

Differentiating natural vs. anthropogenic mercury inputs and subsequent Se/Hg interactions and biogeochemical cycling in Bighorn Lake, Bighorn Canyon National Recreation Area

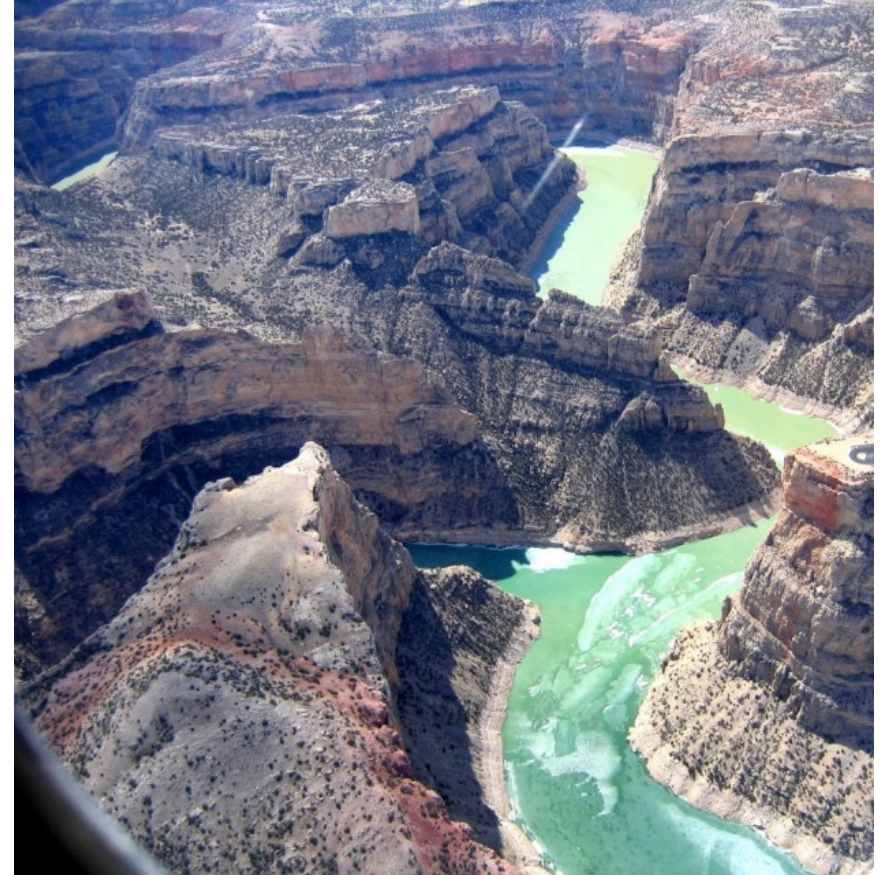
David Naftz, Elliott Barnhart, and David Krabbenhoft (USGS),
and Andrew Ray (NPS)



<http://www.nationalparks.org>

WHY ARE WE HERE?

- ◆ We want to inform BICA stakeholders and regulators about our study
- ◆ We want to obtain feedback about our study objectives/approach
- ◆ We want to develop partnership(s) and increase the applicability of our data for other uses (Lake Powell example)



http://water.usgs.gov/nps_partnership/index.php



This program empowers U.S. Geological Survey scientists and National Park Service resource managers to work in a partnership setting to provide the hydrologic information and understanding needed to preserve unimpaired the natural and cultural resources and values of the national park system for the enjoyment, education, and inspiration of this and future generations.

INTRODUCTION / PROBLEM

- ◆ Bighorn Lake is one of the most fished lakes in the State of Montana, with about 15,000 angler hours/year.
- ◆ Tissue samples collected from selected fish species in BICA contain elevated levels of Hg that restricts consumption by women and children
- ◆ Limited understanding of Hg sources and biogeochemical / microbial processes contributing to the elevated Hg concentrations in the native and sport fisheries in BICA
- ◆ BICA watershed contains natural and anthropogenic Hg sources
- ◆ Se inputs to Bighorn Lake and the associated antagonistic interaction of Se and Hg in fish

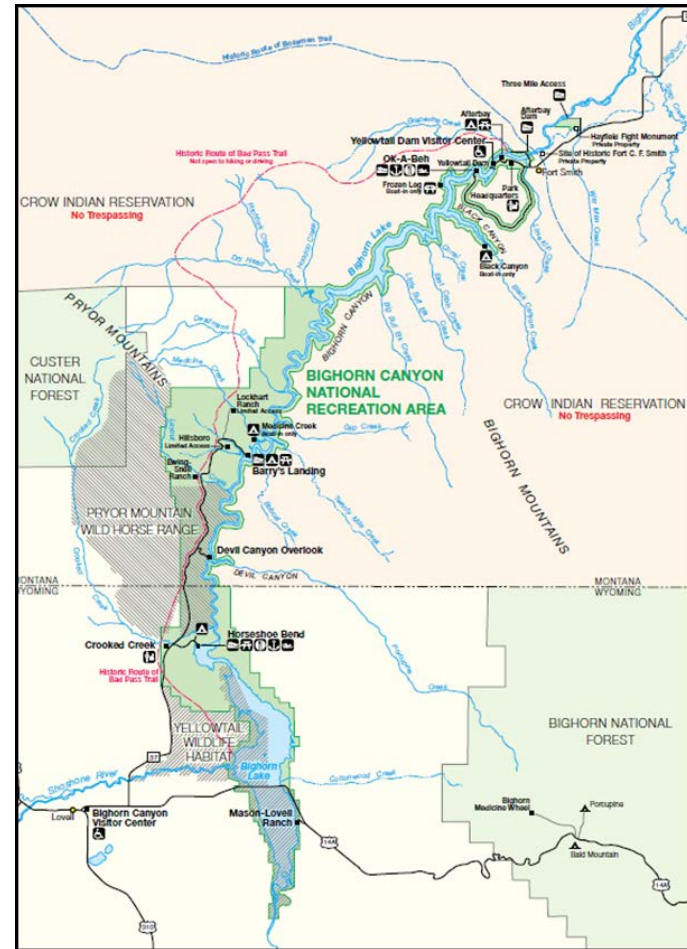


Bighorn Lake study team



STUDY OBJECTIVES

- ◆ Natural versus anthropogenic Hg inputs entering BICA
- ◆ Hg cycling in BICA and potential Hg methylation hotspots
- ◆ Bioaccumulation and transfer of Hg through the food web to top predators



LAKE POWELL EXAMPLE

HOUSEBOATING LAKE POWELL FOR SCIENCE

On Lake Powell, houseboating scientists peer into reservoir's mercury problem.

