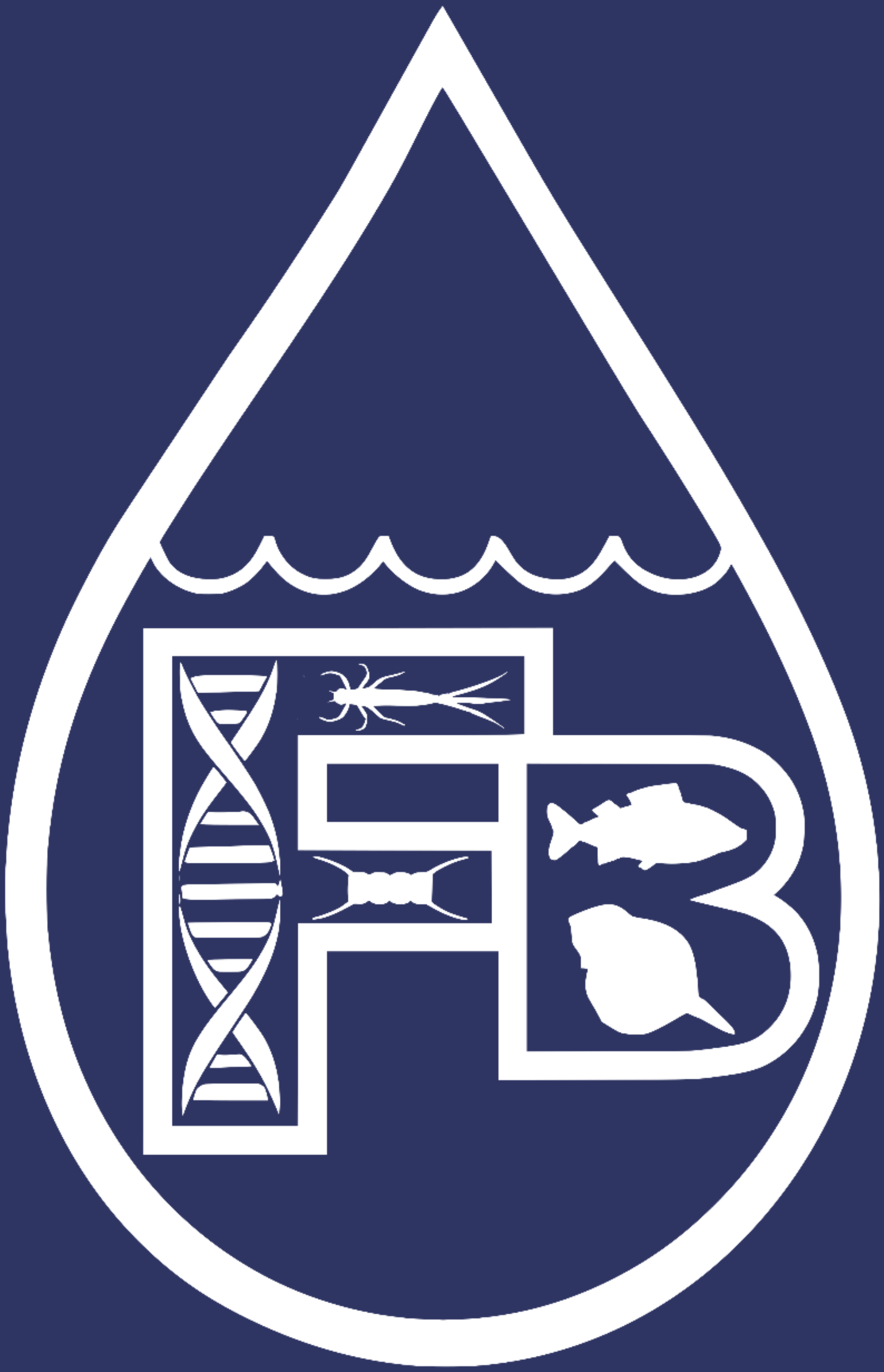
FBFW 2017



5th meeting of
Fresh Blood for FreshWater

9-13 April 2017
České Budějovice

Institute of Hydrobiology

The Institute of Hydrobiology is one of the institutes associated in the Biology Centre of the Czech Academy of Sciences in České Budějovice.

Mission statement

The Institute of Hydrobiology, Biology Centre of Academy of Sciences of the Czech Republic, v.v.i. (public research institution) is the principal institution in the Czech Republic devoted to complex freshwater research of man-made reservoirs and natural lakes. The research portfolio includes the assessment of biotic interrelations and their interactions with abiotic factors. Limnological interactions are studied both within the waterbodies and within whole catchment. The institute performs research on different levels of interactions from the ecosystem, community, population, organismal, through cellular to molecular levels. The investigations combine regular long-term ecological research on selected Czech reservoirs, comparative and methodical studies and different scale experiments that allow scrutinizing the phenomena in different time- and space-scales. The institute applies a holistic approach from elementary chemistry to high trophic levels and societal effects on water systems. It acts as an advisory body for the assessment of the ecological potential of heavily modified and artificial waterbodies. Special investigations going beyond the investigations of lakes and reservoirs involve ponds, running waters and other aquatic environment.

The Institute of Hydrobiology was established in České Budějovice in 1990, building on the long-lasting research activities (since 1959) of the Hydrobiological laboratory of the Czechoslovak Academy of Sciences in Prague, which was relocated to České Budějovice in South Bohemia between 1980 and 1984. The main research areas encompass water chemistry, fish biology, production processes of freshwater ecosystems, microbial processes, interactions and diversity using classical limnological approaches and novel molecular and isotopic techniques.

