Supplementary dataset

**Arsenic cycling and high affinity phosphate uptake gene distribution in shallow submarine hydrothermal sediments**

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| --- | --- | --- | --- | --- | --- | --- |
| **Gene** | **Strain used for curve calibration** | **Primer name** | **Primer sequence** | **Primer concentration (nM)** | **Annealing temperature°C** | **Reference** |
| ***arrA*** | *Geobacter sulfurreducens (DSMZ 12127)* | qArr1F | 5’- GATCCACGCTTCTCCACCTC-3’ | 500 | 60 | Giloteaux et al. 2013 |
|  |  | qARR1R | 5’-CCCCGGCTTTAAAGAGGTTC-3’ | 500 |
| ***aoxB*** | *Marinobacter Santoriniesis(DSM 21262)* | *aoxBM1-2F* | 5’-CCACTTCTGCATCGTGGGNTGYGGNTA-3’ | 500 | 60 | Quéméneur et al. 2010 |
|  |  | aoxBM2-1R | 5’-GGAGTTGTAGGCGGGCCKRTTRTGDAT-3’) | 500 |
| ***arc3-1*** | *Geobacter sulfurreducens (DSMZ 12127)* | qA1-3F | 5’-ATGGCCAGCTCGAAaTTGTT -3’ | 500 | 60 | Giloteaux et al.2013 |
|  |  | qA1-2R | 5'-GCGATGGCCAGCTCRAARTTRTT-3' | 500 | Fahy et al. 2015 |
| ***arc3-2*** | *Rhodoferax ferrireducens (DSMZ 15236)* | qA2-1F | 5’-GGCCAGTTCGAAGAAGTTGG-3’ | 500 | 60 | Giloteaux et al. 2013 |
|  |  | qA2-1R | 5’-GCCGATTTTGATCCAGGTGT-3 | 500 |
| ***arsB*** | *Desulfovibrio tunisiensis (DSMZ 19275)* | darsB1F | 5'-GAACATCGTCTGGAAYGCNAC-3' | 500 | 53 | Poirel et al., 2013 |
|  |  | darsB1R | 5'-GTACACCACCAGRTACATNCC-3' | 500 |
| ***pstB*** | *Geobacter sulfurreducens (DSMZ 12127)* | pstB-310F | 5′-CCGTTCCCCAAATCGATCT-3′ | 500 | 60 | N’Guessan et al. 2010 |
|  |  | pstB-422R | 5′-ATGGCGGCGTTAGTGAGG-3′ | 500 |
| **16S rRNA geobacteraceae** | *Geobacter sulfurreducens (DSMZ 12127)* | GEO-494F | 5′-AGGAAGCACCGGCTAACTCC-3’ | 500 | 60 | Homes et al. 2002 |
|  |  | GEO-825R | 5‘-TACCCGCRACACCTAGT-3‘ | 500 | Andersson et al. 1998 |

Table S1. Genes, pure culture standards and primers used for qPCR analysis. With the exception of the *Geobacteraceae* *pstB* and 16S rRNA-specific gene primers, the remainder of the primers are universal (see the references for the choice of primers).

Table S2. Sediment porewater and seawater chemical analysis in ppm.

Table S3. Total variance explained and matrix of Varimax rotated factor loadings and communalities for normal score transformed geochemical and genomic data. Significant positive and negative factor loadings are indicated in red numbers.