BY JEFF GILLIES

Lake Powell, the canyon-lined, serpentine reservoir that straddles the Utah-Arizona border, draws millions of visitors every year. Vacationers there often take to houseboats for a mellow week on the water amongst the red sandstone cliffs.

That never appealed much to David Nafiz, a U.S. Geological Survey research hydrologist who lived in Utah before taking up a post with the agency's Montana Science Center. But then duty called, in the form of a project to learn more about mercury contamination in the lower half of the 180-mile reservoir.

He and six USGS researchers from across the country — "A lot of the mercury guru," Nafiz said — stayed 12 nights on a 60-foot houseboat on the lake.

"It does sound fun, and it was a fun trip, but there were very long days," Nafiz said. Instead of soaking up empires or launching day trips into one of the reservoir's 90 side canyons, the scientists were collecting samples and working the mobile laboratory that occupied their vessel's top deck.

"There were a few days of the trip where people were processing samples until two or three in the morning and then getting up at six to start over again," Nafiz said.

The trip came about when, after several years of collecting fish with high mercury levels in the southern half of the reservoir, Arizona

and Utah issued consumption advisories for that section of the lake in late 2012. That elevated the mercury issue on the radar of the National Park Service, which operates the Glen Canyon National Recreation Area where the lake lies. High-mercury fish included endangered species, the protection of which is a management priority for the park service.

So the USGS crew, along with another researcher from University of Montana, set off in late May this year to get a better handle on the mercury dynamics in the lake. That includes a look at potential sources and the chemical and biological processes driving the mercury contamination. They're also looking at why the issue is much worse in the southern reservoir than in the northern half.

"Why is the mercury problem restricted geographically? That's basically what the project is trying to address," Nafiz said.

Their work began on the north end of Lake Powell near where the Colorado River flows into the reservoir. They operated two boats: the "mud boat" gathered samples of the bottom sediments, and another collected water samples and additional data with a YSI EXO2 multi-parameter water quality sonde.

The scientists were also running an instrument that continuously analyzed the air for mercury. That data could give an indication of the effects of nearby mercury sources, including a coal-fired power plant near the Glen Canyon Dam of Lake Powell's southern end.

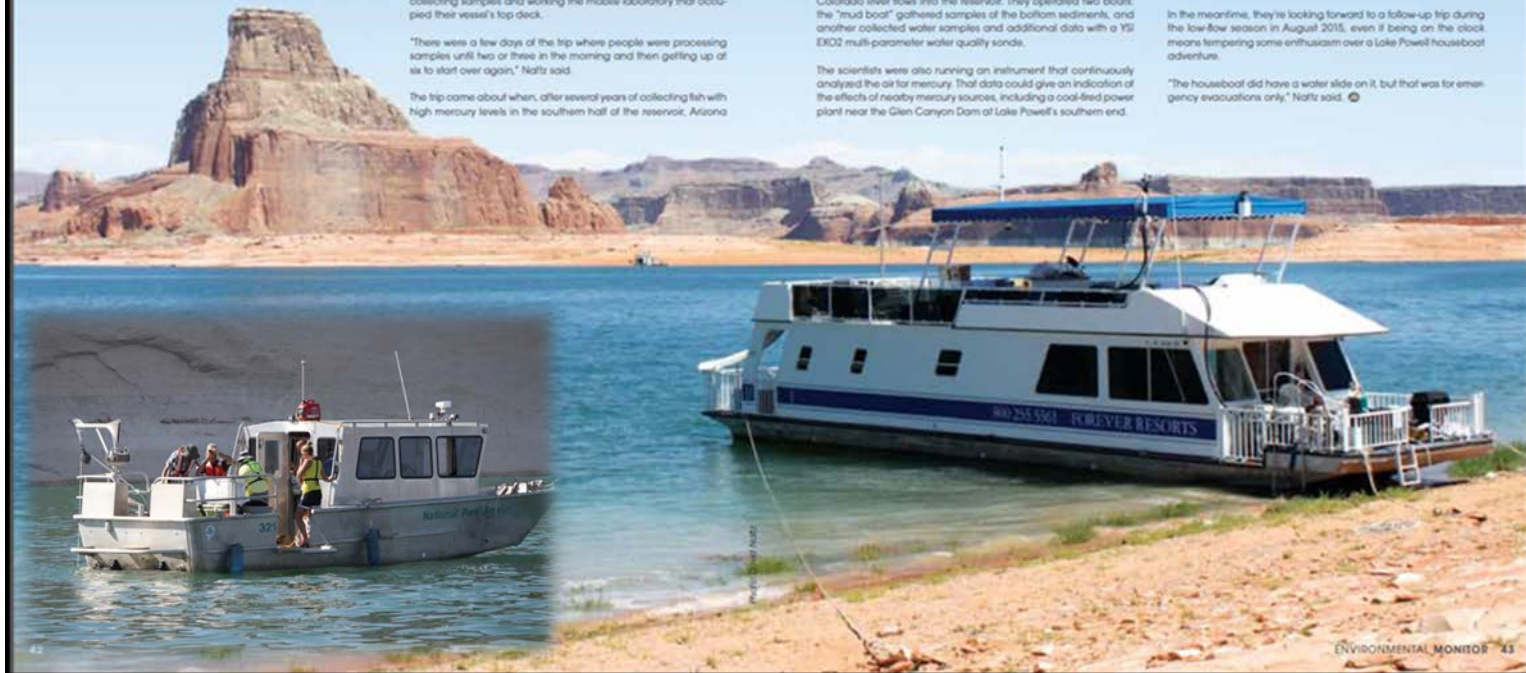
However, it seems more likely that the difference in mercury levels between the two ends of Lake Powell has more to do with what's going on under the water. The thought is, Nafiz said, that particulates cloud the water in the north end of the lake, but the sediment settles out as the water flows south. That clears the water and allows more sunlight to penetrate, fueling phytoplankton growth. Then the plankton die off, which facilitates microbial activity that converts mercury to methylmercury, the toxic form that accumulates in fish tissue.

