Effects of a Strong Static Magnetic Field on Bacterium Shewanella oneidensis: An Assessment by Using Whole Genome Microarray

Weimin Gao,^{1,†} Yongqing Liu,^{1,†} Jizhong Zhou,¹ and Hongjun Pan^{2*}

¹Environmental Sciences Division, Oak Ridge National Laboratory, Oak Ridge, Tennessee ²Department of Chemistry, University of Tennessee, Knoxville, Tennessee

The effect of a strong static 14.1 T magnetic field on log phase cells of bacterial strain *Shewanella oneidensis* MR-1 was evaluated by using whole genome microarray of this bacterium. Although differences were not observed between the treatment and control by measuring the optical density (OD), colony forming unit (CFU), as well as post-exposure growth of cells, transcriptional expression levels of 65 genes were altered according to our microarray data. Among these genes, 21 were upregulated while other 44 were downregulated, compared with control. Bioelectromagnetics 26, 2005. © 2005 Wiley-Liss, Inc.

Key words: DC; magnetic field; gene expression; transcription expression

INTRODUCTION

High static field magnets are widely used in medical and research laboratories such as magnetic resonance imaging (MRI) and nuclear magnetic resonance (NMR). Studies of the biological effect of strong magnetic field have been intensified in recent years due to its possible harmful or beneficial effects on many eukaryote organisms, including human beings [Sakuria et al., 1999; Emura et al., 2003; Iwasaka and Ueno, 2003; Schiffer et al., 2003]. In our previous studies, we found that the strong static magnetic fields had an apparent effect on insect egg hatching, the hatching was delayed by the strong static magnetic fields and the delay nonlinearly increased with the intensity of the magnetic field [Pan, 1996; Pan and Liu, 2004]. The larval development in the strong magnetic field was slower than that in the geomagnetic field. Denegre et al. [1998] reported that a strong magnetic field altered the cleavage planes in frog eggs.

As relatively simple living organisms, bacteria are important research subjects in this field too. Kohno et al. [2000] studied the effect of static magnetic field on bacteria *Streptococcus mutans*, *Staphylococcus aureus*, and *Escherichia coli*. They found that the ferrite magnet caused strength-dependent decreases in the growth rate and maximum number of bacteria for *S. mutans*, *S aureus* when cultured under anaerobic conditions, but their growth was not inhibited under aerobic conditions. Their finding suggested that oxygen related to the growth in the cases of *S. mutans* and *S. aureus*. However, no growth effects were detected in *E. coli* cultures. Stansell et al. [2001] found that exposure of *E. coli* to static magnetic field significantly increased its antibiotic resistance. Horiuchi et al. [2001] found that a high magnetic field (5.2-6.1 T) promoted survival rate of *E. coli* B cells of stationary phase, since the colony forming unit (CFU) number under the high magnetic field (5.2-6.1 T) was 100 000 times higher than that under a geomagnetic field. The same authors also reported that the amount of S factor encoded by the *rpoS* gene under the high magnetic field was larger than that

*Correspondence to: Hongjun Pan, Department of Chemistry, University of Tennessee, Knoxville, TN 37996. E-mail: hpan@utk.edu

Received for review 8 July 2004; Final revision received 8 March 2005

DOI 10.1002/bem.20133

Published online in Wiley InterScience (www.interscience.wiley.com).

[†]Weimin Gao and Yongqing Liu have contributed equally to this work.

Grant sponsor: US Department of Energy (Office of Biological and Environmental Research, Office of Science); Grant sponsor: Genomes to Life program; Grant number: DE-FG02-01ER63220; Grant sponsor: Natural and Accelerated bioremediation Research Program; Grant number: DE-FG02-97ER62492; Grant sponsor: Microbial Genome Program; Grant number: ERKP385; Grant sponsor: Laboratory Directed and Research Development Program.

2 Gao et al.

under control, and thus the activity of the *rpoS* gene was affected by the high magnetic field [Horiuchi et al., 2001].

Shewanella oneidensis MR-1 is a gram-negative, facultative anaerobe bacterial strain. This bacterium can anaerobically respire numerous organic compounds such as fumarate and dimethyl sulfate oxide, and many metal oxides such as Fe(III), Mn(IV), Cr(VI), and U(VI) [Myers and Myers, 1992, 1993a,b; Leblane et al., 2001; Marier and Myers, 2001]. Because of its versatile respiration pathways, which may be applied to the immobilization of environmental pollutants in soil and groundwater (i.e., chromium and uranium), this strain has been intensively investigated as an excellent metal reducing cellular system for studying redox mechanisms [Myers and Myers, 1993; Fries et al., 1994; Glasauer et al., 2001; Johnson et al., 2001; Arnesano et al., 2002; Giometti et al., 2003]. Sequencing the whole genome of this strain is one important step for thoroughly understanding of this complex organism [Glasauer et al., 2001]. In this study, we report our studies of the effect of 14.1 T static magnetic field on the growth of log phase cells of bacterial strain Shewanella oneidensis MR-1, as well as the transcriptional activities of genes evaluated through a whole genome microarray.

EXPERIMENTAL METHOD

Bacterial Cell Preparation

A single colony grown on Luria Broth (LB) agar was picked up and transferred to 10 ml LB liquid medium for culturing overnight at 30 °C. The next morning, 1 ml of culture was pipetted and transferred to 100 ml LB liquid medium in a 250 ml flask, followed by shaking at 150 rpm and 30 °C. When growth reached mid-log phase, cells were inoculated at the ratio 1:100 into each of two sterilized glass vials containing 15 ml fresh LB liquid medium for magnetic field exposure experiment.

14.1 T Magnetic Field Treatment

The glass vials were mounted on a mechanical shaking device that was specially designed for this experiment. One vial was located at the center of the 14.1 T magnet (Varian INOVA 600 NMR spectrometer with Oxford 14.1 T magnet) and the other vial, used as a control, was located at the bottom of the 14.1 T magnet where the fringe field was about 22.8 mT (228 G). The magnetic field at the center was well shimmed by cryoshim coils built into the superconducting magnet; the homogeneity of the magnetic field meets the requirement for high resolution NMR experiments.

Due to the nature of the experiment in the 14.1 T magnetic field, the shaker was made of plastic and copper materials, and all moving parts were made of plastic materials to avoid the eddy current effect; therefore, the effect on the homogeneity of the magnetic field in the center of the magnet is negligible, if any, even during the shaking. We assumed that the fringe field at the bottom of this magnet has no apparent biological effect, as indicated by our previous results [Pan and Liu, 2004] and the temperatures at the both locations were same.

Two experiments were conducted. In the first experiment, the MR-1 was exposed to 14.1 T magnetic field for 1.5 h; and in the second experiment, the MR-1 was exposed to the same magnetic field for 12 h. The samples were mechanically shaken at 120 rpm during the entire period in the magnetic field at a room temperature of 23 °C. The shaking permits bacteria growth under aerobic conditions. However, due to a technological limit of our system, we set the rate of shaking as 120 rpm, not as 150 rpm as before exposure. The ideal growth temperature for MR-1 is 30 °C. Due to the same technical difficulty, the temperature for exposure experiment was set as room temperature 23 °C.

After treatment of the 14.1 T magnetic field, the optical density (OD) value of both the exposed and control samples were measured at wavelength 600 nm using a spectrometer (Spectronic 20D+, Thermo Spectronic). The exposed and control samples (0.5 ml) were transferred to 9.5 ml fresh LB liquid medium for further culturing. The culture conditions were the same as that described in cell preparation. The OD value was measured every 2 h. The OD value is proportional to the amount of bacterial cells in the liquid. Meanwhile, both the treatment and control samples were diluted to 10^{-7} and 0.1 ml of each dilution spread on LB agar plates for CFU counting. Colony counting was performed after the plates were incubated at 30 °C for 2 days.

Microarray Hybridization and Data Analysis

Based on the known sequence [Heidelberg, 2002], we designed a gene-specific primer set for all *S. oneidensis* MR-1 genes whose full or almost full length has less than 75% similarity to another gene. For those genes with more than 75% similarity to another genes, we designed a 50-mer oligo for the region whose similarity to another sequence is less than 75% using the software PRIMEGENS [Xu et al., 2002]. We successfully PCR-amplified and fabricated the whole-genome scale microarray of *S. oneidensis* MR-1 that has a 95% of genome coverage [Liu et al., 2003].

Liquid-cultured cells in exponential growth phase were inoculated at the ratio 1:100 into a vial containing

15 ml fresh LB liquid medium and then subjected to 14 T magnetic field exposure for 12 h at room temperature 23 °C. The samples were mechanically shaken during the entire exposure period in the magnetic field. Cell cultures were harvested from each sample after 12 h exposure followed by a brief centrifugation, resuspended in RNAlater solution, and stored at -70 °C for later RNA extraction. Microarray fabrication, hybridization, probe labeling, image acquisition, and processing were carried out as described in references [Liu et al., 2003].

Gene expression analysis was performed using three independent microarray experiments, with each slide containing two replicate array of *S. oneidensis* MR-1 genome, a collection of 4608 distinct ORFs. Total cellular RNA from 14.1 T magnetic field exposed and control samples was isolated and purified using the TRIzol Reagent (Gibco BRL) according to the manufacturer's instruction. The ratios of the exposed samples over the control were normalized using Pooled-Common Error model provided by the statistical analysis software ArrayStat v. 2.0. Data was gained by the software IMAGINE, normalized by trimmed geometric mean, and statistically analyzed by the software ARRAYSTAT after all outliers were removed [Liu et al., 2003].

