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Supporting Online Material for

## **A Bacterium That Can Grow by Using Arsenic Instead of Phosphorus**

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*Supporting online material for:*

“A bacterium that can grow by using arsenic instead of phosphorus”

## **MATERIALS AND METHODS**

*Field site description and enrichments.* Mono Lake bottom sediment was added to 20-ml sterile glass screw top tubes containing 10 ml autoclaved artificial defined Mono Lake medium (AML60; *S1*) at pH 9.8 with the following constitution: 0.80 mM  $(\text{NH}_4)_2\text{SO}_4$ , 0.20 mM  $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$ , 1.0 M NaCl, 100 mM  $\text{Na}_2\text{CO}_3$ , 50 mM  $\text{NaHCO}_3$ , 10 mM glucose, a full complement of vitamins (*S2*) and trace elements according to Widdel et al. (*S3*) with the addition of 45 nM  $\text{Na}_2\text{WO}_4 \cdot 2\text{H}_2\text{O}$ . All materials were prepared with sterile- and nutrient-clean techniques. Cultures were grown in tubes at room temperature (20 to 22°C) in the dark. Control tubes were set up with added phosphate (P: 0.6 mM  $\text{KH}_2\text{PO}_4$  + 0.9 mM  $\text{K}_2\text{HPO}_4$ ) while experimental tubes had no added  $\text{PO}_4^{3-}$ , and a gradient of added  $\text{Na}_2\text{HAsO}_4 \cdot 7\text{H}_2\text{O}$ : 100 $\mu\text{M}$ , 1mM and 5mM. Seven successive decimal dilution transfers, over the course of three months with an overall dilution of  $10^{-7}$  from the original inocula, resulted in modest increased turbidity in all tubes, as compared with a sterile control. The sixth transfer of the 5mM  $\text{AsO}_4^{3-}$  (no added  $\text{PO}_4^{3-}$ ) condition was closely monitored and demonstrated an approximate growth rate ( $\mu$ ) of  $0.1 \text{ day}^{-1}$ . 5 mM  $\text{AsO}_4^{3-}$  cultures were then spread on plates containing AML60 1.5 % solid agar (10 mM glucose, 5 mM  $\text{AsO}_4^{3-}$ , no  $\text{PO}_4^{3-}$ ). Two types of colony morphologies were observed. Single colonies were picked and reintroduced into defined artificial liquid AML60 with 10 mM glucose, 5 mM  $\text{AsO}_4^{3-}$ , and no  $\text{PO}_4^{3-}$ . All of the isolates are maintained as stock cultures in the laboratory with  $\text{AsO}_4^{3-}$  but no added no  $\text{PO}_4^{3-}$ .

*Isolation of strain GFAJ-1.* Of the colonies picked and cultured back into liquid medium, a single colony, GFAJ-1, was identified as the fastest growing isolate and pursued for further study. After identification of GFAJ-1 by 16S rRNA phylogeny (see below) as a member of the Halomonadaceae and closely related to microbes known to survive high arsenate concentrations, we tested the growth of GFAJ-1 over the range of 10, 20, 40 and 80 mM  $\text{AsO}_4^{3-}$ . We determined the +As/-P condition that elicited the best growth for GFAJ-1 was AML60 amended with 10 mM glucose, 40 mM  $\text{AsO}_4^{3-}$ , no  $\text{PO}_4^{3-}$  and incubated at 28°C. All experimental evidence shown for this study were conducted with GFAJ-1 cells grown under these conditions identified in the main manuscript text as “+As/-P” unless explicitly stated otherwise. Strain GFAJ-1 is maintained as a stock culture for all inocula under the +As/-P condition.

*GFAJ-1 growth experiment.* GFAJ-1 cells were grown in 10 ml total volume in 20-ml screw-top glass tubes in sterile AML60 amended 10 mM glucose and vitamins (as above) under three experimental conditions including +As/-P, 40 mM  $\text{AsO}_4^{3-}$  with no added  $\text{PO}_4^{3-}$ ; -As/+P, 1.5 mM  $\text{PO}_4^{3-}$  with no added  $\text{AsO}_4^{3-}$  and Control, no added  $\text{AsO}_4^{3-}$  nor  $\text{PO}_4^{3-}$ . Six replicates of +As/-P and -As/+P with two replicates of Control experimental tubes were set up. All tubes were incubated at 28°C in the dark. We measured the optical density of all cultures at 680 nm ( $\text{OD}_{680}$ ) on a Spectronic 20 Genesys

spectrophotometer (Spectronic Instruments). Because we had to remove samples for acridine orange direct cell count (AODC) measurements (S4), O.D. was performed on all cultures (n=6 for experimental tubes and n=2 for control tubes) until material was depleted due to sampling as of 262 hours of the experiment. AODCs were done on a subset of the cultures (n=3 for experimental and n=1 for control tubes) to allow enough material for the duration of the experiment. AODCs were done according to standard protocols outlined elsewhere (S5).

*Electron microscopy.* GFAJ-1 was grown +As/-P and -As/+P to stationary phase for EM analyses. For scanning electron microscopy, critical point drying was performed in a Ladd Critical Point Dryer No. 28000 using CO<sub>2</sub> as the transitional fluid. Cells were sputter coated with Au/Pd and imaged at 5 kV with a Leo 982 Digital Field Emission Electron Microscope. Cells volumes were estimated using ImageJ (rsb.info.nih.gov/ij/; S6, S7) with n= 6 cells measured for both +As/-P and -As/+P conditions. Length and width were measured and volume was estimated based on a cylindrical shape. Transmission electron microscopy preparation included negative staining of whole cells performed with 1 % uranyl acetate on Formvar-coated grids. Thin sections of Spurr's embedded samples were prepared following the procedure described by Switzer Blum et al. 1998 (S8). Samples were observed with a transmission electron microscope (100CX; JEOL) at 60 kV.