Research areas

Aquatic Microbial Ecology

Bottom-up (carbon resources and nutrient limitation) and top-down regulations of bacterioplankton community dynamics at fine temporal scales

Species-specific algae-bacterium interactions, effects of algal-derived substrates on shaping bacterioplankton community composition

Genomic and ecophysiological traits of major groups of freshwater *Betaproteobacteria* yielding their contrasting lifestyles and habitat preferences

Specific design of phylogenetic rRNA-probes for detecting non-cultivable and understudied groups of freshwater bacteria

Lineage-specific roles of different bacterial groups in carbon flow to higher trophic levels mediated by protistan grazers

Ecological significance of ectoenzymatic activities in nutrient regeneration and interactions among plankton organisms

Molecular taxonomy, ecophysiology, cultivation, characterization, and biogeography of key groups of aquatic bacteria and cyanobacteria

Effects of extreme rainfalls on phytoplankton structure and composition along the longitudinal gradient in reservoirs

Long-term changes in the phytoplankton in response to ecological changes and global climate change

Polyphasic approach in taxonomic classification of cyanobacteria and detection of cyanotoxin genes and evolution of toxin synthesis in a wide variety of benthic, periphytic and soil nostocacean cyanobacteria

Hydrochemistry and Ecosystem Modelling

Aquatic chemistry of mountain lakes and their catchments recovering from acidification and stress to forests by natural catastrophes (wind throws, bark-beetle infestation)

Eutrophication of water ecosystems as a result of external and internal nutrient loading

Reconstruction and modelling of historical trends in biogeochemical cycling of the macronutrients (organic carbon, nitrogen, phosphorus, sulfur) and other substances (chloride) in aquatic ecosystems

Photochemical processes involved in the transport of macro- and micronutrients via dissolved organic matter from soils to aquatic systems

The role of sediments and organic matter in the internal cycling of nutrients in lakes

The environmental characteristics which can best explain the patterns of nutrient flux to waters in complex catchments

Fish and Zooplankton Ecology

Interactions of trophic state, fish and zooplankton in terms of influence on the species and size composition and space-time distribution of zooplankton

Long-term changes in the zooplankton and fish of model reservoirs

Genetic studies of the populations of the most common European hybrid complex Daphnia longispina and of their links to biotic and abiotic factors

„Priority effect“ of newly colonized biotopes of lakes in former coal quarries and subsequent adaptations to changes caused by fish colonization

Physiological-ecological adaptations of the most common species Daphnia galeata,

Spatio-temporal changes in fish distribution, habitat use, activity and behaviour

Succession and management of fish communities in artificial and heavily modified water bodies

Top down and bottom up interactions in fish communities, feeding, food web role, biomanipulation.

Fish population dynamics, reproduction, recruitment, exploitation and productivity.

Climate change impact on recreational fishery.

Applications and innovations of fish community assessment methods: acoustics, seining, trawling, gillnetting, electrofishing, telemetry, mark recapture.

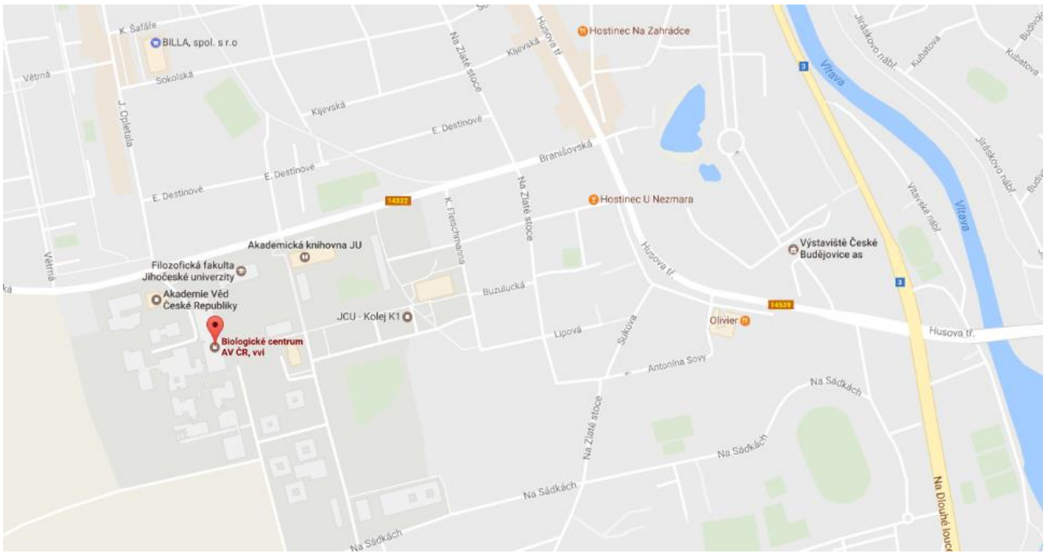
České Budějovice City

České Budějovice or Budweis, with a population of almost 100,000 people, is the largest city in South Bohemia. It was founded during the 13th century by King Přemysl Otakar II near to the junction of two rivers - Malše and Vltava. The city center is characterized by the biggest south bohemian gothic style square with the Samson fountain in the middle. The most impressive remaining of the past are the guard tower and prison known as the Iron Maiden, St Nicholas church, the 72 meter high Black Tower and the City Hall.

Budweis is famous for its brewing tradition dating back to the 13th century. The two famous breweries of the town are Samson and Budvar where the original Budweiser beer is made. Lines of restaurants and pubs offering delicious local food and beers can be found in the narrow cobblestoned backstreets of the old town.

Venue

The meeting will take place in the Congress Hall at the Biology Centre CAS within the campus of the University of South Bohemia.



This project is co-financed by the City of České Budějovice

Fresh Blood for Freshwater 2017

The 5th meeting of Fresh Blood for Freshwater, primarily organized to encourage young limnologists to present their research and exchange ideas with other early career scientists. The meeting covers a broad range of topics in the field of limnology. The 5th FBFW meeting in České Budějovice attracted 57 participants among young limnologists from 10 different countries (Czech Republic, Austria, Germany, Hungary, Slovakia, United Kingdom, Iran, Switzerland, Spain, and Romania).

This project is co-financed by the City of České Budějovice

Program overview

Sunday 9/4/2017

- 16:30-18:00 **Registration**
- 18:00 **Ice Breaking + Beer**

Monday 10/4/2017

- 9:00-11:00 **Registration**
- 11:00-11:40 **Welcome**
- 11:40-12:25 **Keynote Speaker Dr. Sandra Brucet**
- 12:25-13:30 **Lunch**
- 13:30-15:10 Monitoring and global changes
- **Coffee Break**
- 15:50-17:30 Monitoring and global changes
- 16:50-17:30 Sponsored Section SEQme
- 17:30 **Poster Presentation + Beer**

Tuesday 11/4/2017

- 9:00-9:45 **Keynote Speaker Dr. Arnaud Sentis**
- 9:45-10:25 Invertebrates
- **Coffee Break**
- 11:05-12:25 Invertebrates
- 12:25-13:30 **Lunch**
- 13:30-15:10 Invertebrates
- **Coffee Break**
- 15:50-17:10 Fish ecology and fisheries
- 17:10 **Poster Presentation + Beer**

