Subject offered for a contract starting October 2016

SUBJECT TITTLE: Microbial biofilms in basaltic subsurface environments. Diversity studies and impact of CO_2 injections.

Advisor: **MENEZ, Bénédicte, Pr, menez@ipgp.fr**
Second Advisor/ Supervisor:
GERARD, Emmanuelle, IR, emgerard@ipgp.fr
Host lab/ Team :
IPGP- Equipe Géomicrobiologie – UMR7154

Financing: Doctoral contract with or without teaching assignment

For more information go to http://ed560.ipgp.fr, section: Offres de these (PhD offer), You must apply on the Doctoral School website

Team: MENEZ, Bénédicte; GERARD, Emmanuelle; TRIAS, Rosalia; MOORE, Rachael

Project summary:

The microbial communities inhabiting the Earth subsurface are still poorly studied but have to be considered as important contributors to the global C, N and S cycles, notably in basalts where high diversity was revealed (Santelli et al., 2008 Nature; Cowen et al., 2003, Science). With the aim of understanding the diversity and dynamics of microbial communities in the basalt hosted aquifers of Hellisheidi (SW Iceland), our research group has been monitoring the microbial diversity in the different available monitoring wells since 2008. The Hellisheidi site has different strategically located wells, used by Reykjavik Energy, the operator of the associated geothermal plant that has been performing CO_2 and CO_2-H_2-H_2S injections at a depth of 400–800 m and temperatures up to ~ 80°C as mitigation strategy for its main waste products.

Groundwater samples have been used for bacterial and archaeal 16s rRNA gene cloning, 454- pyrosequencing, metagenomics and qPCR. First results obtained show that groundwater harbors a diverse and abundant community that reacts and adapts to gas injections. After CO_2 injections the microbial community changed, decreasing in diversity and richness, but we observed the successive dominance of 2 phyla. First, representatives of the *Gallionellales* order (*Betaproteobacteria*, likely autotrophic iron oxidizers including some genera of the *Gallionellales* with a possible capability to degrade hydrocarbons) became dominant, and two months later *Desulfotomaculum* sp. (recognized as sulfate-reducing bacteria) bloomed along with an increase of bacterial biomass (x500 factor) as measured by qPCR of the bacterial 16S rRNA gene (Trias et al., submitted to Nature Com).

Moreover, during October-November 2014 we had the opportunity to participate to drilling operations that have taken place at Hellisheidi (NSF project PI J. Matter, Columbia

University, USA/Southampton University, UK) during which we collected a series of unique core samples evidencing the presence of a highly developed microbial life that invaded the rock likely as a consequence of the gas injection. In particular, this sampling experience has allowed us to understand that the microbial communities have developed in the form of biofilms after the gas injection, in existing fractures or rock porosity such as basalt vesicles. A greenish layer of biofilm (as confirmed by Confocal Scanning Laser Microscope imaging) has been found as soon as the driller reached the top of the aquifer (i.e. at 400 m depth) and all along its way through the permeable layer which was sampled over 100 m. Variously coloured secondary minerals (from brownish to reddish) are associated, likely resulting from the microbial activity within the biofilm. These ubiquitous biofilms at these depths have not been described before, and are likely a consequence of the CO_2 injection, since deep communities are usually C limited and the injection could have stimulated their development. Knowledge on the diversity of the sampled biofilm would bring relevant information for the subsurface microbiology science and for the development of C sequestration technologies.

The goal of the proposed PhD is to analyse the diversity and structure of the core communities. The collection of about 50 samples obtained includes unaltered basalt and corroded samples, covered in biofilm, which can be used as a model for common basaltic communities, and C altered communities. Massive sequencing techniques such as Illumina and 454 pyrosequencing followed by bioinformatics analyses will be used. In parallel, different microscopy approaches, including Fluorescence In Situ Hybridization (FISH) will be used to determine the biofilm structure. Results will be discussed and integrated within the research team who will provide information about the basalt mineralogy and the metabolic function of the communities, leading to model of microbial biofilms in subsurface in the context of C injections.