



# Targeting mercury bioremediation of marine sediments by using *omics* and culture-driven approaches

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**MER-CLUB**

Mercury clean-up system  
based on bioremediation  
by marine bacteria



Anders Lanzén



Silvia G. Acinas



Olga Sánchez



David  
Amouroux



Ulrich Soltmann



Stefan Bertilsson





## MER-CLUB

Mercury clean-up system  
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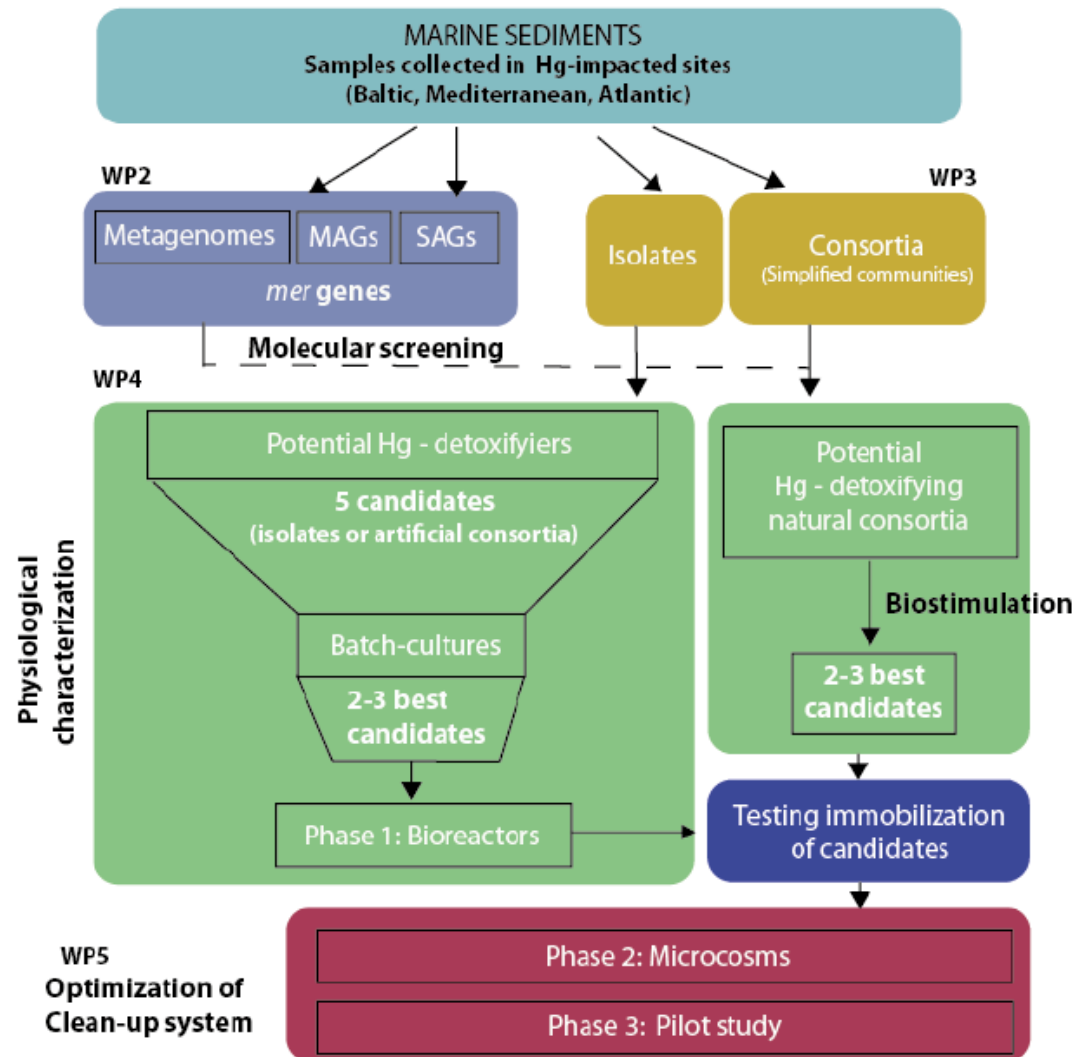
The **objective** of MER-CLUB is to **advance our understanding of mercury biogeochemistry in marine sediments** and design a novel **bioremediation solution** for this complex environmental matrix.



# MER-CLUB

Mercury clean-up system based on bioremediation by marine bacteria

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WHICH BACTERIA ARE INVOLVED IN MERCURY TRANSFORMATION IN MARINE POLLUTED SEDIMENTS?



