2022-01

Microbial selenate detoxification linked to elemental sulfur oxidation: Independent and synergic pathways

Li, L

10.1016/j.jhazmat.2021.126932
Journal of Hazardous Materials
Elsevier BV

Supporting Information

Microbial Selenate Detoxification Linked to Elemental Sulfur Oxidation: Independent and Synergic Pathways

Liuliu Li[a,b], Baogang Zhang[a,b*], Lei Li[a,b], Alistair G.L. Borthwick[c,d,e]

[a] *School of Water Resources and Environment, China University of Geosciences Beijing, Beijing 100083, China*

[b] *Key Laboratory of Groundwater Circulation and Evolution (China University of Geosciences Beijing), Ministry of Education, Beijing 100083, China*

[c] *St Edmund Hall, Queen's Lane, Oxford OX1 4AR, UK*

[d] *School of Engineering, The University of Edinburgh, The King's Buildings, Edinburgh EH9 3JL, UK*

[e] *School of Engineering, Computing and Mathematics, University of Plymouth, Drakes Circus, Plymouth PL4 8AA, UK*

[*]Corresponding author.

Tel.: +86 10 8232 2281; Fax: +86 10 8232 1081. E-mail: baogangzhang@cugb.edu.cn (B. Zhang).

This supporting information contains:

number of pages: 10

number of tables: 2

number of figures: 6

Table S1. Primers with sequences of functional genes used in the present study.

Genes	Primers	Primer sequences (5′→3′)	Function	References
serA	serAF	CCGCTCAAGTCCTATCCCTAC	Se(VI) reduction	Wen et al., 2016
	serAR	ATACTCGCTCACCTGCTCCTC		
tatC	SLDTatB-F	CCCGGTGGTGAAAAATAGTGAAG	Se(VI) reduction	Ma et al., 2007
	638TatD-R	GATGGACTCCCGCCGTTGAC		
napA	napAV17f	TGGACVATGGGYTTYAAYC	NO_3^- reductase	Bru et al., 2007
	napA4r	ACYTCRCGHGCVGTRCCRCA		
nirS	nirScd3aF	GT(C/G)AACGT(C/G)AAGGA(A/G)AC(C/G)GG	NO_2^- reductase	Throbäck et al., 2004
	nirSR3cd	GA(C/G)TTC GG(A/G) TG(C/G)GTCTTGA		
soxB	soxB693F	ATCGGNCARGCNTTYCCNTA	S(-II) oxidation	Meyer et al., 2007
	soxB1164B	AARTTNCCNCGNCGRTA		

Table S2. Bacterial richness and diversity of inoculum and bioreactors.

Sample ID	Reads	OTU	Ace	Chao1	Shannon	Simpson	Coverage
Inoculum	66094	4031	4826	4769	6.97	0.0025	0.98
Stage 1	74258	4086	4791	4713	6.80	0.0041	0.99
Stage 2	73714	2833	3952	3852	4.06	0.13	0.99
Stage 3	67683	1334	3243	2448	1.88	0.52	0.99
Stage 4	48117	2362	4758	3669	4.32	0.065	0.98
Stage 5	41047	2594	3776	3706	5.29	0.046	0.97

