Polar microbes and their implications in the aquatic mercury cycle

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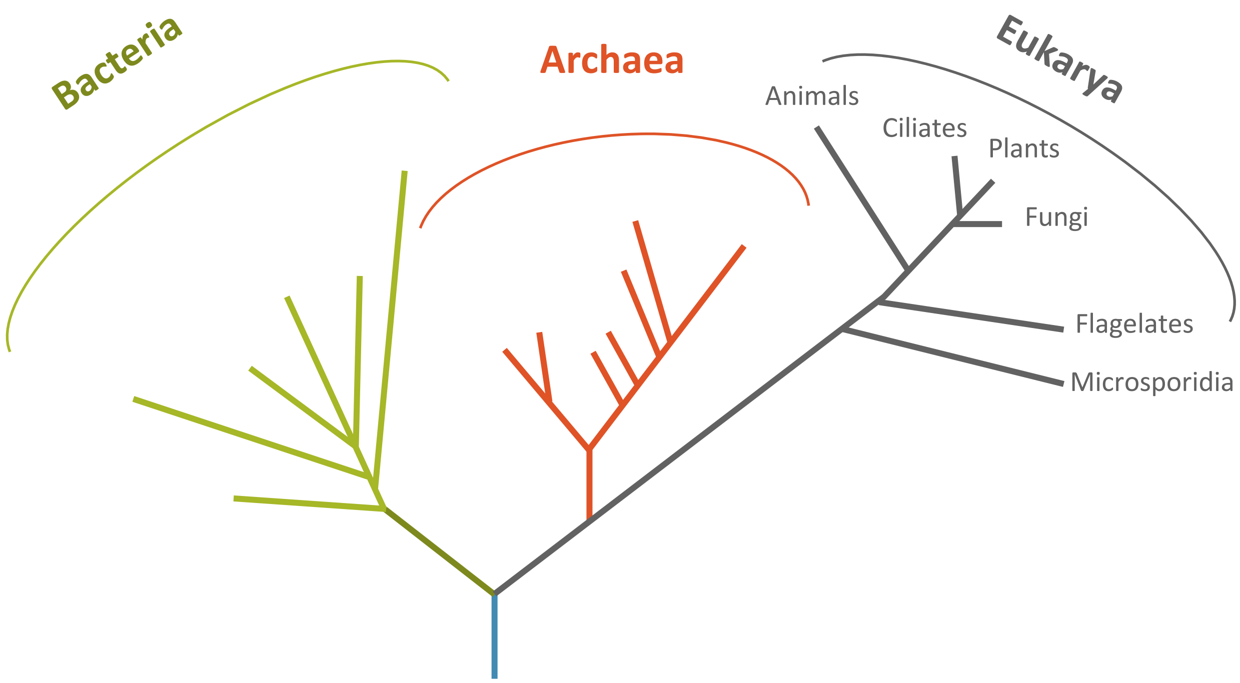
Microorganisms and Hg cycle

Microorganisms able to methylate or demethylate mercury are widespread in the tree of life – among Bacteria and Archaea domains



Woese et al (1990)

Chemotrophic transformation processes of Hg

Hg Methylation

- SRB: sulfate-reducing bacteria
- IRB: iron-reducing bacteria
- Methanogenic Archaea
- *Firmicutes*
- Putatively: *Nitrospirae, Chloroflexi, Phycisphaerae, Aminicenantes, Spirochaetes* and *Elusimicrobia*

With experimental proof (SRB, IRB, Methanogenic Archaea)

Harboring hgcA/B genes (*Firmicutes* and putative groups)

Demethylation

- SRB: sulfate-reducing bacteria
- Methanogenic Archaea

(*Grégoire & Poulain, 2018; Gionfriddo et al., 2020, Villar et al., 2020*)

In polar environments?