RESULTS AND DISCUSSION

Cell Growth

Initially, we started with our 1.5 h exposure to 14.1 T magnetic field of MR-1, and no significant results were obtained, as reflected by OD measurement and colony forming unit (CFU) counting, as well as a growth experiment of cells post-exposure (data not shown). Then we extended the exposure time to 12 h. If there is any apparent effect of 14.1 T magnetic field on the cell growth, then the number of cells in the center of magnetic field would be significantly different from that at the bottom of the magnet after such 12 h exposure, such difference would be detected by the OD measurement and CFU counting, as well as postexposure growth. Our results indicate that 12-h exposure of the 14.1 T magnetic field has no detectable effect on the cell growth of S. oneidensis MR-1, as reflected by OD measurement and CFU counting. Both the treatment and control reached an OD value about 1.0 after 12 h exposure, and the CFU counting showed that the viable cells of both treatment and control reached about 10^{10} /ml. Furthermore, the post-exposure growth curves of both exposed and controlled cells of S. oneidensis MR-1 also failed to show an effect, as indicated in Figure 1. The first point at 0 h represents the



Fig. 1. The post-exposure growth of the *Shewanella oneidensis* MR-1 cells after exposure to 14.1 T magnetic field for 12 h. The initial optical (OD) of post-exposure growth of both treatment and control samples began at about 0.1. The OD value was measured at wavelength 600 nm.

inoculated amount of cells, including both living and dead, just taken out of the magnet.

Our result is different from the results by Horiuchi et al. [2001] on *E. coli* cultured in the 5.2–6.1 T

TABLE 1. Hypothetical Genes With Significant Changes in Gene Expression after Exposure to 14.1 T Magnetic Field for 12 h

	Expression ratio ^{a,b}		
Gene	AVG	P-value	
SO0362	-1.555	*	
SO0683	+3.626	*	
SO0938	-2.096	*	
SO1419	-3.861	*	
SO1757	-1.580	*	
SO1831	-1.548	*	
SO2591	-1.595	*	
SO2603	-1.473	*	
SO2688	+2.657	*	
SO2770	+2.102	*	
SO2832	-1.460	*	
SO2884	-1.502	*	
SO2970	+2.107	*	
SO3062	+5.069	*	
SO3074	+2.086	*	
SO3198	-1.988	*	
SO3313	-1.669	**	
SO3475	+2.734	*	
SO4008	-1.560	*	
SO4560	-1.479	*	

^aThe average (AVG) expression ratio of the treatment sample to the control was calculated from 12 replicates together, a P = .05 standard *t*-test result. All genes are significant in expression changes (*, P < .05; **P < .01; probability in *t*-test).

^bFold increases is marked as (+) and decreases (-).