ISOLATION AND PHYSIOLOGICAL CHARACTERIZATION IN LABORATORY CULTURES



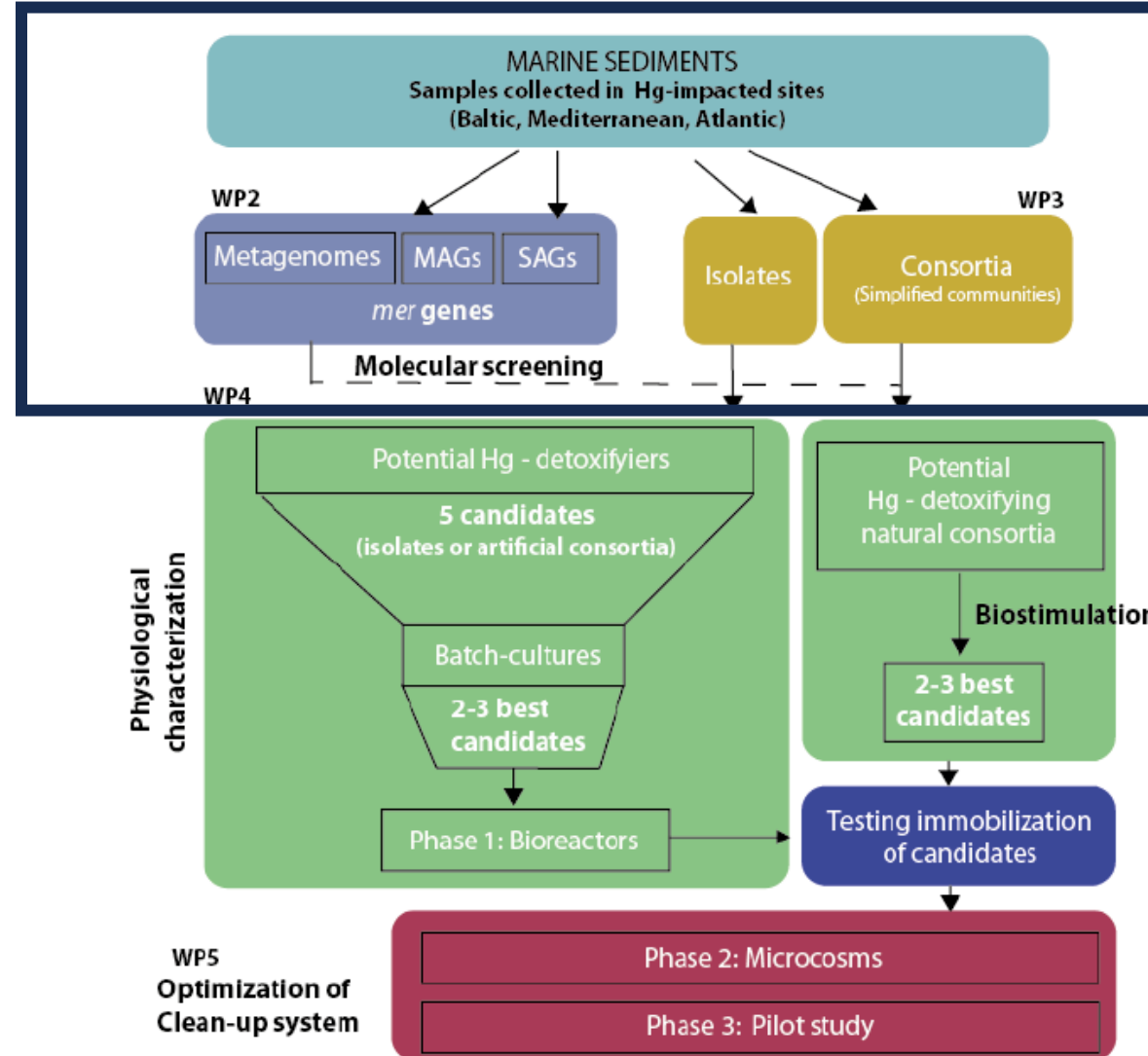
UP-SCALING



# MER-CLUB

Mercury clean-up system based on bioremediation by marine bacteria

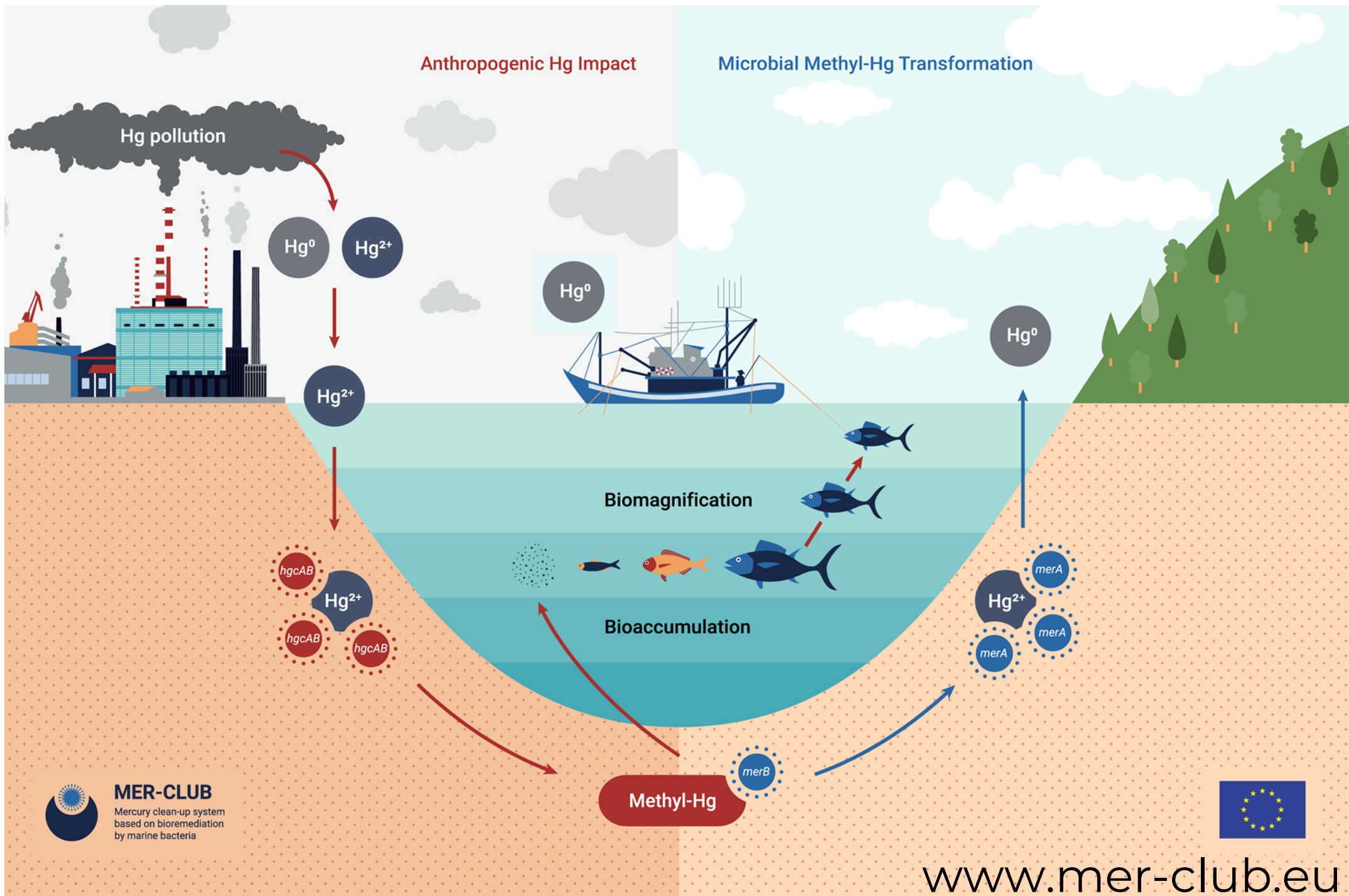
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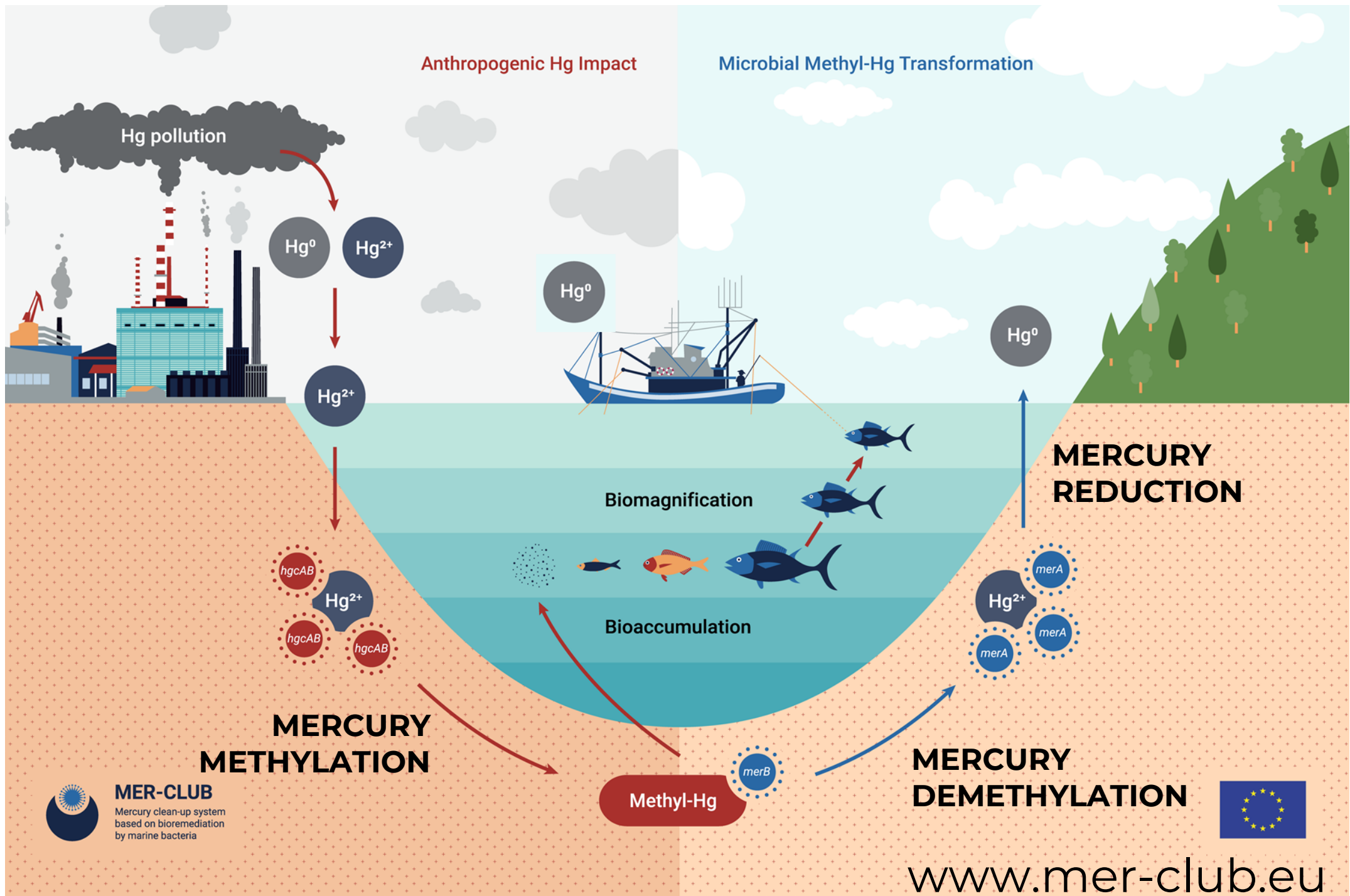


