



## **Enhanced analysis of the community structure of a subsurface radioactive thermal spring in the Austrian Central Alps**

**G. W. Weidler**, M. Dornmayr-Pfaffenhuemer and H. Stan-Lotter

University of Salzburg, Department of Molecular Biology, Division of Microbiology,  
Billrothstrasse 11, A-5020 Salzburg, Austria (gerhard.weidler@sbg.ac.at, Phone: +43 662  
8044-7211)

A molecular analysis of the community structure of the radioactive subsurface thermal spring „Franz-Josef Quelle“ (FJQ) in the Austrian Central Alps was performed (2). Besides the high microbial diversity, ammonia oxidizing *Crenarchaeota* and several bacterial species, which were involved in the nitrogen cycle, were also detected. Additionally several sequences were obtained that were related to sequences from locations, which were e.g. contaminated with radioactivity, suggesting the probable presence of organisms that can interact with the Ra, Rn or U in the spring. Furthermore, biofilms were recognized, which had some similarities to the ones described by Holmes and coworkers (1) in the Nullarbor caves. Holmes suggested that a large part (about 12%) of the microorganisms inhabiting these mats were related to a *Nitrospira* sp. Besides the mats, which were present in the spring FJQ, sequences of *Nitrospira* and related species were found (2). Nitrifiers are known to build biofilms under sub-optimal growth conditions, e. g. the water temperature in the spring is 45°C, but the optimum growth temperature of nitrifiers lies between 25 to 30°C. Preliminary DGGE fingerprinting results of the spring showed the dominance of *Nitrospira* related organisms in biofilms and on glass slides which were placed into the spring for several days. Therefore an extended examination of these natural and artificial biofilms is in progress by addition of DGGE analysis and culturing approaches.

1. Holmes, A. J., Tujula, N. A., Holley, M., Contos, A., James, J. M., Rogers, P., Gillings, M. R. 2001. Environ. Microbiol. 3:256-264.
2. Weidler, G. W., Dornmayr-Pfaffenhuemer, M., Gerbl, F. W., Heinen, W., Stan-

Lotter, H. 2007. *Appl. Env. Microbiol.* 73:259-270.