Wednesday 12/4/2017

- 9:00-12:25 **Workshops**
- 12:25-13:30 **Lunch**
- 13:30-14:15 **Keynote Speaker Dr. Ramiro Logares-Haurie**
- 14:15-15:15 Microbiology and phycology
- **Coffee Break**
- 15:55-16:55 Microbiology and phycology
- 16:55 **Poster Presentation + Beer**
- **Dinner**

Thursday 13/4/2017

- 9:30-10:15 **Keynote Speaker Dr. Pavel Hrouzek**
- 10:15-10:35 Microbiology and phycology
- **Coffee Break**
- 11:15-11:55 Microbiology and phycology
- **Hungarian invitation for next meeting**
- 12:10-12:25 **Awards & Closing words**
- 12:25-13:15 **Lunch**

Keynote speakers

Sandra Brucet

ICREA and University of Vic - Central University of Catalonia

A key focus of my research is the response of aquatic ecosystems and their biodiversity to global changes, particularly the combination of climate change with other anthropogenic stressors such as eutrophication. I am also interested in the study of the body size structure of aquatic organisms and its relationship with ecosystem functioning and environmental change. My research includes the whole trophic structure and I use complementary approaches (experiments, latitudinal comparisons, theoretical ecology).

At the 5th FBFW meeting, I will talk about “Ecological impacts of global warming and water abstraction on freshwater ecosystems.”

Pavel Hrouzek

Institute of Microbiology, Centre Algatech, Czech

Academy of Sciences, Třeboň, Czech Republic

My research concerns primarily cyanobacterial secondary metabolites, which are known to be toxic to humans and/or possess antiviral, antifungal, antibacterial and anticancer activities. I am the head of the Laboratory of Algal Biotechnology at the Institute of Microbiology CAS. Our work consists of the detection and analysis of bioactive cyanobacterial compounds using high-performance liquid chromatography in tandem with high-resolution mass spectrometry, and tests of pharmacological and toxicological effects of cyanobacterial metabolites on human cell lines in vitro.

At the 5th FBFW meeting, I will talk about synthesis of secondary metabolites, their cytotoxic activity against cancer cells, and also about newly discovered compounds and standardized screening established in our lab.

Ramiro Logares-Haurie

Institute of Marine Sciences (ICM-CSIC) in Barcelona

I investigate natural populations of microbes with the final aim of increasing our understanding of the links between microbial life and the functioning of ecosystems. My research occurs in the interface between microbial molecular ecology, molecular evolution and computational biology. I combine multiple omics techniques (e.g. genomics, metagenomics, single-cell genomics) with bioinformatics and High-Performance computing to answer questions with scientific and societal relevance. My career started in 2003 at the Aquatic Ecology unit, Lund University, Sweden, where I got a PhD degree in Limnology & Marine Ecology in 2007. Afterwards, I moved to Uppsala University, Sweden, where I did a Post-Doc (2008-2010) at the Department of Ecology and Genetics (Limnology). After obtaining the Marie Curie fellowship, I moved, in 2010, to the Institute of Marine Sciences (ICM-CSIC) in Barcelona, where I continue now as a Ramón y Cajal fellow.

At the 5th FBFW meeting, I will present results from our research on the genomics of uncultured microbial eukaryotes, based in single-cell genomics and metagenome-assembled genomes.

Arnaud Sentis

University of Toulouse, Toulouse, France.

I am a behavioral ecologist and evolutionary biologist who combine theoretical models and empirical data to understand and predict how biotic and abiotic stresses affect individual phenotype, species interactions and evolution. I am particularly interested in the impacts of global changes (e.g. temperature, enrichment) on individual life history traits, transgenerational epigenetic inheritance, species interactions, and adaptation. I currently hold a postdoctoral position at the University of Toulouse III (France) as a TULIP Fellow, a PRESTIGE Fellow and a Marie Curie Fellow

At the 5th FBFW meeting, I will talk about “Symptoms, acclimation, and adaptation to thermal stress: implication for species and their interactions.”

Workshops

Fish Workshop (8 persons)

The fish workshop will be held at the Římov Reservoir, and will be comprised by three sessions: i) presentation of various standard techniques for sampling of fish in large standing waters (gillnets, beach seine nets, trawls, fyke nets, electrofishing), ii) introduction of a new high-tech method for observation of fish behavior - positioning of the telemetry system, and iii) practical demonstration of the use of gillnets and beach seine nets.

Milan Říha (Fish Ecology group at IHB)

Data management and food web modelling (15 persons)

Part I – Organization and manipulation of lymnological data (Vilem Ded)

This part will focus on general data organization and manipulation in scientific (limnology) fields. First part will be a lecture covering various aspects of data (data types, space, time, organization, software). Common mistakes and pitfalls will be emphasized and real (anonymous) limnology data collected in different projects on IHB will be used for demonstration. Advanced big volume database designs (relational databases) will be mentioned with brief description of basic features (integrity, security, consistency, indexing). Data organization is dependent on personal preferences, for example on favourite software, optimal work-flows, rigorousness, etc… Therefore, any inputs, questions, discussions and ideas from attendants will be more than welcomed.

Next, a fictional project will be presented with all its data inflows (devices, observations, samplings, etc...). Each participant will create its own data design covering all levels of organization (folders -> files -> tables -> columns -> data types). Some of the datasets will be then used in Part II of the workshop.

If you don't know what following terms mean, please come :)

UTC, latlon, UTM, long/wide format of data, merging tables, raster, integer, POSIX time, primary/foreign key, special character, header, NA value, UTF-8...

Part II – Introduction to Food web modelling (Samuel Dijoux)

The workshop aims to present some basics of food web modelling. Applicants will learn simple tips i) to read & understand the use of mathematical equations applied to ecological purposes, ii) and to build simple population dynamic models.

A practical activity will enable applicants to discover some of R packages used for population dynamic (deSolve and PSPM packages). This will also be a good opportunity to discuss openly and share your interest in this topic according to your respective research field.

Vilém Děd (Database management and scientific IT support at IHB)

Samuel Dijoux (Biological system modelling at University of South Bohemia)

Single filament isolation method, a precious tool in genome sequencing (5 persons)

Many cyanobacteria form nuisance water blooms producing harmful metabolites, so called cyanotoxins, posing a risk to the human and animal healt. Establishment of reliable and rapid methods are crucial in detecting potential toxic species. This interactive workshop will provide an insight on how to perform genome sequencing of monoclonal strain culture applying single filament isolation combined with MDA. Investigation of genes responsible for cyanobacteria toxic potential and specific primer design can be used for both easy toxic potential detection method and for future estimation of target-gene expression with help of real time quantitative PCR.

