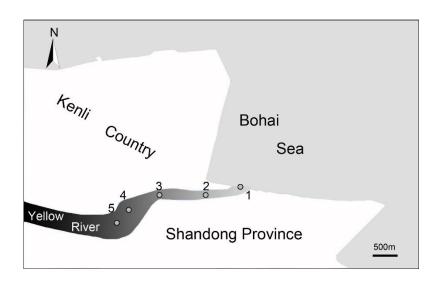
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