Variable Factor1 Factor2 Communality

nscoreAs 0.020 -0.974 0.949

nscoreP 0.345 -0.919 0.964

nscoreFe/S 0.870 -0.090 0.765

nscoreaoxB 0.936 -0.119 0.891

nscorepstB 0.805 -0.391 0.800

nscoreacr3-2 0.980 -0.106 0.972

nscoreacr3-1 0.980 -0.106 0.972

nscorearrA 0.738 -0.402 0.707

nscore16SrRNA 0.883 -0.282 0.858

Variance 5.6455 2.2313 7.8768

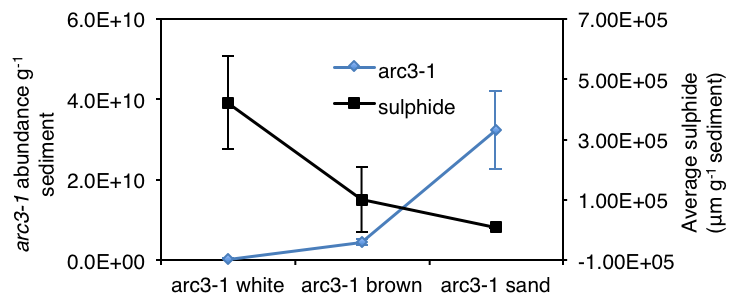
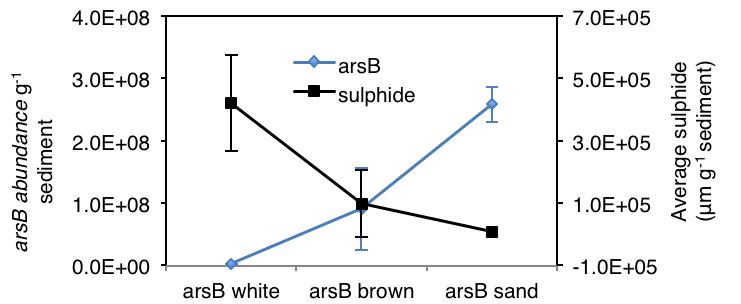
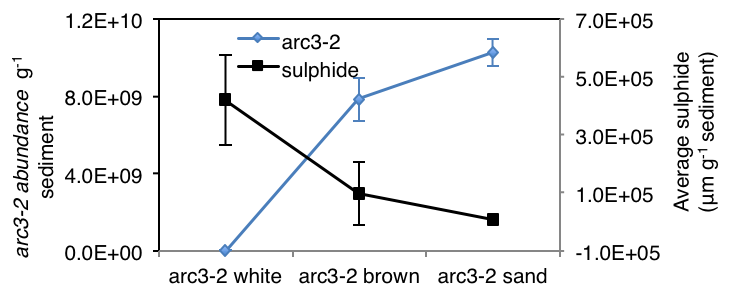
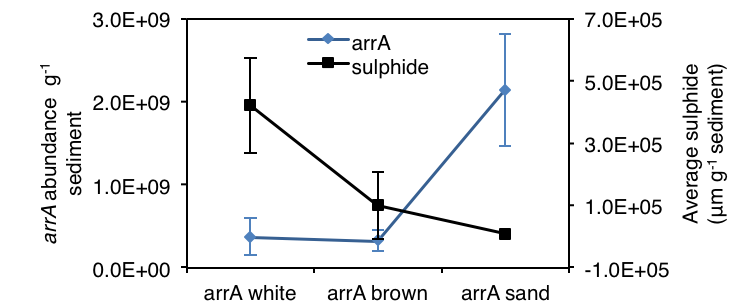
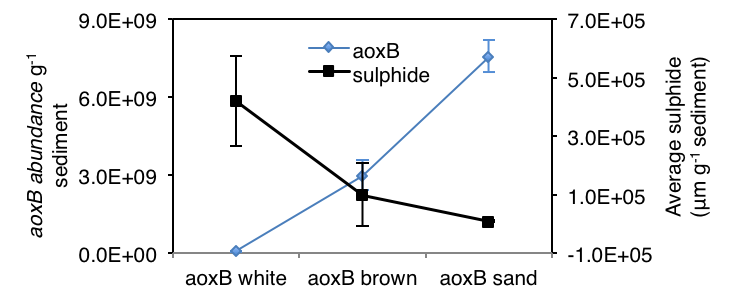
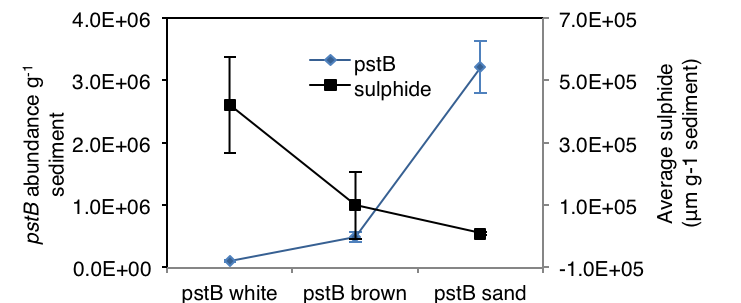
% Var 0.627 0.248 0.875



Fig. S1. Distribution of Fe, P and As in sequential Fe extractions. W, B and S, represent white, brown and sand-capped sediments, arranged according to sediment depth. (a) Fe quantified in different Fe(III)(oxyhydr)oxide phases. (b) As content associated with different Fe(III)(oxyhydr)oxide phases. (c) P content associated with different Fe(III)(oxyhydr)oxide phases. (d) Total sediment Fe, As and P to total Fe(III)(oxyhydr)oxide ratios.



Figure S2. Abundance of the As cycling genes *aoxB*, *arsB*, *arrA*, *arc3-2* and *arc3-1* and high affinity phosphate uptake *pstB* genes with sediment depth (cm) and seawater water depth (m). (A) Sand-capped sediment. (B) Brown-capped sediment. (C) White-capped sediment. (D) Seawater. Data not represented were below detection limit.



(A)

(B)

(C)

(D)

(E)

(F)

Fig. S3.Relationship between sulphide and distribution of As and high affinity phosphate genes in the first 20 cm of sediments at Spathi Bay, Milos Island. Values are average core values for the entire sediment depth for two replicate cores per habitat type. Scale bars for the sulphides are standard deviations across a 20 cm depth profile, while bars on the gene graphs are errors for measurements averaged across the same depth profiles.

**References**

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