4 Gao et al.

GeneSymbolPutative functionAVG $P-value^h$ Energy metabolismSymbolgyAGiycerrol-2-phosphate dehydrogenase -1.965 ****SO0068petAUbiquinol-cytochrome c -1.7645 *SO2021cacQCytuchrome c oxidase, cbbl-type -1.980 **SO2121ansA				Expression ratio ^a	
Interry metabolism gpsA Glycerol-3-phosphate dehydrogenase -1.055 *** S00008 ptA Ubiquinol-cytochrome c reductase -1.157 * S02021 ecolo Cytochrome c voidacase -1.157 * S02178 ecolo Cytochrome c voidacase, cbb3-type -1.080 *** S02121 ansA	Gene	Symbol	Putative function	AVG	P-value ^b
SU0033 gp>A Glycerol-3-phosphate dehydrogenase -1.045 *** SU0008 ptA Ubiquinol-yrochrome c -1.045 * SU0178 omeB Decaheme cytochrome c -1.057 * SU2421 ansA L-asparaginase I -1.587 * SU2513 nnA L-asparaginase I -1.587 * SU112 bf1 Bacteriofernitin subunit 1 -1.701 * SU112 bf1 Bacteriofernitin subunit 1 -1.701 * SU2786 Sulfate permase Family protein +2.124 * SU0303 mine Cell division topological specificity factor MinE -1.848 * SU2786 mine Hethylacotering chonotaxis protein +1.527 * SU3030 mine Cell division topological specificity factor MinE -1.848 * SU3300 mine Type I restriction-modification system, M subunit -1.527 * SU3309 mine Cell division topological specificity factor MinE -1.848 *	Energy metabolism				
S00008 ptA Ubiquinol-cytochrome c reductase -1.645 * S01778 omes B Decahene cytochrome c -1.57 * S02362 eccQ Cytochrome c oxidas, eb3-type -1.980 *** S02421 ansA	SO0053	gpsA	Glycerol-3-phosphate dehydrogenase	-1.965	***
S01778 omeB Decker cytochrome c -1.757 * S02362 ccoQ Cytochrome c vidase, cb3-type -1.987 * S02421 anA L-aspanginase I -1.587 * S02513 NAPDERAFAE family protein -1.587 * S01157 Proton/glutanate symporter +1.527 * S01112 bfr1 Bacterioferritin submit I -1.701 * S02786 Suffate permeses family protein +2.152 * S040913 fic Cell division topological specificity factor MinE -1.148 * S04500 Methyl-accoping chernotaxis protein +3.152 * S01457 * S01457 Type I restriction-modification system, M submit -1.527 * S01401 * * S01431 Diversity protein -1.538 * * S01431 * * S01431 Diversity protein -1.538 * * S0326 * S0230 * S0230 * * <td< td=""><td>SO0608</td><td>petA</td><td>Ubiquinol-cytochrome c reductase</td><td>-1.645</td><td>*</td></td<>	SO0608	petA	Ubiquinol-cytochrome c reductase	-1.645	*
S02362 cccQ Cytochrome'c oxidae, cb3-type -1.587 ** S02421 ansA L-asparnginase I -1.587 * S02131 narport and binding proteins -1.541 * S00157 Proton/glutamate symporter +1.527 * S01112 bf1 -1.541 * S02578 Sulfate permease family protein +2.124 * S02578 mile Cell division topological specificity factor MinE -1.848 * S03800 Methyl-accepting chemotaxis protein +3.152 * * S040013 umuD UmuD protein -1.520 * S03191 Chain length determinant protein -1.520 * S03193 polysaccharide biosynthesis protein -1.520 * S03191 Chain length determinant protein -1.520 * S03192 polysaccharide biosynthesis protein -1.520 * S03193 mole cid biosynthesis -1.520 * * S030244 prBE Ribosona	SO1778	omcB	Decaheme cvtochrome c	-1.757	*
S02421ans. $-issparaginase I-issparaginase I$	SO2362	ccoO	Cytochrome c oxidase, cbb3-type	-1.980	**
S02513 market NgrDE/RnfAE family protein -1.541 * S00157 Proton/glutamate symporter +1.527 * S00157 Bacterioferitin submit 1 -1.701 * S02786 Sulfate permease family protein +2.124 * S02978 mine Cell dimensation protein Fie -1.701 * S0390 mine Cell dimonation protein Fie -1.701 * S0390 mine Cell division topological specificity factor MinE -1.848 * S01407 Type I restriction-modification system, M subunit -1.527 * S01491 Polysaccharide biosynthesis protein -1.583 * S03191 Polysaccharide biosynthesis protein +1.531 * S0321 PiE Type I / pilus biogenesis protein +1.526 * S03231 PiE Type I / pilus biogenesis protein +1.526 * S0324 PiE Type I / pilus biogenesis protein +1.526 * S03030 indA_A_2 Ribosomal protein S -1.508	SO2421	ansA	L-asparaginase I	-1.587	*
Transport and binding proteinsToto of guidancia symports1.1.5.7*SO0157Proto of guidancia symports+1.5.27*SO1112bfr1Bacterioferritin subunit 1-1.701*SO2786Sulfate percess-1.701*SO2787mineCell division topological specificity factor MinE-1.848SO3890Methyl-accepting chemotaxis protein+3.152*DNA metabolismType I restriction-modification system, M subunit-1.527*SO4577Type I restriction-modification system, M subunit-1.527*SO3191Chain length determinant protein-1.520*SO3193politicType I v pilus biogenesis protein-1.585*SO3191Chain length determinant protein-1.526*SO3193politicTransfation initiation factor IF-3-1.508*SO3240pmDRibosonal protein 55-1.508*SO3030infCTransfation kinase-1.634*SO3030gestruk-2Ribosonal protein 59-1.638*SO3030gesttranscriptional regulator, LysR family+1.452*SO3030poltTranscriptional regulator, LysR family+1.452*SO3040pones regulator, LysR family+1.652*So3030php-2Hypoxanthine kinase-1.634*SO2571transcriptional regulator, LysR family+1.418*SO1457transcriptional regulator, LysR family+1.418<	SO2513		NarDE/RnfAE family protein	-1.541	*
	Transport and binding proteins			110 11	
S01112 bf1 Bacterioferritin submit 1 -1.701 * S02786 Sulfate pernease family protein +2.124 * Cellular process -1.701 * S02786 Cell filmentation protein +2.124 * S02877 min Cell division topological specificity factor MinE -1.848 * S03800 Methyl-accepting chemotaxis protein +3.152 * * S01401 UmuD UmuD UmuD protein -1.520 * S03191 Chain length determinant protein -1.520 * S03193 pills togenesis protein Pille -1.701 * S03191 Chain length determinant protein -1.520 * S03193 pills Type IV pillus biogenesis protein Pille -1.701 * S03204 pill Type IV pillus biogenesis protein -1.582 * S00249 rpmD Ribosomal protein S5 -1.582 * * S03393 rpsL Ribosomal protein S9 -1.421 * * S03394 rpsL Ribosomal arge submint psouridine synthetase A -1.721	SO0157		Proton/glutamate symporter	± 1.527	*
S02726 Sulfate permease family protein +2.124 * Cellular process Sulfate permease family protein +2.124 * S00913 fic Cell division topological specificity factor Mine -1.848 * S02578 mine Cell division topological specificity factor Mine -1.848 * S03800 Methyl-accepting chemotaxis protein +3.152 * DNA metabolism UnuuD protein +1.531 * S01457 Type I restriction-modification system, M subunit -1.527 * S03191 Chain length determinant protein -1.526 * S03191 Chain length determinant protein -1.526 * S03192 piE Type IV pilus biogenesis protein PiE -1.701 * S03242 piE Type IV pilus biogenesis protein PiE -1.508 * S00248 rpsE Ribosomal protein S5 -1.508 * S00300 in/C Transcriptional fegulator. LysR family +1.425 * S03040 selsor histidine kinase -1.634 * * S03306 Sensor histidine kinase	SO1112	bfr1	Bacterioferritin subunit 1	-1.701	*
Cellular processControl periodic lamb protein1.215*SO9915ficCell division topological specificity factor MinE-1.701*SO25778mineCell division topological specificity factor MinE-1.848*SO3500Methyl-accepting chemotaxis protein+3.152*SO4A013umuDUmuD protein-1.520*SO3191Chain length determinant protein-1.520*SO32524piEType IV pilus biogenesis protein PilE-1.701*SO32300infCTranslation initiation factor IF-3-1.552*SO3393rpsLRibosomal protein S3-1.552*SO3394rpsLRibosomal protein S9-1.425*SO3395rpsLRibosomal protein S9-1.425*SO3396rpsLRibosomal alrega tabinot pseudine synthetase-1.634*SO3396rpsLRibosomal alrega tabinot, LysR family+1.418*SO2240Transcriptional regulator, LysR family+1.418*SO2571rpmPPolyribonucleotide nucleotidyfiransferase+1.264*SO1426polyribonucleotide nucleotidyfiransferase+1	SO2786	0111	Sulfate permease family protein	± 2.124	*
Clandar packessfcCell dimentation protein Fic-1.701*SOD913fcCell division topological specificity factor MinE-1.848*SO3890Methyl-accepting chemotaxis protein+3.152*DNA metabolismType I restriction-modification system, M subunit-1.527*SOA0013umuDUnuuD protein+1.531*Cell envelope*SO3191Chain length determinant protein-1.520*SO3193Polysaccharide biosynthesis protein-1.526*SO3244pilEType IV pilus biogenesis protein-1.526*SO3254pilEType IV pilus biogenesis protein-1.528*SO3240rpmERibosomal protein S5-1.508*SO3259rpmDRibosomal protein IS0-1.527*SO3306censor histidine kinase-1.634*SO3307rpsERibosomal protein S5-1.634*SO3306censor histidine kinase-1.634*SO3306ranscriptional regulator, LysR family+1.418*SO3451Transcriptional regulator, LysR family+1.418*SO3452polyribonucleotide uncleotidytiransferase+1.284*SO3456Transcriptional regulator, LysR family+1.418*SO2459ppPolyribonucleotide uncleotidytiransferase+1.284*SO3450pp=Polyribonucleotide uncleotidytiransferase+1.284*SO3456 <td>Callular process</td> <td></td> <td>Surface permease family protein</td> <td>12.124</td> <td></td>	Callular process		Surface permease family protein	12.124	