"It just seems like the conditions for the methylation reaction are perhaps more important than having an actual point source in the watershed," Nafiz said.

The researchers were on the water during the spring high-flow season, and Nafiz said that the signs of runoff faded and the water cleared as they moved closer to the dam. Now researchers are waiting to see how clearly the contrast shows up in the data.

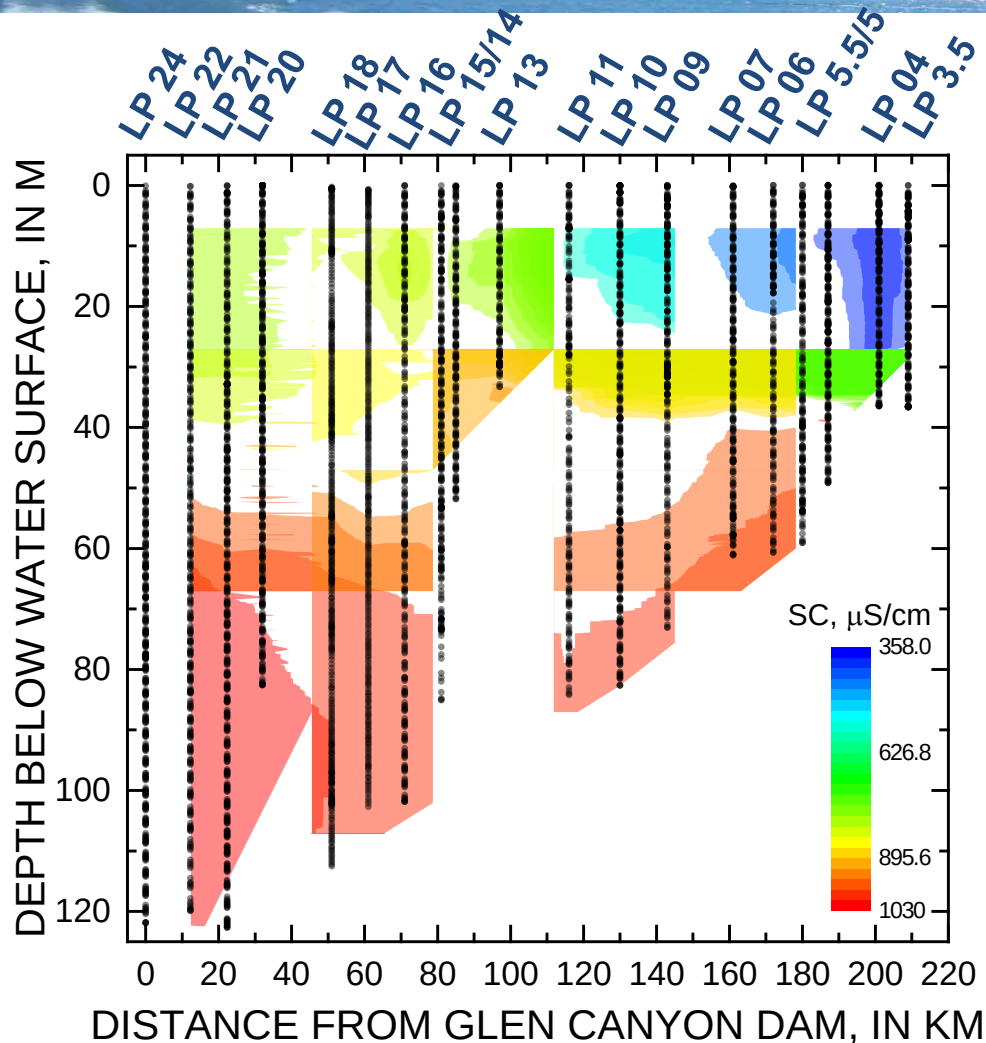
In the meantime, they're looking forward to a follow-up trip during the low-flow season in August 2015, even if being on the clock means tempering some enthusiasm over a Lake Powell houseboat adventure.

"The houseboat did have a water slide on it, but that was for emergency evacuations only," Nafiz said. ☺

