



Investigation of a microbial community involved in dolomite formation, Lagoa Vermelha, Brazil

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Sedimentary dolomite is found throughout the geologic record whereas in the present time dolomite is rarely formed at Earth's surface conditions. The origin of primary dolomite remains a subject of geological debate. In this study, we investigate the structure of the microbial community mediating dolomite formation in Lagoa Vermelha, a shallow hypersaline lagoon 100 km east of Rio de Janeiro, Brazil. Dolomite precipitates in the anoxic organic matter-rich layer at the sediment surface. Lagoa Vermelha can be considered as a modern analogue for ancient environments with conditions that may have dominated during certain periods in Earth's history when anoxia was more prevalent. Whereas it has proven difficult to precipitate dolomite inorganically, precipitation in laboratory culture experiments at low temperature is now routinely accomplished (Vasconcelos & McKenzie 1997, Warthmann et al. 2000). Sulfate-reducers like *Desulfovibrio brasiliensis* and heterotrophs in aerobic and anaerobic conditions were shown to be capable of dolomite biomineralization, in both natural environments and culture experiments. Methanogenesis is also a metabolism suggested to be linked to dolomite precipitation.

To get insight into the microbial processes involved in dolomite formation, cultivation-independent techniques based on the analysis of the 16S ribosomal RNA genes were used to explore the prokaryotic diversity in the upper anaerobic dolomite-forming sediments from Lagoa Vermelha. Total DNA was extracted from dolomitic sediments. Bacterial and archaeal 16S rDNA were amplified by PCR using universal primers, then cloned and sequenced.

Some of the identified bacteria may be involved in dolomite precipitation through sulphate-reduction (*δ -Proteobacteria*) as well as aerobic and anaerobic heterotrophy

(γ -Proteobacteria, Firmicutes, CFB). Actinobacteria, Chloroflexi and Candidate Division OP8 were also evidenced. Archaeal sequences belong to Eury- and Crenarchaeota. They are mostly affiliated to uncultured microorganisms detected in saline environments, marine mud volcanoes, deep seafloor and methane-rich sediments. Methane was also detected in Lagoa Vermelha sediments indicating that some archaea retrieved in this study are most likely methanogenic. A large prokaryotic diversity associated with dolomite was highlighted in this study through the analysis of 16S rRNA genes. The rarefaction curves showed that the diversity, especially among bacteria, was not completely accessed. However, the function of these microorganisms can not always be deduced, especially when belong to uncultured groups. To further investigate the functional diversity inside the prokaryotic community, sulphate reducers and methanogens diversity were analysed through the use of specific genes: dsrA (dissimilatory sulfite reductase subunit A) and mcrA (Methyl-coenzyme M reductase A). The analysis of the dsrA sequences demonstrated so far a low diversity. Most of the sequences were affiliated to "uncultured sulfate-reducing bacterium" originating for example from sulfate and methane zones of a marine sediment (Black Sea) and deep-sea chimneys. Some sequences were affiliated to *Desulfosarcina* spp. and *Desulfovibrio* spp. No mcr A sequences could be directly amplified from the total DNA extracted from the sediments. To find out if the methane production is related with the microbial activity, enrichment culture experiments were performed to grow methanogenic microorganisms from the cores. Various media were designed and the cultivated methanogens identified so far correspond to methylotrophic *Methanolobus* spp..

Further comparisons of the microbial diversity in different dolomite-containing sediments (from deeper dolomite concretions in Lagoa Vermelha and sediments from deep marine subsurface) may provide insights to identify the microorganisms and the biological processes mediating dolomite biomineralization.

References

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