*Radiolabel <sup>73</sup>AsO<sub>4</sub><sup>3-</sup> experiment.* Cells were grown in duplicate 100 ml cultures in 250-ml screw top glass flasks in the dark at 28°C in AML60 with 10 mM glucose, 20 mM AsO<sub>4</sub><sup>3-</sup>, without added PO<sub>4</sub><sup>3-</sup> and amended with 111 kBq ml<sup>-1</sup> of the radiolabel <sup>73</sup>AsO<sub>4</sub><sup>3-</sup> (carrier-free, Oak Ridge National Laboratory, Oak Ridge, TN). To determine uptake and cellular distribution of <sup>73</sup>AsO<sub>4</sub><sup>3-</sup> cells were grown to stationary phase, collected by centrifugation and washed three times with AML60 containing no PO<sub>4</sub><sup>3-</sup>, AsO<sub>4</sub><sup>3-</sup>, vitamins or glucose so as to remove any adsorbed radiolabel. Cell pellets were processed for nucleic acid extraction (see below). The radiolabel was quantified by gamma spectrometry (S9, S10) to determine radiolabel distribution in all subcellular fractions of the extraction including the phenol subnatant, three phenol:chloroform subnatants, chloroform subnatant, final aqueous supernatant and DNA/RNA pellet. To estimate the total As associated with a genome, we downloaded the size of all sequenced bacterial genomes and calculated a conservative estimate for the total P associated with the number of base pairs in a bacterial genome on average. These data are publically available from the JGI website.

*Nucleic acid extraction.* To separate cellular fractions and isolate DNA and RNA, cell pellets were disrupted using a buffer containing 1.2 % SDS, 30 mM EDTA, 50 mM Tris-HCl (pH 8.0), 220 mM NaCl and 50 mM β-mercaptoethanol. Extractions were initiated with a phenol addition (pH 6.6), briefly vortexed, and separated by centrifugation. The extraction was further clarified by three phenol:chloroform (1:1, pH 6.7) additions and centrifugation, where the supernatant (aqueous) fraction was serially removed and extracted with phenol:chloroform. The third aqueous supernatant from the phenol:chloroform steps was combined with equal part chloroform and centrifuged. The DNA/RNA was precipitated from the chloroform step supernatant by addition of one-tenth volume 3

M sodium acetate (pH 5.5) and pre-chilled 100 % ethanol. The nucleic acids were pelleted by centrifugation and the supernatant removed. For downstream molecular biology applications, the DNA/RNA pellet was resuspended in sterile molecular biology grade water.

*Phylogenetic analyses.* Cells were harvested that had been grown under four conditions: +As/-P, -As/+P, +As/+P and -As/-P (control). DNA extractions were done as explained above. The 16S ribosomal gene was amplified by PCR using the universal primers Bact 8F 5'-AGA GTT TGA TCC TGG CTC AG-3' and Univ 1517R 5'-ACG GCT ACC TTG TTA CGA CTT-3' (Integrated DNA Technologies, Inc. Coralville, IA). PCR products were run out on 1% agarose gels, bands cut, and gel purified using QIAquick Gel Extraction Kit (#28704, Qiagen, Inc. Valencia, CA). Gene fragments were then cloned into *E. coli* (pCR4 TOPO-TA kit #K4575-01, Invitrogen, Inc. Carlsbad, CA) and a total of forty clones were picked for sequencing (ten clones for each PCR product). Positive clones were isolated using QIAprep Sping Miniprep Kit (#27106, Qiagen, Inc. Valencia, CA) verified by PCR for correct insert and sent for sequencing (Sequetech, Inc. Mountain View, CA). All conditions produced identical 16S ribosomal gene sequences; hence a single sequence was used representing GFAJ-1 for tree construction (Figure S1). 16S rRNA sequences were aligned employing the NAST alignment tool (S11) as part of the Greengenes Database and Tools (S12). The sequences were also tested to identify any possible PCR produced chimeras using the Bellerophon package (S13) and preliminary taxa identification was done using the Ribosomal Database Project tools and pipeline (S14). After the final alignment was manually adjusted using BioEdit (S15) the tree was constructed using a maximum likelihood analysis with PhyML (S16) through the PhyML software package accessed through the Phylemon online tools suite (phylemon.bioinfo.cipf.es). Sequences used for analysis are listed in Table S3. The sequence for GFAJ-1 has been deposited with GenBank (accession HQ449183).

*Total elemental composition of GFAJ-1, medium and buffers by ICP-MS.* Phospho-molybdenum blue has lower detection limits for phosphate concentrations, but was not used due to the arsenate interference (S17). Batch cultures were grown until early stationary phase and harvested by centrifugation. Cell pellets were gently washed three times by resuspension in AML60 containing no added  $\text{PO}_4^{3-}$ ,  $\text{AsO}_4^{3-}$ , vitamins, glucose or trace metals to wash any potentially adsorbed inorganic minerals from the cell surfaces. Cells were then flash frozen until acid digestion. Cell pellets were digested in concentrated nitric acid until completely dissolved, dried and then re-dissolved in 0.32 M nitric acid. Other washed cell pellets were processed as for nucleic acid extraction (see above section) and the “phenol” and “final aqueous and pellet” fractions were dried, dissolved and acidified in a similar manner to the whole cell pellets (presence of the DNA in the samples was confirmed by measuring the absorption properties of the sample at 260 nm prior to processing). DNA/RNA fractions were also run out on 1 % agarose gels, positive and control (not containing DNA or RNA) bands excised and subject to the same ICP-MS preparation (dried, dissolved and acidified) as the cell pellets. Details below.

