Silicate reactivity and microbial diversity promoted by water-basalt interactions under subsurface conditions

JULIETTE BAS-LORILLOT¹, BASTIEN WILD², BENEDICTE MENEZ³, DAMIEN DAVAL⁴, ANDRI STEFÁNSSON⁵, JÓHANN GUNNARSSON-ROBIN⁶, ANNA BRÍET BJARKADÓTTIR⁵, SIGRÍÐUR MARÍA AÐALSTEINSDÓTTIR⁵, GUILLAUME BORREL⁷ AND EMMANUELLE GÉRARD³

¹ISTerre, CNRS

²CNRS - Université Grenoble Alpes

³Université Paris Cité, Institut de physique du globe de Paris, CNRS, UMR 7154
⁴ISTerre - CNRS
⁵University of Iceland
⁶Nordic Volcanological Center, Institute of Earth Sciences, University of Iceland
⁷Institut Pasteur

Presenting Author: juliette.bas-lorillot@univ-grenoble-alpes.fr

Silicate reactivity and microbial diversity promoted by waterbasalt interactions under subsurface conditions

Authors: Juliette Bas-Lorillot, Bastien Wild, Bénédicte Ménez, Damien Daval, Andri Stefánsson, Jóhann Gunnarsson-Robin, Anna Bríet Bjarkadóttir, Sigríður María Aðalsteinsdóttir, Guillaume Borrel, Emmanuelle Gérard

Microorganisms are well known to occupy the deep Earth's crustal environments. Yet, it remains unclear whether these microbial communities rely solely on the abiotic release of nutrients and chemosynthetic energies upon water-rock interaction, or whether they actively contribute to the elemental mobilization, and thus play an important role in rock alteration. In order to assess the contribution of subsurface microorganisms to silicate alteration, the main factors shaping microbial diversity in such environments need to be characterized, and quantitative understanding of the water-rock reactions under the conditions that prevail at depth needs to be established.

Here we focus on the microbial diversity of deep basaltic environments. Field campaigns were carried out in Iceland to sample groundwater in basaltic aquifers with contrasting physicochemical properties (temperatures and pH ranging from 30 to ~100°C and from 7 to 11, respectively). Microbial biomass was collected by filtration (0.22 μ m pore size) for DNA extraction and Illumina MiSeq tag sequencing of the 16S rRNAencoding gene for microbial community profiling. Our preliminary results show that dominant archaea belong to the Crenarchaeota phylum while dominant bacteria belong to the Nitrospirota phylum. To the first order, archaeal diversity is primarily driven by temperature, while bacterial diversity seems to be shaped by pH. Our current work aims to ascertain whether microbial species with known alteration capability are present in the groundwater microbial communities collected during our field campaigns.

In parallel, the reactivity of olivine and basaltic glass at conditions relevant to these groundwater systems has been investigated using batch experiments combined with non-invasive techniques, including vertical scanning interferometry, which assesses the nanotopography of the sample surfaces. Our preliminary results show unexpectedly low reactivity for olivine at these conditions (especially at pH > 10), while the reactivity of basaltic glass is consistent with previously published work.