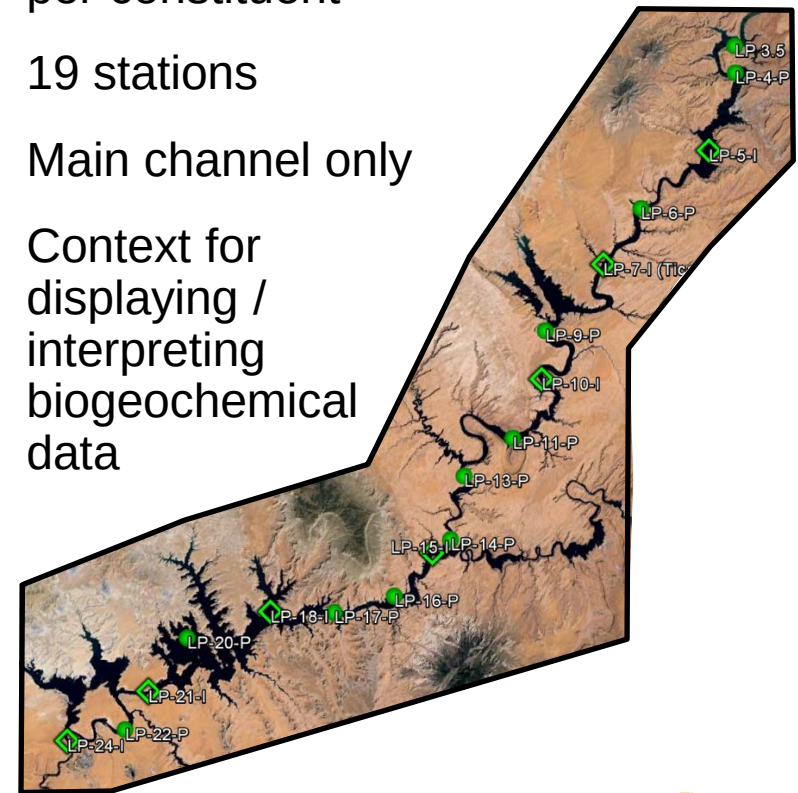


ENVIRONMENTAL MONITOR 43

VERTICAL CONTOUR MAPS

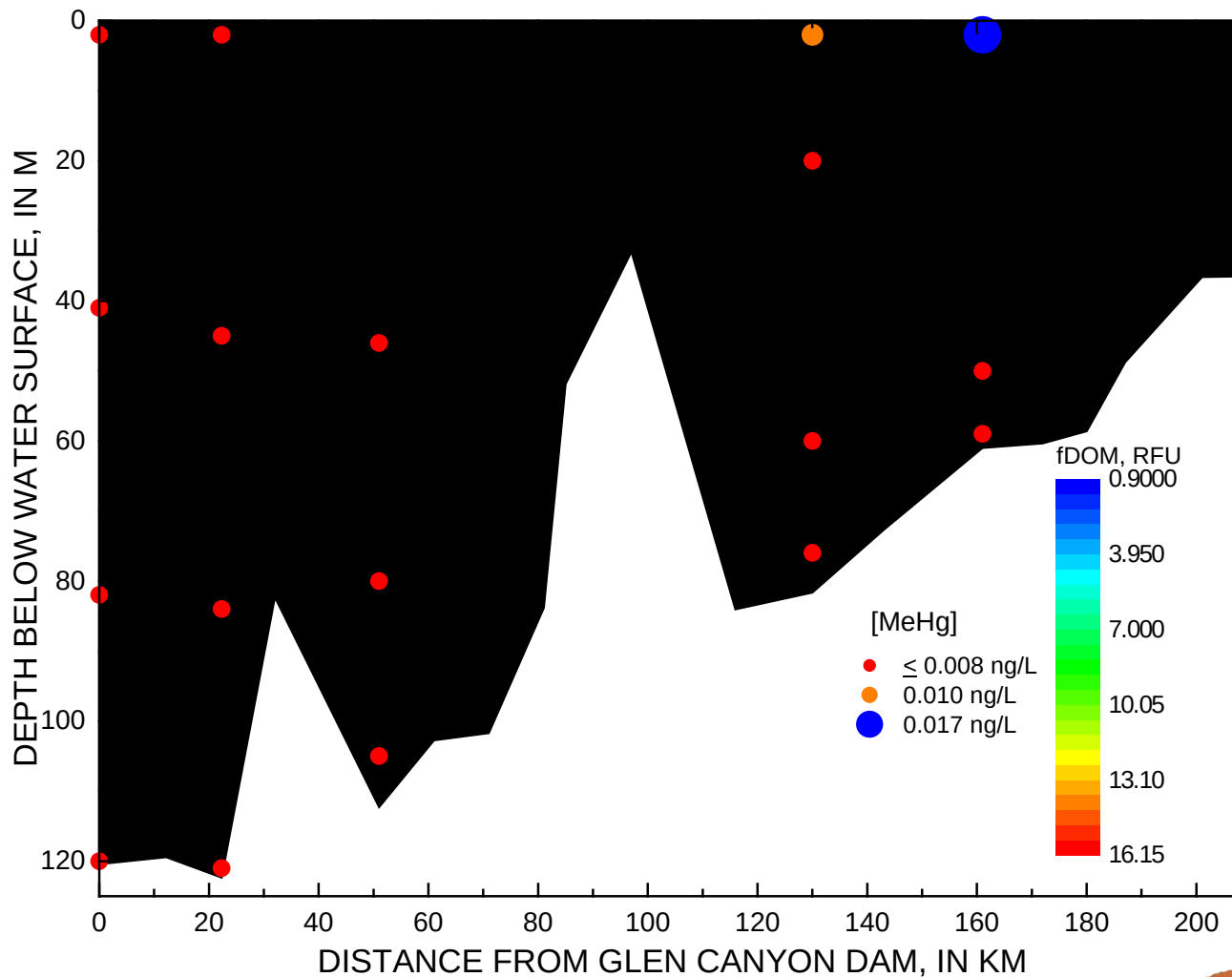


- ◆ ~ 5,700 data points per constituent
- ◆ 19 stations
- ◆ Main channel only
- ◆ Context for displaying / interpreting biogeochemical data