Antartic

- Still isolated from the majority of anthropic sources 
- Low organic matter content in soils and sediments

Sub-Antarctic beaver ponds

- Low anthropic impact

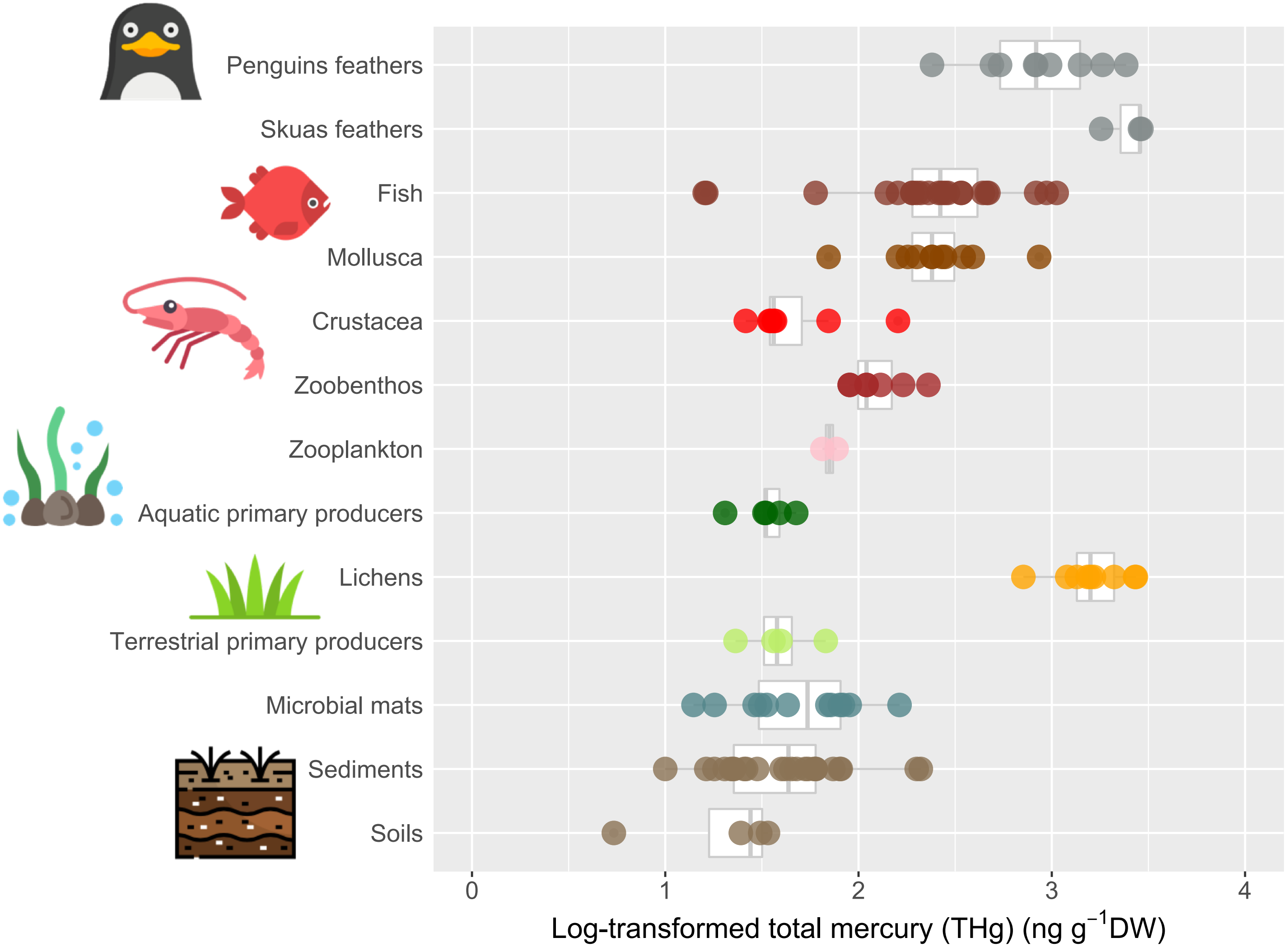
Why studying mercury cycle there?