Andreja Kust (Aquatic Microbial Ecology group at IHB)

In the footsteps of heterotrophic nanoflagellates, small but powerful predators (5 persons)

Heterotrophic nanoflagellates (HNF) are important members of the food chain in most aquatic environments. These protists are often selectively controlling bacterial populations, and play a role in carbon flow to higher trophic levels. Despite this, only small amount of microbial ecologists is working with HNF. In our workshop, we will present simple but informative methods, which can help you to learn more about HNF population from environment of your interest: (1) We will estimate the grazing rate of HNF community using fluorescently labelled bacteria (FLB). (2) We will provide examples of catalyzed reporter deposition fluorescent in situ hybridization (CARD-FISH) of flagellates groups with explanation of methodology, as well as examples of combined CARD-FISH of flagellates and bacterial populations in the same sample.

Tatiana Shabarova & Vesna Grujčić (Aquatic Microbial Ecology group at IHB)

Monday 10/4/2017

9:00	**Registration**	
11:00	**Welcome**	
11:40	**Sandra Brucet,** ICREA and University of Vic - Central University of Catalonia **Ecological impacts of global warming and water abstraction on freshwater ecosystems**	
12:25	**Lunch**	
13:30	**Monitoring and global changes**	How design and connectivity of shoreline habitats control carbon cycling in large rivers **Eva Pölz**, WasserCluster Lunz, Boku Wien, Austria
13:50		Methane (CH4) and carbon dioxide (CO2) emissions from paddy rice ecosystems – Investigations for the potential mitigation options **Saw Min Min**, Department of Ecology and Environmental Sciences, Faculty of Science, Palacký University, Czech republic
14:10		Aquatic methane emissions in urban areas **Sonia Herrero**, Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB), Germany
14:30		Primary production under multiple stress: effects of experimental lake browning and nutrient enrichment in large-scale enclosures **Susanne Stephan**, Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB), Germany
14:50		Effects of browning and nutrient enrichment on alkaline phosphatase activity in lake plankton: a test in a large-scale enclosure experiment **Cleo Stratmann**, Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB), Germany
15:10	**Coffee Break**	
15:50	**Monitoring and global changes**	Biomonitoring and water quality **Vladyslav Bozhynov**, Laboratory of Signal and Image Processing, Institute of Complex Systems, FFPW, USB, Czech republic
16:10		Lago d'Iseo – the peculiar way a deep lake responds to a warming climate **Lau Maximilian**, Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB), Germany
16:30		Disentangling the seasonal and depth-related long-term differential warming in a mountain lake **Georg H. Niedrist**, River Ecology and Conservation Research Group, Institute of Ecology, University of Innsbruck, Austria
16:50	**SEQme**	**Identification of viral genotypes in wastewater using NGS** **NGS sequencing with SEQme** **Petr Vácha, SEQme Company**
17:30	**Poster Presentation + Beer**	

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Tuesday 11/4/2017		
9:00		**Arnaud Sentis,** University of Toulouse, Toulouse, France **Symptoms, acclimation, and adaptation to thermal stress: implication for species and their interactions**
9:45	**Invertebrates**	Searching for keystone species in aquatic food webs **Anett Endrédi**, Danube Research Institute, MTA Centre for Ecological Research, Hungary
10:05		Genomic causes of large intraspecific genome size variation in a species of rotifer **Julie Blommaert**, Research Institute for Limnology, Mondsee, University of Innsbruck, Austria
10:25		**Coffee Break**
11:05	**Invertebrates**	When lumbriculids (Annelida: Clitellata: Lumbriculidae) have power: clitellate assemblages in some Carpathian spring fens **Martina Bílková**, Department of Botany and Zoology, Masaryk University, Brno, Czech Republic
11:25		Growth and survival of pearl mussel (Margaritifera margaritifera) for bioindication **Eva Niedlová**, Departments of Biological Disciplines, Faculty of Agriculture, University of South Bohemia, České Budějovice, Czech Republic
11:45		Demographic differences in the Keratella cochlearis species complex **Adam Cieplinski**, Edmund Mach Foundation (FEM), San Michele all'Adige, Italy & Research Institute for Limnology, University of Innsbruck, Austria
12:05		How many ways can an aquatic beetle spend its time? Study on the movement and breathing behavior of Cybister lateralimarginalis De Geer, 1774 **Péter Mauchart**, Department of Hydrobiology, University of Pécs, Hungary
12:25		**Lunch**
13:30	**Invertebrates**	Behavioural types in aquatic insects and their potential effects on the food web structure and stability **Joacim Näslund**, Department of Ecosystem Biology, Faculty of Science, University of South Bohemia, České Budějovice, Czech Republic
13:50		Turbidity mediates the relative importance of herbivory and carnivory in a fairy shrimp **Dunja Lukić**, WasserCluster Lunz, Austria
14:10		Unexpected nonlinear effect of habitat complexity on functional responses **Pavel Soukup**, Faculty of Science of the University of South Bohemia, České Budějovice Czech Republic
14:30		Multiple biotic influences on functional response in an intraguild predation system **Julien Mocq**, Department of Ecosystem Biology, Faculty of Science, University of South Bohemia, České Budějovice, Czech Republic
14:50		Temperature, prey availability and predator diversity jointly influence surplus killing in a freshwater food web **Lukáš Veselý**, Faculty of Fishery and Protection of Waters, South Bohemian Research Centre of Aquaculture and Biodiversity of Hydrocenoses, University of South Bohemia, České Budějovice, Czech Republic
15:10		**Coffee Break**

15:50	**Fish ecology and fisheries**	Top or bottom? Habitat measures aimed at boosting salmonid populations may be outweighed by associated increases in predation pressure **Joe Huddart**, Imperial College London, England
16:10		Do Great Cormorants Phalacrocorax carbo target fish of the same species and sizes as anglers? **Roman Lyach**, Institute for Environmental Studies, Faculty of Science, Charles University in Prague, Czech republic
16:30		Environmental DNA as a fish monitoring tool for Alpine rivers **Dominik Kirschner**, Workgroup Applied and Trophic Ecology, Institute of Ecology, University of Innsbruck, Austria
16:50		
17:10	**Poster Presentation + Beer**	