All reagent acids were trace metal grade; pipette tips and centrifuge tubes were pre-cleaned by soaking in dilute Citranox overnight, washed three times in 18.2 MΩ water, soaked in 20% (v/v) reagent grade nitric acid for several days, washed three times in 18.2 MΩ water, soaked in 20% (v/v) reagent grade hydrochloric acid for several days, washed three times in 18.2 MΩ water and dried in a designated HEPA-filtered hood. Savillex Teflon digestion vessels were cleaned by soaking in dilute Micro90 detergent, rinsed three times in 18.2 MΩ water, heated to sub-boiling in 50% (v/v) reagent grade nitric acid for 24 hours, rinsed three times in 18.2 MΩ water, heated to sub-boiling in 50% (v/v) reagent grade hydrochloric acid for 24 hours, rinsed three times in 18.2 MΩ water, heated to sub-boiling in 18.2 MΩ water for 18 hours, dried in a designated HEPA-filtered hood. An additional cleaning step of 50% (v/v) trace metal grade nitric acid heating for each container on a hot plate was completed to reduce any potential contamination or blank contribution.

Media samples were diluted and analyzed as received. The DNA/RNA gel samples, the DNA/RNA extracts, the phenol extracts and the washed cell pellets were digested in a class 10 hood in a trace metal clean lab. The samples were weighed, transferred into Savillex Teflon digestion vials, dried under filtered air at low temperature and weighed again. 2 ml of trace metal clean nitric acid was added to each sample, and they were digested in a closed vessel overnight at ~150°C. Samples from the +As/-P, -As/+P and -As/-P conditions were prepared on separate hot plates with digestion process blanks on each hot plate to monitor for contamination (see “digestion process blank in Table S1”). The digestion process was repeated several times until solutions were clear with no precipitate. The phenol samples were digested in aqua regia until they were clear with no precipitate.

Samples were analyzed on a Thermo X-series quadrupole ICP-MS with Collision Cell Technology (CCT) option at the W.M. Keck Foundation Laboratory for Environmental Biogeochemistry at Arizona State University in Tempe, AZ. Low P and As sample concentrations, combined with the high ionic strength of media (Na/P ratio up to 10<sup>6</sup>) and samples can cause plasma suppression. Hence, the following precautions were taken to assure accuracy and validity of measured concentrations: a) multiple calibration curves, b) standard addition for As and P for most samples except in cases of sample limitation, c) independent single element check standards at concentrations similar to samples, d) independent sample matrix-matched check standards e) frequent analytical blanks f) multiple process blanks g) replicate digestions from the same sample and h) repeat analyses of samples over multiple analytical sessions. The calibration curve used a multi-element standard solution, and was analyzed at the beginning, end and approximately every fifty samples during the runs. Sc, Ge, Y, In and Bi were used as internal standards. As was analyzed using a 7% H<sub>2</sub> in He gas mixture to reduce polyatomic interferences. Blanks and secondary single element standards of similar concentration of As and P as the samples were analyzed as check standards every five samples. Matrix matched secondary standards were designed to evaluate accuracy of low P and As concentration determinations in the high salt matrix of many samples and included A) 100 ppm Na, B) 700 ppb Na 10 ppb P 1 ppb As, C) 50 ppm Na 3 ppm P 10 ppb As, D) 50 ppm Na 5 ppb P, and E) 50 ppm Na 5 ppm P 140 ppb As; these samples showed good reproducibility within error. From the reproducibility

of single element and matrix-matched check standards, limit of detection is approximately 1 ppb for both As and P.

Digested samples were diluted by gravimetry to a dilution factor of 30 and analyzed by ICP-MS to obtain a rough estimate of As and P concentrations. Subsequently, each sample was measured by standard addition of As and P in amounts appropriate to that sample. Depending on sample availability, each sample was measured using a standard addition curve comprised of with three to five measurements per curve. The correlation coefficient of 18 of the 22 phosphorus standard addition curves was better than 0.95; the other four were 0.52, 0.71, 0.88 and 0.93. The correlation coefficient of 19 of the 22 arsenic standard addition curves was better than 0.95; the other three were 0.58, 0.82 and 0.93. The data for the three P standard addition curves and two As standard addition curves with correlation coefficients less than 0.9 are denoted in italics in Table S1. Samples not analyzed by standard addition due to limited sample quantities are in italics in Table S1. “Repeat” in Table S1 indicates a replicate digestion and analysis.

