

Combining 454-Pyrosequencing, Q-PCR and FISH to characterize deep-sea sediment microbiomes

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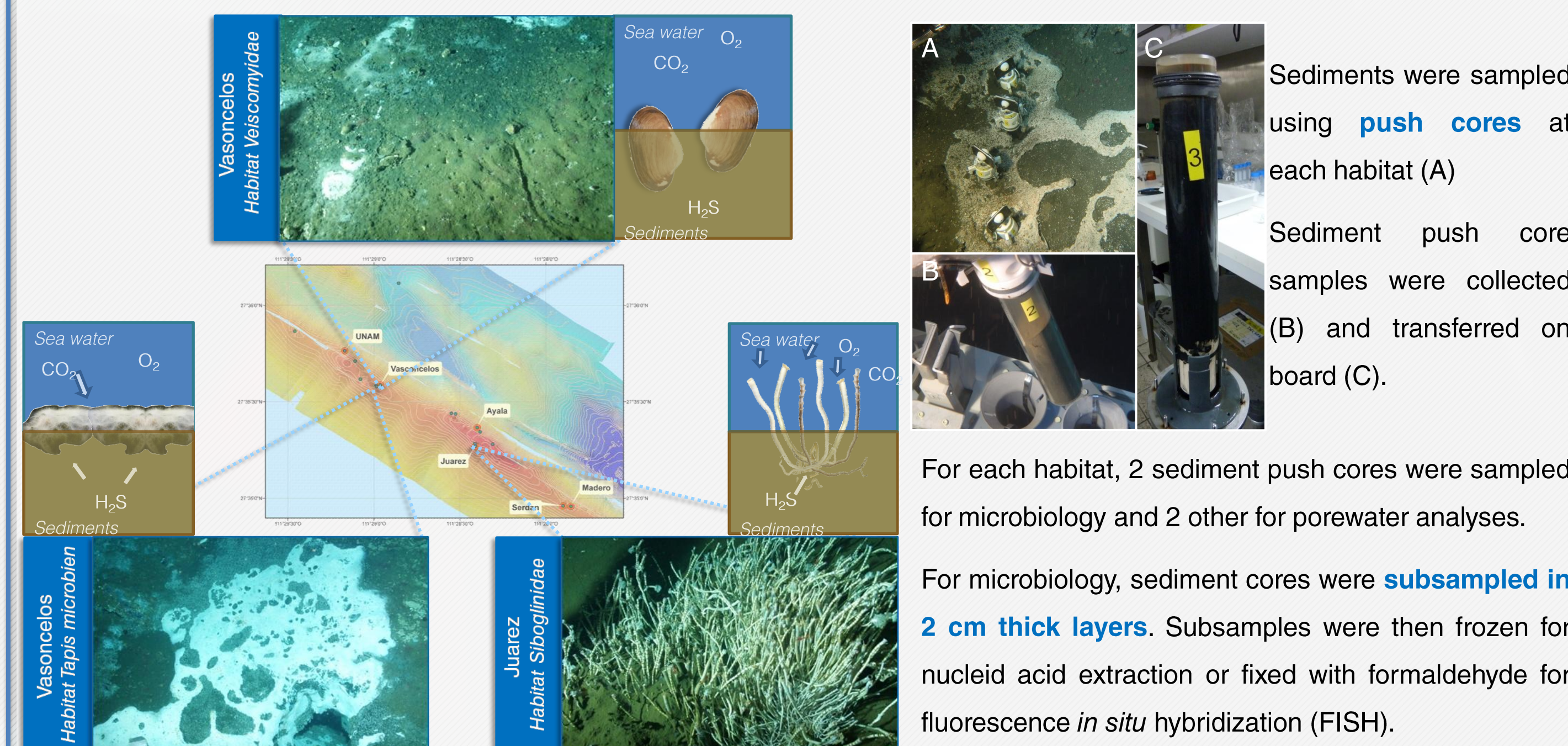
Continental margins accumulate large amounts of sedimented organic matter that are progressively degraded and transformed into deeply buried hydrocarbons, such as methane. In specific areas, named **cold seeps**, these hydrocarbons rise to the seafloor and fuel microbial communities and various faunal assemblages.