**WHICH BACTERIA ARE INVOLVED IN MERCURY TRANSFORMATION IN MARINE POLLUTED SEDIMENTS?**

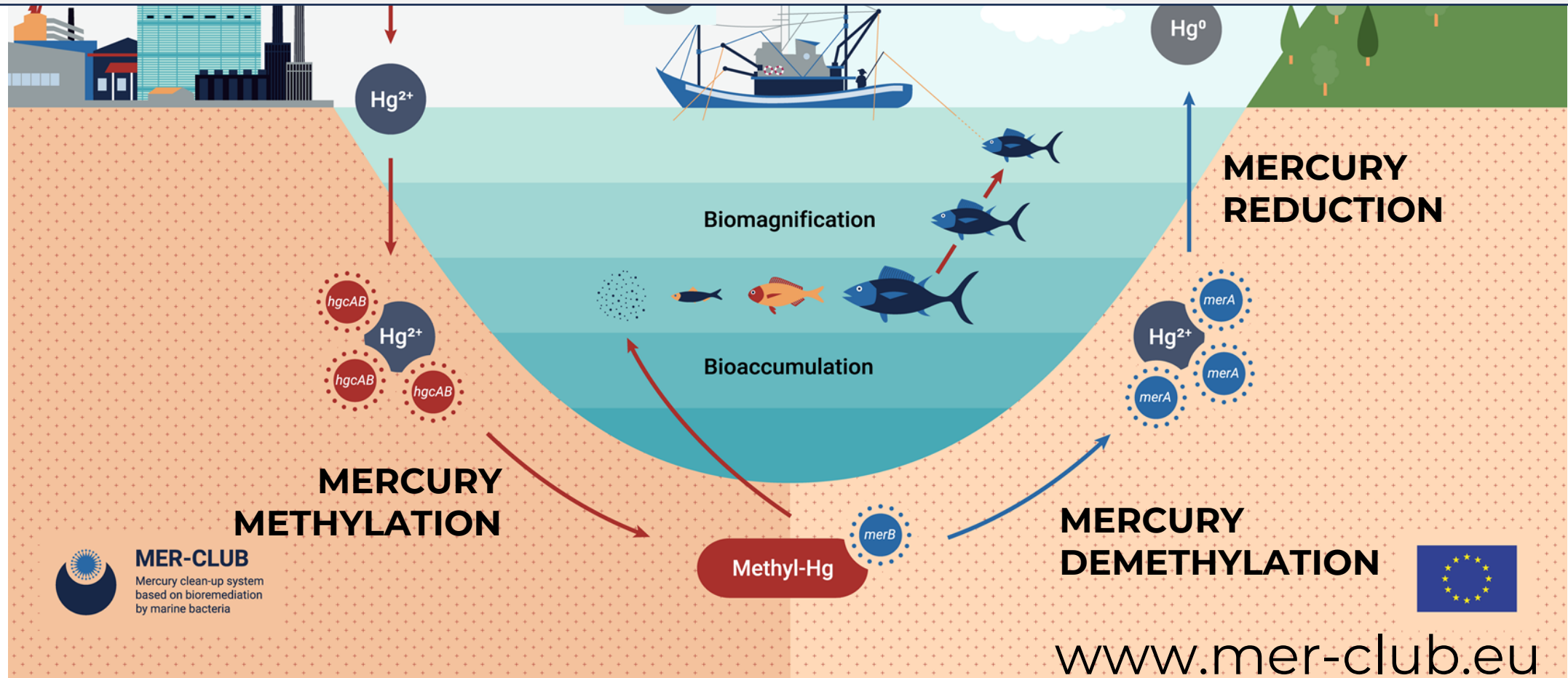
Anthropogenic Hg Impact

Microbial Methyl-Hg Transformation





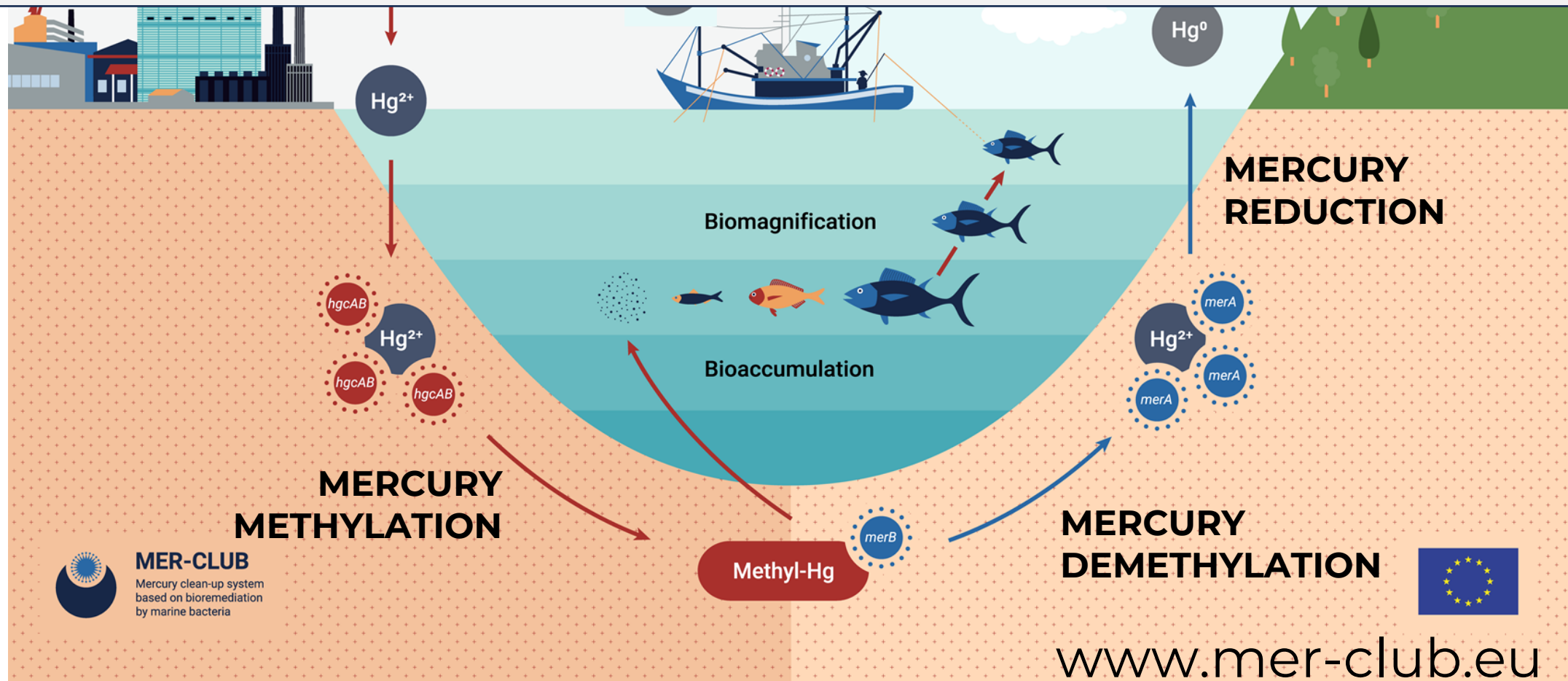
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Identification of bioindicators of Hg pollution



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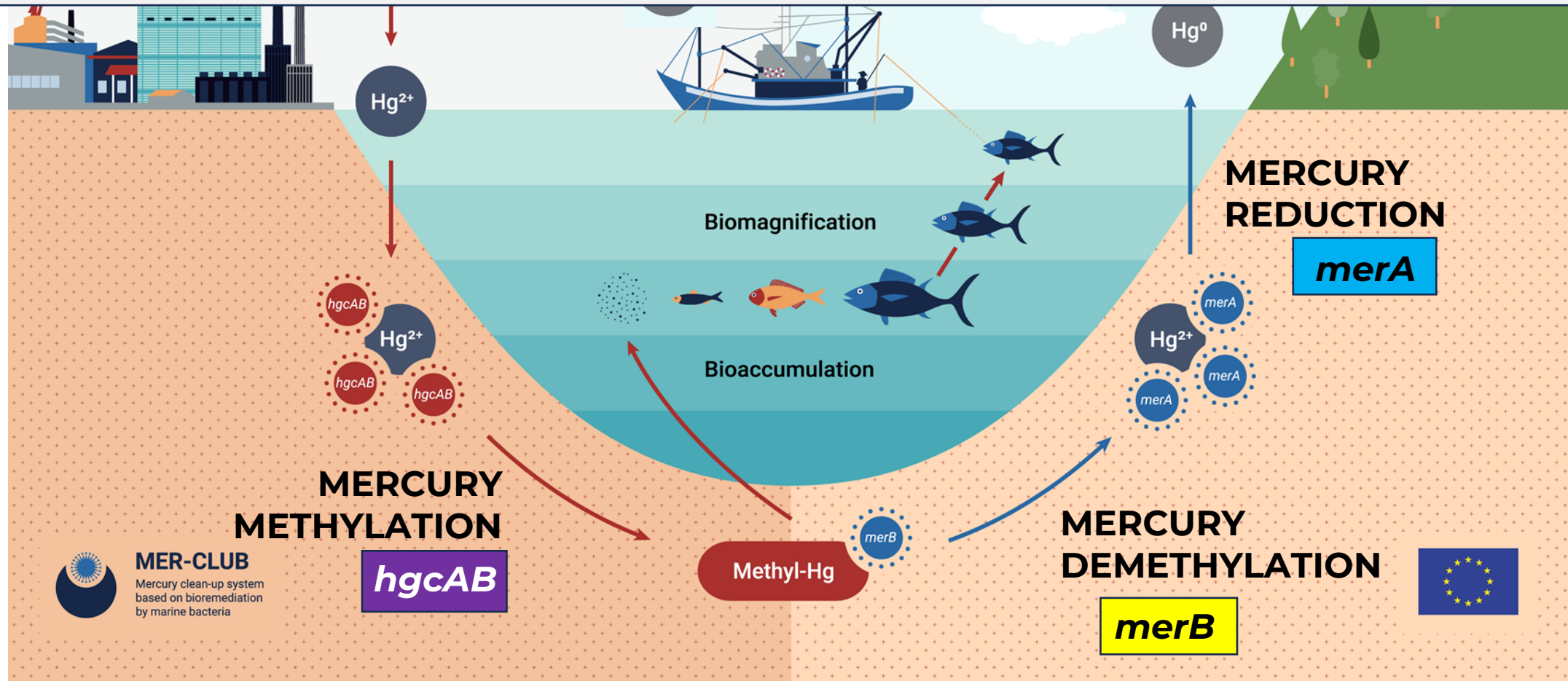
Identification of bioindicators of Hg pollution

Identification of bacteria harbouring Hg-related genes

*hgcAB*

*merA*

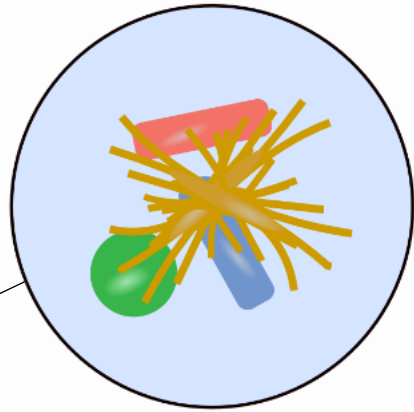
*merB*



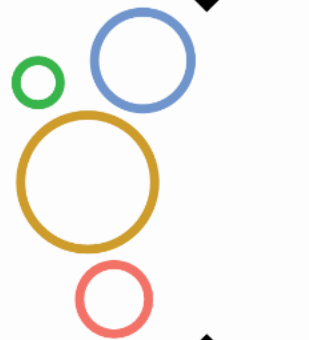
# Methodology



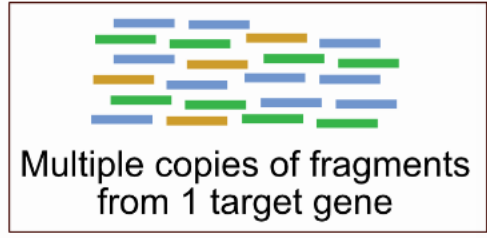
Mixed microbial community



DNA  
Extraction



**Amplicon sequencing**



Multiple copies of fragments  
from 1 target gene

**Metagenomics sequencing**



Short sequence  
fragments from "all" DNA

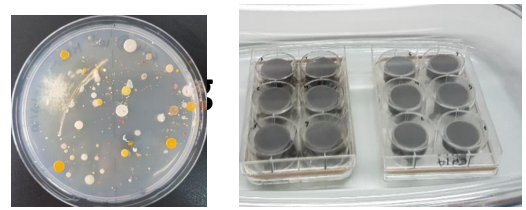
**Taxonomy**

Metabarcoding  
(16S rRNA genes)

