

Martian permafrost might hypothetically record genetic signatures of preexisting life, which has long since vanished. Best Earth's analogue of Mars is permafrost, which studying gives an understanding of our possibilities to find life on Mars. Among the various microorganisms observed in the permafrost, methanogenic archaea is one of very important group of anaerobic lithotrophs. The main goal of this work was the investigation of methanogens in Arctic permafrost. We also tried to get answer how methanogens have been preserved during geological time and maintain viability. Samples from typical Arctic permafrost horizons of different age (modern, 10 and 20 to 50 Kyr and

0.6 to 3 Myr) and genesis were studied. Culture and culture-independent methods were employed to characterize the culturable and unculturable microbial populations. Three cultures of methanogenic archaea were isolated from Holocene and late Pliocene horizons. New species *Methanobacterium veterum* sp. nov and strain *Methanosarcina mazei* JL01 were isolated and described. tDNA were extracted and amplified with archaea-specific primers. Positive results were observed with tDNA from modern soil to 50 Kyr old permafrost samples. It was shown domination of order Methanosarcinales in majority of analyzed permafrost samples.

Phenomenon of the Black Sea Smoker

V. Kutny, O. S. Potashko, and I. Shnyukov

*Department of Marine Geology and Sedimentary Ore-Formation, The National Academy of Sciences of Ukraine, ul. 55-b Gonchara, Kyiv, 01054, Ukraine
e-mail: ale-potas@bigmir.net*

In 2001 from a bottom of Black sea the fragment of the smoker has been lifted From depth 1600 m. The raising has been carried out by a drag, the sizes of fragment: 1.0 × 0.5 m. The external part chimney has been covered by organic gel in the thickness of 10 mm. The basic part of the lifted smoker is exhibited at Central Museum of

Natural History in Kiev. The object owns the astrobiological aspects due to extreme living conditions of bacterial floor-mats which cover outside wall. It has been carried out radio carbon dating. Element, isotopic, mineral and microbiological floor-mats structure defined using analyses: spectral, sonde, Roentgen-fluorescent.

Astrobiological Lessons from the Ancient Iron-Oxidizing Genus *Gallionella*

M. Meola^a, N. M. Lee^a, Ch. Heim^b, N.-V. Quéric^b, O. Braissant^c, D. Ionescu^d, D. de Beer^d,
F. E. Löffler^e, V. Thiel^b, J. Reitner^b, and W. Liebl^a

^a*Technische Universität München, Lehrstuhl für Mikrobiologie, Emil-Ramann-Str. 4, München, Freising, 85354 Germany*

^b*Göttingen University, Geobiology, Geoscience Centre, Goldschmidtstraße 3, Göttingen, 37077 Germany*

^c*University of Basel, Lab. for Biomechanic and Biocalorimetry, Klingelbergstrasse 50-70 Base, 4056 Switzerland*

^d*Max Planck Institute for Marine Microbiology, Celsiusstrasse 1, Bremen, D-28359 Germany*

^e*Department of Microbiology and Department of Civil & Environmental Engineering, University of Tennessee Biosciences Division, Oak Ridge National Laboratory, P.O. Box 2008 Oak Ridge, TN, 37831 USA
e-mail: marco_meola@hotmail.com*

The biology of iron transforming microorganisms is of fundamental importance for our understanding of past and present biogeochemical processes on Earth, as iron is the most abundant element. This abundance promoted a fascinating evolution of a diverse group of prokaryotes metabolizing different iron compounds in various ecosystems, encompassing chemolithotrophic and heterotrophic species, as well as different types of extremophiles from both prokaryotic domains. Iron metabolizing prokaryotes like the iron-oxidizing *Gallionella* thus constitute interesting models for our emerging comprehension of past and present prokaryotic evolution in iron-based environments and its current role in our biosphere as well as in astrobiology in general. Not only does *Gallionella* species belong to

one of the few current species whose ancestors can be traced back to the eldest prokaryotic fossil records on our planet (Hofmann et al., 2008), they still play a fundamental role in many ecosystems, e.g. in the vast unknown subsurface. Although the genus *Gallionella* was already described in 1836, our knowledge about its biodiversity is scarce. So far, only one strain, *Gallionella capsiferriiformans* T, has been deposited in a type culture collection and just recently the draft for the genome sequence of *Gallionella ferruginea* subsp. *capsiferriiformans* ES-2 was released. However, a recent inventory of hundreds of 16S rRNA gene sequences affiliated to *Gallionella* suggests that an unexplored diversity exists. Here, we describe our efforts to explore the global biodiversity of *Gallionella*