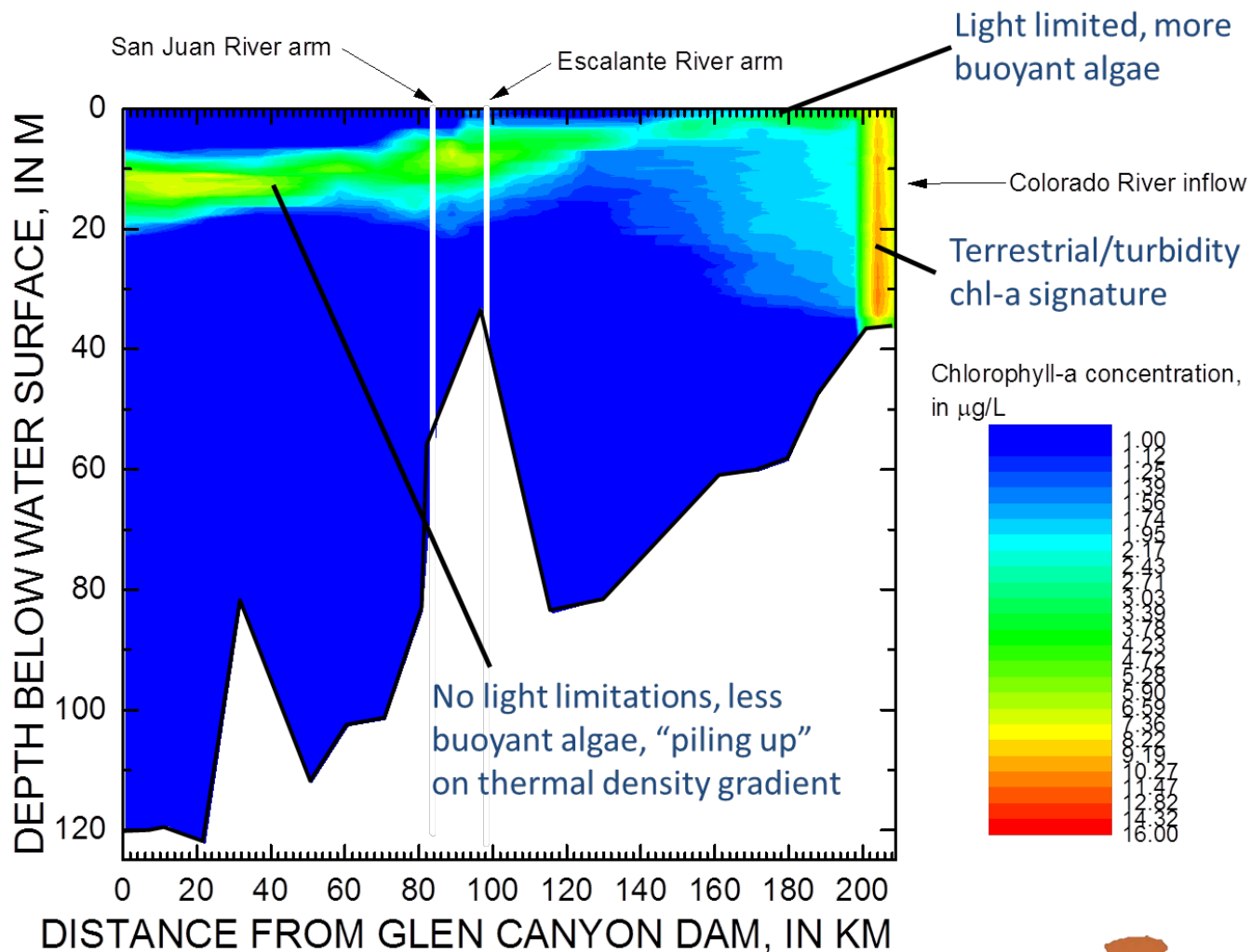


Lake Powell study team

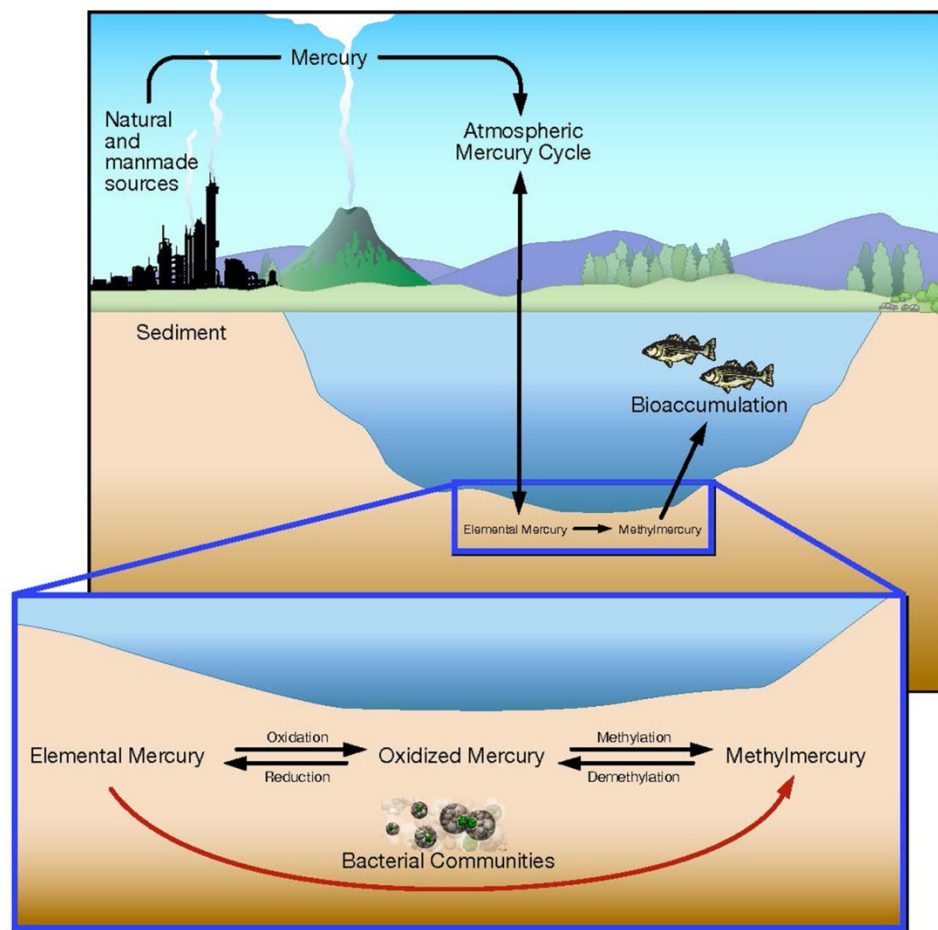
fDOM_{raw} VS [MeHg]



Chlorophyll



Sources and Methylation of Mercury



Oak Ridge National Laboratory website
<http://www.ornl.gov/ornl/news/news-releases/2013/ornl-research-reveals-new-challenges-for-mercury-cleanupfrom>

Research

- Ferredoxin
 - Iron-sulfur proteins that mediate electron transfers
- Cobalamin
 - Stabilize methyl transfer

Scienceexpress

The Genetic Basis for Bacterial Mercury Methylation

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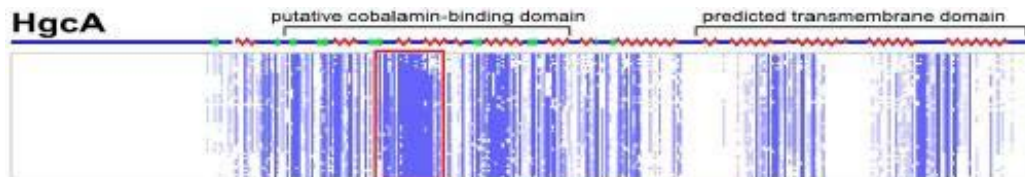
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Methylmercury is a potent neurotoxin produced in natural environments from inorganic mercury by anaerobic bacteria. However, until now the genes and proteins involved have remained unidentified. Here, we report a two-gene cluster, *hgcA* and *hgcB*, required for mercury methylation by *Desulfovibrio desulfuricans* ND132 and *Geobacter sulfurreducens* PCA. In either bacterium, deletion of *hgcA*, *hgcB* or both genes abolishes mercury methylation. The genes encode a putative corrinoid protein, HgcA, and a 2[4Fe-4S] ferredoxin, HgcB, consistent with roles as a methyl carrier and an electron donor required for corrinoid cofactor reduction, respectively. Among bacteria and archaea with sequenced genomes, gene orthologs are present in confirmed methylators but absent in non-methylators, suggesting a common mercury methylation pathway in all methylating bacteria and archaea sequenced to date.