**Functional genes**

Metagenomics

**Cultures**

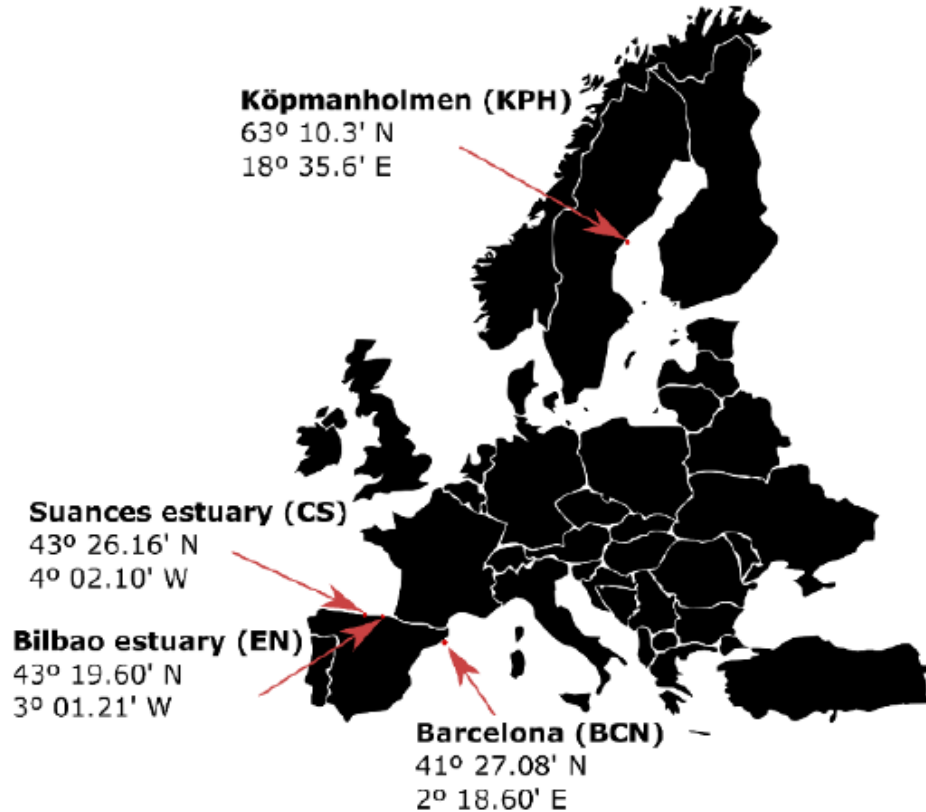




**MER-CLUB**

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# Sampling sites



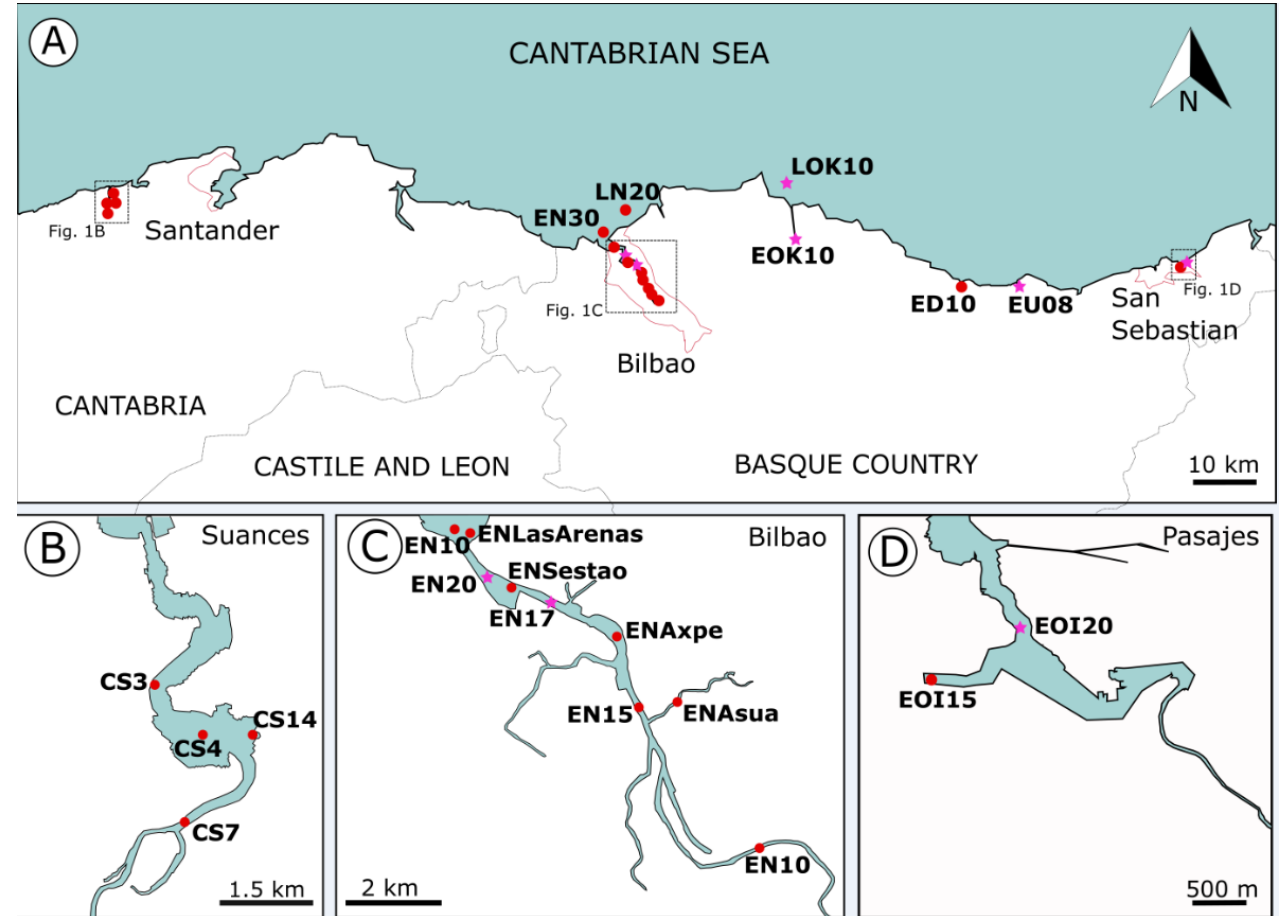
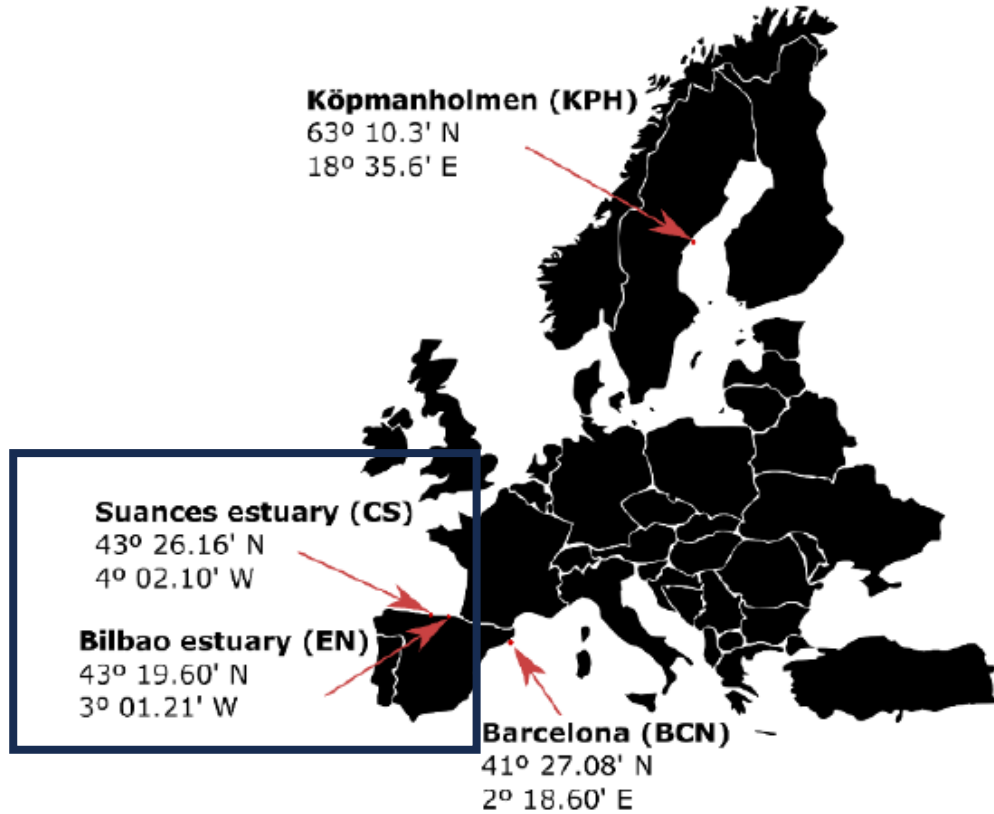
Sample	Hg tot ± sd (ng/g dw)	
BCN1	118	8
BCN4	1785	189
CS3	827	89
CS4	3173	203
CS7	1315	214
CS14	5049	124
EN15	412	174
EN17	6601	179
EN Asua	2398	20
EN Axpe	496	3



# MER-CLUB

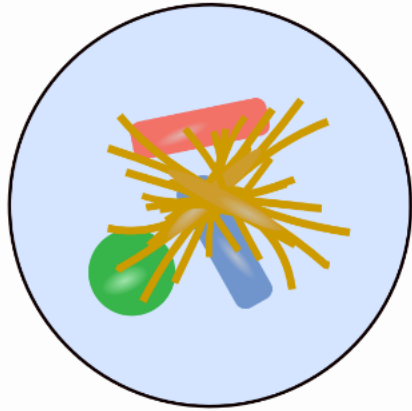
Mercury clean-up system based on bioremediation by marine bacteria

