



## **Microbial diversity and activity in a pristine aquifer**

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Microbial diversity was investigated through cell numeration and 16S rRNA gene analyses, in a pristine aquifer of Brittany (France). A metaproteomic approach is also performed to analyze this microbial community functional response to modifications of forcing parameters. The pristine aquifer is defined as an oligotrophic environment where heterotrophic processes are dominant despite the lack of organic carbon and the high nitrate concentration. Bacterial diversity is abundant and unique with approximately 80% of its phylotypes being unknown and a bacteria numeration quite large ( $2 \cdot 10^5$  to  $2 \cdot 10^6$  cells per mL). From the 27 phylogenetic species found by sequences analyses, 6 belong to new classes or phyla. The diversity discovered in this aquifer should be considered as highly original. This may be the result of: (i) the use of new primers and (ii) the very limited number of published studies about microbial diversity within such environment. With the same microbial community, nitrate reducing microbial activity is tested, in laboratory conditions with acetate and glucose as sources of carbon. Microbial activity is accessed by monitoring nitrate concentration and protein expression determination. This study shows preferential acetate consumption (over glucose) linked to a complete nitrate reduction and a high proteins expression. We demonstrate that the nature of carbon is fundamental to reduce nitrate concentration efficiently and that community reacts specifically to environmental pressures. The metaproteomic approach indicates a clear divergence among activated metabolic pathways expressed in microorganisms' communities as a result of the na-

ture of the carbon added (forcing variable).