

## Carbon fixation in microbial communities from the shallow serpentinite-hosted system of Prony Bay, New Caledonia

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The beginnings of life remain one of the most outstanding scientific issues. For the development and maintenance of biological activity, electrochemical disequilibria are of central importance. In marine serpentinite-hosted systems, abiotic redox gradients develop between the ultrabasic hydrothermal fluid rising from the deep subsurface, and the surface waters. They are maintained across the porous hydrothermal chimney wall, which can be compared to an osmotic membrane. It is hypothesized that this rudimentary proton motive force has driven chimney nanopores to develop into protocells at the emergence of life [1]. In serpentinite-hosted systems, ultrabasic hydrothermal fluids enriched in abiotic hydrogen, methane, and small organic molecules are produced. The hyperalkaline milieu poses a great challenge for metabolic energy and nutrient acquisition, curbing the cellular membrane potential and limiting electron acceptor, phosphorous and dissolved inorganic carbon availability [2]. Nevertheless, diverse microbial communities are found in modern serpentinite-hosted systems. Their metabolic makeup might provide a glimpse into early life forms [1]. One of the greatest questions regarding microbial metabolism in a serpentinization context revolves around the carbon source for primary production in the absence of dissolved inorganic carbon. Potential carbon sources are formate and acetate produced abiotically or via acetogenesis [3] and fermentation [4], as well as abiotically produced amino acids such as glycine [5]. Some microorganisms have also been shown to grow on calcium carbonate, presumably by local redissolution into bicarbonate [6]. Here, we present a metagenomic study on the fixation of those carbon compounds in the shallow Prony Bay Hydrothermal Field, located on the Southern coast of New Caledonia [7]. We assess the abundance of respective functional genes along a transect from land to sea, their presence in taxonomic groups typically associated with serpentinization, as well as the completeness of relevant carbon fixation pathways. Subsequently, we compare the metagenomic results to preliminary experimental evidence obtained from microbial consortia grown on the different carbon compounds. Implications for the metabolic functioning of the community as well as the methodological approach are discussed.

### Références

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