The **Sonora Margin** cold seeps, located in the Guaymas Basin (Gulf of California), harbour microbial mats and different faunal assemblages, such as *Vesicomyidae* and *Siboglinidae*.

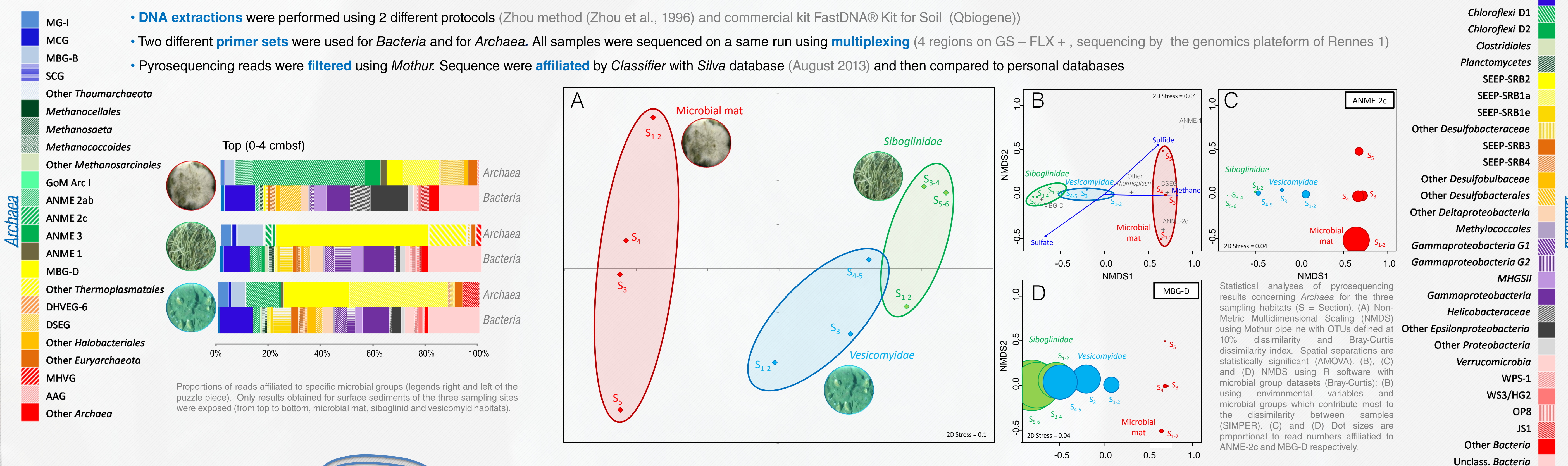
Problematic :

- Is the **microbial diversity** of the Sonora Margin cold seeps similar to those usually found in these type of ecosystems ?
- Are there differences between microbial communities according to the type of **surface colonizers** ?
- How do they interact with each other?
- How does the microbial communities vary with **depth** and **geochemical gradients** ?
- Are there some **interactions** between the different microbial groups ?