Wednesday 12/4/2017		
9:00	**Workshops**	
12:25	**lunch**	
13:30	**Ramiro Logares-Haurie,** Institute of Marine Sciences (ICM-CSIC) in Barcelona **Genomics of uncultured microbial eukaryotes, based in single-cell genomics and metagenome-assembled genomes**	
14:15	**Microbiology and phycology**	Grazing of Nuclearia thermophila and Nuclearia delicatula (Nucleariidae, Opisthokonta) on the toxic cyanobacterium Planktothrix rubescens **Sebastian Dirren**, Limnological Station, Department of Plant and Microbial Biology, University of Zurich, Switzerland
14:35		Common stress me out – how stressors affect freshwater communities **Julia Nuy**, Department of Biodiversity, University of Duisburg, Essen, Germany
14:55		Diversification and coherence in a species of pelagic freshwater bacteria **Matthias Hoetzinger**, Research Institute for Limnology, Mondsee, University of Innsbruck, Austria
15:15		**Coffee Break**
15:55		Novel and abundant streamlined Synechococcus sp. genomes assembled from freshwater reservoirs **Pedro J Cabello-Yeves**, Department of Microbiology. Universidad Miguel Hernández. San Juan de Alicante, Spain
16:15		Beta-diversity and the main drivers of benthic diatom communities in soda pans of the Carpathian Basin **Beáta Szabó**, University of Pannonia, Department of Limnology, Hungary
16:35		The microbiology of cave water pools and dripping points – aspects from Romanian show caves **Bercea Silviu**, Emil Racoviţă Institute of Speleology, Cluj-Napoca, Romania
16:55	**Poster Presentation + Beer**	
Dinner		

Thursday 13/4/2017		
9:30	**Pavel Hrouzek,** Institute of Microbiology, Centre Algatech, Czech Academy of Sciences, Třeboň, Czech Republic **Synthesis of secondary metabolites, their cytotoxic activity against cancer cells, newly discovered compounds and standardized screening methods**	
10:15	**Microbiology and phycology**	Metagenomic analysis reveals the role of two submerged macrophyte species in shaping water column and sediment bacterial community **Yanran Dai**, Institute of hydrobiology, Chinese Academy of Sciences and WasserCluster Lunz GmbH
10:35		**Coffee Break**
11:15		Functional identity matters to ecosystem functioning in natural phytoplankton communities **András Abonyi**, MTA Centre for Ecological Research, Danube Research Institute, Hungary
11:35		Temperature- and light intensity preference of four freshwater green algae from different habitats **Tamás Pálmai**, University of Pannonia, Department of Limnology, Hungary
11:55	**Hungarian invitation for the next meeting of FBFW**	
12:10	**Goodbye**	
12:25	**Lunch**	

Poster Presentation

Burbot ecology in Central European reservoirs

Blabolil Petr, Biology Centre of the Czech Academy of Sciences, Institute of Hydrobiology, České Budějovice, Czech Republic

The effects of different DOM-sources from agricultural catchments on microbial activity in stream sediments

Campostrini Lena, University of Natural Resources and Life Sciences, Vienna, Austria

Relative roles of environmental control and spatial structuring on different macroinvertebrate dispersal mode groups within a metacommunity in small streams and higher order rivers

Csercsa András, University of South Bohemia, Faculty of Science, Department of Biology of Ecosystems, Czech Republic

Spectroscopic and phylogenetic studies of the phototrophic microbial communities in a geothermal spring in Rupite, Bulgaria

Dachev Marko, Institute of Microbiology CAS, Center Algatech, Třeboň, Czech Republic

Historical changes and phenotypic variation in Daphnia longispina species complex in Lago Maggiore

Faktorová Zuzana, Charles University, Faculty of Science, Department of Ecology, Czech Republic

Fish schooling behavior in the pelagic habitat of a freshwater temperate reservoir

Holubová Michaela, Biology Centre of the Czech Academy of Sciences, Institute of Hydrobiology, České Budějovice, Czech Republic

Mayflies of the Caucasus Mountains: diversity and perspectives

Hrivniak Ľuboš, Institute of Entomology, Biology Centre CAS, České Budějovice, Czech Republic Faculty of Sciences, University of South Bohemia, České Budějovice, Czech Republic

Shoreline morphology as a controlling factor for epilithic algal communities (Danube River, Austria)

Ivanković Marina, WasserCluster Lunz - Biologische Station GmbH, Lunz am See, Austria

Biodiversity of aerobic heterotrophic microorganisms of the Caspian Sea

Kangarani Farahani Homa, Extremophiles Laboratory, Department of Microbiology, Faculty of Biology and Center of Excellence in Phylogeny of Living Organisms, College of Science, University of Tehran, Tehran, Iran

Microhabitat use of fishes in submontane streams – size matters

Maroda Ágnes, Department of Hydrobiology, University of Pécs, Hungary

The effects of different DOM-sources from agricultural catchments on microbial activity in stream sediments

Masic Damir, University of Natural Resources and Life Sciences, Vienna, Austria

Valuation of Ecosystem services at the Biharugra Fishponds

Palásti Peter, NARIC-HAKI, Szarvas, Hungary

Breeding site use of protected amphibian species in Hungary

Péntek Attila László, Department of Zoology and Animal Ecology, Szent István University, H-2100 Gödöllő, Páter Károly u. 1. Hungary

Double origin of fairy shrimp Eubranchipus grubii in Central European vernal pools

Pešek Pavel, Department of Ecology, Faculty of Science, Charles University in Prague, Czech Republic

The Green Tetrahymena utriculariae n. sp. (Ciliophora, Oligohymenophorea) with its Endosymbiotic Algae (Micractinium sp.), Living in Traps of a Carnivorous Aquatic Plant

Pitsch Gianna, Limnological Station, Department of Plant and Microbial Biology, University of Zurich, Switzerland

Assimilation of organic matter by natural microbial communities in light and dark

Piwosz Kasia, Institute of b Microbiology CAS, Centre ALGATECH, Třeboň, Czech Republic

Cryptic diversity of the Gammarus fossarum species complex (Amphipoda) across the Bohemian Massif and Western Carpathians: phylogeny and lineage distribution

Rutová Tereza, Charles University in Prague, Faculty of Science, Department of Ecology, Czech Republic

Effects of the chrysophyte Uroglena americana on the zooplankton secondary production in the alpine Lake Lunz, Austria

Schneider Claudia, WasserCluster Lunz, Dr. Carl Kupelwieser Promenade 5, A-3293 Lunz am See, Austria