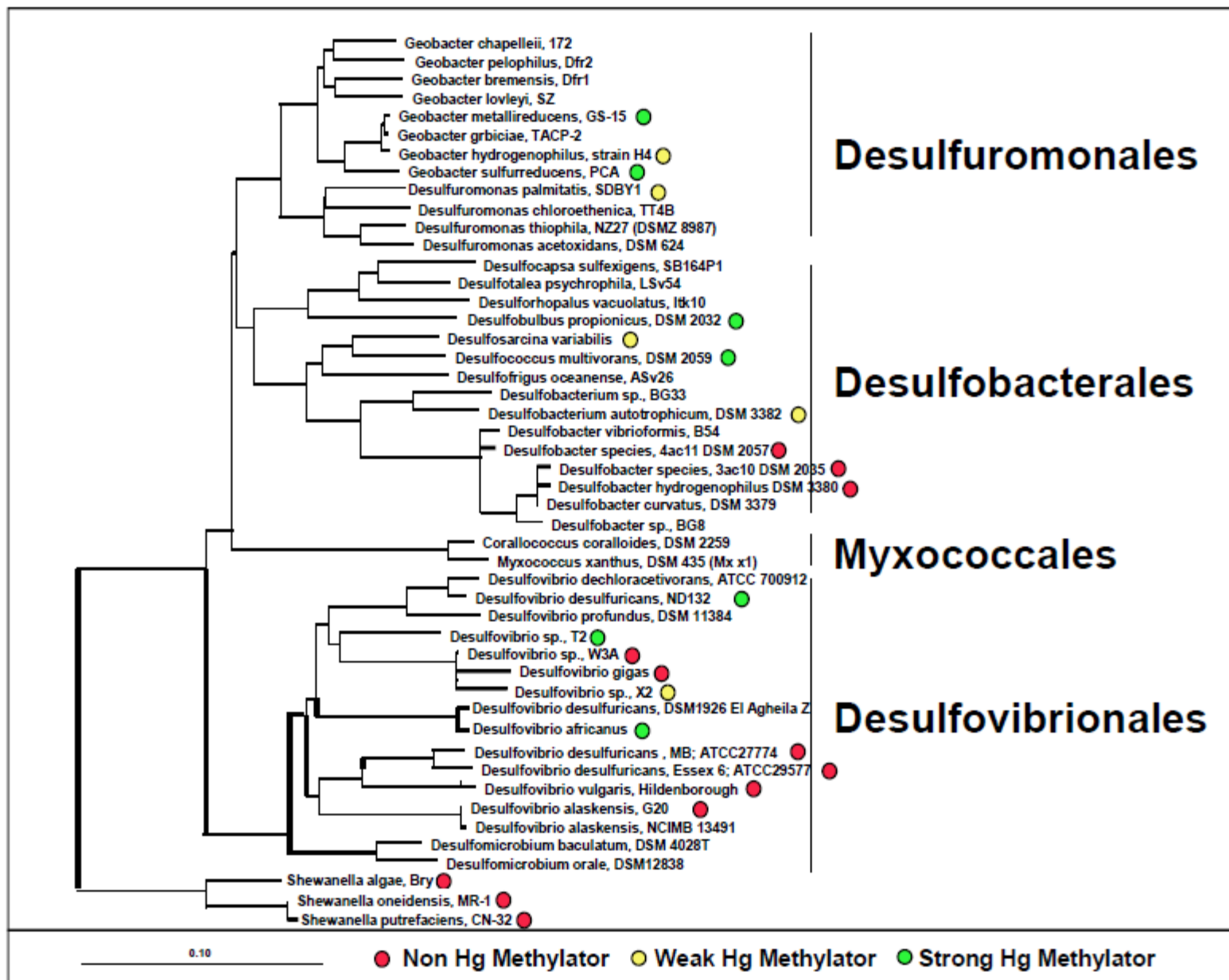
HgcA



HgcB

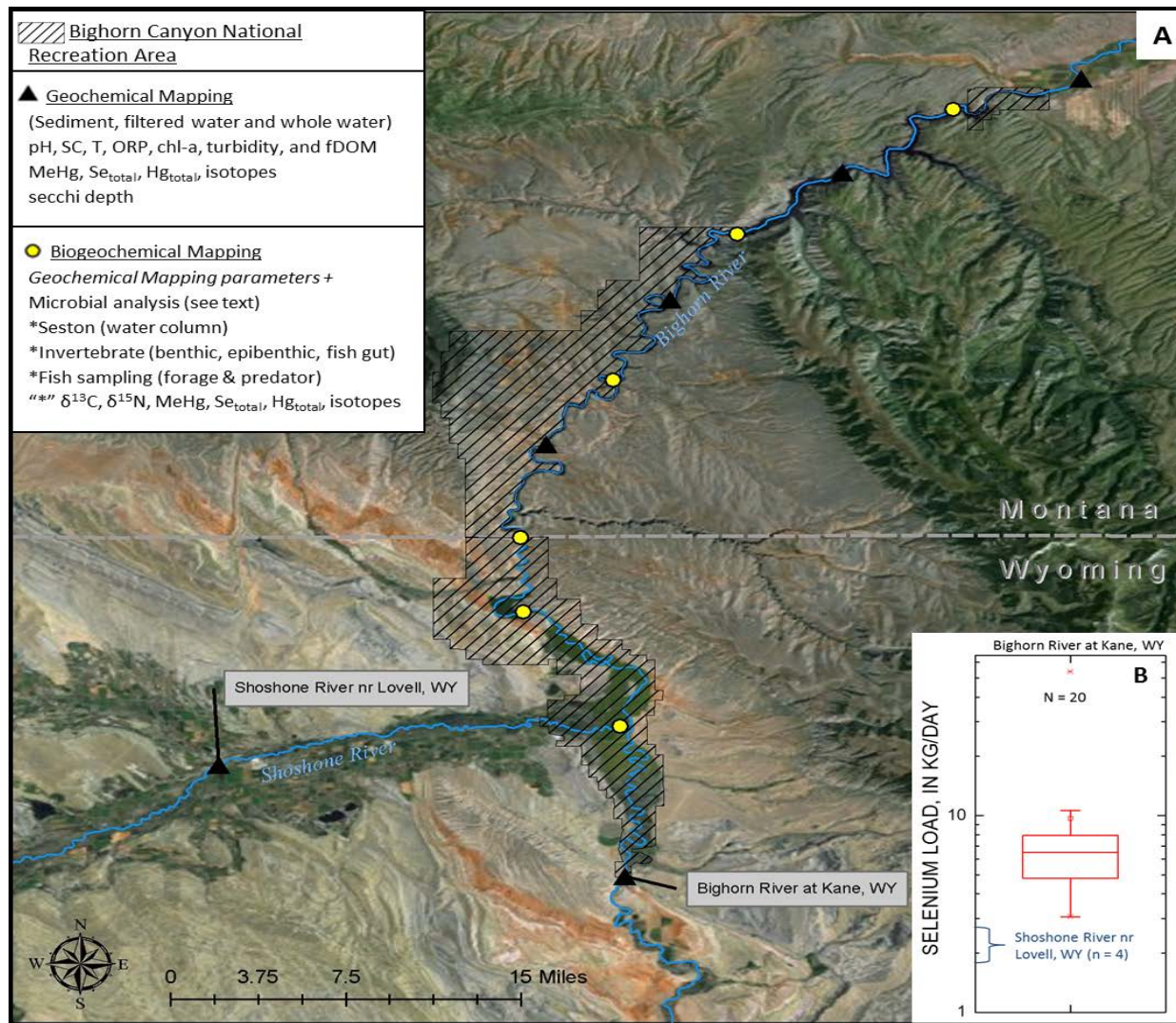


Proteobacteria	-	<i>Desulfotomicrobium desulfuricans</i> ND132	AWLVLVDTRGINVWCAAGKGLFTASEVA	CVGCGSCVDVCP	CMECGACARNCF	-CC
	-	<i>Desulfotomicrobium aestuarii</i> Asp-2	AWLVADTRGNIWCAAGKGLFTSEDEVA	CVGCGMCTATVCP	CMECGACARNCF	-CC
	-	<i>Desulfotomicrobium africanus</i> str. Walvis Bay	AWLVLDITKGYNVWCAAGKGTFTSAEIIIV	CACGGMCTVACP	CMECGACALNCF	-CC
	-	<i>Desulfotomicrobium baculum</i> X	LWLLVLTDRGINWCAAGKGTINAAGIA	CVGCGICATVCP	CMECGACALNCF	-CC
	-	<i>Desulfonatronosphaera thiodismutans</i> ASO3-1	CWLLVVEITYGNVWCAAGKQSNAAEIVA	CMGCGSCVDVCP	CMECGACALNCF	S00
	-	<i>Desulfonatronum lacustre</i> Z-7951	AWLVADTRGINVWCAAGKQSNAAEAVA	CVGCGCLCVAVCP	CMECGACALNCF	-CC
	-	<i>Desulfotomicrobium oxyhalinae</i> DSM 11498	VWLLVIDTRGINVWCAAGKSLSTDEVI	CVGCGMCLAVCP	CMECGACALNCF	G00
	-	<i>Desulfococcus propionicus</i> DSM 2032	AWLLVYDTRGINVWCAAGKGTFTWEVI	CIGCGICTTVCP	CMECGACARNCF	G00
	-	uncultured <i>Desulfobacterium</i> sp.	VWLLVLEITYGNVWCAAGKGTFTSQELV	CIGCGRCLEVCP	CMECGACALNCF	K00
	-	<i>Geobacter sulfurreducens</i> PCA	IWLLVLEITHGNVWCAAGKGTFTGDELIV	CVGCGMCVEVCP	CMECGACAVNCF	R00
	-	<i>Geobacter sulfurreducens</i> DL-1 KN400	IWLLVLEITHGNVWCAAGKGTFTGDELIV	CVGCGMCVEVCP	CMECGACAVNCF	R00
	-	<i>Geobacter metallireducens</i> GS-15	VWFLVLEIFDGINVWCAAGKGTFTGDELIV	CIGCGMCLAVCP	CMECGACAVNCF	G00
	-	<i>Geobacter metallireducens</i> RCH3	VWFLVLEIFDGINVWCAAGKGTFTGDELIV	CIGCGMCLAVCP	CMECGACAVNCF	G00
	-	<i>Geobacter</i> sp. duttonii FRC-32	VWLLVLEITHGNVWCAAGKGTFTGTELIV	CIGCGRCLEVCP	CMECGACARNCF	G00
	-	<i>Geobacter</i> sp. M18	VWLLVLEITYGNVWCAAGKGTFTGTELIV	CVGCGRCLEVCP	CMECGACALNCF	G00
	-	<i>Geobacter</i> sp. M21	VWLLVLEIFDGINVWCAAGKGTFTGDELIV	CVGCGRCLEVCP	CMECGACALNCF	G00
	-	<i>Geobacter uranireducens</i> R64	VWLLVLEIFDGINVWCAAGKGTFTGDELIV	CIGCGRCLEVCP	CMECGACAKNCF	G00