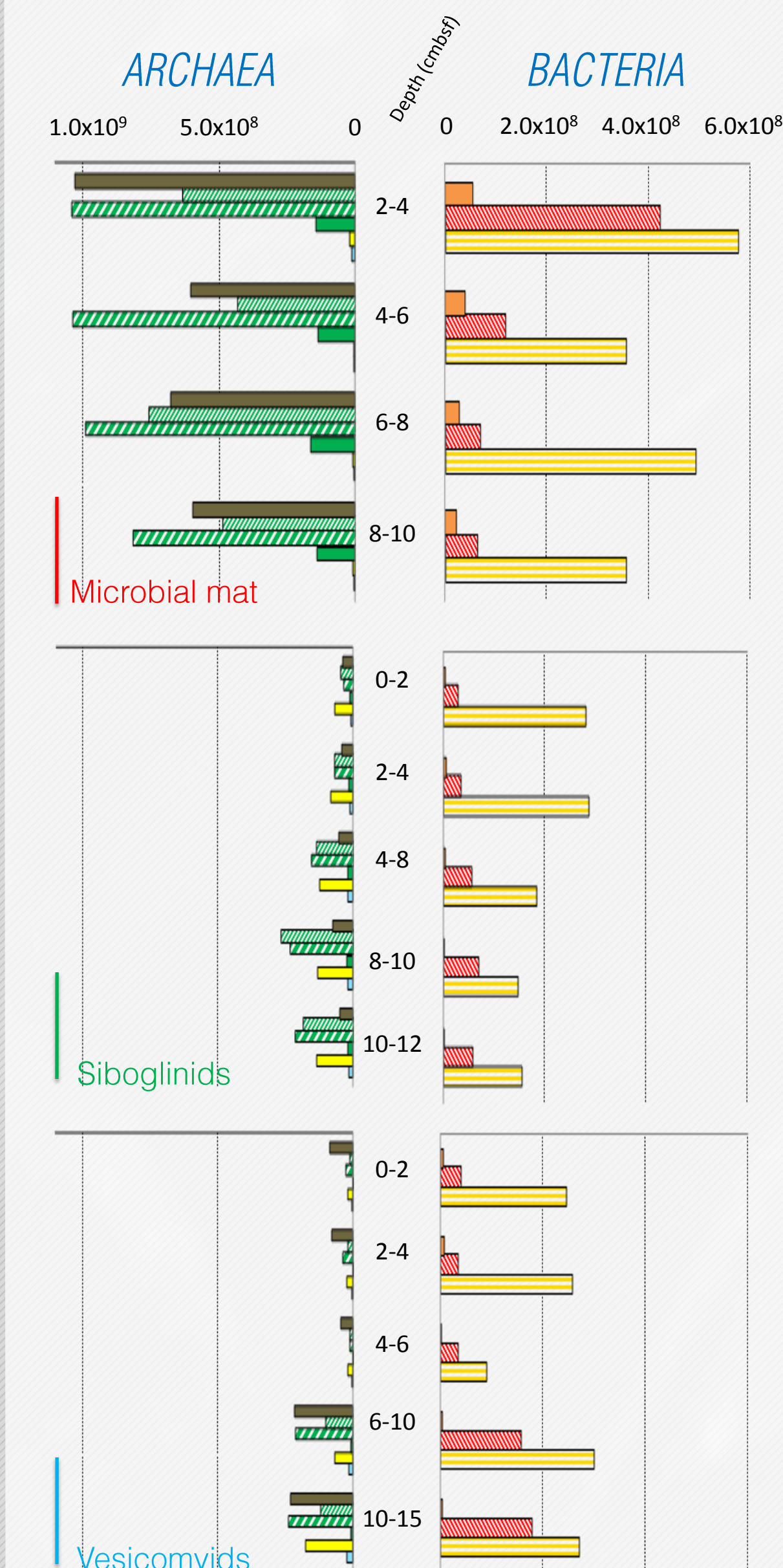
Sampling :



454-Pyrosequencing :



Q-PCR:



- Specific primer sets** were used to target dominant microbial groups highlighted by pyrosequencing
- Unit : 16S rRNA copies per gram of sediments
- Higher relative abundance was detected in microbial mat habitats.
- ANME-2 and -1** seemed to be more abundant in sediment underlying microbial mat than below the faunal assemblages.
- In contrast, **MBG-D** appeared to be more abundant in sediment underlying vesicomyids and siboglinids.
- These results were congruent with pyrosequencing analyses except for ANME / MBG-D proportions in sediments underlying animals.

Conclusions et hypothesis...

- Microbial communities **distribution** varied significantly according to the sampling habitat
- Anaerobic methanotrophs** (ANME) were more abundant in sediments underlying microbial mats whereas **MBG-D** lineages were more abundant below animal colonizers
- Higher methane and sulfide concentrations were measured in microbial mat sediments. **Geochemical composition** of the up-raising fluid could impact on the microbial community structure, distribution and abundance
- Microbial communities could also influence **the fluid chemical composition** (sulfate reduction, methane oxidation) and fuel the **surface colonizers**
- Surface colonizers** could modify the **sediment geochemistry** (oxygen, sulfur oxidation, bioturbation) and thus impact the microbial community distribution, diversity and abundance

FISH

