Microbial calcification in the rock record: learning from field- and laboratory-based studies down to the nm-scale

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A large abundance of microfossils and biogenic minerals are preserved in the geological record as Ca-carbonates and phosphates [e.g., 1; 2]. Recent progresses in microscopy and spectroscopy have allowed to characterize these biogenic traces with an unprecedented level of details. However, interpreting these fossil traces in terms of phylogenetic affiliation or metabolic capabilities is limited by our understanding of their transformations during ageing as well as the assessment of the diversity of modern microbial populations and mechanisms of biomineralization.

In this talk, I will first review the results of recent studies on a wild-type and mutant strains of *E. coli* inducing Ca-phosphate biomineralization. I will show that the calcification activity of these strains is related to the total phosphatase activity of the cells and that resulting mineralogical patterns depend on the localization of the enzyme [3]. I will also show that calcification impacts the preservation of organic molecules upon ageing based on taphonomy experiments [4].

In a second stage, I will discuss the extracellular vs intracellular formation of Ca-carbonates by cyanobacteria. These different biomineralization pathways likely result in the formation of different traces in the geological record, which can be discussed based on laboratory-based experiments [5]

While these studies using single strains are meaningful, they capture only a limited extent of biological diversity and I will elaborate on this issue and discuss how analyses of genomes and metagenomes might provide useful clues to assess the biomineralization capabilities of bacteria [6].

[1] Cosmidis *et al*. (2013) *Geobiology* 11, 139-153.

[2] Couradeau *et al* (2013) *Biogeosci*. 10, 5255-5266.

[3] Cosmidis J *et al*. (2015) *Front. Earth Sci*, 3, #00084.

[4] Li J *et al* (2014) *Earth Planet. Sci. Lett*., 400, 113-122

[5] Li J *et al* (2016) *Minerals*, 6, #10.

[6] Saghaï A *et al* (2015) *Front.Microbiol*, 6, #797.