*NanoSIMS analyses.* Individual cells and DNA in high purity agarose gel sections were analyzed for As and P abundance by high-resolution secondary ion mass spectrometry (SIMS) on a Cameca NanoSIMS 50 at Lawrence Livermore National Laboratory (LLNL) in Livermore, California. The NanoSIMS 50 allows the simultaneous collection of 5 isotopes with high spatial resolution (up to 50 nm) and high mass resolution. Glutaraldehyde preserved washed GFAJ-1 cells were first coated with 5 nm of iridium (agarose slices were gold coated to ~20 nm) to make them conductive, then a focused Cs<sup>+</sup> primary beam was rastered over the sample surfaces to generate secondary ions (<sup>12</sup>C<sup>-</sup>, <sup>12</sup>C<sup>14</sup>N<sup>-</sup>, <sup>31</sup>P<sup>-</sup>, <sup>34</sup>S<sup>-</sup>, and <sup>75</sup>As<sup>-</sup> for the cell analyses and <sup>12</sup>C<sup>-</sup>, <sup>29</sup>Si<sup>-</sup>, <sup>31</sup>P<sup>-</sup>, <sup>70</sup>Ge<sup>-</sup>, and <sup>75</sup>As<sup>-</sup> for agarose analyses) along with secondary electron (SE) images. Cells were sputtered with Cs<sup>+</sup> at high beam current before measurements to achieve sputtering equilibrium. For cell analyses, a 2.2 pA Cs<sup>+</sup> primary beam focused to a nominal spot size of 100-150 nm was stepped over the sample in a 128 x 128 pixel raster to generate secondary ions, collected by electron multipliers with a dead time of 44 ns. Dwell time was 1ms/pixel, and raster size was either 3 x 3 μm or 8 x 8 μm. DNA gel samples were sputtered with Cs<sup>+</sup> at moderately high beam current (~100 pA) to a depth of ~100 nm before performing the analyses with ~10 pA Cs<sup>+</sup> on a 5 x 5 μm, 128 x 128 pixel raster with 2 ms/pixel dwell time and 14 cycles. To resolve As from neighboring isobaric interferences at mass 75, the mass spectrometer was tuned to ~8000 mass resolving power and the <sup>75</sup>As<sup>-</sup> peak was aligned on a GaAs wafer. Samples were simultaneously imaged by secondary electrons which yields a reference image useful for comparison to the secondary ion images. Secondary ions were detected in simultaneous collection mode by pulse counting to generate 30-60 serial quantitative secondary ion images (*i.e.* layers). Measurements were repeated on 10 to 25 individual cells per treatment (+As/-P, -As/+P), and at 4 to 7 different locales in the DNA-loaded agarose gels. For the cell analysis, each was defined as a region of interest (ROI) by encircling pixels where <sup>12</sup>C<sup>14</sup>N<sup>-</sup> counts > 30% of the maximum counts in the image. The As:C and P:C composition of each ROI was calculated by averaging over all replicate layers where both <sup>12</sup>C<sup>-</sup> and <sup>12</sup>C<sup>14</sup>N<sup>-</sup> count rates were stable (*i.e.*, at sputtering equilibrium). Data were processed as quantitative

elemental ratio images using LIMAGE software, developed by L. Nittler (Carnegie Institution of Washington, Washington, D.C.), and were corrected for detector dead-time and image shift from layer to layer (due to drift in the location of the ion beam). Concentration estimates of As and P were calculated with:

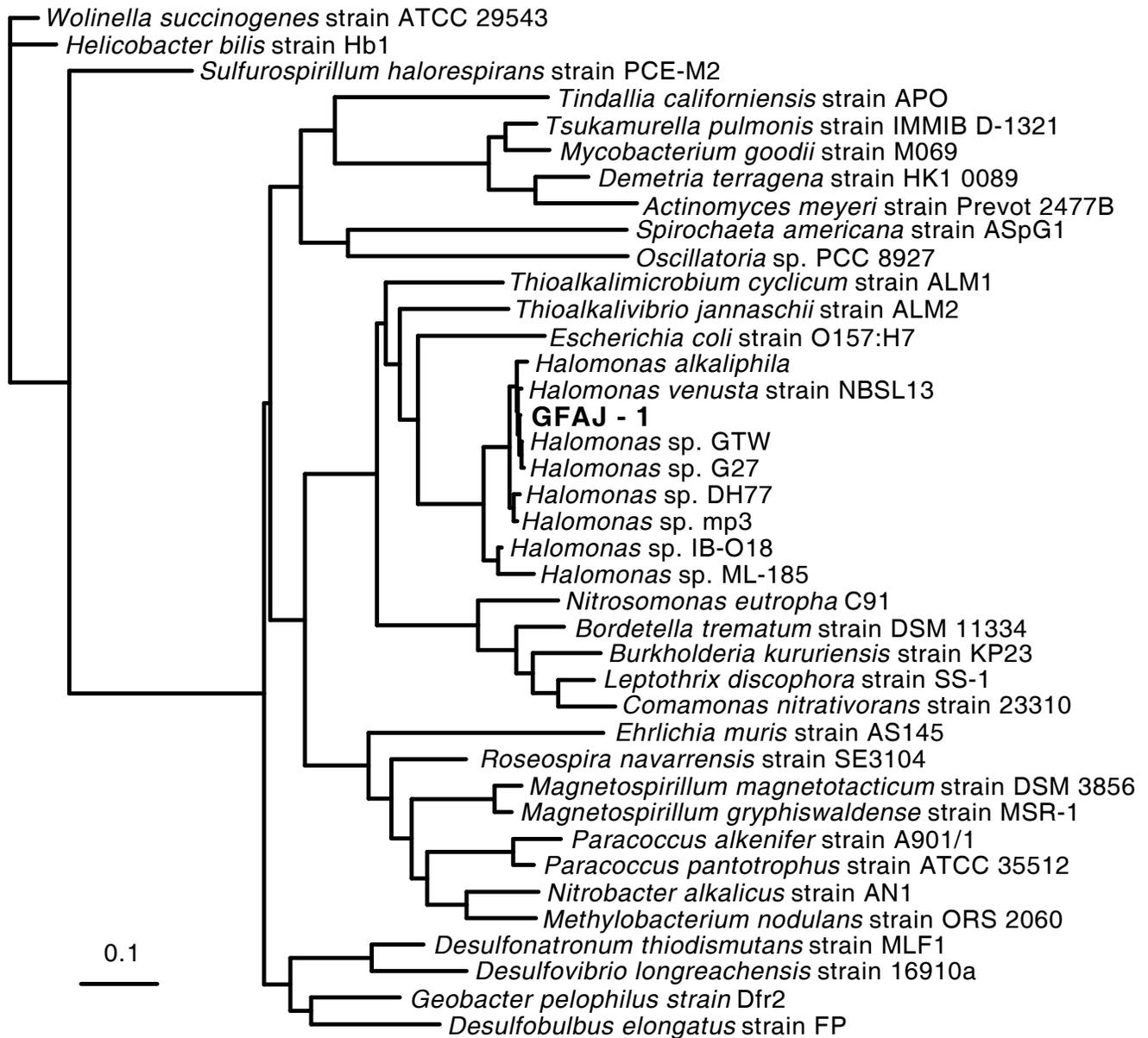
$$[X] = \text{RSF}_{X/C} * (^nX^-/^{12}C^-)$$