# Sampling sites



High organic matter content (5-7% dry weight)  
Anoxic conditions

Mixed microbial community



DNA  
Extraction



Amplicon sequencing



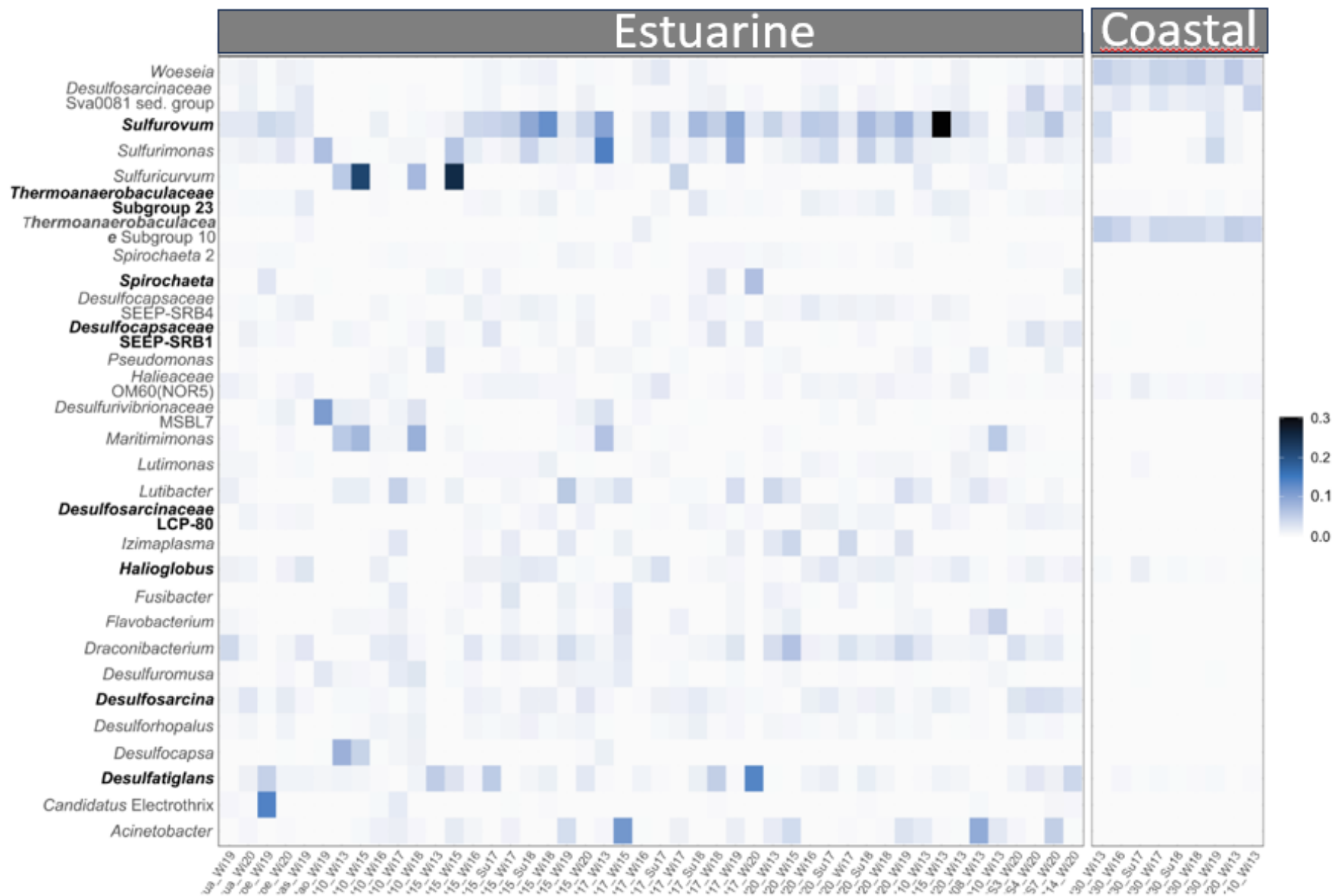
Multiple copies of fragments  
from 1 target gene

**Taxonomy**

Metabarcoding  
(16S rRNA genes)



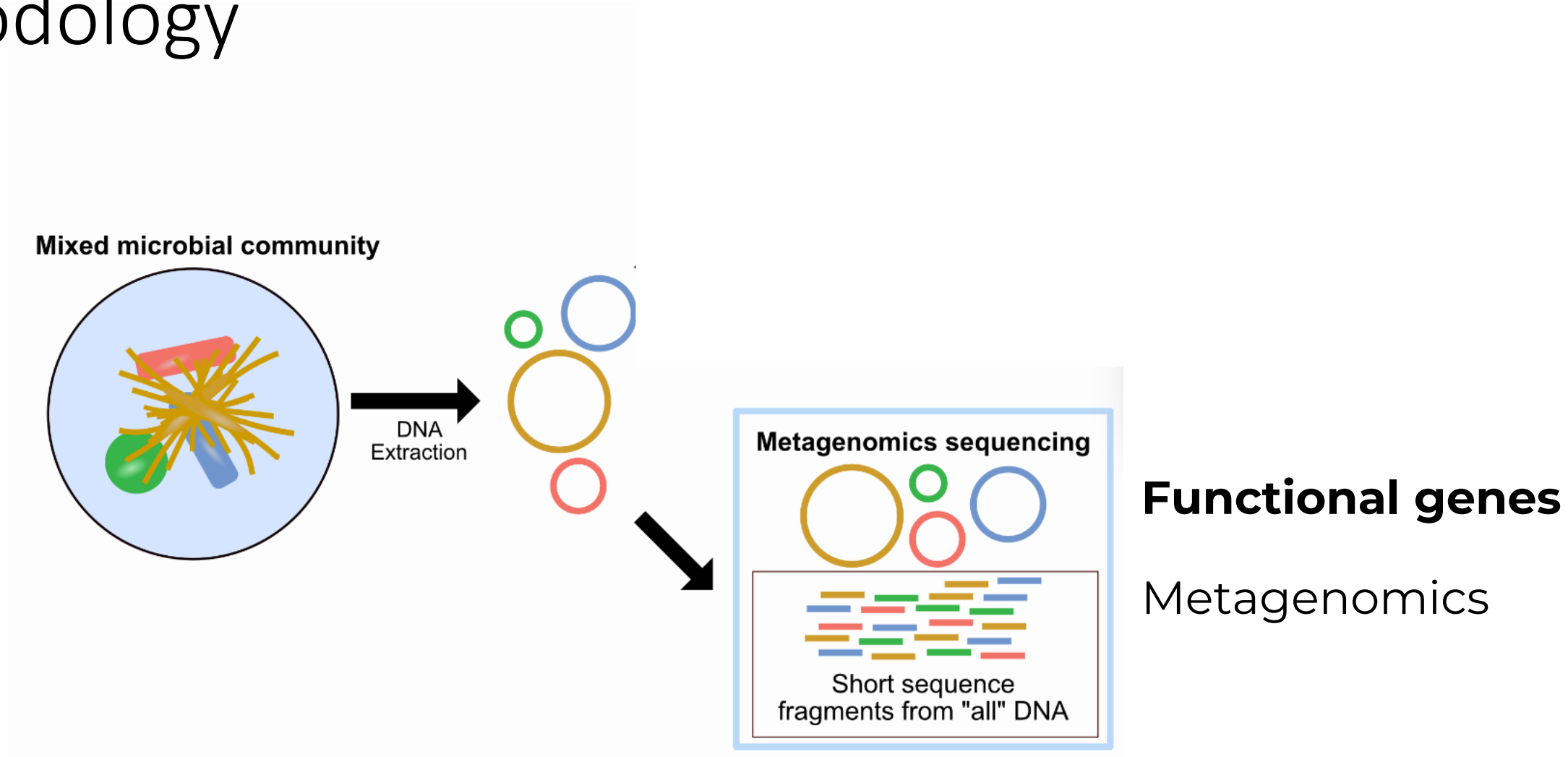
# Top-abundant taxa in the samples and Hg-bioindicators as identified by TITAN (Threshold Indicator Taxa Analysis, Baker & King 2010)



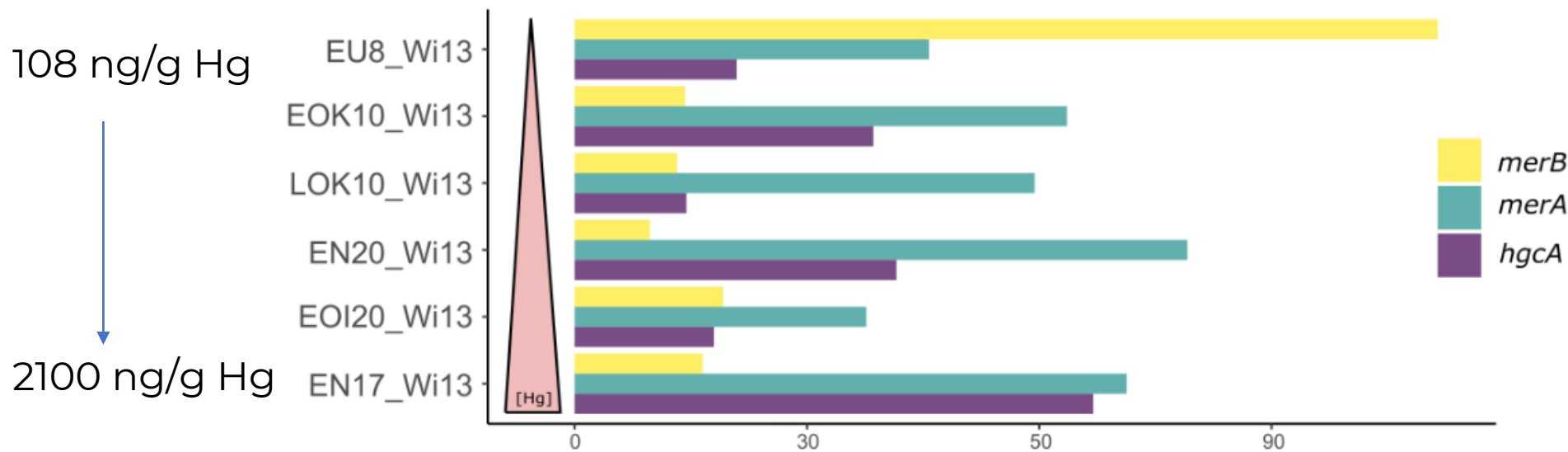
Many Hg-bioindicators were involved in the S cycle