Distribution of Crucigenioid Algae in the Classes Chlorophyceae & Trebouxiophyceae

Štenclová Lenka, University of South Bohemia, Faculty of Science, Czech Republic

Potency of water bloom lipopolysaccharide (LPS) to induce pro-inflammatory effects in vitro

Švihálková Lenka, Department of Free Radical Pathophysiology, Institute of Biophysics, Academy of Sciences of the Czech Republic, v. v. i., Brno, Czech Republic

The effects of puwainaphycin F on Caco-2 cell line as a model of the intestinal barrier

Vasicek Ondrej, Institute of Biophysics, Academy of Sciences, Brno, Czech Republic International Clinical Research Center – Centre of Biomolecular and Cellular Engineering, St. Anne's University Hospital, Brno, Czech Republic Institute of Experimental Pharmacology and Toxicology, Slovak Academy of Sciences, Bratislava, Slovak Republic

A farewell to distance-based clustering: Accurate reconstruction of rRNA gene diversity in environmental samples by radical denoising

Villiger Joerg, Limnological Station, University of Zurich, Switzerland

Fish Behavior and Fish Color Monitoring

Urbanová Pavla, Laboratory of Signal and Image Processing, Institute of Complex Systems, FFPW, USB, Czech Republic

Unexpected and diverse lifestyles within the genus Limnohabitans

Kasalický Vojtěch, Biology Centre CAS, Institute of Hydrobiology, Czech Republic

First record of a putative pederin-type gene cluster and its product in a free-living cyanobacterium Cuspidothrix issatschenkoi

Andreja Kust, Biology Centre CAS, Institute of Hydrobiology, Czech Republic, Centre Algatech, Institute of Microbiology, Třeboň, Czech Republic, University of South Bohemia, Faculty of Science, České Budějovice, Czech Republic

Influence of body size and habitat productivities on trophic energetic flows: insights on a size-dependent freshwater food web and apparent competition

Samuel Dijoux, Department of Ecosystem Biology, Faculty of Science, University of South Bohemia, Ceske Budejovice, Czech Republic, Institute of Entomology, Biology Centre, Czech Academy of Science

Metagenomic recovery of phage genomes of uncultured freshwater actinobacteria

Maliheh Mehrshad, Biology Centre CAS, Institute of Hydrobiology, Czech Republic

Participants’ E-mail address

Name	e-mail
Adam Cieplinski	adam.cieplinski@fmach.it
Ágnes Maroda	maroda.agnes@gmail.com
András Abonyi	abonyiand@gmail.com
András Csercsa	andras.csercsa@gmail.com
Anett Endrédi	endredi.anett@okologia.mta.hu
Attila László Péntek	attila.petak@gmail.com
Beáta Szabó	szabobea@almos.uni-pannon.hu
Bercea Silviu	Silviu.Bercea@gmail.com
Birnstiel Emil	emil.birnstiel@uzh.ch
Claudia Schneider	claudia_schn@hotmail.com
Cleo Stratmann	stratmann@igb-berlin.de
Damir Masic	damir.masic@students.boku.ac.at
Dominik Kirschner	dominik.Kirschner@student.uibk.ac.at
Dunja Lukić	dunjalkc@gmail.com
Eva Niedlová	Evickaniedlova@seznam.cz
Eva Pölz	Eva-Maria.Poelz@wcl.ac.at
Georg H. Niedrist	g.niedrist@student.uibk.ac.at
Gianna Pitsch	gianna.pitsch@uzh.ch
Homa Kangarani Farahani	Homafarahani1987@gmail.com
Joacim Näslund	joacim.naslund@gmail.com
Joe Huddart	jeh113@ic.ac.uk
Joerg Villiger	villiger@limnol.uzh.ch
Julia Nuy	Julia.nuy@uni-due.de
Julie Blommaert	julie.blommaert@uibk.ac.at
Julien Mocq	julien.mocq@gmail.com
Kasia Piwosz	piwosz@alga.cz
Lena Campostrini	lena.campostrini@hotmail.com
Lenka Štenclová	stenclova.lenca@gmail.com
Lenka Švihálková	sindler@ibp.cz
Ľuboš Hrivniak	lubos.hrivniak@gmail.com
Lukáš Veselý	veselyl@frov.jcu.cz
Marina Ivanković	marina.ivankovic90@gmail.com
Marko Dachev	dachev@alga.cz
Martina Bílková	maty.bilkova@seznam.cz
Matthias Hoetzinger	matthias.hoetzinger@uibk.ac.at
Maximilian Lau	Maximilian_lau@yahoo.de
Michael Kolmar	office@sanako-koi.com
Michaela Holubová	Michaela.Holubova@centrum.cz
Ondrej Vasicek	ondrej.vasicek@ibp.cz

Pavel Pešek	pesek.pa@seznam.cz
Pavel Soukup	pavsoukup@gmail.com
Pavla Urbanová	purbanova@frov.jcu.cz
Pavla Urbanová	purbanova@frov.jcu.cz
Pedro J Cabello-Yeves	pedrito91vlc@gmail.com
Péter Mauchart	mauchart@gamma.ttk.pte.hu
Peter Palásti	palasti.peter@haki.naik.hu
Petr Blabolil	Blabolil.Petr@seznam.cz
Saw Min Min	sawminster@gmail.com
Sebastian Dirren	s.dirren@limnol.uzh.ch
Sonia Herrero	herrero@igb-berlin.de
Susanne Stephan	s.stephan@igb-berlin.de
Tamás Pálmai	palmait@almos.uni-pannon.hu
Tereza Rutová	trutova@seznam.cz
Vladyslav Bozhynov	vbozhynov@frov.jcu.cz
Yanran Dai	yanrandai@hotmail.com
Zuzana Faktorová	faktorovazuzana@seznam.cz

Organizers’ E-mail address

Vojta Kasalický	vojtech.ves@post.cz
Dijoux Samuel	dijoux.samuel@gmail.com
Zuzana Frkova	zuzabluz@gmail.com
Andreja Kust	andreja.kust@gmail.com
Vesna Grujcic	grujcicV@gmail.com
Říha Milan	mriha00@gmail com
Tatiana Shabarova	shabrik@gmail.com
Maliheh Mehrshad	chaji.ml@gmail.com

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Abstract text:

There are many ways how to use NGS technologies in studies of nature around us or inside us. We have used NGS sequencing and following data analysis (whole genome mapping and genotyping) to look for certain kind of viruses in human intestinal microflora and waste waters. With the use of very small sequencing capacity we have found the kind of virus we were expecting to find. Moreover, we have very easily determined with high accuracy variations of its segmented genome and thus we have very accurately described the type of virus found in the sample. This study is the first step of evaluation method of fast, accurate and versatile identification of virus types in human intestinal microflora and/or in waste waters.

