

Supporting Information

Effect of Antibiotics on Redox Transformations of Arsenic and Diversity of Arsenite-Oxidizing Bacteria in Sediment Microbial Communities

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Table S1. Chemical components of the sediments used in this study^a

	Small pond	Lake Kasumigaura
As (mg/kg)	10.1 (0.4)	11.7 (0.2)
Total C (g/kg)	41.6 (0.2)	51.9 (0.1)
Total N (g/kg)	3.0 (0.0)	5.4 (0.0)
P (g/kg)	0.8 (0.0)	1.6 (0.0)
Fe (g/kg)	61.9 (2.5)	57.5 (1.4)
Al (g/kg)	112.9 (7.4)	94.8 (3.3)
Mn (g/kg)	0.5 (0.0)	1.3 (0.0)
Ca (g/kg)	4.8 (0.6)	7.5 (0.2)
K (g/kg)	6.2 (0.3)	9.1 (0.2)
Mg (g/kg)	7.9 (0.8)	6.5 (0.2)
Na (g/kg)	4.2 (0.2)	4.6 (0.2)

^aFive samples were assayed in this study. Figures in parentheses indicate the standard deviations.

Table S2. Diversity indices for the *aioA* gene sequences in clone libraries of 0-, 2- and 4-day cultures of the control and antibiotics-amended experiments (N = control; TC = tetracycline; EM = erythromycin; LCM = lincomycin; ABPC = ampicillin). For experimental conditions, see Figure 4.

	<u>0 d</u>		N	TC	EM	LCM	ABPC
Chao1	35.0	<u>2 d</u>	70.3	7.0	22.2	30.0	24.0
		<u>4 d</u>	58.0	22.5	30.3	54.3	49.0
ACE	44.5	<u>2 d</u>	74.6	9.8	23.8	54.7	27.2
		<u>4 d</u>	60.3	24.0	33.6	48.5	47.4
Shannon index	2.6	<u>2 d</u>	2.6	0.7	2.3	1.4	2.2
		<u>4 d</u>	2.8	1.8	2.2	2.5	1.5
Simpson index	0.9	<u>2 d</u>	0.9	0.3	0.8	0.5	0.8
		<u>4 d</u>	0.9	0.7	0.8	0.8	0.6
Pielou index	0.9	<u>2d</u>	0.8	0.4	0.8	0.5	0.8
		<u>4d</u>	0.9	0.7	0.7	0.8	0.6