where [X] is the concentration of the element of interest in hydrated agarose,  $\text{RSF}_{X/C}$  is the relative sensitivity factor for element X relative to carbon, and  $^nX^-$  and  $^{12}C^-$  are the measured isotopes.  $\text{RSF}_{X/C}$  is estimated based on NanoSIMS and ICP-MS data for bulk gel samples in this study, based on wet weight ( $\text{RSF}_{As/C} \sim 1.2 \times 10^{-3} \text{ g As} \cdot \text{g}^{-1} \text{ agarose} \cdot (^{75}\text{As}^-/^{12}\text{C}^-)^{-1}$ ;  $\text{RSF}_{P/C} \sim 1.2 \times 10^{-3} \text{ g P} \cdot \text{g}^{-1} \text{ agarose} \cdot (^{31}\text{P}^-/^{12}\text{C}^-)^{-1}$ ). Because of significant uncertainty in bulk gel P and particularly As concentrations, the precisions of the RSF and subsequent concentration estimates are low relative to the precisions of the ion ratios and therefore the relative concentrations. The relative ratio of  $\text{RSF}_{As/C}$  to  $\text{RSF}_{P/C}$  is  $\sim 2$  compared to 7 based on published values for silicon wafer (S18).

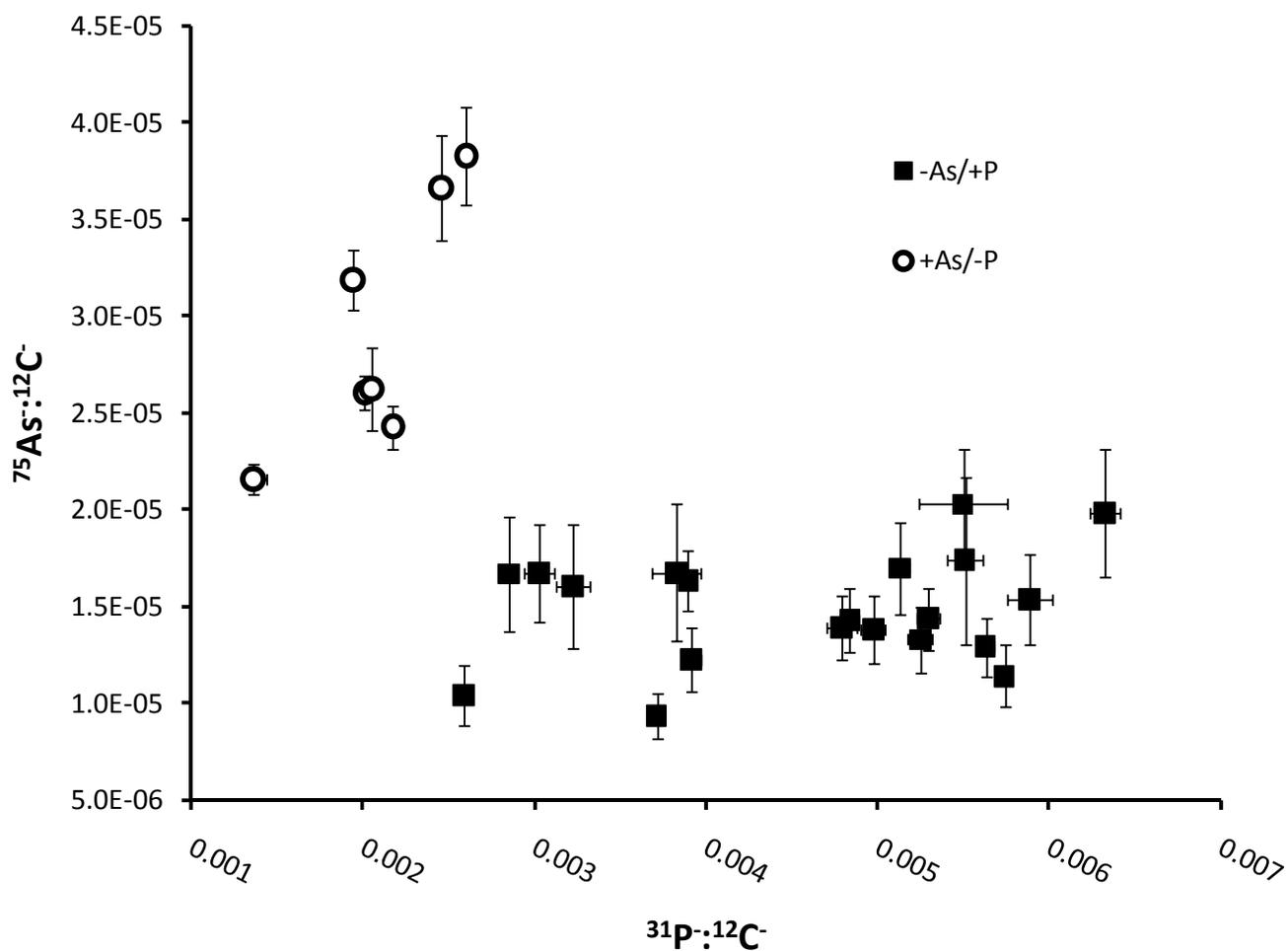
*Synchrotron Studies.* GFAJ-1 cells were collected by centrifugation and washed two times with AML60 with no added  $\text{PO}_4^{3-}$ ,  $\text{AsO}_4^{3-}$ , vitamins or glucose and fixed at a final concentration of 0.25% glutaraldehyde. Samples were air dried on Nucleopore 0.2  $\mu\text{m}$  polycarbonate filters and directly subjected to beam radiation. Data were recorded at the As K-edge (11867 eV) on beam line 2-3 at the Stanford Synchrotron Radiation Lightsource (SSRL). The beam at BL2-3 is micro-focused using Kirkpatrick-Baez mirrors to a size of 2x2 microns. The sample was rastered across the x-ray beam and the elemental fluorescence at each pixel was measured in a continuous manner. Areas of interest were selected by identifying groups of cells on the sample. EXAFS data were collected at several points of interest, from 200 eV below the edge to 650 eV above the edge (k of 13). X-ray absorption spectra were averaged, background subtracted and processed using the SIXPACK software (S19). The extracted EXAFS data were fit using shell-by-shell fitting in SIXPACK, using algorithms from IFEFFIT (S20), and theoretical phase and amplitude calculations obtained from FEFF7 (S21).