S0015IteCell manentation protein Pic -1.01 S02578mineCell division topological specificity factor MinE -1.548 S03800Methyl-accepting chemotaxis protein $+3.152$ S01457Type I restriction-modification system, M subunit -1.527 S01457Type I restriction-modification system, M subunit -1.527 S03191UmuD protein -1.584 S03191Chain length determinant protein -1.585 S03193Polysaccharide biosynthesis protein -1.585 S0324pilEType IV pilus biogenesis protein Pile -1.701 S04321OmpA family protein $+1.526$ *Amino acid biosynthesismitCTranslation initiation factor IF-3 -1.582 S00249rpmERibosomal protein S0 -1.582 S03306Sensor histidine kinase -1.634 *S03306Sensor histidine kinase -1.634 *S03060Sensor histidine kinase -1.633 *S01407Transcriptional regulator, LuxR family $+1.562$ *S01408Transcriptional regulator, LysR family $+1.284$ *S01429ppppPolyribonacleotide mecleotidyltransferase $+1.284$ *S014371Transcriptional regulator, LysR family -1.633 *S01420ppppPolyribonacleotide mecleotidyltransferase $+1.284$ *S01410hereDecoxpribose-prosphate synthase, large summit -1.435 *S01420polyribonacleotide	sooo12	fie	Call filomentation protein Fig	1 701	*
SO2390 Methyl-accepting chemotaxis protein -1.946 SO3890 Methyl-accepting chemotaxis protein -1.527 DNA metabolism Type I restriction-modification system, M subunit -1.527 SO1457 UmuD UmuD protein +1.531 Cell envelope	SO0913 SO2579	mina	Cell division tonological apositioity factor MinE	-1.701	*
SO:S90wettry-accepting chemotaxis protein+.1.52SOAType I restriction-modification system, M subunit-1.527SOA0013umuDUmuD proteinCell envelope-1.520SO3191Chain length determinant protein-1.520SO3193Polysaccharide biosynthesis protein-1.585SO324pilEType IV pilus biogenesis protein Pile-1.701SO4231OmpA family protein+1.526SO0248rpmERibosomal protein S5-1.508SO0249rpmDRibosomal protein S5-1.508SO0230infCTranslation initiation factor IF-3-1.527SO3798rluk-2Ribosomal protein S9-1.425SO306Sensor histidine kinase-1.634*SO306Sensor histidine kinase-1.634*SO1965Transcriptional regulator, LuxR family+1.562*SO1964Transcriptional regulator, LuxR family+1.633*SO2400Transcriptional regulator, LuxR family+1.633*SO2571Transcriptional regulator, LyxR family-1.633*SO3303hpt-2Hyorikonucleotide mcleotidyltransferase+1.284*SO142carBCarbamoyl-phosphate synthase, large summit-1.425*SO171deoCDeoxyribose-phosphate synthase, large summit-1.633*SO3303hpt-2Hyorikonucleotide mcleotidyltransferase+1.284*SO33175asnBAsparagine synthetase, large summit-1.435*	502376	mme	Methyl accepting showstonic metain	-1.040	*
DAVA metabolism SO1457 Type 1 restriction-modification system, M subunit 1.527 * SOA0013 unuD UmuD protein - 1.528 * SO3191 Chain length determinant protein - 1.528 * SO3191 Polysaccharide biosynthesis protein - 1.528 * SO3524 pilE Type IV plus biogenesis protein PilE - 1.701 * SO0481 rpsE Ribosomal protein S5 - 1.508 * SO0249 rpmD Ribosomal protein L30 - 1.582 * SO0249 rpmD Ribosomal protein L30 - 1.582 * SO3399 rpsL Ribosomal protein S9 - 1.527 * SO3399 rpsL Ribosomal protein S9 - 1.638 * SO3306 Sensor histidine kinase - 1.634 * SO1965 Transcriptional regulator, Laxf family + 1.562 * SO19664 Transcriptional regulator, Laxf family + 1.562 * SO1965 Transcriptional regulator, Laxf family + 1.563 * SO2440 Transcriptional regulator, Laxf family + 1.563 * SO2440 Transcriptional regulator, Laxf family + 1.737 * SO3306 Sensor histidine kinase - 1.634 * SO1965 Transcriptional regulator, Laxf family + 1.737 * SO14571 Transcriptional regulator, Laxf family + 1.737 * SO1290 pnp Polyribonucleotide nucleotidyltransferase + 1.284 * SO1290 pnp Polyribonucleotide nucleotidyltransferase + 1.284 * SO1291 doc Deoxyribose-phosphate atdolase + 1.566 * SO3303 hpt-2 Hypoxanthine phosphoribosyltransferase + 1.566 * SO3304 hpt-2 Hypoxanthine phosphoribosyltransferase + 1.566 * SO3304 hpt-2 Hypoxanthine phosphoribosyltransferase + 1.566 * SO3304 hpt-2 Hypoxanthine phosphoribosyltransferase + 1.186 * SO3314 thrB Homoserine kinase + 1.566 * SO3303 hpt-2 Hypoxanthine phosphoribosyltransferase + 1.566 * SO330414 thrB Homoserine kinase + 1.566 * SO3304 hpt-2 Hypoxanthine phosphoribosyltransferase + 1.566 * SO3305 hpt-2 Hypoxanthine phosphoribosyltransferase + 1.668 * SO3305 hpt-2 Hypoxanthine phosphoribosyltransferase + 1.668 * SO3305 hpt-2 Hypoxanthine phosphoribosyltransferase + 1.668 * SO3305 hpt-2 Hypoxanthine phospho	SU3890		Methyl-accepting chemotaxis protein	+5.152	-1-
SO1457Type I restriction-modification system, M subunit-1.527*Cell envelope	DNA metabolism			1 507	-te
SOA0013umuDUmuD forein $+1.531$ *S03190Chain length determinant protein -1.520 *S03191Polysaccharde biosynthesis protein -1.585 *S0321pilEType IV pilus biogenesis protein PilE -1.701 *S00421OmpA family protein $+1.526$ *S00248rpsERibosomal protein S5 -1.582 *S00249rpmDRibosomal protein L30 -1.582 *S02300infCTranslation initiation factor IF-3 -1.527 *S03798rhu-2Ribosomal protein S9 -1.425 *S03399rpsLRibosomal protein S9 -1.425 *S03306Sensor histidine kinase -1.634 *S00464Transcriptional regulator, LuxR family $+1.562$ *S01965Transcriptional regulator, LysR family $+1.1418$ *S01966Transcriptional regulator, LysR family $+1.653$ *S04381DNA-binding response regulator -1.623 *S04382DPPolyribonucleotide nucleotidyltransferase $+1.284$ *S0147deoCDeoxyribose-phosphate synthase, large sununit -1.425 *S0147deoCDeoxyribose-phosphate adolase $+1.666$ *S0147deoCDeoxyribose-phosphate adolase $+1.666$ *S0147deoCDeoxyribose-phosphate adolase $+1.497$ *S03175asnBAsparagine synthetase, glutamine hydrolyzing -1.742	SO1457	D	Type I restriction-modification system, M subunit	-1.527	*
Cell envelope S03191 Chain length determinant protein -1.520 * S03193 Polysaccharide biosynthesis protein -1.520 * S03524 pilE Type IV pilus biogenesis protein PilE -1.701 * S04321 OmpA family protein PilE -1.701 * S04321 S0249 pmD Ribosomal protein S5 -1.508 * S00249 pmD Ribosomal protein L30 -1.527 * S03390 prL Ribosomal protein L30 -1.527 * S03390 prL Ribosomal protein S9 -1.425 * S03390 prL Ribosomal protein S9 -1.425 * S03306 Sensor histidine kinase -1.634 * S03306 Transcriptional regulator, LuxR family +1.562 * S03306 Transcriptional regulator, LuxR family +1.418 * S02440 Transcriptional regulator, LuxR family +1.418 * S02430 Transcriptional regulator, LuxR family +1.418 * S02440 Transcriptional regulator, LuxR family +1.418 * S02430 Transcriptional regulator, LuxR family +1.418 * S02430 Transcriptional regulator, LuxR family +1.418 * S02440 Transcriptional regulator, LuxR family +1.418 * S024571 Transcriptional regulator, LuxR family +1.418 * S01209 pm Polyribonucleotide nucleotidyItransferase +1.284 * S01142 carB Carbamoyl-phosphate synthase, large sunnit -1.435 * S01142 carB Carbamoyl-phosphate synthase, large sunnit -1.435 * S01142 carB Carbamoyl-phosphate synthase, large sunnit -1.435 * S01142 boxyribuse +1.266 * S03175 asnB Asparagine synthetase, glutamine hydrolyzing -1.742 * S03175 asnB Asparagine synthetase, glutamine hydrolyzing +1.768 * S03175 protein fate	SOA0013	umuD	UmuD protein	+1.531	*
S03191Chain length determinant protein-1.520*S03193Polysaccharide biosynthesis protein-1.585*S03524pilEType IV pilus biogenesis protein PilE-1.701*Amino acid biosynthesismpA family protein+1.526*S00248rpsERibosomal protein S5-1.508*S00249rpmDRibosomal protein L30-1.582*S03798rlu4.2Ribosomal protein S9-1.721***S03939rpsLRibosomal protein S9-1.634*S03306Sensor histidine kinase-1.634*S01461Transcriptional regulator, LuxR family+1.562*S01965Transcriptional regulator, LuxR family+1.562*S01965Transcriptional regulator, LysR family+1.737*S04388DNA-binding response regulator-1.633*S01209pnpPolyribonucleotide nucleotidyltransferase+1.284*S01217deoCDeoxyribose-phosphate synthase, large summit-1.435*S01217deoCDeoxyribose-phosphate synthase, large summit-1.435*S03175asnBAsparagine synthetase, glutamine hydrolyzing-1.742*S03175asnBAsparagine synthetase, glutamine hydrolyzing-1.742*S03175asnBAsparagine synthetase, glutamine hydrolyzing-1.742*S03175asnBAsparagine synthetase, glutamine hydrolyzing-1.742*S03176Glyo	Cell envelope				
S03193Polysaccharide biosynthesis protein-1.585*S03524pilEType IV pilus biogenesis protein PilE-1.701*S04321OmpA family protein+1.526*Amino acid biosynthesis**S00248rpsERibosomal protein S5-1.508*S00249rpmDRibosomal protein L30-1.582*S03798rluA-2Ribosomal protein GS-1.721**S03798rluA-2Ribosomal protein S9-1.425*S03306Sensor histidine kinase-1.634*Regulatory function***S00864Transcriptional regulator, LvR family+1.562*S0450Transcriptional regulator, LvRs family+1.737*S04511Transcriptional regulator, LySR family+1.737*S04571Transcriptional regulator, LySR family-1.623*S02571Transcriptional regulator, LySR family-1.629*Volt209pnpPolyribonucleotide nucleotidyltransferase+1.284*S01457carBCarbamoyl-phosphate synthase, large sununit-1.435*S0144thrBHooserine kinase+1.484*S0127deoCDeoxyribose-phosphate aldolase+1.566*S03303hpt-2Hypoxanthine phosphoribosyltransferase-1.600*S0144thrBHomoserine kinase+1.487*S033175asnBAsparagine synthetase, glutamine hydrolyzig	SO3191		Chain length determinant protein	-1.520	*