- Natural processes (volcanism)
- Storage of Hg in ice and release during melting season
- long-range atmospheric transport (Equator-polar)

- High organic matter content in pond sediments
- Contaminants can be trapped with organic matter before the dam

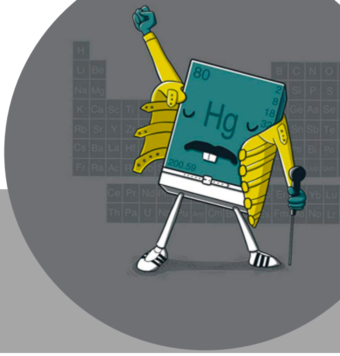
(Perez-Rodriguez et al., 2019)

Mercury in the trophic webs of Antartica



Similar values in Arctic *(Braune et al., 2015)*

References used in the plot: Bargagli et al., 1993; Niemistö and Perttilä 1995; Sun et al., 2000; Favaro et al., 2004; Riva et al., 2004; Bargagli et al., 2005; dos Santos et al., 2006; Negri et al., 2006; Nie et al., 2012; Zverina et al., 2014; Calle et al., 2015; Camacho et al., 2015; Zheng et al., 2015



Objective

Explore and compare the concentrations of total mercury in aquatic ecosystems of King George Island (Antarctic Peninsula) and Tierra del Fuego (Chile) and identify sites with highest mercury methylation potential

Studied sites

Antartic aquatic systems

AK - Kitiesh Lake

P - Ardley Island

ALB - Fildes Bay

Sub-Antarctic beaver ponds

BP4 – Karukinka Park

BP1

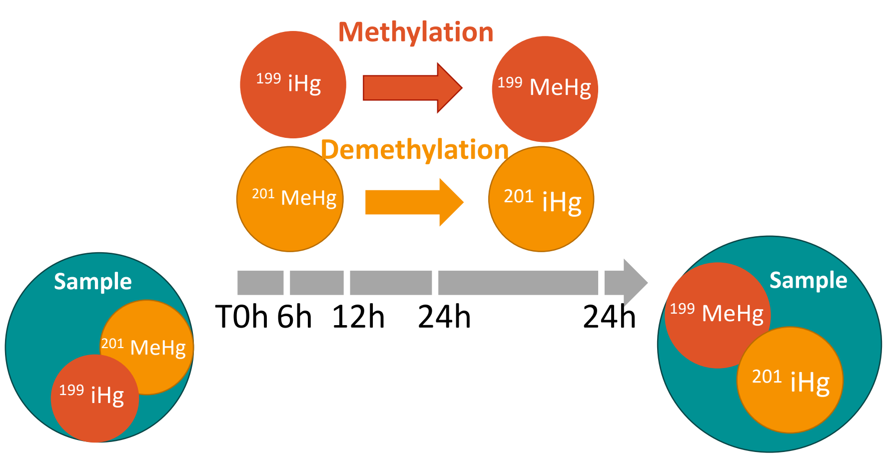
Mercury measurement procedures

Sediments

- **Total mercury**: CV-AAS (US EPA, Method 7473, 2007; AMA LECO 254)

Water

- **Total mercury:** CV-AFS, Brooks Rand Model III, USA
- **Methylmercury**: isotope dilution (ID) applied to a high sensitivity coupled gas chromatography – sector field ICP-MS (GC-SF-ICP-MS) method (*Heimbürger et al., 2015)*
- **Mercury Methylation/Demethylation rates:** kinetics in microcosms, using species specific isotope dilution (ID) gas chromatography – sector field ICP-MS (GC-SF-ICP-MS) *(Lehnherr et al., 2011; Rodriguez-Gonzalez et al., 2013)*



Microbial diversity

DNA extraction

PowerSoil (QIAGEN)

PowerWater (QIAGEN)

