

Open postdoc position

The Department of Aquatic Microbial Ecology, Institute of Hydrobiology, Biology Centre of the Czech Academy of Sciences, invites applications from a prospective postdoctoral scientist

One postdoc position is open in the Department of Aquatic Microbial Ecology, Institute of Hydrobiology, České Budějovice, Czech Republic to study the diversity of freshwater prokaryotes using high-throughput isolation, comparative genomics and experimental approaches. The position is in the framework of the 5-year grant PELAGICS with multinational collaboration partners (see abstract below).

Background: Small prokaryotes with reduced genomes are the most abundant organisms in freshwater lakes. However, their ecology and evolutionary history remains largely elusive because of problems in cultivating environmentally relevant microbes. One major focus of this project lies in eco-genomics of freshwater prokaryotes aiming at a large collection of environmentally abundant strains. Semi-automated high-throughput isolation with media mimicking natural conditions will be combined with cultivation experiments and comparative genomics. Whole genome sequencing of >500 strains and deep sequencing of metagenomes gained from lakes all over Europe will allow comparative population

genomics (e.g., microdiversity, biogeography, evolutionary history, etc.).

This project is planned in collaboration with other members of the institute – especially the Laboratory of Microbial Ecology and Evolution – and a large consortium from 16 European countries. We will apply a polyphasic approach, combining sampling of 70 lakes across Europe, high-throughput isolation and cultivation, comparative (meta-)genomics, lab and in-situ experiments of environmentally relevant strains and environmental quantification via e.g. specific FISH probes targeting the major players in lakes to disentangle the ecology and evolution of freshwater microbes aiming at a pan-European “inventory” of abundant freshwater prokaryotes.

Requirements: Applicants for the postdoc position should have a PhD in Biological Sciences (e.g. Limnology, Microbiology, Ecology) and must be strongly motivated to work in an ecogenomics laboratory. The majority of the work is expected to be computational (60%) and laboratory based (40%). Prior experience in microbial cultivation and linux/unix/perl/python programming might be favourably considered but is not a prerequisite for selection. Candidates must be proficient in English.

Please submit 1) a detailed CV, 2) a brief statement of your research interests and work performed and 3) the name and contact information for at least one referee (preferably all this information combined into a single PDF file). The position will remain open until a suitable candidate is found; applications will be evaluated monthly starting September 2021. Target starting date is Jan 2022, the position is initially for 2 years with a possibility of extension by 1 year.

Contact: Please send your application to **michaelasalcher@gmail.com** and indicate “Postdoc Application” in the subject. Please don’t hesitate to contact me for further information about the position.

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Links

<https://www.hbu.cas.cz/en/structure/ame/michis-page/>

https://www.researchgate.net/profile/Michaela_Salcher

České Budějovice (Budweis) is a medium-sized city ca. 150 km south of Prague with 100,000 inhabitants, a relaxed atmosphere, and a growing expat community at the Biology Centre and the University. Both the town and the surrounding countryside provide numerous opportunities for research and leisure activities. Living costs are low by international standards. Postdocs and PhD students have access to accommodation in dormitories at the campus shared by the Biology Centre and the University. Czech courses are available for foreign staff and students to reach a basic level of proficiency in everyday situations.

The Department of Aquatic Microbial Ecology (Institute of Hydrobiology, Biology Centre of the Czech Academy of Science) is an internationally recognized high-class institution for studying freshwater microbes. The Laboratory of Microbial Cultivation and Ecogenomics focuses on isolating and cultivating abundant freshwater prokaryotes and comparative genomics. There are four well-equipped microbiological laboratories: one lab for bacterial isolation and cultivation, two for molecular biology, one for working with radioisotopes and two walk-in climate-controlled chambers for cultivation and experiments. A new lab for cultivation purposes is currently under reconstruction and will be opened in autumn. Instrumentation: A fully automated fluorescence microscope with image analysis (Zeiss AxioImager) for high-throughput evaluation of CARD-FISH stained samples, three fluorescence microscopes equipped with image analysis systems, a flow cytometer equipped with an autosampler for 96-well plates, standard equipment for cultivation and molecular biology, full equipment for sampling. A MinION and MinIT (Oxford Nanopore) for generating ultra-long sequencing reads, three 128-core Unix servers (768 Gb RAM), two 64-core Unix servers (512 Gb RAM) and three 100/160 Tb NAS storage are available with all relevant software installed for analyses of (meta-)genomic data.

Pan-European Lake Sampling - Microbial Eco-genomics (PELAGICS) EXPRO-project granted by the Czech Science Foundation (GACR)

Freshwater habitats are critical for all terrestrial life, yet the vast majority of their microbial inhabitants (pro- and eukaryotes) remain enigmatic, outside the bounds of cultivation. The recent development of novel cultivation methods, coupled with advances in sequencing now provides an opportunity to finally unravel freshwater microbial diversity. The PELAGICS project plans a coordinated pan-European sampling campaign (70 lakes) with 24 collaborating scientists from 16 European countries. With novel media mimicking natural conditions and semi-automated high-throughput isolation we aim for stable cultivation and whole-genome sequencing of 500 prokaryotes and 50 unicellular eukaryotes. Moreover, terabyte scale deep-metagenomic sequencing (ca. 15 TB) will allow recovery of thousands of metagenome-assembled genomes for pro-, eukaryotes and viruses. This large-scale effort will finally uncover the microbial diversity (pro- and eukaryotes), their natural interactions and ecological roles in aquatic food webs.