

# **Investigating the diversity and metabolic interactions in hydrogen-powered microbial consortia cultures from a shallow marine serpentinite-hosted ecosystem, the Prony Bay Hydrothermal Field (PBHF), New Caledonia.**

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Serpentinization, the alteration of (Fe, Mg)-minerals of mantle rocks (peridotites) into serpentinites, and the accompanied reduction of CO<sub>2</sub> generate reduced fluids enriched in H<sub>2</sub>, CH<sub>4</sub>, and small organic molecules (mainly formate). These compounds are potential energy and carbon sources for microbial life. However, serpentinization also generates environmental conditions hostile to life: high pH (>11), low availability of oxidants to serve as electron acceptors, and very low concentration of dissolved inorganic carbon. These extreme environments have been the object of considerable scientific interest over the last two decades [1]. Most of our current knowledge of this particular microbial ecosystem is derived from metagenomic studies [2]. They have highlighted the importance of dihydrogen metabolisms and revealed the prevalence of new lineages of bacteria or archaea that are currently uncultivated. Indeed, cultural approaches, so far, have allowed the isolation of only a small fraction of the detected diversity [3-5]. Hence, most of the dominant members of the serpentinite-hosted microbiomes have so far escaped culture attempts. This lack has hampered the true understanding of the functioning of these ecosystems because metagenomic-based hypotheses lack experimental evidence. To fill this gap, we reduce the complexity of the natural system by carrying out cultures of consortia in bioreactor mimicking the in-situ conditions but where the effect of environmental parameters on the specific or functional diversity of the cultivated community can be more easily tested. Cultured consortia were established from samples of a carbonate chimney from the PBHF, in a semi-batch bioreactor supplied with H<sub>2</sub> and formate at pH 10 under the four tested electrons acceptors (O<sub>2</sub>, nitrate, sulfate, or CO<sub>2</sub>). The total microbial diversity and truly active members of the communities were monitored by DNA or RNA sequencing of a marker gene, respectively, along with the growth and metabolic activity measurement (HPLC, GC-MS, IRMS). The main results and their ecological significance will be presented and discussed.

[1] Schrenk, M. *et al.* (2013) *Rev. Mineral. Geochem.*, [2] Lecoivre, A. *et al.* (2021) *ISME J.*, [3] Suzuki S., *et al.* (2014) *Nat. Commun.* [4], Mei, N. *et al.* (2016) *IJSEM* [5], Postec A., *et al.* (2021) *System Appl Microbiol.*