Library preparation

V4-V5 region of the 16S rRNA gene

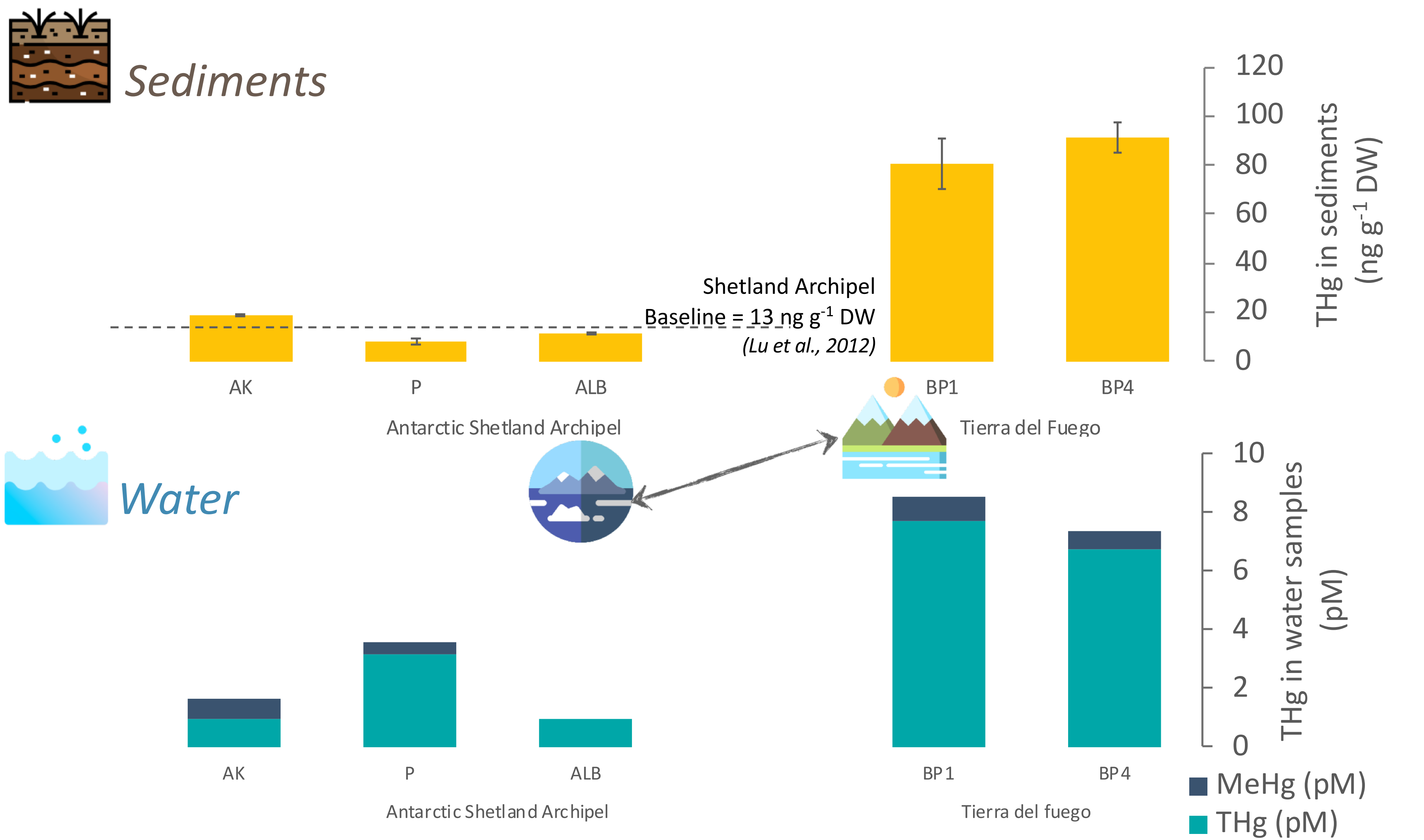
High throughput sequencing

Illumina MiSeq (Genotoul, France)