Correlation plots (Figure S3) were created by plotting the concentrations of each element at each pixel in the map. Elemental concentrations were determined by calibration of the fluorescence intensity of each element excited with 12 keV x-rays. A total of 400 pixels were used for each elemental calibration. Metal foil standards were obtained from Micromatter (Vancouver Canada). Due to the low response of some of the elements, the pixel intensities were “smoothed” using an adjacent averaging kernel, i.e. the intensity of a pixel was averaged with the 8 other pixels that are adjacent. This process reduces the pixelation of single photon counting.

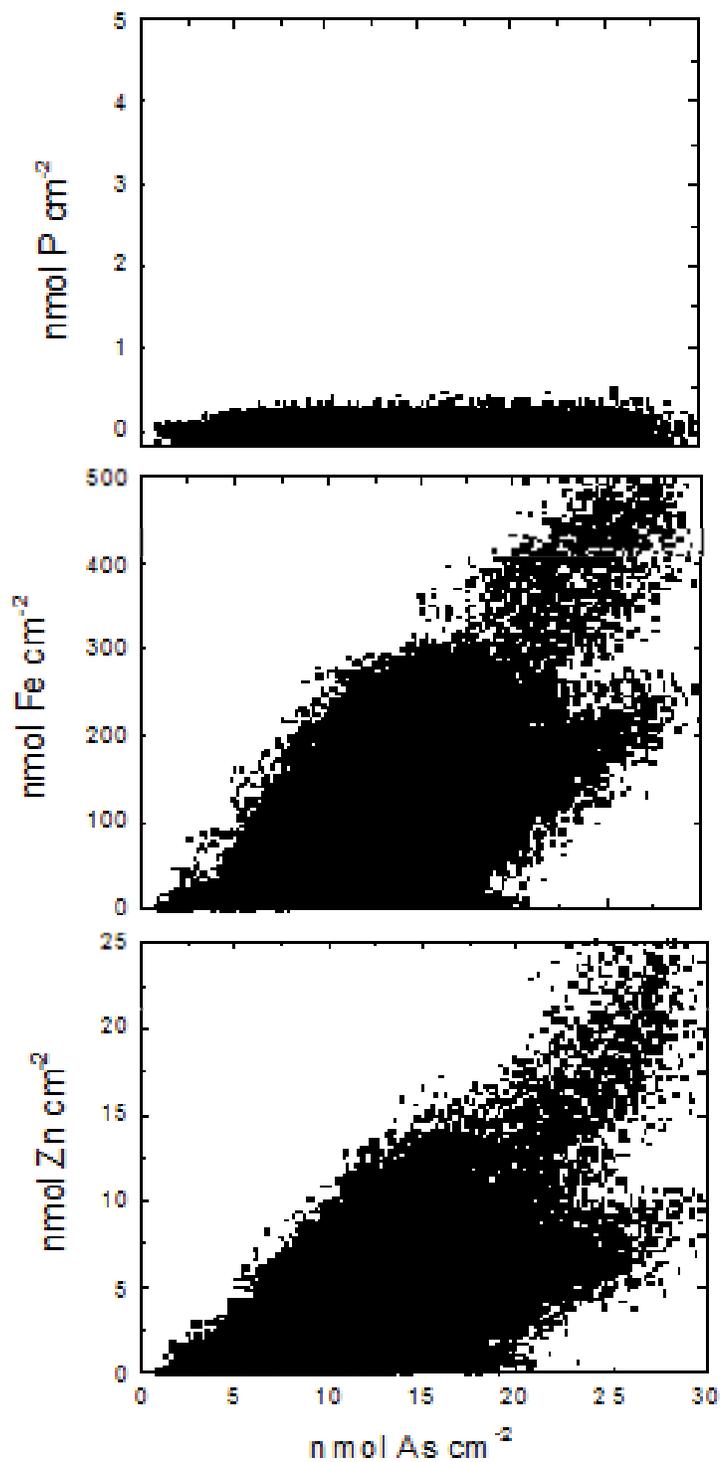
Supplementary Figures.



**Figure S1. Phylogenetic analysis of strain GFAJ-1.** Maximum likelihood phylogenetic tree based on 16S rRNA genes identified GFAJ-1 as a member of the Halomonadaceae family in the Gammaproteobacteria.



**Figure S2.**  $^{75}\text{As} : ^{12}\text{C}$  versus  $^{31}\text{P} : ^{12}\text{C}$  ratio plot from GJAJ-1 cells by NanoSIMS. Data showing the relationships between As, P and C for GFAJ-1 cells grown +As/-P (open circles) and -As/+P (closed squares). Error bars represent 1 standard deviation of analytical variance during a single measurement.