How design and connectivity of shoreline habitats control carbon cycling in large rivers

***Eva-Maria Pölz*[1, 2]*, Gabriele Weigelhofer*[1, 2]*, Xiaoxiong Zheng*[1]*, Elisabeth Bondar-Kunze*[1, 2]*,*
and Thomas Hein[1, 2]

[1] WasserCluster Lunz Biologische Station GmbH, Lunz am See, Austria

[2] Institut für Hydrobiologie und Gewässermanagement, Universität für Bodenkultur, Vienna, Austria

Abstract text:

River systems have been viewed as simple drainage pipes transporting terrestrial matter, but are actually active players in the carbon cycle - a key ecosystem property - and large amounts of carbon and nutrients are not only stored in river sediments, but are also degraded, transformed and mineralized due to microbial activity in the water column and sediments. However, like most large rivers in Europe and North America, the Danube has been morphologically modified to a large extent for flood protection, navigation and hydropower production during the last century. Nowadays channelization and straightening of fluvial corridors has increased the flow of surface waters and minimized contact time and space between the active channel and riparian subsystems. Instead of extended floodplains and heterogeneous river banks, artificial shoreline habitats, such as groines or artificial side arms, have to take over important function in the carbon and nutrient cycle.

In this study we wanted to know, if and to what extend these artificial and altered shoreline habitats play a role in the carbon cycle of the river. We compared six different artificial shoreline habitats as to the turnover and degradation of organic matter and studied the effects of hydrological connectivity and retention on microbial activities (respiration, extracellular enzymatic activities, bacterial secondary production) and carbon accumulation.

Benthic respiration and carbon stocks showed a strong (but non-linear) positive response to an increasing share of fine sediment, which is linked to hydrologic retention. Non-linear statistics and regression splines revealed for example a significant and strong, negative relation between glucosidase activity and flow velocity. Other influencing factors for microbial activities were the depth of the water body and the type of connection of the water body with the main channel. An understanding of the relationship between the function and design of artificial shoreline habitats are therefore required for ecologically orientated planning and management of large rivers.

Methane (CH_4) and carbon dioxide (CO_2) emissions from paddy rice ecosystems –Investigations for the potential mitigation options

***Saw Min Min*[1]**, *Martin Rulik*[1]

[1]Department of Ecology and Environmental Sciences, Faculty of Science, Palacký University

Abstract text:

Global warming is one of the critical issues and could be of significance in an environmental consequence due to the increasing greenhouse gases in the atmosphere. The effect of greenhouse gases was increasing globally and atmospheric concentration of carbon dioxide (CO_2) and methane (CH_4) has been increasing rapidly in recent year. Methane is the most important one among greenhouse gases, while having higher global warming potential than carbon dioxide. Rice is the major food source for the world especially in Asia which was cultivated intensively under flooded condition. Flooded rice field are listed among the most important sources of methane emission for a global greenhouse budget. Methane is the final product of microbial breakdown of organic matter, produced by a group of strictly anaerobic *methanogenic archaea*in rice paddies, swamps, sludge digesters, rumens and sediments. There are large spatial and temporal variations of CH_4 fluxes from the rice fields due to different soil types, and various agricultural practices, such as rice cultivar, water management, application of organic manures and fertilizers. However, the mechanism and magnitude behind the CO_2 flux exchange between the rice paddies and atmosphere is still now unclear.

This research will estimateCH_4 and CO_2emissions from paddy rice by conducting greenhouse experiment and subsequent actual field measurements in Myanmar. For greenhouse experiment, we will quantify $CH_4$and CO_2 gas emission in different rice growth stages, different water and mineral fertilizer management practices for finding suitable mitigation options of CH_4/CO_2emissions from rice ecosystems. For field experiment in Myanmar, we will estimate spatial and diurnal distribution of methane (CH_4) emission based on target locations (Central and Lower Myanmar). Methane will be sampled by fibre glass (Acrylic sheet) air-tight chambers and analysed with gas chromatography (GC) while carbon dioxide fluxes will be measured by using portable Sensor Module CO_2 Engine ®ELG.

Based on the results of this research, we can quantify the amount of both CH_4 and CO_2 from the rice growing systems and different water/nutrient management to identify appropriate mitigation potentials.

Aquatic methane emissions in urban areas

***Sonia Herrero*[1]**, *Clara Romero*[2], *Peter Casper*[1], *Birgit Kleinschmit*[3], *Gabriel Singer*[2] *and Mark. O. Gessner*[1,4]

[1] Department of Experimental Limnology, Leibniz Institute of Freshwater Ecology and Inland Fisheries (IGB), Stechlin, Germany

[2] Department of Ecohydrology, Leibniz Institute of Freshwater Ecology and Inland Fisheries (IGB), Berlin, Germany

[3] Department of Landscape Architecture and Environmental Planning, Geoinformation in Environmental Planning Lab, Berlin Institute of Technology (TU Berlin), Berlin, Germany

[4] Department of Ecology, Berlin Institute of Technology (TU Berlin), Berlin, Germany

Abstract text:

Greenhouse gases (GHG) from inland waters are getting more attention due to their role in global warming. Methane (CH_4) released from fresh waters accounts for 1.4–13.2% of the global emissions of this potent greenhouse gas (GHG). However, the focus has been almost invariably on natural ecosystems, so that little is known about CH_4 dynamics in urban fresh waters, where environmental conditions could be particularly conducive to CH_4 formation. In particular, chemical composition of freshwaters in cities is highly modified, e.g. eutrophication and waste water effluents. Here we report on CH_4 emissions from a total of 32 freshwater bodies covering the metropolitan area of Berlin, Germany. They represent surface waters typically affected by multiple stressors, including alterations of hydrological regimes and morphology as well as water and sediment pollution by nutrients and micropollutants. Four types of water bodies (lakes, ponds, rivers and streams/ditches) differing in the degree of human modification were repeatedly studied over an entire year to estimate Berlin´s aquatic CH_4 footprint. Our tentative analysis of data from spring and summer 2016 suggests considerable spatial and seasonal variation in CH_4 emissions. Variation was highest in lakes and rivers, where emissions appear to be influenced by the degree of human modification, whereas ponds and ditches had the highest average emission rates (approximately 214 mg CH_4 m^{-2} d^{-1} in summer). Our results on CH_4 emissions from surface waters in the city of Berlin support the notion that considering urban areas is important when assessing aquatic GHG emissions at global scale.