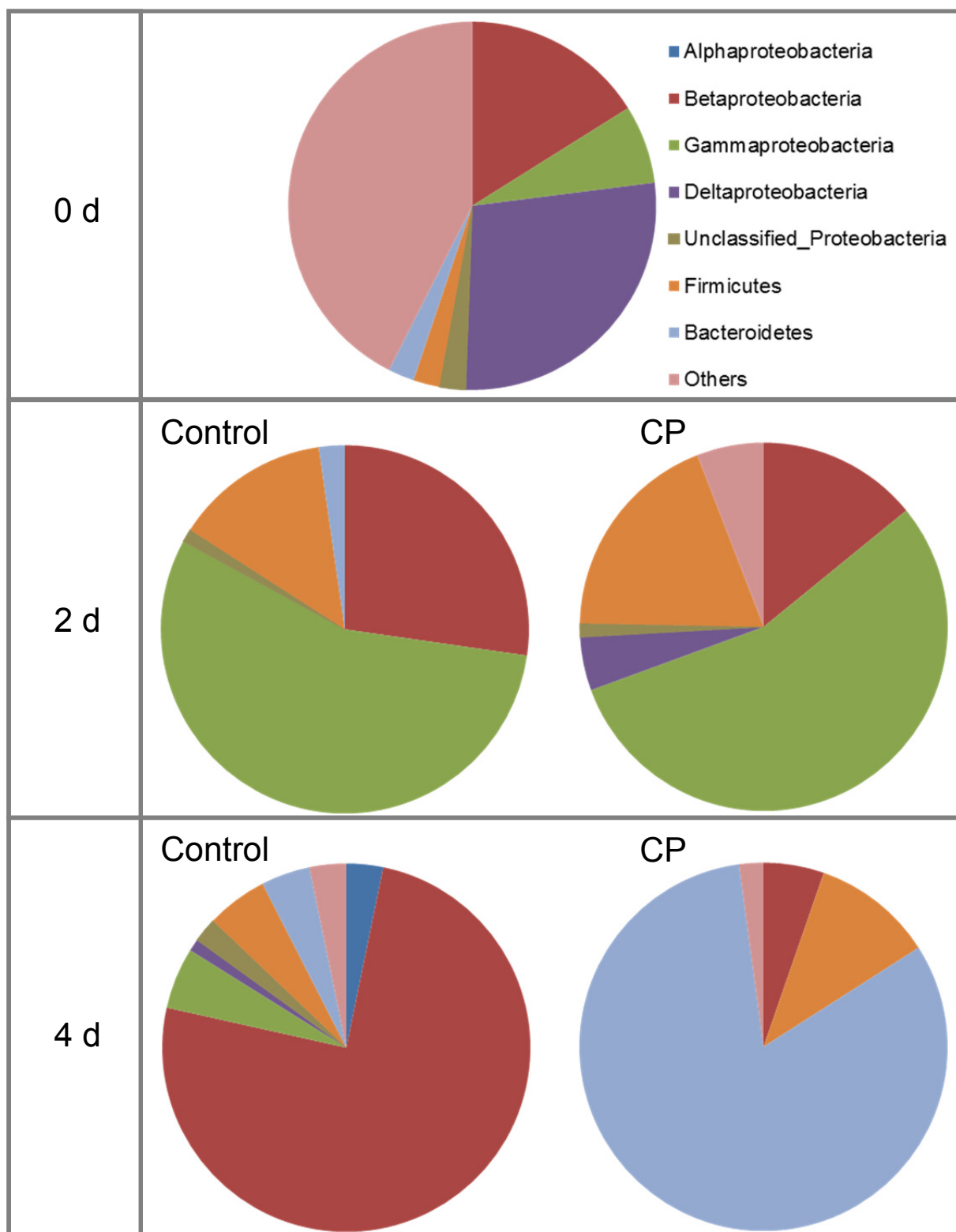


Figure S1. Compositions of bacterial communities determined from 16S rRNA gene clone libraries of 0-, 2- and 4-day cultures of the control and CP-amended experiments (where CP denotes chloramphenicol). For experimental conditions, see Figure 4.

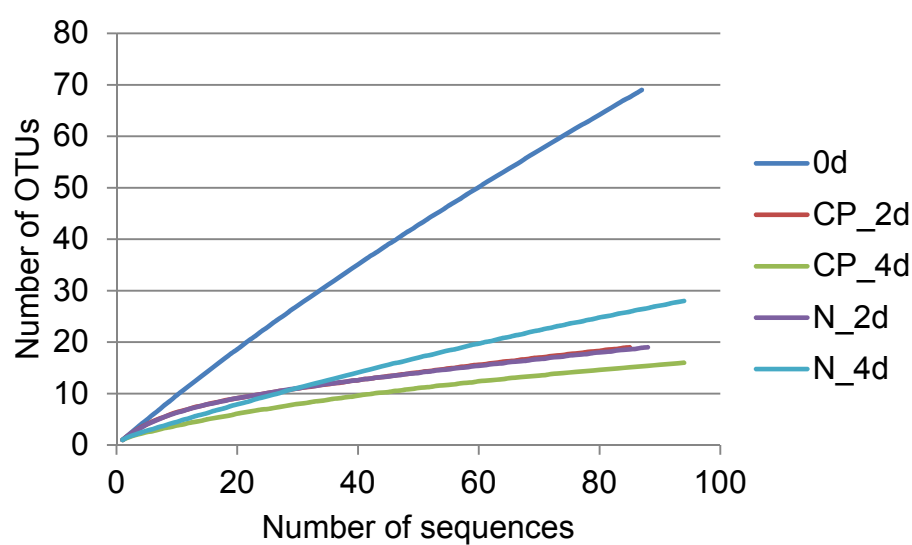


Figure S2. Rarefaction curves obtained for the 16S rRNA gene sequences in clone libraries of 0-, 2- and 4-day cultures of the control and CP-amended experiments (N = control; CP = chloramphenicol). The vertical axis indicates the number of OTUs clustered at 97% similarity. For experimental conditions, see Figure 4.

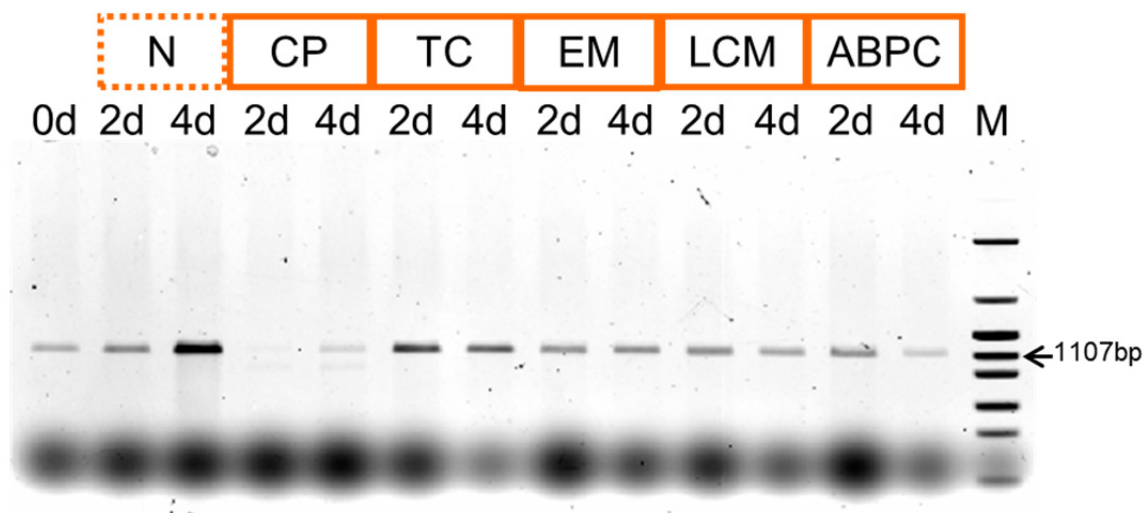


Figure S3. PCR amplification of *aioA* genes from the control (no antibiotics; N) and antibiotics-amended cultures. Lane M, molecular mass markers. For experimental conditions, see Figure 4.