**Figure S3. Correlation plots of P, Fe, and Zn versus As XRF mapping data for GFAJ-1 cells.**

Correlation plots showing the relationship of the spatial distribution of phosphorus (top), iron (middle) and zinc (bottom) with respect to arsenic for the images and data shown in Figure 3B. Strong correlations exist between Fe, Zn and As while there is no correlation between As and P.

## Supplementary Tables

**Table S1. ICP-MS analyses.\***

<b>BLANKS</b>	<b>P ng</b>	<b>+/-<sup>c</sup></b>	<b>As ng</b>	<b>+/-<sup>c</sup></b>	<b>As/P</b>	<b>+/-<sup>d</sup></b>
<i>sterile falcon tube blank</i>	<1		<1			
<i>repeat</i>	<1		<1			
<i>+As/-P digestion process blank</i>	<1		<1			
<i>repeat</i>	<1		<1			
<i>-As/+P digestion process blank</i>	<1		<1			
<i>repeat</i>	<1		<1			
<i>+As/+P digestion process blank</i>	<3		<1			
gel blank	795 <sup>a</sup>	80	42.5 <sup>a</sup>	9		
repeat	1,066	107	<2			
repeat	599	60	<2			
<b>MEDIA</b>	<b>μM</b>		<b>μM</b>			
<i>water blank</i>	<0.03		<0.01			
<i>repeat</i>	<0.03		<.01			
-P/-As media (-vitamins, - arsenic, -phosphate, - glucose) 5 Apr 2010 batch	3.7	0.4	0.26	0.03		
-P/-As media (-vitamins, - arsenate -phosphate, - glucose) 11 June 201 batch	<0.3		0.43	0.04		
-P/+As media (+vitamins, +10 mM glucose, + arsenate) 29 July 2010 batch	2.9	0.3	33,520	3,352		
-P/+As media (+ vitamins, +10 mM glucose, +arsenate) 5 Apr 2010 batch	2.7	0.3	39,920	3,992		
+P/-As media (+ vitamins, +10 mM glucose, + phosphate) 5 Apr 2010 batch	2,003	200	0.16	0.02		
cell wash solution -P/-As media (-vitamins, - arsenic, -phosphate, - glucose, - trace metals), 3 July 2010 batch	7.4 <sup>a</sup>	23	<0.01 <sup>a</sup>			

**Table S1continued. ICP-MS analyses.\***

<b>DNA/RNA EXTRACTS, GELS AND PHENOL SAMPLES</b>	<b>P ppb</b>	<b>+/-<sup>c</sup></b>	<b>As ppb</b>	<b>+/-<sup>c</sup></b>	<b>As/P</b>	<b>+/-<sup>d</sup></b>
<i>+As/-P DNA/RNA extract GFAJ</i>	2,081	174	<20			
<i>-As/+P DNA/RNA extract</i>	266,000 <sup>d</sup>	26,600	118	35.3		
<i>+As/-P DNA/RNA GFAJ gel</i>	2,339	117	89	18	0.038	0.008
<i>+As/-P RNA gel</i>	455	46	<1		-	
<i>-As/+P DNA/RNA GFAJ gel</i>	1,820	180	12	2	0.007	0.0015
<i>-As/+P RNA gel</i>	4,063	406	6.3	1.3	0.002	0.0003
<i>-As/+P gel</i>	6,110	610	<1		-	
<i>-As/+P phenol</i>	241,100	12,100	3,650	365	0.02	0.0017
<i>repeat</i>	269,100	29,100	3,717	370	0.01	0.002
<i>+As/-P phenol</i>	4,170	830	4,880	770	1.17	0.30
<i>repeat</i>	4,670	930	4,570	460	0.98	0.22
<b>CELLS</b>	<b>dry wt %</b>	<b>dry wt %</b>				
<i>+As/-P cells<sup>b</sup></i>	0.023	0.002	0.114	0.011	4.91	0.69
<i>repeat<sup>b</sup></i>	0.023	0.002	0.200	0.020	8.55	1.21
<i>repeat<sup>b</sup></i>	0.024	0.002	0.624	0.062	26.56	3.76
<i>repeat<sup>b</sup></i>	0.036	0.004	0.550	0.055	15.19	2.15
<i>+As/-P cells</i>	0.014	0.001	0.010	0.001	0.76	0.08
<i>repeat</i>	0.011	0.001	0.010	0.001	0.97	0.11
<i>repeat</i>	0.011	0.001	0.009	0.001	0.83	0.09
<i>repeat</i>	0.011	0.001	0.011	0.001	0.95	0.11
<b>average</b>	0.019	0.009	0.191	0.25	<b>7.3</b>	<b>9.3</b>
<i>-As/+P cells<sup>b</sup></i>	0.66	0.07	0.0006	0.0001	0.0004	0.0001
<i>repeat<sup>b</sup></i>	0.23	0.02	0.0005	0.00005	0.0011	0.0002
<i>-As/+P cells</i>	0.63	0.06	0.0015	0.0001	0.0023	0.0003
<i>repeat</i>	0.65	0.06	0.0015	0.0001	0.0022	0.0003
<b>average</b>	0.542	0.210	0.0010	0.00053	<b>0.0015</b>	<b>0.0009</b>

\*<sup>a</sup>Correlation coefficient of sample addition curve was between 0.58 and 0.9. <sup>b</sup>Sample was from batch grown in June 2010. All other samples were grown in a separate batch in July 2010. <sup>c</sup>Errors are calculated as the standard deviation on replicate analyses or 10%, whichever is larger. <sup>d</sup>Error is the expanded error including uncertainties on measurements. "Repeat" indicates a replicate sample digestion and analysis. Sample names in italics designates that the sample was analyzed in several dilutions and on multiple analytical sessions with separate calibration curves, but not as standard addition curves.