Bioinformatic analysis using QIIME pipeline

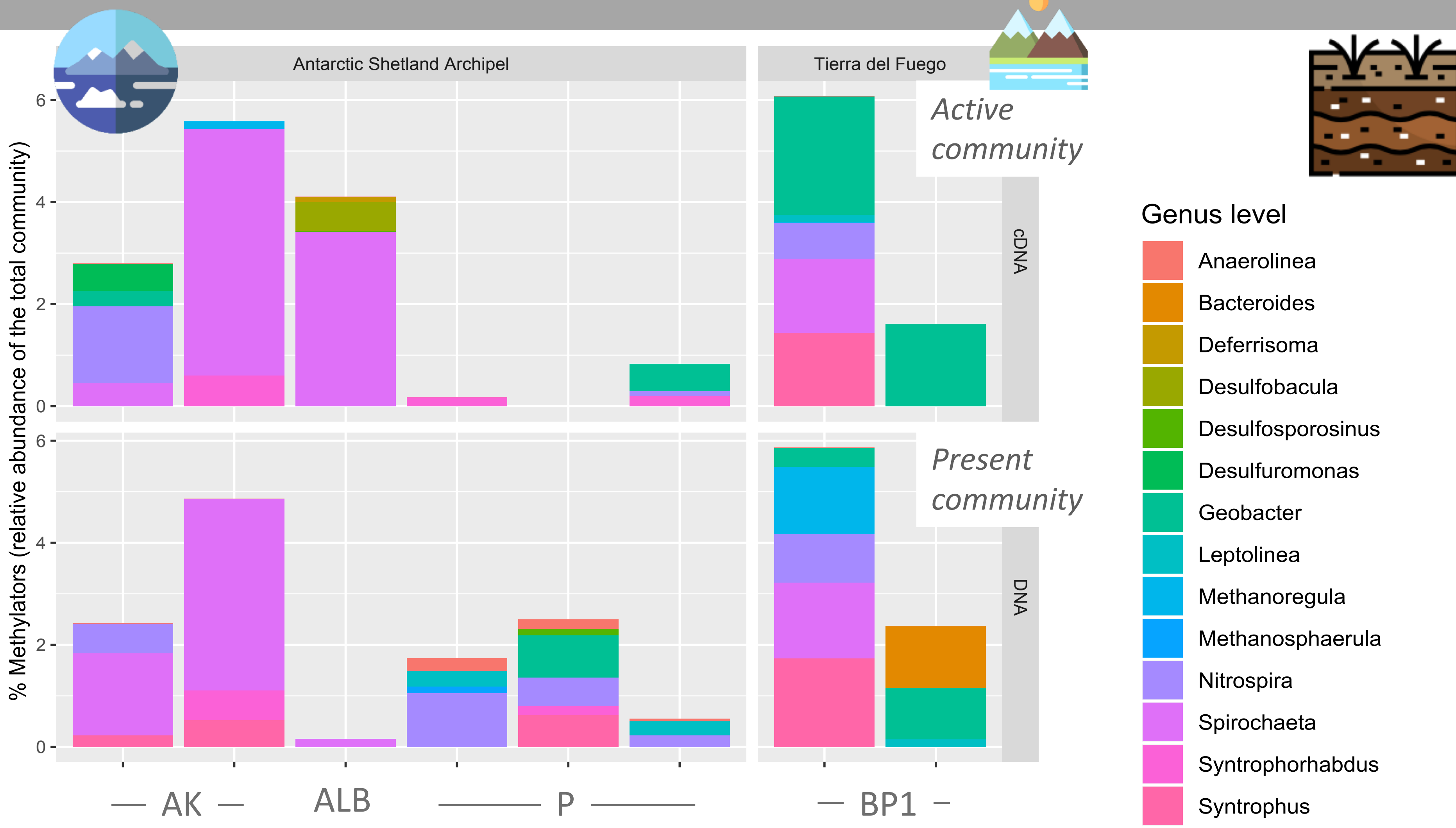
+ multivariate analysis with R

Total mercury in both Antarctic and sub-Antarctic ecosystems



