Methanogens: principal methylators of mercury in lake periphyton

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Table S1 Physico-chemical proprieties of the water at Girodeau station

Phytoplankton biomass $mg.L^{-1}$	3.98-13.22
% light penetration	5.26-50.00
pH	7.45-8.09
DOC $mg.L^{-1}$	4.89-5.82
NO_3 $mg.L^{-1}$	0.15-0.94
TP $mg.L^{-1}$	0.04-0.06
SO_4 $mg.L^{-1}$	13.16-20.70
THg $ng.L^{-1}$	0.36-3.3
MeHg $ng.L^{-1}$	0.05-0.30
T^oC	21.6-23.2
O2 $mg.L^{-1}$	7.43-12.88

Figure S1 Supplementary informations for water samples collection and analysis

Water samples for THg and MeHg were collected in duplicate and stored in Teflon bottles that had previously been acid-washed and thoroughly rinsed with ultrapure water. Preservation was assured by adding 0.4% ultraclean hydrochloric acid and samples were kept in the dark and refrigerated (4°C) until analysis. Analysis were carried out using an automated Tekran 2600 following U.S. Environmental Protection Agency method 1631.

Samples of all other analytes were collected in duplicate in Nalgene HDPE bottles. DOC, NO3 and SO4 were determined in filtered samples using 0.45 μm polyethersulfone (PES) membranes. Colorimetric method following potassium persulfate oxidation at 120°C was used to measure TP (Astoria 2; MDL: 0.2 µg L-1). The DOC concentration was measured by high-temperature combustion on a platinum catalyst using a Shimadzu TOC-5000 Analyser (MDL: 0.10 mg L-1). NO3 was measured by an auto-sampler (Lachat, FIA) with respective MDLs of 5 and 1 µg L-1. SO4 was analysed by ion chromatography using a DIONEX-DX500 (MDLs: 0.05 and 0.03 mg L-1 respectively).

Table S2: Clones representing active Bacteria and Archaea in periphyton samples from MHg/DHg incubations with and without metabolic inhibitors. Bacterial clones were obtained from bacterial library with primers 27f/519r and archaeal clones were obtained from archaeal library with primers 344f/ 907r.

Treatment	Clone	Most similar to the 16S rRNA gene of (% identity)	Lineage: kingdom, order, family
Control	LSP_periphyton_1	*Streptococcus sp.,* (98%)	Bacteria, Lactobacilliales, Streptococcaceae
	LSP_periphyton_2	*Neisseria sp.,* (99%)	Bacteria, Neisseriales, Neisseriaceae
	LSP_periphyton_3	*Halobacterium sp.,* (99%)	Archaea, Halobacteriales, Halobacteriaceae
	LSP_periphyton_4	*Streptococcus sp.,* (99%)	Bacteria, Lactobacilliales, Streptococcaceae
	LSP_periphyton_5	*Acidobacteria sp*., (98%)	Bacteria, Acidobacteriales, Acidobacteriacea
	LSP_periphyton_6	*Actinomycetales* (99%)	Bacteria, Actinomycetales
	LSP_periphyton_7	*Oscillatoria sp*., (99%)	Bacteria, Oscillatoriales, Oscillatoriaceae
	LSP_periphyton_8	*Oscillatoria sp*., (99%)	Bacteria, Oscillatoriales, Oscillatoriaceae
	LSP_periphyton_9	*Actinomycetales* (99%)	Bacteria, Actinomycetales
BESA	LSP_periphyton_10	*Actinomycetales* (99%)	Bacteria, Actinomycetales
	LSP_periphyton_11	*Methanococcales* (98%)	Archaea, Methanococcales
	LSP_periphyton_12	*Francisella sp.,* (100%)	Bacteria, Thiotricales, Francisellaceae
	LSP_periphyton_13	*Actinomycetales* (98%)	Bacteria, Actinomycetales
	LSP_periphyton_14	*Alishewanella sp.,* (97%)	Bacteria, Enterobacteriales, Enterobacteriaceae
	LSP_periphyton_15	*Methanobacteriales* (98%)	Archaea, Methanobacteriales
	LSP_periphyton_16	*Methanosarcinales* (97%)	Archaea. Methanosarcinales
	LSP_periphyton_17	*Actinomycetales,* (98%)	Bacteria, Actinomycetales
	LSP_periphyton_18	*Neisseria sp.,* (99%)	Bacteria, Neisseriales, Neisseriaceae
	LSP_periphyton_19	*Sphingomonas sp.*, (99%)	Bacteria, Sphingomonadales, Sphingomonadaceae
Molybdate	LSP_periphyton_20	*Vogesella sp.* (98%)	Bacteria, Neisseriales, Neisseriaceae
	LSP_periphyton_21	*Ideonella sp.,* (98%)	Bacteria, Burkholderiales, Comamonadaceae
	LSP_periphyton_22	*Pseudomonas sp.,* (98%)	Bacteria, Pseudomonadales, Pseudomonadaceae
	LSP_periphyton_23	*Francisella sp.,* (100%)	Bacteria, Thiotricales, Francisellaceae
	LSP_periphyton_24	*Escherichia coli* ,(99%)	Bacteria, Enterobacteriales, Enterobacteriaceae
	LSP_periphyton_25	*Corynebacterium sp.,* (100%)	Bacteria, Actinomycetales, Corynebacteriaceae
	LSP_periphyton_26	*Exiguobacterium sp.,* (98%)	Bacteria, Bacilliales, Bacilliaceae
	LSP_periphyton_27	*Methanobacteriales* (98%)	Archaea, Methanobacteriales
	LSP_periphyton_28	*Methanococcales,* (99%)	Archaea, Methanococcales
	LSP_periphyton_29	*Neisseriaceae* (98%)	Bacteria, Neisseriales, Neisseriaceae
	LSP_periphyton_30	*Actinomycetales,* (100%)	Bacteria, Actinomycetales
	LSP_periphyton_31	*Neisseria sp.,* (98%)	Bacteria, Neisseriales, Neisseriaceae