S03524pilEType IV plus biogenesis protein PilE-1.701*S0431OmpA family protein+1.526*Amino acid biosynthesisS0248rpsERibosomal protein S5-1.508*S0249rpmDRibosomal protein L30-1.527*S02300infCTranslation initiation factor IF-3-1.527*S03798rluA-2Ribosomal protein S9-1.425*S0306Sensor histidine kinase-1.634*S0306Sensor histidine kinase-1.634*S00864Transcriptional regulator, LvxR family+1.562*S04318DNA-binding response regulator-1.635*S0438DNA-binding response regulator-1.636*S0438DNA-binding response regulator-1.636*S0438DNA-binding response regulator-1.637*S01405Transcriptional regulator, LysR family-1.770*TranscriptionalTranscriptional regulator, LysR family-1.636*S01209pnpPolyribonucleotide nucleotidyltransferase+1.284*S01412carBCarbamoyl-phosphate synthase, large sununit-1.435*S01421deoCDecxyribose-phosphate aldolase+1.566*S01421deoCDecxyribose-phosphate aldolase+1.466*S0142carBAsparagine synthetase, glutamine hydrolyzing-1.742*S0143hpt-2Hypoxantline phosphoribosyltransferase+1.666 <td< td=""><td>SO3193</td><td></td><td>Polysaccharide biosynthesis protein</td><td>-1.585</td><td>*</td></td<>	SO3193		Polysaccharide biosynthesis protein	-1.585	*
S04321OmpA family protein+1.526*Amino acid biosynthesisrpsERibosomal protein S5-1.508*S00248rpmDRibosomal protein L30-1.882*S02300infCTranslation initiation factor IF-3-1.527*S03798rluA-2Ribosomal protein S9-1.425*S03306Sensor histidine kinase-1.721**S03306Sensor histidine kinase-1.634*Regulatory functionTranscriptional regulator, LysR family+1.562*S0484Transcriptional regulator, LysR family+1.737*S04388DNA-binding response regulator-1.653*S04388DNA-binding response regulator-1.653*S01965Transcriptional regulator, LysR family-1.770*Transcription-1.770**S01209pnpPolyribonucleotide nucleotidyltransferase+1.284*S01217deoCDeoxyribose-phosphate synthase, large sununit-1.435*S03303hpt-2Hypoxanthine phosphoribosyltransferase+1.566*S03414thrBHomoserine kinase+1.497*S01679Acyl-CoA dehydrogenas family+2.227*Protein fate-1.605**S01679Glycaalase family protein-1.637*S01679Glycaalase family protein-1.618*S01679Feptidase, putative-1.587*S01679Reyl-CoA dehydro	SO3524	pilE	Type IV pilus biogenesis protein PilE	-1.701	*
Amino acid biosynthesisSO0248rpsERibosomal protein S5-1.508*SO0249rpmDRibosomal protein L30-1.582*SO2300infCTranslation initiation factor IF-3-1.527*SO3798rluA-2Ribosomal large subunit psecuridine synthetase A-1.721**SO3939rpsLRibosomal large subunit psecuridine synthetase A-1.721**SO306Sensor histidine kinase-1.634*Regulatory functionTranscriptional regulator, LyR family+1.562*SO1965Transcriptional regulator, LyR family+1.737*SO2640Transcriptional regulator, Mark family+1.737*SO4388DNA-binding response regulator-1.633*SO1209pnpPolyribonucleotide nucleotidyltransferase+1.284*SO1209pnpPolyribonucleotide nucleotidyltransferase+1.284*SO1142carBCarbamoyl-phosphate synthase, large sununit-1.435*SO1142carBCarbamoyl-phosphate synthase, large sununit-1.435*SO3175asnBAsparagine synthetase, glutamine hydrolyzing-1.742*Amino acid biosynthesis*SO2223Peptidase, putative-1.587*SO2030cmDHimoserine kinase+1.166*SO223So243Peptidase, putative-1.587*SO2431thrBHomoserine kinase+1.166*SO31	SO4321		OmpA family protein	+1.526	*
SO0248rpsERibosomal protein S5-1.508*SO0249rpmDRibosomal protein L30-1.582*SO2300infCTranslation factor IF-3-1.527*SO3798rluA-2Ribosomal large subunit psecuridine synthetase A-1.721**SO3306Resor histidine kinase-1.634*Regulatory function*SO0864Transcriptional regulator, LuxR family+1.562*SO1965Transcriptional regulator, LysR family+1.737*SO4380DNA-binding response regulator-1.653*SO4571Transcriptional regulator, LysR family+1.737*SO1209pnpPolyribonucleotide nucleotidyltransferase+1.284*SO1217deoCDeoxyribose-phosphate aldolase+1.566*SO1303hpt-2Hypoxanthine phosphoribosyltransferase+1.666*SO1375asnBAsparagine synthetase, glutamine hydrolyzing-1.742*SO4375asnBAsparagine synthetase, glutamine hydrolyzing-1.742*SO309lysADiamiopinelate decarboxylase+1.668*SO2230Peptidase, putative-1.587*SO2231Petidase, putative-1.587*SO2231Petidase, putative-1.587*SO3175asnBAsparagine synthetase, glutamine hydrolyzing-1.742*SO2331Npt-2Petidase, putative-1.587*SO3167CercD <td>Amino acid biosynthesis</td> <td></td> <td></td> <td></td> <td></td>	Amino acid biosynthesis				
SO0249rpmDRibosomal protein L30-1.522*S02300infCTranslation initiation factor IF-3-1.527*S03798rluA-2Ribosomal large subunit pseouridine synthetase A-1.721**S03939rpsLRibosomal protein S9-1.425*S0306Sensor histidine kinase-1.634*Regulatory function-*S01965Transcriptional regulator, LuxR family+1.562*S01965Transcriptional regulator, Mark family+1.418*S02640Transcriptional regulator, Mark family+1.737*S04388DNA-binding response regulator-1.653*S04388DNA-binding response regulator-1.653*S01209pnPolyribonucleotide nucleotidyltransferase+1.284*S02571ATP-dependent RNA helicase, DEAD box family-1.629*Purines, pyrimidines, nucleosides, and nucleotides-1.630*S01142carBCarbamoyl-phosphate synthase, large sunnit-1.435*S0375asnBAsparagine synthetase, glutamine hydrolyzing-1.742*S03175asnBAsparagine synthetase, glutamine hydrolyzing-1.742*S04399lysADiaminopimelate decarboxylase+1.166*S03175asnBAsparagine synthetase, glutamine hydrolyzing-1.742*S04399lysADiaminopimelate decarboxylase+1.667*S04309lysADiaminopimelate decar	SO0248	rpsE	Ribosomal protein S5	-1.508	*
SO2300infCTranslation initiation factor IF-3-1.527*S03798rluA-2Ribosomal large subunit pseouridine synthetase A-1.721***S03939rpsLRibosomal protein S9-1.425*Signal transductionSensor histidine kinase-1.634*Regulatory functionTranscriptional regulator, LuxR family+1.562*S00864Transcriptional regulator, LyxR family+1.418*S02640Transcriptional regulator, LyxR family+1.737*S04571Transcriptional regulator, LyxR family-1.623*Transcriptional regulator, LyxR family-1.623*S04571Transcriptional regulator, LyxR family-1.629*Transcription-1.629**S01209pnpPolyribonucleotide nucleotidyltransferase+1.284*S01210carBCarbamoyl-phosphate synthase, large sununit-1.435*S01412carBCarbamoyl-phosphate synthase, large sununit-1.435*S01217deoCDeoxyribose-phosphate aldolase+1.566*S0303hpt-2Hypoxanthine phosphoribosyltransferase-1.600*S0144thrBHomoserine kinase+1.497*S04309lysADiaminopimelate decarboxylase+1.768*S03175asnBAsparagine synthetase, glutamine hydrolyzing-1.742*S01679Acyl-CoA dehydrogenas family+2.227*Protein fate1.605 <td>SO0249</td> <td>rpmD</td> <td>Ribosomal protein L30</td> <td>-1.582</td> <td>*</td>	SO0249	rpmD	Ribosomal protein L30	-1.582	*
SO3798rluA-2Ribosomal large subunit pseouridine synthetase A-1.721**SO3939rpsLRibosomal protein S9-1.425*SO3306Sensor histidine kinase-1.634*Regulatory functionTranscriptional regulator, LvxR family+1.562*SO0864Transcriptional regulator, LvxR family+1.418*SO2640Transcriptional regulator, LvxR family+1.737*SO4388DNA-binding response regulator-1.653*SO4388DNA-binding response regulator-1.663*SO2571Transcriptional regulator, LyxR family-1.770*TranscriptionaTranscriptional regulator, LyxR family-1.629*SO1209pnpPolyribonucleotide nucleotidyltransferase+1.284*SO2571ATP-dependent RNA helicase, DEAD box family-1.629*Purines, pyrimidines, nucleosides, and nucleotidesEocoryphose-phosphate aldolase+1.566*SO3175asnBAsparagine synthetase, glutamine hydrolyzing-1.742*SO3175asnBAsparagine synthetase, glutamine hydrolyzing-1.742*SO4309lysADiaminopimelate decarboxylase+1.667*SO2223Peptidase, putative-1.587*SO2206ccmDHeme exporter protein CrmD-1.605*OthersSO310OmpA-like transmembrane domain protein-1.618*SO310OmpA-like transmembrane domain protein-1.618*SO310<	SO2300	infC	Translation initiation factor IF-3	-1.527	*
SO3939rpsLRibosomal protein S9-1.425*Signal transductionSensor histidine kinase-1.634*S03306Sensor histidine kinase-1.634*Regulatory functionTranscriptional regulator, LuxR family+1.562*S01965Transcriptional regulator, LuxR family+1.418*S02640Transcriptional regulator, MarR family+1.737*S04388DNA-binding response regulator-1.653*SO4571Transcriptional regulator, LysR family-1.770*Transcription-1.629**S01209pnpPolyribonucleotide nucleotidyltransferase+1.284*S02571ATP-dependent RNA helicase, DEAD box family-1.629*Purines, pyrimidines, nucleosides, and nucleotides1.600*S0142carBCarbamoyl-phosphate aldolase+1.566*S03175asnBAsparagine synthetase, large sununit-1.425*S03175asnBAsparagine synthetase, glutamine hydrolyzing-1.742*S0414thrBHomoserine kinase+1.497*S02223peptidase, putative-1.587*S0223Peptidase, putative-1.605*S03175Glyxalase family protein-1.615*S0223Peptidase, putative-1.587*S0260ccmDHeme exporter protein CcmD-1.605*Others	SO3798	rluA-2	Ribosomal large subunit pseouridine synthetase A	-1.721	**
Signal transduction-1.634SO3306Sensor histidine kinase-1.634Regulatory function-SO0864Transcriptional regulator, LuxR family+1.562SO1965Transcriptional regulator, LysR family+1.1418SO2640Transcriptional regulator, LysR family+1.737SO4388DNA-binding response regulator-1.653SO4571Transcriptional regulator, LysR family-1.770Transcription-1.629*SO1209pnpPolyribonucleotide nucleotidyltransferase+1.284SO2571ATP-dependent RNA helicase, DEAD box family-1.629Purines, pyrimidines, nucleosides, and nucleotides-*SO1142carBCarbamoyl-phosphate synthase, large sununit-1.435SO303hpt-2Hypoxanthine phosphoribosyltransferase+1.266SO3175asnBAsparagine synthetase, glutamine hydrolyzing-1.742Amino acid biosynthesis*SO4309lysADiaminopimelate decarboxylase+1.768Fatty acid and phospholipid metabolism*SO223Peptidase, putative-1.587*SO2260ccmDHeme exporter protein CcmD-1.613*Others*SO310OmpA-like transmembrane domain protein-1.637*SO4238TPR domain protein-1.618*SO4206Cloy Heme exporter protein CcmD-1.618*SO310OmpA-like transmembrane domain prot	SO3939	rpsL	Ribosomal protein S9	-1.425	*