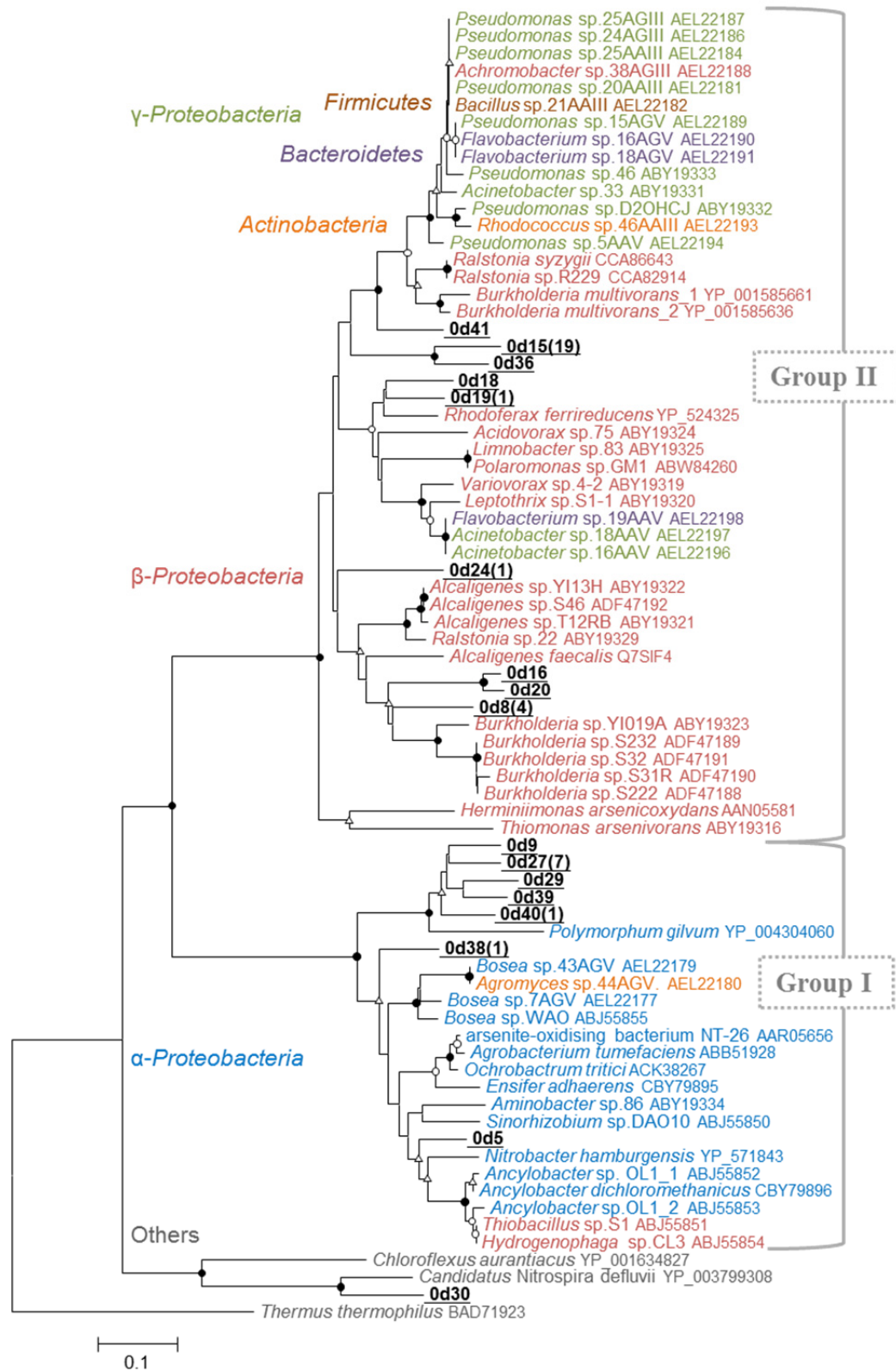


Figure S4. Neighbor-joining phylogenetic trees of bacterial AioA protein sequences retrieved from initial (0 d) cultures. The sequences obtained in this study are shown in underlined bold font. Numbers in parentheses indicate the number of closely related sequences obtained. Reference

sequences of *Alphaproteobacteria*, *Betaproteobacteria*, *Gammaproteobacteria*, *Actinobacteria*, *Bacteroidetes*, and *Firmicutes* are shown in *blue*, *red*, *green*, *orange*, *purple*, and *brown*, respectively. The reference sequences are of As(III) oxidases encoded by cultivated bacteria. Circles and triangles at the branch nodes represent bootstrap percentages: filled circles, 90–100%; open circles, 70–90%; open triangles, 50–70%. Values less than 50% are not shown. The scale bar represents the estimated number of substitutions per site.