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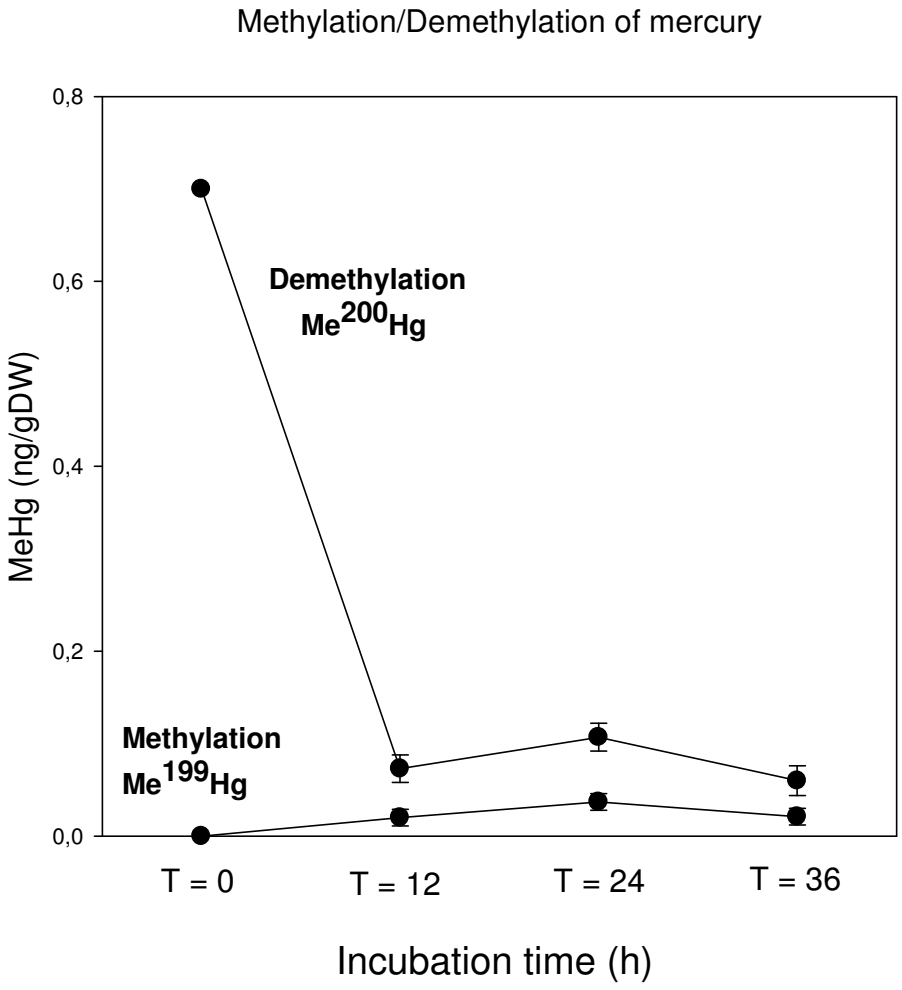

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3 Figure S2: Course of isotopic MeHg during 48h methylation/demethylation incubation using $Me^{200}Hg$ and $Me^{199}Hg$

Table S3 Mean mercury methylation and demethylation rates following 48h incubation with and without addition of metabolic inhibitors

Treatment	Mean Km ± Std error (in d^{-1})	Mean Kd ± Std error (in d^{-1})
Control	0.0017 ± 0.0002	0.1873 ± 0.0301
DCMU	0.0008 ± 0.0001	0.1650 ± 0.0310
BESA	nd	0.1949 ± 0.0269
Chloramphenicol	0.0007 ± 0.0003	0.1500 ± 0.0363
Molybdate	0.0753 ± 0.0031	nd