	-	<i>Geobacter hemidjensis</i> Blem	VWLLVLEIFDGINVWCAAGKGTFTGDELIV	CVGCGRCLEVCP	CMECGACALNCF	G00
	-	<i>Syntrophorhabdus aromaticivorans</i> Ull	GWILLVLDTLGINVWCAAGKGTFTGDELIV	CNCGICLTVCP	CIECGACARNCF	-CC
	Firmicutes	-	<i>Desulfomonile tiedjei</i> DCB-1	AWLVLDITOGYNVWCAAGKGTFTGDELIV	CSCCGMCLQVCP	CMECGACAKNCF
-		<i>Syntrophus aciditrophicus</i> SB	AWLVLDITNGINVWCAAGKGAFTGTEEVV	CIGCGMCLVCP	CIECGACARNCF	-CC
-		delta proteobacterium MLMS-1	AWLVLDITDGINVWCAAGKGSFOTANLV	CVGCGTGLEVCP	CMECGACMHNCF	S00
-		delta proteobacterium NaphS2	VWLLVLDITDGINVWCAAGKGTFTGTELIV	CVGCGMCLMVCP	CMECGACARNCF	G00
-		<i>Delfiaformosa carmini</i> S3R1	AWLVLDITWGYNVWCAAGKGTFTGDELIV	CVGCGLCETVCP	CMECGACARNCF	G0-
-		<i>Acetivibrio cellulolyticus</i> CD2	AWLVLDITRGYNVWCAAGKGTFTGTRIV	CKGCGRCLEVCP	CMECGACARNCF	G00
-		<i>Dehalobacter restrictus</i> DSM 9455	AWLVLDITKGYNVWCAAGKGTFTGTAELS	GTGCGRCLEVCP	CMECGACARNCF	G00
-		<i>Dehalobacter</i> sp. CF	AWLVLDITKGYNVWCAAGKGTFTGTAELS	GTGCGRCLEVCP	CMECGACARNCF	G00
-		<i>Dehalobacter</i> sp. DCA	AWLVLDITKGYNVWCAAGKGTFTGTAELS	GTGCGRCLEVCP	CMECGACARNCF	G00
-		<i>Dehalobacter</i> sp. FTH1	TWILLVLDITKGYNVWCAAGKGTFTGTELL	CTGCGKCIEVCS	CIECGACVNCF	S00
-		<i>Desulfatobacterium dehalogenans</i> ATCC 51507	TWILLVLDITKGYNVWCAAGKGTFTGTELL	CTGCGKCIEVCS	CIECGACVNCF	S00
-		<i>Desulfatobacterium dichloroelimians</i> LMG P-21439	TWILLVLDITKGYNVWCAAGKGTFTGTELL	CTGCGKCIEVCS	CIECGACVNCF	S00
-		<i>Desulfatobacterium metalloreducens</i> DSM 15288	TWILLVLDITKGYNVWCAAGKGTFTGTELL	CTGCGKCIEVCP	CMECGACVNCF	-CC
-		<i>Desulfatobacterium</i> PCE1 DSM 10344	AYIMVLDITKGYNVWCAAGKGTFTGTELL	CTGCGKCIEVCP	CIECGACVNCF	-CC
-		<i>Desulfosporosinus acidiphilus</i> SJ4	AWLVLDITKGYNVWCAAGKGTFTGTELL	CTGCGKCIEVCP	CIECGACVNCF	-CC
-		<i>Desulfosporosinus orientis</i> DSM 765	AWLVLDITKGYNVWCAAGKGTFTGTELL	CTGCGKCIEVCP	CMECGACVNCF	G00