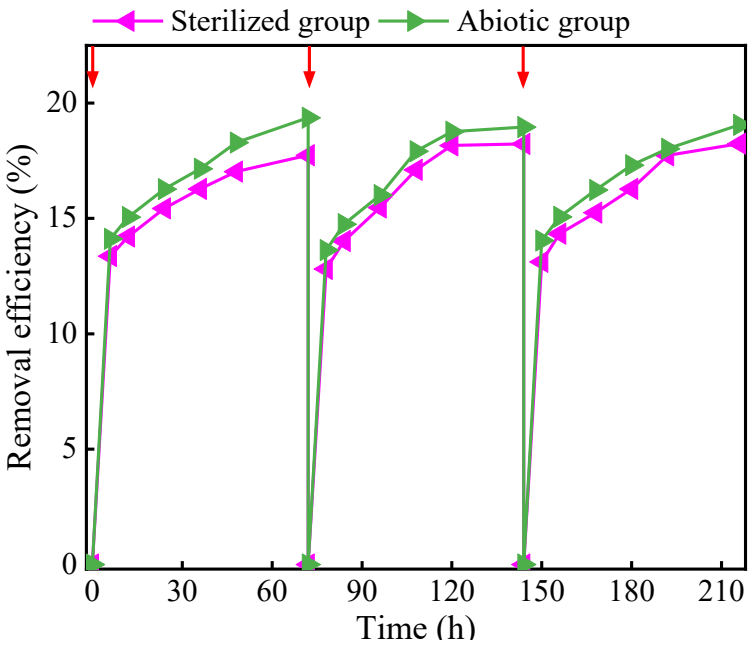

Fig. S1. Time histories of Se(VI) concentration during three consecutive operating cycles in batch trial (Sterilized group and Abiotic group). Red arrows indicate replacement of synthetic groundwater.

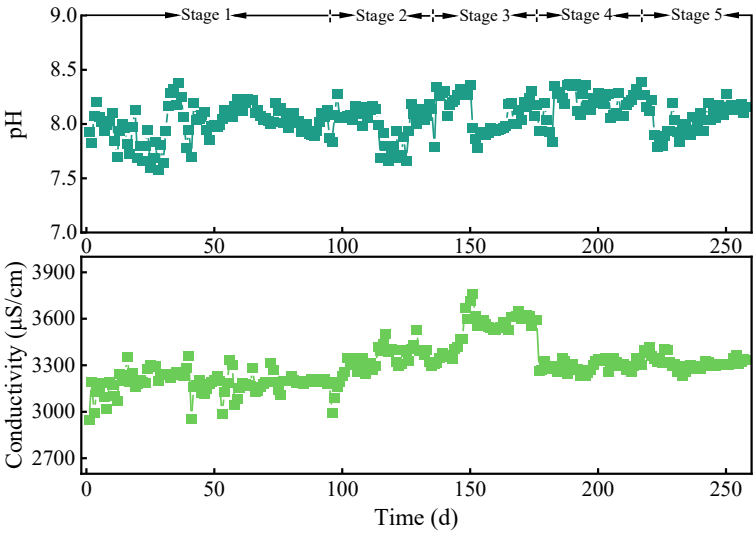

Fig. S2. Time histories of pH and conductivity during 258 d operation of the column trial.

Fig. S3. Images of bioreactor before and after the experiment.

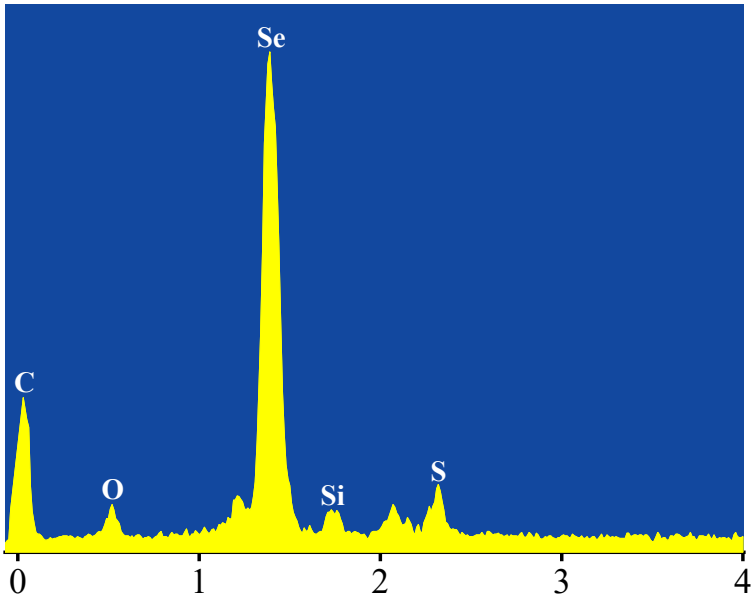

Fig. S4. EDS analysis of precipitates after reaction. EDS: Energy Dispersive Spectrometer.