**Table S2. NanoSIMS gel elemental concentrations and ion ratios.<sup>†</sup>**

	P		As		As/P	As/P	<sup>31</sup> P/ <sup>12</sup> C <sup>-</sup>	+/-	<sup>75</sup> As/ <sup>12</sup> C <sup>-</sup>	+/-	<sup>75</sup> As/ <sup>31</sup> P <sup>-</sup>
	ppb <sup>a</sup>	+/- <sup>b</sup>	ppb <sup>c</sup>	+/-	g/g	atom/atom					
+As/-P DNA	299	36	27	5	0.09045	0.03738	2.52E-04	3.06E-05	1.34E-05	2.48E-06	5.31E-02
-As/+P DNA	1017	237	14	3	0.01361	0.00562	8.58E-04	2.00E-04	6.85E-06	1.56E-06	7.99E-03
-As/+P RNA	1202	93	5	1	0.00411	0.00170	1.01E-03	7.81E-05	2.45E-06	5.25E-07	2.41E-03
Blank <sup>d</sup>	820	143	15	3	0.01829	0.00756	6.92E-04	1.21E-04	7.43E-06	1.50E-06	1.07E-02

<sup>†</sup>Measurements are mean values for splits of excised agarose gel bands loaded with purified GJAJ-1DNA and RNA; the other portion was run by ICP-MS. <sup>a,c</sup>Elemental concentrations are for hydrated agarose. <sup>b</sup>All error values reported in this table are 2 \* standard error. <sup>d</sup>Blank values were measured on agarose gel segments excised from outside of electrophoresis lanes; these are an upper limit of expected background ion concentrations caused by trace impurities in agarose, loading dye or ethidium bromide stain.

**Table S3. Various bond length distances of typical phosphate containing biomolecules between phosphorus, oxygen and carbon atoms.<sup>‡</sup>**

<i>Compound (PDB ID)</i>	<i>Type</i>			
	P-O	P-C	P-P	P-C <sub>2</sub>
ATP (ANP)	1.69 1.75 1.76	2.91	3.24	-
NAD (NAD)	1.65 1.78	2.70	2.86	4.24
Glucose-6-phosphate (B6G)	1.49 1.62	2.45	-	3.86
acetyl-CoA (ACO)	1.50 1.64	2.49	2.63	3.65 3.91
Glycogen synthase kinase-3 $\beta$ inhibitor complex(3F88)	1.46 1.55 1.56 1.58	2.51	-	3.35 3.38
DNA (7BNA)	1.47 1.58	2.52 2.66	-	3.36 3.76 3.97 4.14

<sup>‡</sup>These structures were taken directly from the protein databank ([www.pdb.org](http://www.pdb.org), S22) and are “ligand structures” standards in the PDB while 3F88 is an example of a phosphorylated protein. They have been identified in a range of biomolecules.

**Table S3: Sequences used for phylogenetic tree construction**

<b>Taxon</b>	<b>Accession</b>
<i>Actinomyces meyeri</i> strain Prevot 2477B	NR_029286
<i>Bacillus selenitireducens</i> strain MLS10	NR_028707
<i>Bordetella trematum</i> strain DSM 11334	NR_025404
<i>Burkholderia kururiensis</i> strain KP23	NR_024721
<i>Comamonas nitrativorans</i> strain 23310	NR_025376
<i>Demetria terragena</i> strain HK1 0089	NR_026425
<i>Desulfobulbus elongatus</i> strain FP	NR_029305
<i>Desulfonatronum thiodismutans</i> strain MLF1	NR_025163
<i>Desulfovibrio longreachensis</i> strain 16910a	NR_029364
<i>Ehrlichia muris</i> strain AS145	NR_025962
<i>Escherichia coli</i> strain O157:H7	EU118103
<i>Geobacter pelophilus</i> strain Dfr2	NR_026077
<i>Halomonas alkaliphila</i>	AJ640133
<i>Halomonas</i> sp. DH77	FJ404755
<i>Halomonas</i> sp. G27	EF554887
<i>Halomonas</i> sp. GTW	DQ279849
<i>Halomonas</i> sp. IB-O18	AM490136
<i>Halomonas</i> sp. ML-185	AF140007
<i>Halomonas</i> sp. mp3	AJ551117
<i>Halomonas venusta</i> strain NBSL13	FJ973521
<i>Helicobacterbilis</i> strain Hb1	NR_029182
<i>Leptothrix discophora</i> strain SS-1	NR_025916
<i>Magnetospirillum gryphiswaldense</i> strain MSR-1	NR_027605
<i>Magnetospirillum magnetotacticum</i> strain DSM 3856	NR_026381
<i>Methylobacterium nodulans</i> strain ORS 2060	NR_027539
<i>Mycobacterium goodii</i> strain M069	NR_029341
<i>Nitrobacter alkalicus</i> strain AN1	NR_024920
<i>Nitrosomonas eutropha</i> C91	NR_027566
<i>Oscillatoria</i> sp. PCC 8927	GQ351575
<i>Paracoccus alkenifer</i> strain A901/1	NR_026424
<i>Paracoccus pantotrophus</i> strain ATCC 35512	NR_026457
<i>Roseospira navarrensis</i> strain SE3104	NR_025440
<i>Spirochaeta americana</i> strain ASpG1	NR_028820
<i>Sulfurospirillum halorespirans</i> strain PCE-M2	NR_028771
<i>Thioalkalimicrobium cyclicum</i> strain ALM1	NR_028806
<i>Thioalkalivibrio jannaschii</i> strain ALM2	NR_028807
<i>Tindallia californiensis</i> strain APO	NR_025162
<i>Tsukamurella pulmonis</i> strain IMMIB D-1321	NR_029302
<i>Wolinella succinogenes</i> strain ATCC 29543	NR_025942

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