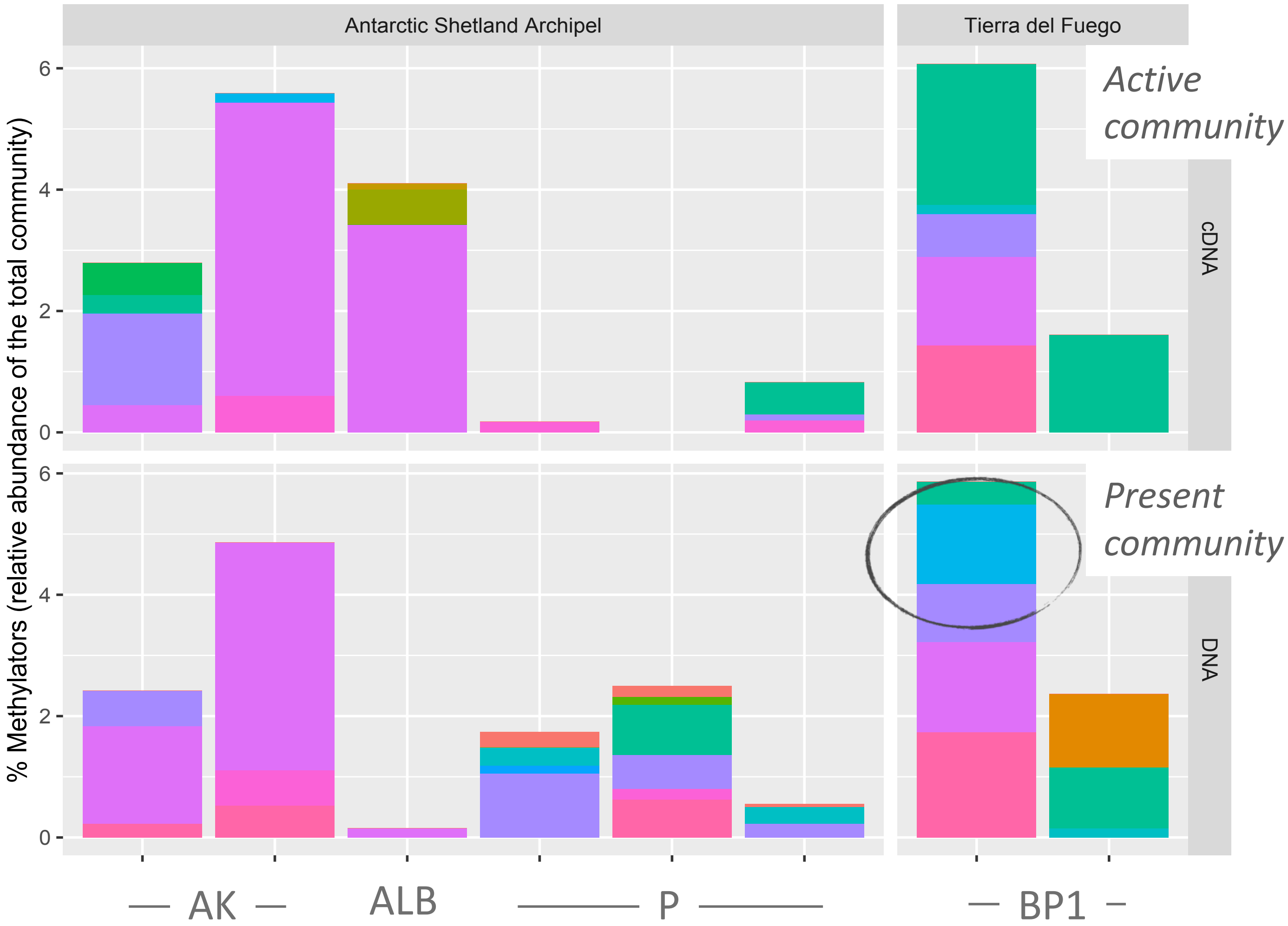
Beaver pond sediments contained > 6-times more total mercury than Antarctic ones. In water, until 29% of total mercury was methylmercury in the Antarctic Kitiesh lake.