# Methodology

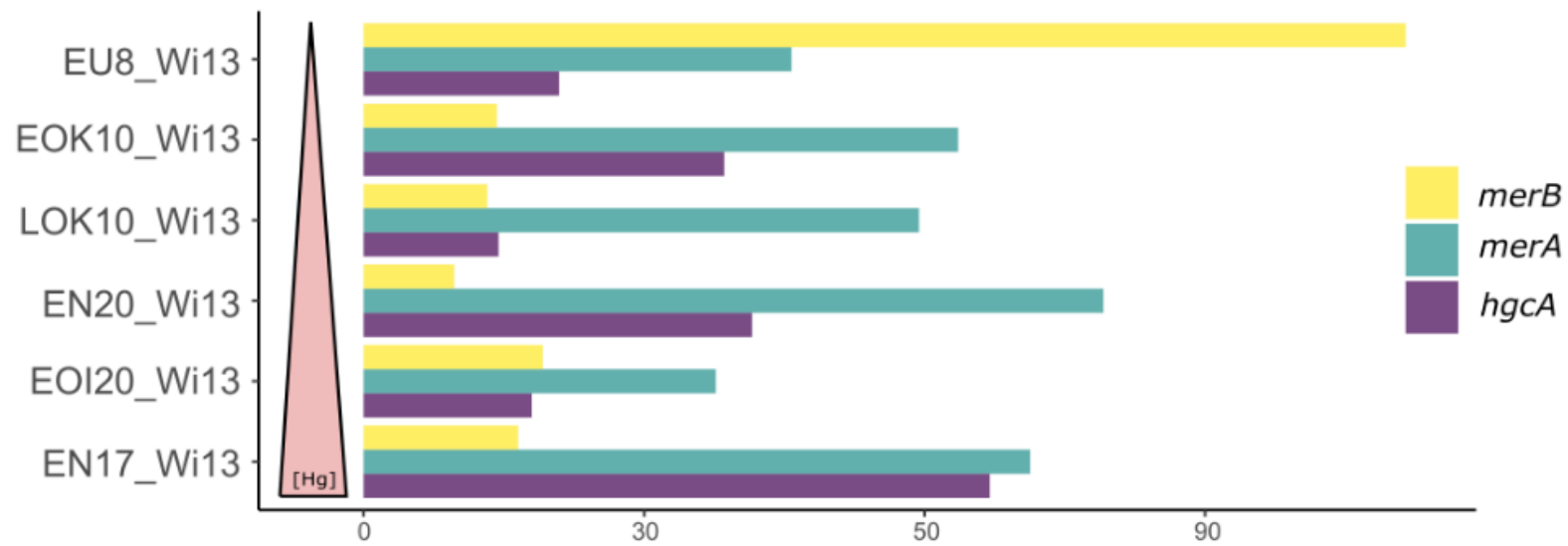


# Normalized **abundance** of *merA*, *merB* and *hgcA* genes

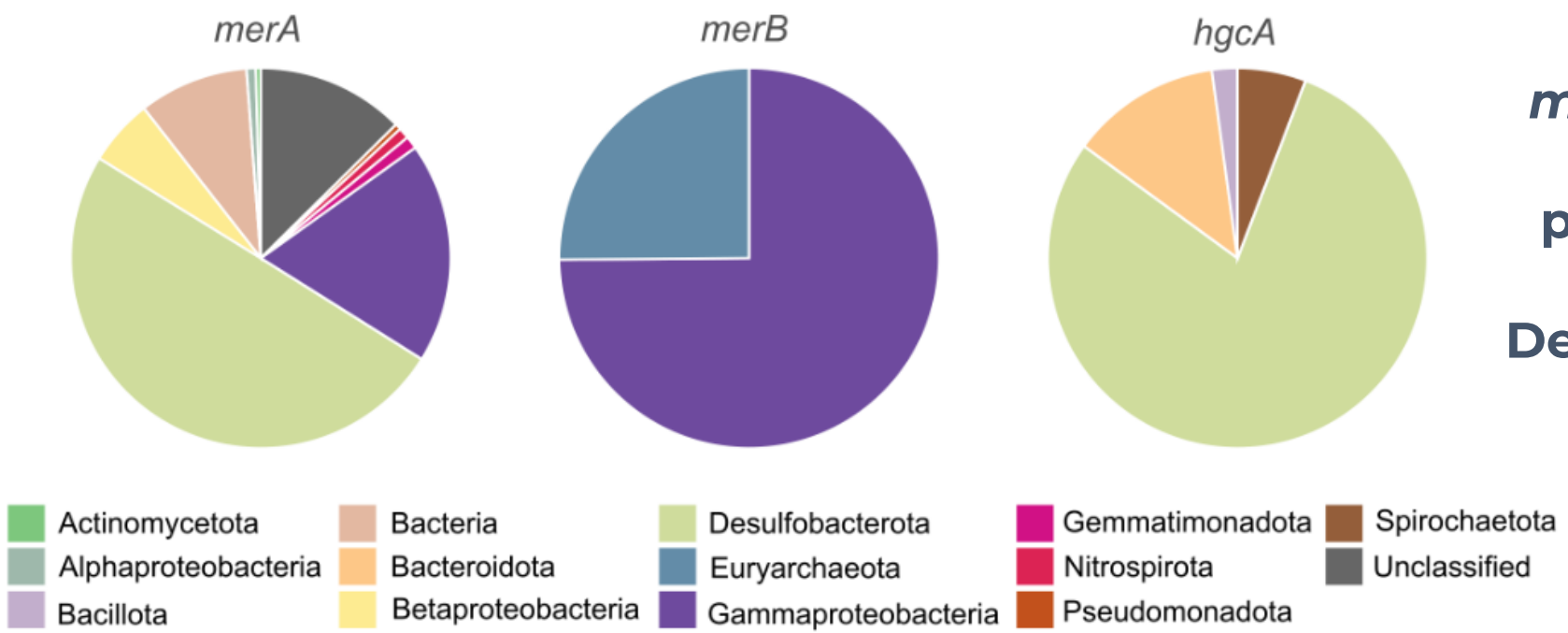


***merA* genes  
highly  
abundant in  
anoxic  
polluted  
sediments**

# Normalized abundance of *merA*, *merB* and *hgcA* genes

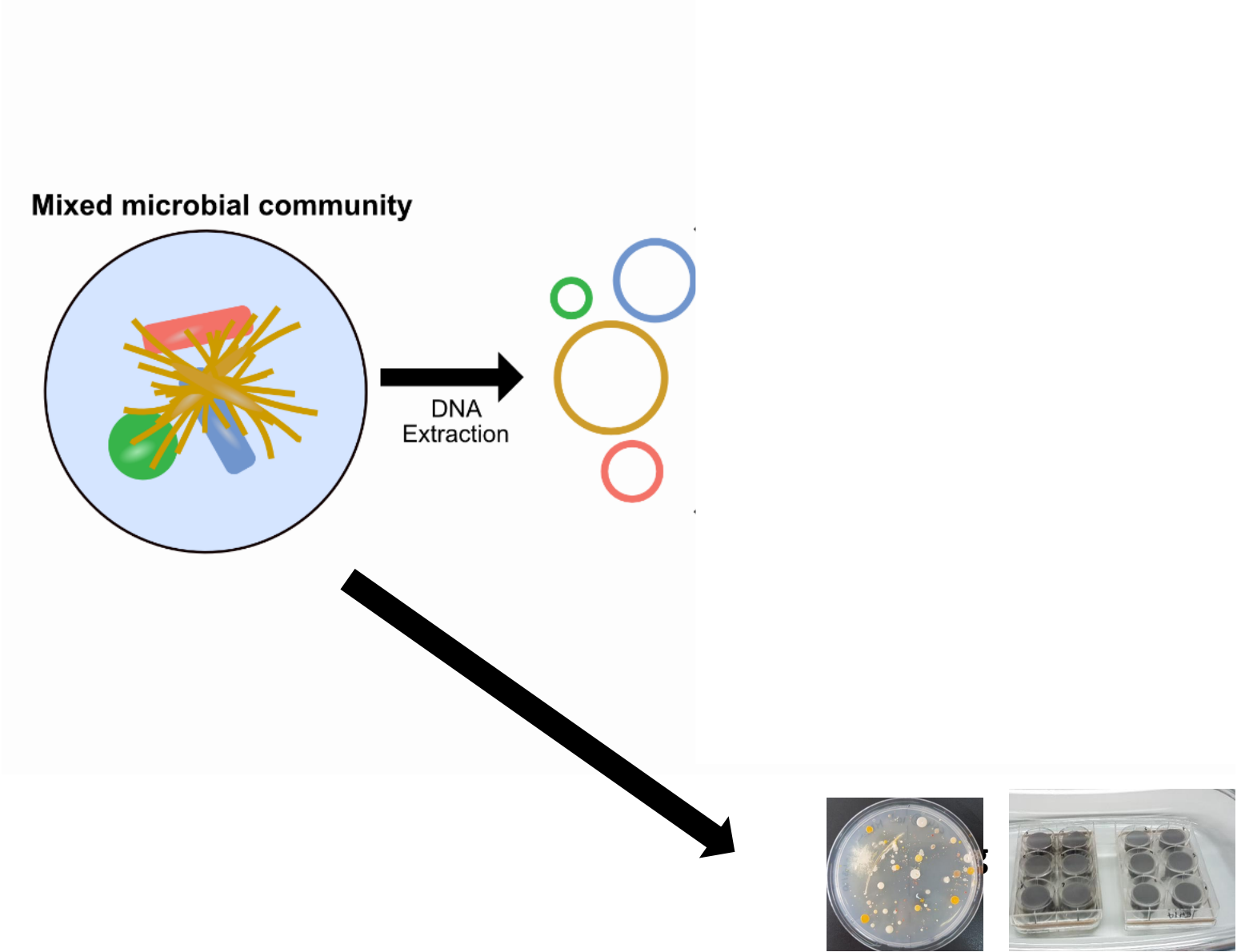


## Taxonomic affiliation of *merA*, *merB* and *hgcA* genes

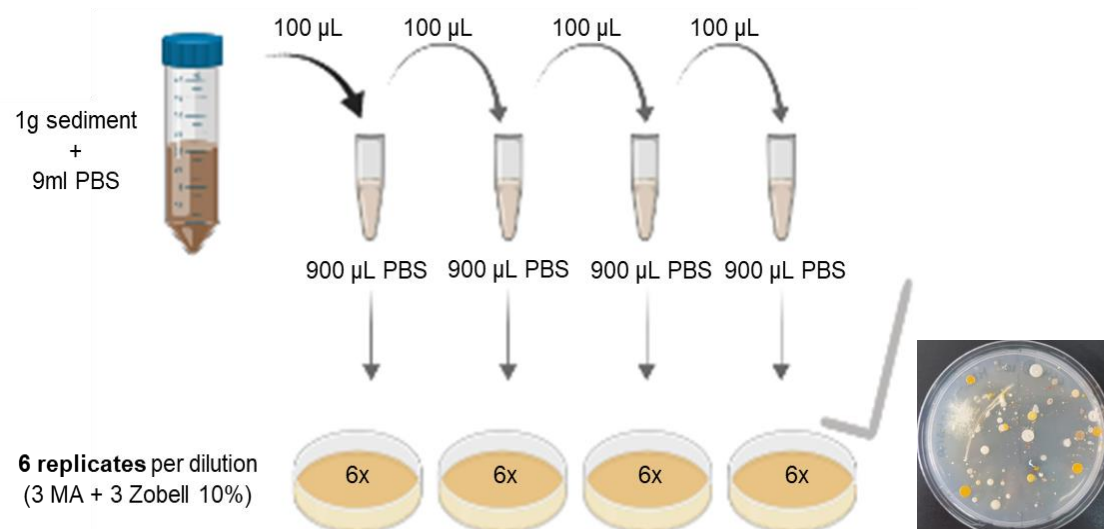


***merA* and *hgcA* genes predominately assigned to Desulfobacterota**

# Which bacteria did we retrieve in culture?

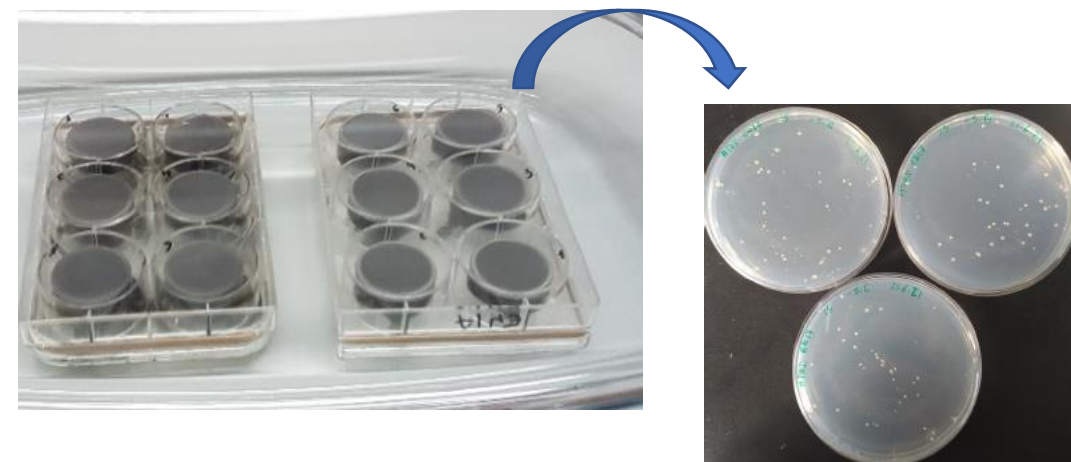