SO3306Sensor histidine kinase-1.634*Regulatory functionTranscriptional regulator, LuxR family+1.562*SO0864Transcriptional regulator, LysR family+1.418*SO2640Transcriptional regulator, LysR family+1.737*SO4388DNA-binding response regulator-1.653*SO43871Transcriptional regulator, LysR family-1.770*Transcription*SO1209pnpPolyribonucleotide nucleotidyltransferase+1.284*SO2571ATP-dependent RNA helicase, DEAD box family-1.629*Purines, pyrimidines, nucleosides, and nucleotidesCarbamoyl-phosphate synthase, large sununit-1.435*SO1217deoCDeoxyribose-phosphate aldolase+1.566*SO3803hpt-2Hypoxanthine phosphoribosyltransferase-1.600*Amino acid biosynthesis**SO175asnBAsparagine synthetase, glutamine hydrolyzing-1.742*SO1679Acyl-CoA dehydrogenas family+2.227*Protein fate*SO223Peptidase, putative-1.605*SO260ccmDHeme exporter protein CcmD-1.605*Others*SO3175Glyxalase family protein-1.618*SO2404Iron-containing alcohol dehydrogenase+1.665*SO250ComDHeme exporter protein CcmD-1.605* </td <td>Signal transduction</td> <td>1</td> <td>I I I I I I I I I I I I I I I I I I I</td> <td></td> <td></td>	Signal transduction	1	I I I I I I I I I I I I I I I I I I I		
Regulatory functionInternational negulator, LuxR family+1.562SO0864Transcriptional regulator, LuxR family+1.418SO2640Transcriptional regulator, MarR family+1.418SO2640Transcriptional regulator, MarR family+1.737SO4388DNA-binding response regulator-1.653SO4571Transcriptional regulator, LysR family-1.770TranscriptionSO1209pnpSO1209pnpPolyribonucleotide nucleotidyltransferase+1.284SO2571ATP-dependent RNA helicase, DEAD box family-1.629Purines, pyrimidines, nucleosides, and nucleotides-SO1142carBCarbamoyl-phosphate synthase, large sununit-1.435SO1217deoCDeoxyribose-phosphate aldolase+1.566SO3803hpt-2Hypoxanthine phosphoribosyltransferase-1.600Amino acid biosynthesisSO3175asnBAsparagine synthetase, glutamine hydrolyzing-1.742SO4309lysADiaminopimelate decarboxylase+1.768Fatty acid and phospholipid metabolism*SO1679Acyl-CoA dehydrogenas family+2.227*Protein fate*SO223Peptidase, putative-1.587*SO260ccmDHeme exporter protein CcmD-1.605*OthersSO310OmpA-like transmembrane domain protein-1.618*SO3810OmpA-like transmembrane d	SQ3306		Sensor histidine kinase	-1.634	*
SousserTranscriptional regulator, LuxR family+1.562*SO0864Transcriptional regulator, LysR family+1.418*SO2640Transcriptional regulator, LysR family+1.418*SO4388DNA-binding response regulator-1.653*SO4388DNA-binding response regulator-1.653*SO2571Transcriptional regulator, LysR family-1.770*TranscriptionS01209pnpPolyribonucleotide nucleotidyltransferase+1.284*SO2571Carba Carbamoyl-phosphate synthase, large sununit-1.629*Purines, pyrimidines, nucleosides, and nucleotidesCarba moyl-phosphate aldolase+1.566*SO1142carBCarbamoyl-phosphate synthase, large sununit-1.435*SO117deoCDeoxyribose-phosphate aldolase+1.660*SO3803hpt-2Hypoxanthine phosphoribosyltransferase-1.600*SO3175asnBAsparagine synthetase, glutamine hydrolyzing-1.742*SO4309lysADiaminopinelate decarboxylase+1.768*Fatty acid and phospholipid metabolismSo223Peptidase, putative-1.587*SO223Peptidase, putative-1.653*SO223Peptidase, putative-1.605*SO223Peptidase, putative-1.605*SO260ccmDHeme exporter protein CcmD-1.605*OthersSO3810OmpA-like transmembrane domain protein-1.618*S	Regulatory function				
SO1965Transcriptional regulator, LysR family+1.418SO2640Transcriptional regulator, MarR family+1.737SO4388DNA-binding response regulator-1.653SO4571Transcriptional regulator, LysR family-1.770Transcription-1.770SO2571Transcriptional regulator, LysR family-1.770SO1209pnpPolyribonucleotide nucleotidyltransferase+1.284SO2571ATP-dependent RNA helicase, DEAD box family-1.629Purines, pyrimidines, nucleosides, and nucleotides-1.435*SO1142carBCarbamoyl-phosphate synthase, large sununit-1.435SO1217deoCDeoxyribose-phosphate aldolase+1.566SO3803hpt-2Hypoxanthine phosphoribosyltransferase-1.600Amino acid biosynthesis*SO4509IysADiaminopimelate decarboxylase+1.778SO4309IysADiaminopimelate decarboxylase+1.768Fatty acid and phospholipid metabolismSO2223Peptidase, putative-1.587SO2204ccmDHeme exporter protein CcmD-1.605OthersSO1756Glyxalase family protein-1.637SO3810OmpA-like transmembrane domain protein-1.637SO4238TPR domain protein-1.618SOA00164Iron-containing alcohol dehydrogenase+1.486SOA00136ISSod3, transposase-1.538	SO0864		Transcriptional regulator LuxR family	+1.562	*
SO2640Transcriptional regulator, MarR family+1.737SO2640Transcriptional regulator, MarR family+1.737SO4388DNA-binding response regulator-1.653SO4388DNA-binding response regulator-1.653SO4381Transcriptional regulator, LysR family-1.770TranscriptionSO2571-1.770SO1209pnpPolyribonucleotide nucleotidyltransferase+1.284SO2571ATP-dependent RNA helicase, DEAD box family-1.629Purines, pyrimidines, nucleosides, and nucleotides-1.435*SO1142carBCarbamoyl-phosphate synthase, large sununit-1.435SO1217deoCDeoxyribose-phosphate aldolase+1.566SO3803hpt-2Hypoxanthine phosphoribosyltransferase-1.600Amino acid biosynthesis1.629*SO3175asnBAsparagine synthetase, glutamine hydrolyzing-1.742SO4309lysADiaminopimelate decarboxylase+1.497SO1679Acyl-CoA dehydrogenas family+2.227Protein fate-1.605*SO2223Peptidase, putative-1.587SO2223Peptidase, putative-1.605SO176Glyxalase family protein-1.637SO3810OmpA-like transmembrane domain protein-1.637SO3810OmpA-like transmembrane domain protein-1.618SO400164Iron-containing alcohol dehydrogenase+1.468SOA00164Iron-containing alcohol dehydrogenase-1.538	SO1965		Transcriptional regulator, LysR family	+1.302 +1.418	*
SO438DNA-binding response regulator11.57SO4388DNA-binding response regulator-1.653SO4571Transcriptional regulator, LysR family-1.770TranscriptionSO1209pnpPolyribonucleotide nucleotidyltransferase+1.284SO2571ATP-dependent RNA helicase, DEAD box family-1.629Purines, pyrimidines, nucleosides, and nucleotidesSO142carBCarbamoyl-phosphate synthase, large sununit-1.435SO1217deoCDeoxyribose-phosphate aldolase+1.566SO3803hpt-2Hypoxanthine phosphoribosyltransferase-1.600Amino acid biosynthesisSO3175asnBAsparagine synthetase, glutamine hydrolyzing-1.742SO3414thrBHomoserine kinase+1.497SO4309lysADiaminopimelate decarboxylase+1.768Fatty acid and phospholipid metabolismSO2223Peptidase, putative-1.657SO2204ccmDHeme exporter protein CcmD-1.605OthersSO1756Glyoxalase family protein-1.637SO3810OmpA-like transmembrane domain protein-1.618SOA00164Iron-containing alcohol dehydrogenase+1.468SOA00136ISSod3, transposase-1.538	SO2640		Transcriptional regulator, MarR family	+1.710 +1.737	*
SO4500Driventum regulator1.000SO4501Transcriptional regulator, LysR family-1.770Transcription*SO209pnpPolyribonucleotide nucleotidyltransferase+1.284SO2571ATP-dependent RNA helicase, DEAD box family-1.629Purines, pyrimidines, nucleosides, and nucleotidesCarbamoyl-phosphate synthase, large sununit-1.435SO1217deoCDeoxyribose-phosphate aldolase+1.566SO3803hpt-2Hypoxanthine phosphoribosyltransferase-1.600Amino acid biosynthesiss-1.772*SO3175asnBAsparagine synthetase, glutamine hydrolyzing-1.742*SO4309lysADiaminopimelate decarboxylase+1.768*SO1679Acyl-CoA dehydrogenas family+2.227*Protein fate-1.605**SO2223Peptidase, putative-1.587*SO1756Glyoxalase family protein-1.603*SO1756Glyoxalase family protein-1.637*SO3810OmpA-like transmembrane domain protein-1.618*SO4238TPR domain protein-1.618*SO400164Iron-containing alcohol dehydrogenase+1.468*	SO2340		DNA-binding response regulator	-1.653	*
SO451TranscriptionTranscriptional regulator, Lysk rainity-1.770SO1209pnpPolyribonucleotide nucleotidyltransferase+1.284*SO2571ATP-dependent RNA helicase, DEAD box family-1.629*Purines, pyrimidines, nucleosides, and nucleotidesCarba moyl-phosphate synthase, large sunnit-1.435*SO1142carBCarbamoyl-phosphate synthase, large sunnit-1.435*SO1217deoCDeoxyribose-phosphate aldolase+1.566*SO3803hpt-2Hypoxanthine phosphoribosyltransferase-1.600*Amino acid biosynthesisSo3175asnBAsparagine synthetase, glutamine hydrolyzing-1.742*SO3175asnBAsparagine synthetase, glutamine hydrolyzing-1.742*SO4309lysADiaminopimelate decarboxylase+1.768*Fatty acid and phospholipid metabolismSO2223Peptidase, putative-1.587*SO21756Glyoxalase family protein-1.605**SO1756Glyoxalase family protein-1.6157*SO3810OmpA-like transmembrane domain protein-1.618*SO4238TPR domain protein-1.618*SO40136ISSod3, transposase-1.538*	SO4571		Transcriptional regulator LycP family	-1.770	*
NatisciptionpnpPolyribonucleotide nucleotidyltransferase+1.284*SO120pnpPolyribonucleotide nucleotidyltransferase+1.284*Purines, pyrimidines, nucleosides, and nucleotides-1.629*SO1142carBCarbamoyl-phosphate synthase, large sununit-1.435*SO1217deoCDeoxyribose-phosphate aldolase+1.566*SO3803hpt-2Hypoxanthine phosphoribosyltransferase-1.600*Amino acid biosynthesis**SO3175asnBAsparagine synthetase, glutamine hydrolyzing-1.742*SO4309lysADiaminopimelate decarboxylase+1.768*Fatty acid and phospholipid metabolism**SO2223Peptidase, putative-1.587*SO2060ccmDHeme exporter protein CcmD-1.605*OthersGlyoxalase family protein-1.637*SO3810OmpA-like transmembrane domain protein-1.637*SO4238TPR domain protein-1.618*SOA00164Iron-containing alcohol dehydrogenase+1.468*SOA00136ISSod3, transposase-1.538*	Transcription		Transcriptional regulator, Lysk family	-1.770	