-		<i>Desulfosporosinus</i> sp. OT	AWLVLDITKGYNVWCAAGKGTFTGTELL	CTGCGRCLEVCP	CMECGACVNCF	S00
-		<i>Desulfosporosinus youngiae</i> DSM 17734	AWLVLDITKGYNVWCAAGKGTFTGTELL	CTGCGRCLEVCP	CMECGACVNCF	S00
-		<i>Elithanlogenens herbinense</i> YUAN-3	AWLVLDITKGYNVWCAAGKGTFTGTELL	CTGCGMCLNVCP	CMECGACAKNCF	N00
Euryarchaeota		-	<i>Syntrophobacillus glycolicus</i> DSM 8271	CWLLVLDITKGYNVWCAAGKGTFTGDELIV	CVGGERCTVCP	CMECGACAMNCF
	-	<i>Dethiobacter alkilophilus</i> AHT 1	LWILLVLDITRGYNVWCAAGKGTFTGTAELI	CSCGRLCTVCP	CMECGACARNCF	- - -
	-	<i>Acetoneema longum</i> DSM 6540	LWILLVLDITRGYNVWCAAGKGTFTGDELIV	CIGCGMCLNVCP	CMECGACAQNCF	S00
	-	<i>Methanohalobius limnatis</i> GKZPZ	GYILLVLDITRGYNVWCAAGKGTFTGDEVV	CINCRRCLEVCP	CMECGACARNCF	S00
	-	<i>Methanoregula boonei</i> BAB	AWLVLDITKGYNVWCAAGKGTFTGTELL	CINCRRCLEVCP	CMECGACAKNCF	S00
	-	<i>Methanoregula formicum</i> SMSP	AWLVLDITKGYNVWCAAGKGTFTGTELL	CINCRRCLEVCP	CMECGACAKNCF	S00
	-	<i>Methanomassiliicoccus luminyensis</i> B10	GYILLVLDITKGYNVWCAAGKGTFTGTELL	CVNGCGRSEVCP	CMECGCGMNCF	-CC
	-	<i>Methanopyrus aerophilus</i> pabstii F 1-Ac	VYILLVLDITRYNWCAAGKGTFTGDELIV	CVNGCGRSEVCP	CMECGACVNCF	-CC
	-	<i>Methanospirillum hungatei</i> JF-1	AYILLVLDITKGYNVWCAAGKGTFTGTELL	CINCRRCLEVCP	CMECGACALNCF	S00
	-	<i>Methanolobus tindarius</i> DSM 2278	CYILLVLDITKGYNVWCAAGKGTFTGDELIV	CINCLMCTNVCP	CMECGACAGNCF	G00
	-	<i>Methanomethylotrophicus hollandica</i> DSM 15078	GYILLVLDITKGYNVWCAAGKGTFTGTELL	CINCLRCTHVCP	CMECGACARNCF	S00
	-	<i>Methanolobus psychrophilus</i> R15	CYILLVLDITKGYNVWCAAGKGTFTGTELL	CINCLRCTHVCP	CMECGACVNCF	S00
-	<i>Methanocella arroyensis</i> MRE50 RC-I	CYILLVLDITRYGNVWCAAGKGTFTGDELIV	CVGCGMCLNVCP	CMECGACALNCF	-CC	
-	<i>Methanocella paludicola</i> SANAE	CYILLVLDITKGYNVWCAAGKGTFTGTELL	CTGCGMCLNVCP	CMECGACALNCF	G00	



(Parks et al., 2013)

Investigating MeHg Sources



Effect of Investigating Management Strategies on Activity