## Direct plating in agar plates

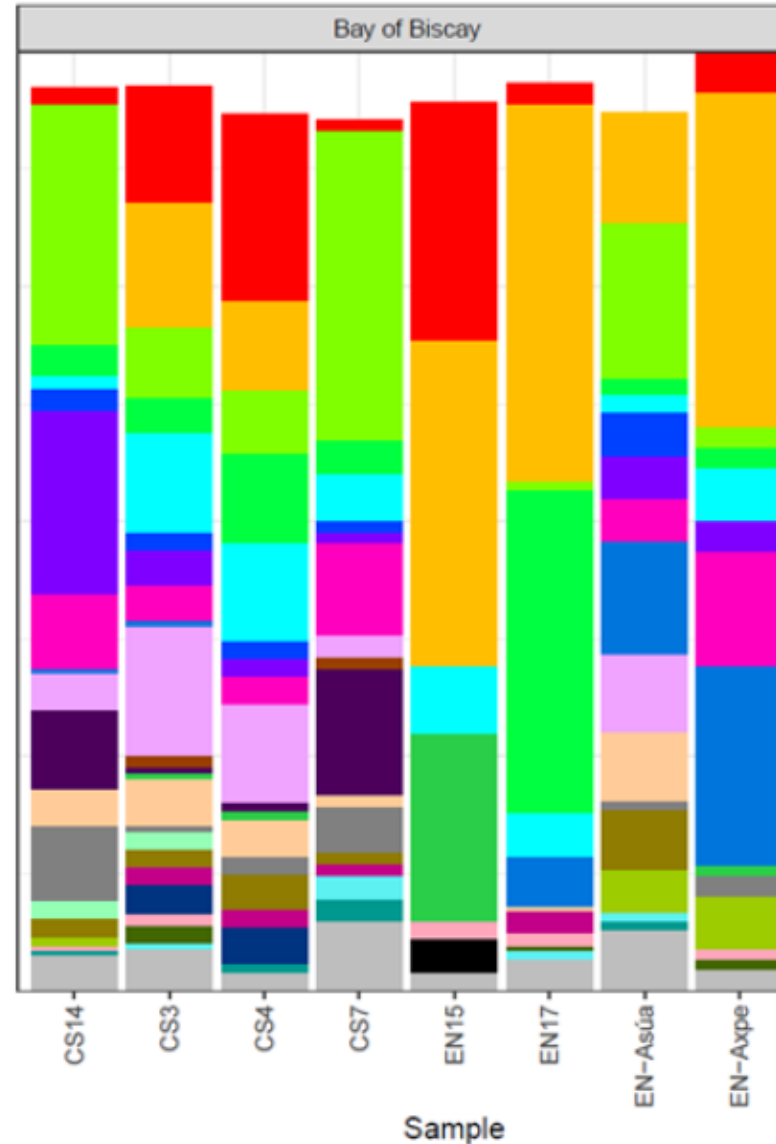
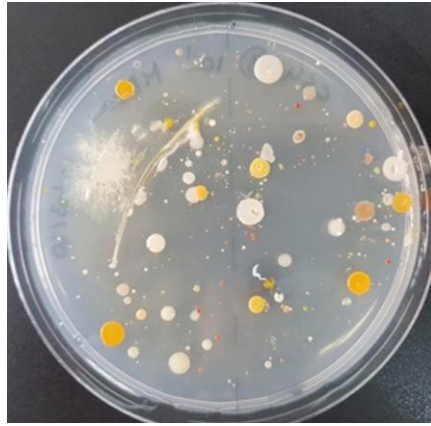


## Soil-substrate membrane system

Rasmussen et al., 2008

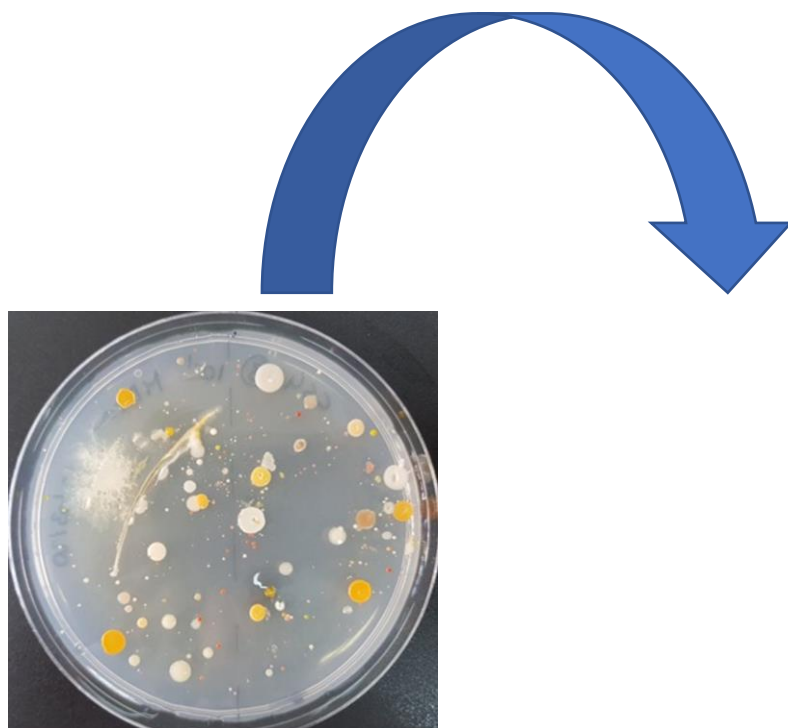


- Culture collection with > 1000 bacterial isolates

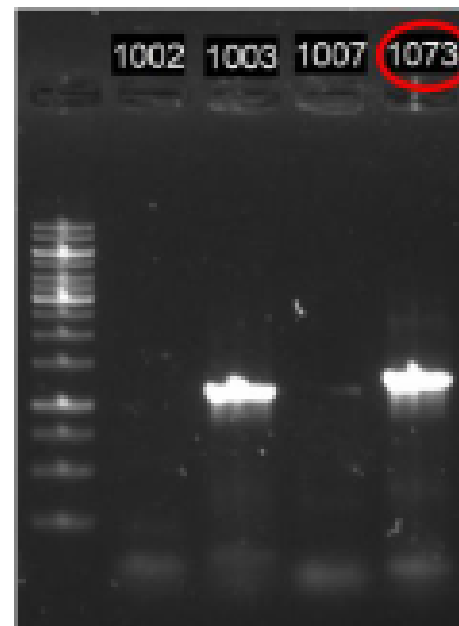


**Most isolates were affiliated with Gamma-proteobacteria**

- Culture collection with > 1000 bacterial isolates
- >50 isolates with *merA* genes



