

Publication MIO : Eleonore Frouin, Meline Bes, Bernard Ollivier, Marianne Quéménéur, Anne Postec, Didier Debroas, Fabrice Armougom, Gaël Erauso (tous du MIO, excepté D. Debroas) - Diversity of rare and abundant prokaryotic phylotypes in the Prony Hydrothermal Field and comparison with other serpentinite-hosted ecosystems published in *Frontiers in Microbiology*, section Extreme Microbiology.



Abstract :

The Bay of Prony, South of New Caledonia, represents a unique serpentinite-hosted hydrothermal field due to its coastal situation. It harbors both submarine and intertidal active sites, discharging hydrogen- and methane-rich alkaline fluids of low salinity and mild temperature through porous carbonate edifices. In this study, we have extensively investigated the bacterial and archaeal communities inhabiting the hydrothermal chimneys from one intertidal and three submarine sites by 16S rRNA gene amplicon sequencing. We show that the bacterial community of the intertidal site is clearly distinct from that of the submarine sites with species distribution patterns driven by only a few abundant populations, affiliated to the Chloroflexi and Proteobacteria phyla. In contrast, the distribution of archaeal taxa seems less site-dependent, as exemplified by the co-occurrence, in both submarine and intertidal sites, of two dominant phylotypes of Methanosarcinales previously thought to be restricted to serpentinizing systems, either marine (Lost City Hydrothermal Field) or terrestrial (The Cedars ultrabasic springs). Over 70% of the phylotypes were rare and included, among others, all those affiliated to candidate divisions. We finally compared the distribution of bacterial and archaeal phylotypes of Prony Hydrothermal Field with those of five previously studied serpentinizing systems of geographically distant sites. Although sensu stricto no core microbial community was identified, a few uncultivated lineages, notably within the archaeal order Methanosarcinales and the bacterial class Dehalococcoidia (the candidate division MSBL5) were exclusively found in a few serpentinizing systems while other operational taxonomic units belonging to the orders Clostridiales, Thermoanaerobacterales, or the genus Hydrogenophaga, were abundantly distributed in several sites. These lineages may represent taxonomic signatures of serpentinizing ecosystems. These findings extend our current knowledge of the microbial diversity inhabiting serpentinizing systems and their biogeography.

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