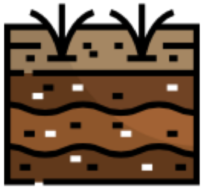
Diversity of putative methylating microorganisms

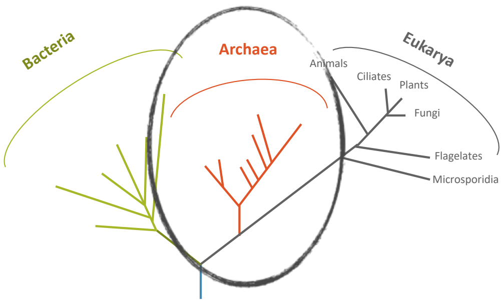


Methylating bacteria and archaea represented until 6.1% and 5.9% of the total microbial community active and present, respectively.

Diversity of putative methylating microorganisms







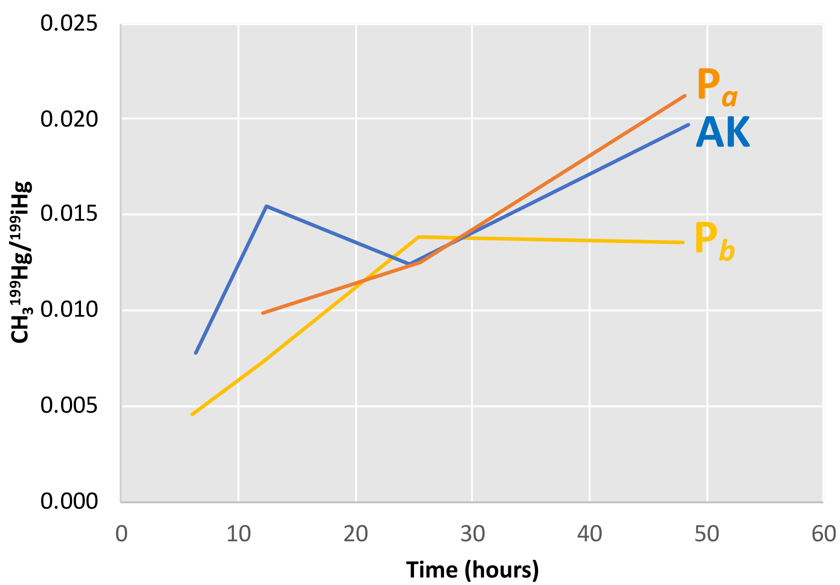
Putative mercury methylating methanogenic archaea *Methanoregula* and *Methanosphaerula* were present in the beaver pond sediments but not active.

Mercury methylation rates in water

In water from Antarctic pond and lakes, while less than 1% of microbial communities are putative methylating microorganisms (i.e. mainly *Nitrospira* and *Bacteroidetes),* mercury methylation is still detected at high levels

AK - Kitiesh Lake

Km (d^{-1})= 0.021 ±0.012

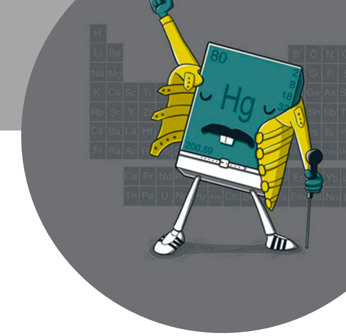


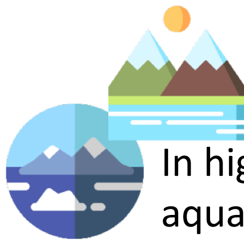
P - Ardley Island

Km (d^{-1})= 0.014 ±0.004

Km estimated following Monperrus et al., 2007

Conclusions





In high-latitude aquatic systems

Methylating bacteria and archaea are present and potentially active in sediments

Hg

Between 10 and 29% of total mercury in water is methylmercury

Hg(II) → MeHg

Methylation occurred in high-latitude waters at rates comparable to low-latitude marine waters

! Necessity to improve our knowledge on microbial mercury dynamics

CONICYT
Ministerio de Educación
Gobierno de Chile

INACH

INACH RT-14-15 (2016-2018)

ECA54-ECA55

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Fernanda Rodriguez

Lars-Eric Heimbürger-Boavida
Marie-Maëlle Desgranges
Aurélie Dufour
Malo Bernard

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