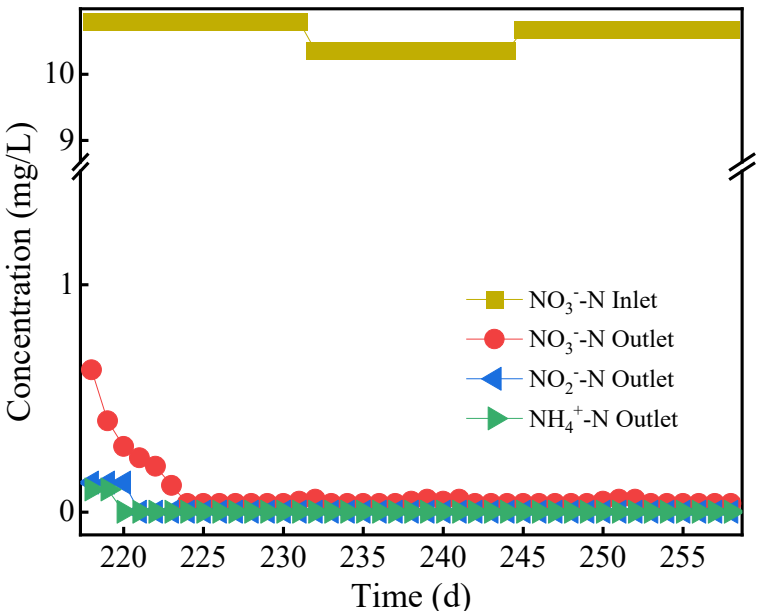

Fig. S5. Concentration of NO_3^--N in influent, and concentrations of NO_3^--N, NO_2^--N and NH_4^+-N in effluent.

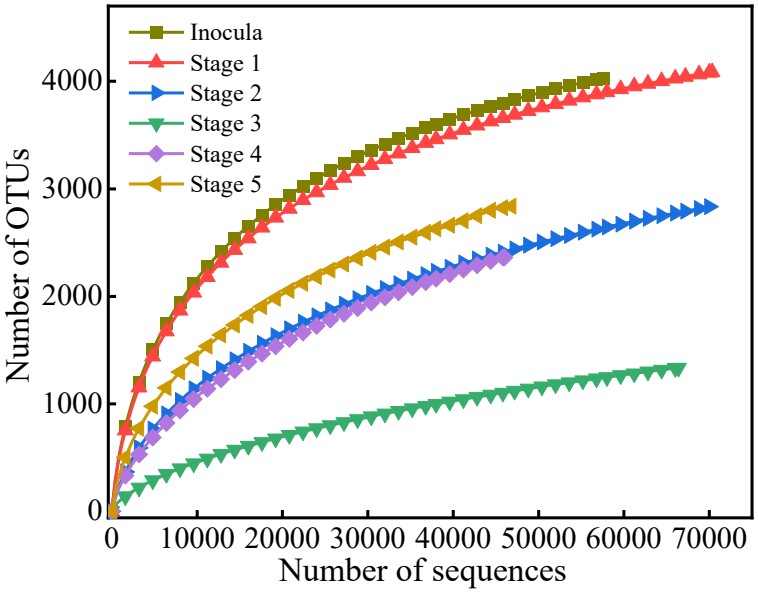

Fig. S6. Rarefaction curves of species abundance in inoculated sludge and post-treated samples.

References

Bru, D., Sarr, A., Philippot, L., 2007. Relative abundances of *Proteobacterial* membrane-bound and periplasmic nitrate reductases in selected environments†. Appl. Environ. Microb. 73, 5971-5974.

Ma, J., Kobayashi, D.Y., Yee, N., 2007. Chemical kinetic and molecular genetic study of selenium oxyanion reduction by *Enterobacter cloacae* SLD1a-1. Environ. Sci. Technol. 41, 7795-7801.

Meyer, B., Imhoff, J.F., Kuever, J., 2007. Molecular analysis of the distribution and phylogeny of the *soxB* gene among sulfur-oxidizing bacteria-evolution of the Sox sulfur oxidation enzyme system. Environ. Microbiol. 9, 2957-2977.

Throbäck, I.N., Enwall, K., Jarvis, Å., Hallin, S., 2004. Reassessing PCR primers targeting *nirS*, *nirK* and *nosZ* genes for community surveys of denitrifying bacteria with DGGE. FEMS Microbiol. Ecol. 49, 401-417.

Wen, L.L., Lai, C.Y., Yang, Q., Chen, J.X., Zhang, Y., Ontiveros-Valencia, A., Zhao, H.P., 2016. Quantitative detection of selenate-reducing bacteria by real-time PCR targeting the selenate reductase gene. Enzyme Microb. Tech. 85, 19-24.