



Effects of Elevated CO₂ Concentrations on Microbial Populations at a Terrestrial CO₂ Vent at Latera, Italy

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CO₂ capture and geologic storage offer a new option for reducing greenhouse gas emissions that could complement strategies like improving energy efficiency and increasing the use of non-fossil energy resources. A technically feasible way of limiting CO₂ emission is storage in deep, saline aquifers or depleted gas and oil reservoirs. Our study aims at investigating the environmental impact of CO₂ leakage from deep reservoirs into near-surface terrestrial environments. To understand the effect of CO₂ leakage on such an ecosystem, detailed knowledge on the abundance and functional diversity of microorganisms and their metabolic products is essential. Consequently, an inventory of dominant microbial communities and their functional groups is required including their analysis and cultivation. These and similar topics need a deeper understanding for the establishment of a legal European framework and authorisation permits for the safe sequestration of CO₂ in the deep subsurface. Understanding the physiology of these CO₂-adapted microorganisms is important because microbes – possibly together with plants - might act as indicators for CO₂-leakage into the environment.

As study site, a CO₂ seep located on an agriculturally used meadow near the Italian city of Latera was chosen. The determination of environmentally important microbial

activities in the Latera soil samples showed significant differences between the CO₂-rich (>90 % of soil gas) “vent” and “vent+H₂S” sites and the control with background CO₂ concentrations. These showed that the presence of high CO₂ concentrations can completely inhibit acetate-dependent methanogenesis at this site.

In accordance with the microbial activities, also total numbers of microorganisms, determined via quantitative PCR, showed significant differences between control site and the center of the vent. Cell numbers of both, *Archaea* and *Bacteria*, generally were highest at the control site (Figure 2) and substantially lower at the vent. Group-specific qPCR assays were carried out to reveal, whether certain functional groups, like the methane oxidising or sulphate reducing bacteria, were absent or stimulated at the CO₂-rich sites. Furthermore, a detailed lipid biomarker analysis was conducted to investigate differences in microbial community composition between the different CO₂-influenced habitats. These information were completed with isotopic studies to reveal biosynthetic pathways used and to enhance knowledge of the relationship between different microbial groups. In combination, these data sets show a shift towards anaerobic microorganisms under elevated CO₂ concentrations. The differences in the community composition between the sites were well in accordance with the activity data.

In summary, significant effects of high CO₂ concentrations were observed on microbial activities, lipid biomarker inventory, and cell numbers at the terrestrial CO₂ vent at Latera. These preliminary results already indicate the stimulation (sulphate reduction) or inhibition (acetate-dependent methanogenesis) of distinct groups of microorganisms as a consequence of the long-term exposure of the soil environment to high CO₂ concentrations. At the end, this study should identify possible candidates in the microbial kingdoms, whose presence or absence provide easily detectable and accurate indicators for the leakage of CO₂ from deep reservoirs into near-surface terrestrial ecosystems.