



## **Interaction between deep-fluids and microbial communities at “Continental Smokers” of northern Greece**

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Greece is characterised by extensive tectonics that facilitates the upflow of mantle-derived fluids and their discharge from thermal manifestations. Crossey et al. (2016) defined as “continental smokers” sites of mantle degassing through continental crust. These are analogous to the black smokers on the ocean bottom where intense hydrothermal activity involves mantle fluids. As well as the geochemistry, the analogy between oceanic and continental smokers can be extended to the peculiar microbial communities they sustain. Microbial phylogenetic analysis suggested that continental smokers contain organisms closely related to chemolithoautotrophs present at marine vents and iron-oxidizing biofilms (Colman et al., 2014, Crossey et al., 2016).

This study, carried out within the CoDL program of the DCO Community, aims to investigate the role of deeply-sourced fluids in niche ecosystem differentiation in European continental smokers. Eleven thermal manifestations located along northern Greece were selected. The sites were characterized by different temperatures (15-77 °C), pH (6.11-8.46), Eh (-289 – 40 mV), salinities (TDS 0.4-38 g/L), and available energy sources for microbial life, like H<sub>2</sub> (up to 0.8 μmol/L), CH<sub>4</sub> (up to 400 μmol/L), NH<sub>4</sub> (up to 112 μmol/L), total sulfide (up to 103 μmol/L), Fe (up to 130 mmol/L), or elements like Ba (up to 38 mmol/L), or As (up to 11.4 mmol/L)

Helium isotope analyses revealed that all of the sites but one show a distinct contribution of mantle fluids (R/R<sub>a</sub> values from 0.4 to 1.2) allowing us to classify them as “continental smokers”. Bacterial and Archaeal communities of the sites were investigated by Illumina sequencing of hypervariable regions V4-V5 of the 16S rRNA gene. All sites showed relatively paucispecific microbial communities (only 1-6 genera represented above 10%) dominated by Actinobacteria, Bacteroidetes, Firmicutes and Proteobacteria, and negligible presence of Archaea. The hottest sites were dominated by the Phylum *Deinococcus-Thermus*, with a high abundance of thermophiles belonging to other phyla, such as the the genera *Rhodothermus* and *Bacteroides*. On the contrary, chemoautotrophic genera (e.g. *Sulfurovum* and *Sulfurimonas*) are abundant in the most reducing H<sub>2</sub>S-rich waters. Noteworthy, two of the eleven sites were characterized by low Eh values and high total sulfur content, the latter being present mostly as sulfate. Such chemical-physical features support the activity of a number of bacteria able to use various sulfur compounds, whose overall abundance exceeds 82% in one site. Signatures of deep-sea vent microbial ecosystems were detected in most assemblages, together with novel taxa. In fact, a number of unassigned sequences, with relative abundances up to 5.4%, were retrieved in 7 out of 11 samples.

This study confirms that continental smokers, despite harsh conditions, by determining abundant availability of high-energy electron donors and acceptors, can host a large variety of microorganisms and rule the distribution of bacterial diversity at taxonomic and functional levels.

Colman et al., 2014. *Geobiology* 12, 83–98.

Crossey et al., 2016, *EPSL* 435, 22-30.