SO1205pipPolymonucleoide nucleoid/maintenage+1.284SO2571ATP-dependent RNA helicase, DEAD box family-1.629*Purines, pyrimidines, nucleosides, and nucleotidesCarbamoyl-phosphate synthase, large sununit-1.435*SO1142carBCarbamoyl-phosphate synthase, large sununit-1.435*SO1217deoCDeoxyribose-phosphate aldolase+1.566*SO3803hpt-2Hypoxanthine phosphoribosyltransferase-1.600*Amino acid biosynthesisSO3175asnBAsparagine synthetase, glutamine hydrolyzing-1.742*SO3175asnBAsparagine synthetase, glutamine hydrolyzing-1.742*SO3414thrBHomoserine kinase+1.497*SO4309lysADiaminopimelate decarboxylase+1.768*Fatty acid and phospholipid metabolismSO1679Acyl-CoA dehydrogenas family+2.227*SO220ccmDHeme exporter protein CcmD-1.605*OthersSO3810OmpA-like transmembrane domain protein-1.617*SO4238TPR domain protein-1.618*SOA00164Iron-containing alcohol dehydrogenase+1.468*SOA00136ISSod3, transposase-1.538*	SO1200		Deluribanuelactida nuelactidultrensforaça	1 2 2 4	*
Arr-dependent KNA nercase, DEAD box failing-1.029Purines, pyrimidines, nucleosides, and nucleotidesArr-dependent KNA nercase, DEAD box failing-1.029SO1142carBCarbamoyl-phosphate synthase, large sununit-1.435SO1217deoCDeoxyribose-phosphate aldolase+1.566SO3803hpt-2Hypoxanthine phosphoribosyltransferase-1.600Amino acid biosynthesis-1.600*SO3175asnBAsparagine synthetase, glutamine hydrolyzing-1.742SO3414thrBHomoserine kinase+1.497SO4309lysADiaminopimelate decarboxylase+1.768Fatty acid and phospholipid metabolismSO1679Acyl-CoA dehydrogenas family+2.227Protein fateSO260ccmDHeme exporter protein CcmD-1.605OthersSO1756Glyoxalase family protein-1.637SO4238TPR domain protein-1.618SOA00164Iron-containing alcohol dehydrogenase+1.468SOA00136ISSod3, transposase-1.538	SO1209 SO2571	pup	ATD dependent DNA belieses DEAD her femily	+1.204	*
Functions, purification of the context of the second state of the seco	Durings pyrimidings pueloosidas	and nucleotides	AIF-dependent KINA hencase, DEAD box family	-1.029	
SO1142CarbCarbanoyr-phosphate synthase, rarge sultuit-1.433*SO1217deoCDeoxyribose-phosphate aldolase+1.566*SO3803hpt-2Hypoxanthine phosphoribosyltransferase-1.600*Amino acid biosynthesisSO3175asnBAsparagine synthetase, glutamine hydrolyzing-1.742*SO3414thrBHomoserine kinase+1.497*SO4309lysADiaminopimelate decarboxylase+1.768*Fatty acid and phospholipid metabolismSO2223Peptidase, putative-1.587*SO22060ccmDHeme exporter protein CcmD-1.605*OthersSO1756Glyoxalase family protein-1.617*SO3810OmpA-like transmembrane domain protein-1.618*SO4238TPR domain protein-1.618*SOA00164Iron-containing alcohol dehydrogenase+1.468*SOA00136ISSod3, transposase-1.538*	Furnies, pyriniumes, nucleosides		Contrary and the contrary counting and the countrary is	1 425	*
SO1217deoCDeoxyribose-pnospnate adolase+1.506*SO3803hpt-2Hypoxanthine phosphoribosyltransferase-1.600*Amino acid biosynthesisSO3175asnBAsparagine synthetase, glutamine hydrolyzing-1.742*SO3414thrBHomoserine kinase+1.497*SO4309lysADiaminopimelate decarboxylase+1.768*Fatty acid and phospholipid metabolismSO1679Acyl-CoA dehydrogenas family+2.227*Protein fateSO2223Peptidase, putative-1.587*SO2600ccmDHeme exporter protein CcmD-1.605*OthersGlyoxalase family protein-1.617*SO3810OmpA-like transmembrane domain protein-1.618*SO4238TPR domain protein-1.618*SOA00164Iron-containing alcohol dehydrogenase+1.468*SOA00136ISSod3, transposase-1.538*	501142	CarB	Carbamoyi-phosphate synthase, large sunum	-1.455	*
SO3803npt-2Hypoxantnine prosphorioosyltransferase-1.600Amino acid biosynthesisSO3175asnBAsparagine synthetase, glutamine hydrolyzing-1.742SO3414thrBHomoserine kinase+1.497SO4309lysADiaminopimelate decarboxylase+1.768Fatty acid and phospholipid metabolismSO1679Acyl-CoA dehydrogenas family+2.227Protein fateSO2223Peptidase, putative-1.587SO260ccmDHeme exporter protein CcmD-1.605OthersGlyoxalase family protein-1.637SO3810OmpA-like transmembrane domain protein-1.618SO4238TPR domain protein-1.618SOA00164Iron-containing alcohol dehydrogenase+1.468	SO1217	deoC	Deoxyribose-phosphate aldolase	+1.500	*
Amino acid biosynthesisSO3175asnBAsparagine synthetase, glutamine hydrolyzing-1.742*SO3414thrBHomoserine kinase+1.497*SO4309lysADiaminopimelate decarboxylase+1.768*Fatty acid and phospholipid metabolism*SO1679Acyl-CoA dehydrogenas family+2.227*Protein fate*SO2223Peptidase, putative-1.587*SO260ccmDHeme exporter protein CcmD-1.605*OthersGlyoxalase family protein-1.637*SO3810OmpA-like transmembrane domain protein-1.618*SO400164Iron-containing alcohol dehydrogenase+1.468*SOA00136ISSod3, transposase-1.538*	503803	npt-2	Hypoxantnine phosphoribosyltransferase	-1.600	*
SO3175asnBAsparagine synthetase, glutamine hydrolyzing-1.742*SO3414thrBHomoserine kinase+1.497*SO4309lysADiaminopimelate decarboxylase+1.768*Fatty acid and phospholipid metabolism*SO1679Acyl-CoA dehydrogenas family+2.227*Protein fate*SO2223Peptidase, putative-1.587*SO260ccmDHeme exporter protein CcmD-1.605*OthersGlyoxalase family protein-1.637*SO3810OmpA-like transmembrane domain protein-1.618*SO4238TPR domain protein-1.618*SOA00164Iron-containing alcohol dehydrogenase+1.468*SOA00136ISSod3, transposase-1.538*	Amino acid biosynthesis			. =	
SO3414thrBHomoserine kinase+1.497SO4309lysADiaminopimelate decarboxylase+1.768Fatty acid and phospholipid metabolismSO1679Acyl-CoA dehydrogenas family+2.227Protein fateSO2223Peptidase, putative-1.587SO0260ccmDHeme exporter protein CcmD-1.605OthersSO1756Glyoxalase family protein-1.637SO3810OmpA-like transmembrane domain protein-1.618SO4238TPR domain protein-1.618SOA00164Iron-containing alcohol dehydrogenase+1.468SOA00136ISSod3, transposase-1.538	SO3175	asnB	Asparagine synthetase, glutamine hydrolyzing	-1.742	*
SO4309lysADiaminopimelate decarboxylase+1.768*Fatty acid and phospholipid metabolismAcyl-CoA dehydrogenas family+2.227*Protein fate-1.587*SO2223Peptidase, putative-1.587*SO0260ccmDHeme exporter protein CcmD-1.605*OthersSO3810OmpA-like transmembrane domain protein-1.637*SO4238TPR domain protein-1.618*SOA00164Iron-containing alcohol dehydrogenase+1.468*SOA00136ISSod3, transposase-1.538*	SO3414	thrB	Homoserine kinase	+1.497	*
Fatty acid and phospholipid metabolismSO1679Acyl-CoA dehydrogenas family+2.227*Protein fate-1.587*SO2223Peptidase, putative-1.587*SO0260ccmDHeme exporter protein CcmD-1.605*Others-1.587***SO1756Glyoxalase family protein-1.637*SO3810OmpA-like transmembrane domain protein-1.618*SO4238TPR domain protein-1.618*SOA00164Iron-containing alcohol dehydrogenase+1.468*SOA00136ISSod3, transposase-1.538*	SO4309	lysA	Diaminopimelate decarboxylase	+1.768	*
SO1679Acyl-CoA dehydrogenas family+2.227*Protein fate+2.227*SO2223Peptidase, putative-1.587*SO260ccmDHeme exporter protein CcmD-1.605*Others </td <td>Fatty acid and phospholipid meta</td> <td>abolism</td> <td></td> <td></td> <td></td>	Fatty acid and phospholipid meta	abolism			
Protein fate SO2223Peptidase, putative-1.587*SO0260ccmDHeme exporter protein CcmD-1.605*OthersGlyoxalase family protein-1.912***SO3810OmpA-like transmembrane domain protein-1.637*SO4238TPR domain protein-1.618*SOA00164Iron-containing alcohol dehydrogenase+1.468*SOA00136ISSod3, transposase-1.538*	SO1679		Acyl-CoA dehydrogenas family	+2.227	*
SO2223Peptidase, putative-1.587*SO0260ccmDHeme exporter protein CcmD-1.605*OthersGlyoxalase family protein-1.912***SO3810OmpA-like transmembrane domain protein-1.637*SO4238TPR domain protein-1.618*SOA00164Iron-containing alcohol dehydrogenase+1.468*SOA00136ISSod3, transposase-1.538*	Protein fate				
SO0260ccmDHeme exporter protein CcmD-1.605*OthersGlyoxalase family protein-1.912***SO3810OmpA-like transmembrane domain protein-1.637*SO4238TPR domain protein-1.618*SOA00164Iron-containing alcohol dehydrogenase+1.468*SOA00136ISSod3, transposase-1.538*	SO2223		Peptidase, putative	-1.587	*
OthersGlyoxalase family protein-1.912***SO1756Glyoxalase family protein-1.637*SO3810OmpA-like transmembrane domain protein-1.637*SO4238TPR domain protein-1.618*SOA00164Iron-containing alcohol dehydrogenase+1.468*SOA00136ISSod3, transposase-1.538*	SO0260	ccmD	Heme exporter protein CcmD	-1.605	*
SO1756Glyoxalase family protein-1.912***SO3810OmpA-like transmembrane domain protein-1.637*SO4238TPR domain protein-1.618*SOA00164Iron-containing alcohol dehydrogenase+1.468*SOA00136ISSod3, transposase-1.538*	Others				
SO3810OmpA-like transmembrane domain protein-1.637*SO4238TPR domain protein-1.618*SOA00164Iron-containing alcohol dehydrogenase+1.468*SOA00136ISSod3, transposase-1.538*	SO1756		Glyoxalase family protein	-1.912	***
SO4238TPR domain protein-1.618*SOA00164Iron-containing alcohol dehydrogenase+1.468*SOA00136ISSod3, transposase-1.538*	SO3810		OmpA-like transmembrane domain protein	-1.637	*
SOA00164Iron-containing alcohol dehydrogenase+1.468*SOA00136ISSod3, transposase-1.538*	SO4238		TPR domain protein	-1.618	*
SOA00136 ISSod3, transposase -1.538 *	SOA00164		Iron-containing alcohol dehydrogenase	+1.468	*
	SOA00136		ISSod3, transposase	-1.538	*

