

## MASTER PROJECT

### MICROBIAL LIFE IN SIBERIAN PERMAFROST – WHO ARE THE KEYPLAYERS?

The Arctic permafrost region plays a key role in the Earth's climate systems. The main reasons are that (i) global warming is predicted to be highest in polar regions and (ii) a significant part of the global carbon pool is stored in Arctic ecosystems. Warming of the upper permafrost might have tremendous consequences and lead to a dramatic increase in microbial activity and organic matter decomposition. The huge carbon reservoir in permafrost may thus become a **future source of a large amount of the greenhouse gases carbon dioxide and methane to the atmosphere**. Soil ecosystems harbor the most complex and diverse microbial communities on Earth, but very little is known about their composition and structure. That is particularly true for permafrost soils. The flexibility of the microbial community in permafrost (= their genetic potential) to react on temperature fluctuation and other physical and chemical changes will determine whether permafrost environments will become net sources or sinks of greenhouse gases following warming.



This master project is appropriate for a highly motivated and responsible candidate that is interested in both microbial ecology and environmental issues (climate change) and is eager to learn and apply molecular techniques (cloning, sequencing, quantitative PCR) as well as bioinformatic tools.



The master project will be part of the CryoCARB project (Long-term Carbon Storage in Cryoturbated Soils), which is a European PolarCLIMATE project involving six European countries and Russia. The **aim of the project** will be to describe the community structure and functional potential of microbes inhabiting different soil horizons, including organic and mineral soil, as well as cryoturbated and permafrost soil. Soil samples will be obtained from the Taymyr Reserve, one of the largest Russian reserves ([www.taimyrsky.ru/ENG/frame.htm](http://www.taimyrsky.ru/ENG/frame.htm)), by the supervisor in summer 2011. Besides 16S rRNA-based analyses, microbes involved in climate-relevant processes, e.g. methane production and consumption, will be specifically targeted using a functional gene approach to (i) estimate their diversity and abundance, and to (ii) assess their potential feedback to a changing local and global climate.

#### INTERESTED IN THIS PROJECT?

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