PCR screening of  
*merA* genes



***Marinobacter***

*Thalassospira*

***Pseudomonas***

*Bacillus*

*Shewanella*

*Arthrobacter*

*Vibrio*

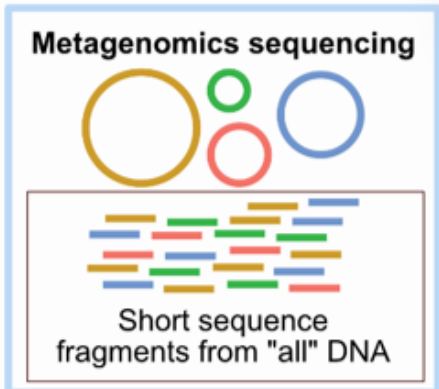
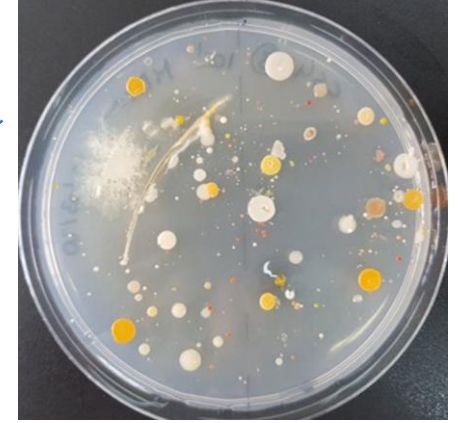
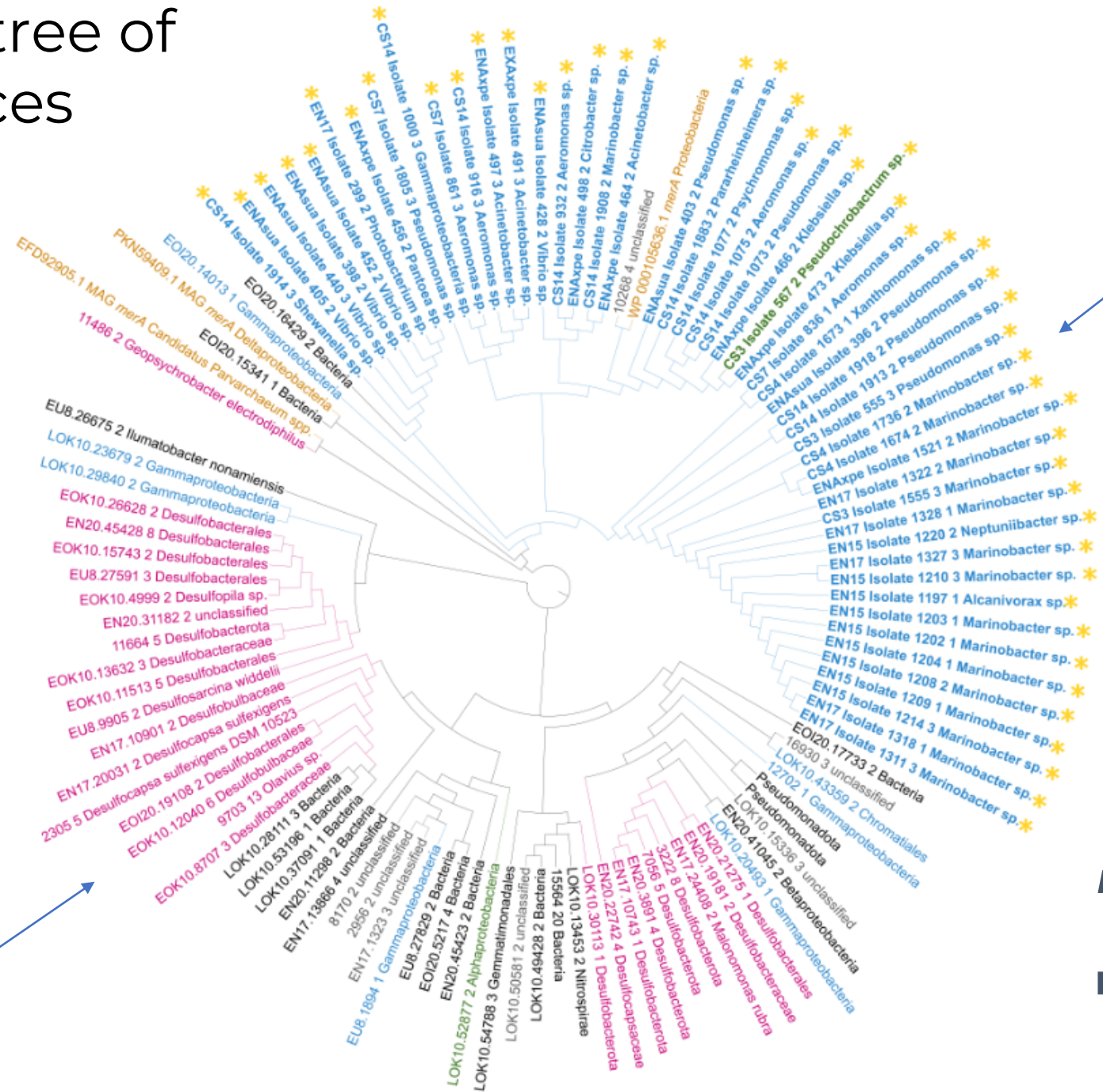
*Acinetobacter*

***Aeromonas***

*Pseudoalteromonas*

*Xanthomonas*

# Phylogenetic tree of *merA* sequences



*merA* genes from cultures and metagenomes do not overlap

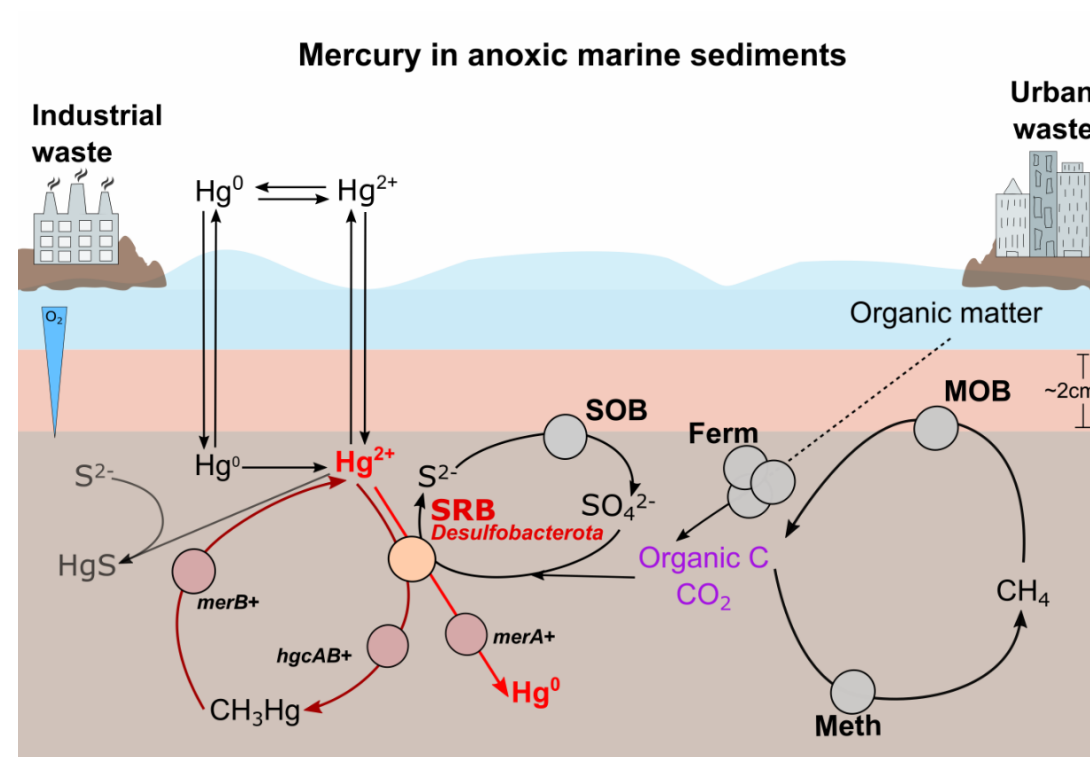


# TAKE HOME MESSAGES

✓ Mercury reduction genes are abundant in anoxic marine sediments

✓ The current known diversity of environmental mercury reducers is highly biased by the fact that a large fraction of them originate from oxic culturing approaches

✓ Sulfate-reducers (Desulfobacterota) may have a predominant role in mercury transformations in anoxic sediments, not only as mercury methylators but also as mercury reducers



# Acknowledgements



## **The MER-CLUB research team!**

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**Questions?**  
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