TABLE 2. Known Functional Genes With Significant Changes in Gene Expression after exposure to 14.1 T Magnetic Field for 12 h

^aThe average (AVG) expression ratio of the treatment sample to the control was calculated from 12 replicates together, a P = .05 standard *t*-test result. All genes are significant in expression changes (*, P < .05; **, P < .01; ***, P < 0.001; probability in *t*-test.) ^bFold increases is marked as (+) and decreases (-).

magnetic field. In that study, Horiuchi et al. [2001] found that the number of viable cells of *E. coli* B in the stationary phase after 48 h under the magnetic field of 5.2-6.1 T was 100 000 times higher than that under a geomagnetic field. Such a difference may be due to different experiment design, since our experiment only observed growth of cells exposed under strong magnetic field for 12 h and the bacteria is still in its log phase stage, whereas Horiuchi's experiment lasted over two days at a different magnetic field strength. The physiological status of bacteria between log phase and stationary phase is very different, and bacterial cells in stationary phase much more easily to give rise to mutants adaptive to stress environments. Indeed, this may explain why the effect of strong magnetic field on viable cell of E. coli only appeared during stationary phase in the study of Horiuchi et al. [2001].

Gene Expression

Among a total of 4583 genes assayed following 12 h, 14.1 T magnetic field exposure, total 65 genes were significantly changed in expression, compared to the non-exposed control. The magnitude of change ranges from 1.5 to 5 times. Out of these 65 genes, 21 were upregulated whereas the other 44 genes were repressed. According to TIGR gene annotation of S. onedensis MR-1, 20 of these 65 genes encode conserved hypothetical proteins and thus their exact functions are unknown (Table 1). Table 2 lists all other genes whose functions are known and that were significantly changed in the gene expression against the control. Five genes are identified as transcriptional regulator and they include SO1965 (LysR family member), SO0864 (LuxR family member), SO4571 (LysR family member), SO4388 (DNA-binding response regulator), and SO2640 (MarR family member). Among these transcriptional regulators, SO1965, SO0864, and SO2640 were upregulated, whereas both SO4571 and SO4388 were downregulated under the magnetic stress condition. Previously, a couple of studies reported that *rpoS* gene, which encodes a sigma factor and plays a role as a transcriptional regulator of some genes, had increased activities in stationary stage [Tsuchiya et al., 1999; Horiuchi et al., 2001]. Here, we reported the activities of other transcriptional regulators were affected by strong static magnetic fields under log phase stage of bacterial growth. However, the mechanism underpinning such expression alterations is not clear.

Under the category of energy metabolism, six genes showed altered expression levels under the magnetic stress (Table 2). They are SO1778 (omcB, encoding decaheme cytochrome c), SO0608 (petA, encoding iron sulfur subunit of ubiquinol-cytochrome c reductase), SO0053 (gpsA, glycerol-3-phosphate dehydrogenase), SO2513 (encoding a NqrDE/RnfAE family protein), SO2421 (ansA, L-asparaginase I), and SO2362 (ccoQ). It is worthwhile to note that SO1778 (omcB), SO0608 (petA), and SO2362 (ccoQ) are ironcontaining proteins. Similarly, SO1112 (bfr1), encoding bacterioferritin subunit I was also transcriptional suppressed under the same condition. In contrast, SOA00164, which encodes an iron-containing alcohol dehydrogenase was upregulated under the same condition. Since the expression of these iron-containing proteins involved in energy metabolism was affected by the strong magnetic field, it is reasonable to suppose that the strong magnetic field perhaps influenced the iron metabolism and then energy metabolism of MR-1, although the exact mechanism remains unknown at this moment.

As shown in Table 2, genes encoding other functional proteins also showed altered expression level. For instance, under the category of transport and binding protein, SO0157 and SO2578, encoding a proton/glutamate symportor and sulfate permease family protein, respectively, were upregulated. In contrast, several genes involved in protein biosynthesis (SO0248, 249, 2300, 3798, and 3939) were downregulated. However, the mechanism underpinning such changes is not clear. Also, the changes at transcriptional levels were not reflected at organism level, as our growth experiments showed. This may suggest that log phase cells of MR-1 were capable of maintaining their physiological homeostasis under such stress, even though they had to experience some transcriptional changes at molecular level.

CONCLUSION

We studied the possible effect of 14.1 T static magnetic field on the growth and transcriptional expression of log phase cells of bacterium *Shewanella oneidensis* MR-1. The results conclude that while little effects on cell growth at log phase were observed, apparent changes at transcriptional levels were detected in some genes of *S. onedensis* MR-1. However, mechanism underpinning such changes was not clear.

ACKNOWLEDGMENTS

The part of this research was conducted at Oak Ridge National laboratory, which is funded by US Department of Energy (Office of Biological and Environmental Research, Office of Science) Grants DE-FG02-01ER63220 from the Genomes to Life program, DE-FG02-97ER62492 from the Natural and Accelerated bioremediation Research Program, and 6 Gao et al.

ERKP385 from Microbial Genome Program, and by the Laboratory Directed and Research Development Program at Oak Ridge National Laboratory. Oak Ridge National laboratory is managed by the University of Tennessee-Battelle LLC for the Department of Energy under the contract DOE-AC05-00OR22725.

REFERENCES

- Arnesano F, Banci L, Barker PD, Bertini I, Rosato A, Su XC, Vierzzoli MS. 2002. Solution structure and characterization of the heme chaperone CcmE. Biochemistry 41:13587– 13594.
- Denegre J, Valles J, Jr., Lin K, Jordan W, Mowry K. 1998. Cleavage planes in frog eggs are altered by strong magnetic fields. Proc Natl Acad Sci USA 95:14729–14732.
- Emura R, Takeuchi T, Nakaoka Y, Higashi T. 2003. Analysis of anisotropic diamagnetic susceptibility of a bull sperm. Bioelectromagnetics 24:347–355.
- Fries MR, Zhou J, Chee-Sanford J, Tiedje JM. 1994. Isolation, characterization, and distribution of denitrifying toluene degraders from a variety of habitats. Appl Environ Microbiol 60:2802–2810.
- Giometti C, Khare T, Tollaksen SL, Tsapin A, Zhu W, Yates JR III, Nealson KH. 2003. Analysis of the *Shewanella oneidensis* proteome by two-dimensional gel electrophoresis under nondenaturing conditions. Proteomics 3:777–785.
- Glasauer S, Langley S, Beveridge TJ. 2001. Sorption of Fe (hydr) oxides to the surface of *Shewanella putrefaciens*: Cell-bound fine-grained minerals are not always formed de novo. Appl Environ Microbiol 67:5544–5550.
- Heidelberg JF, Paulsen IT, Nelson KE, Gaidos EJ, Nelson WC, Read TD, Eisen JA, Seshadri R, Ward N, Methe B, Clayton RA, Meyer T, Tsapin A, Scott J, Beanan M, Brinkac L, Daugherty S, DeBoy RT, Dodson RJ, Durkin AS, Haft DH, Kolonay JF, Madupu R, Peterson JD, Umayam LA, White O, Wolf AM, Vamathevan J, Weidman J, Impraim M, Lee K, Berry K, Lee C, Mueller J, Khouri H, Gill J, Utterback TR, McDonald LA, Feldblyum TV, Smith HO, Venter JC, Nealson KH, Fraser CM. 2002. Genome sequence of the dissimilatory metal ionreducing bacterium *Shewanella oneidensis*. Nat Biotechnol 20:1118–1123.
- Horiuchi S, Ishizaki Y, Okuno K, Ano T, Shoda M. 2001. Drastic high magnetic field effect on suppression of *Escherichia coli* death. Bioelectrochemistry 53:149–153.
- Iwasaka M, Ueno S. 2003. Detection of intracellular macromolecule behavior under Strong magnetic fields by linearly polarized light. Bioelectromagnetics 24:564–570.
- Johnson H, Pelletier D, Spormann AM. 2001. Isolation and characterization of anaerobic ethylbenzene dehydrogenase, a novel Mo-Fe-S enzyme. J Bacteriol 183:4536–4542.

- Kohno M, Yamazaki M, Kimura I, Wada M. 2000. Effect of static magnetic fields on bacteria: *Streptococcus mutans*, *Staphylococcus aureus*, and *Escherichia coli*. Pathophysiology 7:143–148.
- Leblane L, Gouffi K, Leroi F, Hartke A, Blanco C, Auffray Y, Pichereau V. 2001. Uptake of choline from salmone flesh and its conversion to glycine betaine in response to salt stress in *Shewanella putrefaciens*. Int J Food Microbiol 65:93–103.
- Liu Y, Zhou J, Omelchenko M, Beliaev A, Venkateswaran A, Stair J, Wu L, Thompson D, Xu D, Rogozin IB, Gaidamakova EK, Zhai M, Makarova KS, Koonin EV, Daly MJ. 2003. Transcriptome dynamics of *Deinococcus radiodurans* recovering from ionizing radiation. Proc Natl Acad Sci USA 100(7):4191–4196.
- Marier TM, Myers CR. 2001. Isolation and characterization of a *Shewanella putrefaciens* MR-1 electron transport regulator etrA mutant: Reassessment of the role of EtrA. J Bacteriol 183:4918–4926.
- Myers CR, Myers JM. 1992. Fumarate reductase is a soluble enzyme in anaerobically grown *Shewanella putrefaciens* MR-1. FEMS Microbiol Lett 98:13–20.
- Myers CR, Myers JM. 1993a. Ferric reductase is associated with the outer membrane of anaerobically grown *Shewanella putre-faciens* MR-1. MEFS Microbiol Lett 108:15–22.
- Myers CR, Myers JM. 1993b. Role of menaquinone in the reduction of fumarate, nitrate, iron(III) and manganese (IV) by *Shewanella putrefaciens* MR-1. FEMS Microbiol Lett 114: 215–222.
- Pan H. 1996. The effect of a 7 T magnetic field on the egg hatching of *Heliothis virescens*. Magn Reson Imaging 14:673–677.
- Pan H, Liu X. 2004, Apparent biological effect of strong magnetic field on mosquito egg hatching. Bioelectromagnetics 25:84– 91.
- Sakuria H, Okuno K, Kubo A, Nakamura K, Shoda M. 1999. Effect pf a 7-tesla homogeneous magnetic field on mammalian cells. Bioelectrochemistry and Bioenergetics 49:57–63.
- Schiffer IB, Schreiber WG, Graf R, Schreiber EM, Jung D, Rose DM, Hehn M, Gebhard S, Sagemuller J, Spieβ HW, Oesch F, Thelen M, Hengstler JG. 2003. No influence of magnetic fields on cell cycle progression using conditions Relevant for patients during MRI. Bioelectromagnetics 24:241–250.
- Stansell M, Winters W, Doe R, Dart B. 2001. Increased antibiotic resistance of *E. coli* exposed to static magnetic fields. Bioelectromagnetics 22:129–137.
- Tsuchiya K, Okuno K, Ano T, Tanaka K, Takahashi H, Shoda M. 1999. High magnetic field enhances stationary phase-specific transcription activity of *Escherichia coli*. Bioelectrochemistry and Bioenergetics 48:383–387.
- Xu D, Li G, Wu L, Zhou J, Xu Y. 2002. Primegens: Robust and efficient design of gene-specific probes for microarray analysis. Bioinformatics 18:1432–1437.