Primary production under multiple stress: effects of experimental lake browning and nutrient enrichment in large-scale enclosures

Stephan, Susanne[1] *Stella A. Berger* [1], *Darren P.Giling*[1,2], *Jens C. Nejstgaard*[1], *Erik Sperfeld*[1,3], *Anne Lyche Solheim*[4], *Mark O. Gessner*[1,5]

[1]Department of Experimental Limnology, Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB), Alte Fischerhütte 2, 16775 Stechlin, Germany

[2]Experimental Interaction Ecology, German Centre for Integrative Biodiversity Research (iDiv), Deutscher Platz 5e, 04103 Leipzig, Germany

[3]Centre for Ecological and Evolutionary Synthesis, University of Oslo, Blindernveien 31, 0371 Oslo, Norway

[4]Norwegian Institute for Water Research (NIVA), Gaustadalléen 21, 0349 Oslo, NORWAY

[5]Department of Ecology, Berlin Institute of Technology (TU Berlin), Ernst-Reuter-Platz 1, Berlin, Germany

Abstract text:

Elevated levels of humic substances and nutrients resulting from climate and land-use change are widespread and increasing threats to fresh waters. These stressors often act simultaneously. To unravel how primary production and phytoplankton biomass respond to both stressors in combination, we performed a seven-week experiment with natural lake plankton. We used a large enclosure facility (www.lake-lab.de) to create a nutrient gradient corresponding to phosphorus levels ranging from oligo-mesotrophic to eutrophic conditions crossed with three levels of humic substances. Rates of primary production (^{14}C method) and algal biomass (chlorophyll *a*) were initially high in control enclosures without humic substances. Subsequently, both variables tended to respond positively to the addition of nutrients, although the overall variation in the responses was high. In the enclosures receiving humic substances, the biomass and production rates of three major size classes of phytoplankton went through rather distinct phases during the experiment, mostly driven by light availability. Rates of primary production declined sharply immediately after experimental addition of humic substances, whereas declines of phytoplankton biomass were slower. Bleaching gradually improved the underwater light conditions in the enclosures that had received the humic substances. As a consequence, the ratio of euphotic to mixing depth (z_{eu}/z_{mix}), which was strongly depressed directly after experimental browning, began to exceed unity again after one month. The biomass of the picoplankton fraction started to increase concomitantly, most likely because the larger size fractions were heavily grazed by zooplankton. Overall, our results demonstrate that lake browning is a dominant stressor of planktonic primary producers, switching nutrient to light limitation even in oligo-mesotrophic conditions.

Effects of browning and nutrient enrichment on alkaline phosphatase activity in lake plankton: a test in a large-scale enclosure experiment.

***Cleo N. Stratmann*[1]**, *Stella A. Berger*[1], *Darren P. Giling*[1,2], *Lars Ganzert*[1], *Jens C. Nejstgaard*[1], *Mark O. Gessner*[1,3]

[1]Department of Experimental Limnology, Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB), Stechlin, Germany

[2]German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Germany

[3]Department of Ecology, Berlin Institute of Technology (TU Berlin), Berlin, Germany

Abstract text:

Climate and land-use changes have increased the leaching of humic substances and nutrients from catchments into surface waters within the last decades. The resulting browning of lake water by coloured dissolved organic matter and elevated nutrient supply have both well-documented ecosystem consequences. However, the effects of the combined stressors (i.e. browning and eutrophication) on lakes remain poorly known. We investigated these effects on the exoenzymatic activity of alkaline phosphatase (AP), a critical enzyme to provide bioavailable (inorganic) phosphorus to autotrophic and heterotrophic lake plankton for growth. In a large-scale enclosure experiment conducted in a deep clear-water lake (http://www.lake-lab.de), we crossed three levels of browning (clear, meso-, polyhumic) with seven levels of nutrient supply that corresponded to a gradient from oligo- to eutrophic conditions. We determined Michaelis-Menten kinetics of AP at least weekly over a period of 6 weeks by incubating bulk plankton samples using a fluorogenic model substrate. Both stressors independently reduced the enzymatic activity of AP and also affected enzyme kinetics interactively. Specifically, the observed reduction of AP activity with increasing nutrient supply was weakened at elevated levels of browning. Furthermore, the kinetic results indicate that browning led to non-competitive inhibition, whereas elevated nutrient supply caused competitive inhibition of the enzyme. This implies that both stressors reduce the inorganic phosphorus provision from organic matter, although their effects are due to different mechanisms. Overall, our results suggest that browning and nutrient enrichment can notably influence AP kinetics and thus affect phosphorus cycling in lake plankton under future global change.

Biomonitoring and water quality

***Vladyslav Bozhynov*[1]**, *Pavla Urbanová*[1], *Antonín Bárta*[1], *Pavel Souček*[1], *Jan Urban*[1], *Dalibor Štys*[1]

[1]Institute of Complex Systems, Faculty of Fisheries and Protection of Waters, University of South Bohemia in České Budějovice, Zamek 136, Nove Hrady, 37333, Czech republic

Abstract text:

The water quality is an important question for the environment as well as for the aquaculture. The precise monitoring could be done using advanced laboratory techniques (e.g. mass spectrometry, spectrophotometers, capillary electrophoresis). However, quick response and event alerts require automatic and online solutions for monitoring of the basic parameters and their evaluation. The crucial nutrients, secondary metabolites, dissolved gases, pollutions could be detected using simple techniques. The combination of appropriate probes, microPC control and GUI software application or web solution could be extended by bioWes protocol manager to describe the experiments and use proper ontology. The novel approach is also to evaluate the correlation between the water quality and its color measurement.

Lago d'Iseo – the peculiar way a deep lake responds to a warming climate

Maximilian Lau[1], *Juliane Roth*[1], *Marco Pilotti*[2], *Michael Hupfer*[1]

[1]Leibniz Institute of Freshwater Ecology and Inland Fisheries, Berlin, Germany

[2]University of Brescia, Dipartimento di Ingegneria Civile, Architettura, Territorio, Ambiente e di Matematica, Italy

Abstract text:

In many lakes of the boreal and temperate zone, a warming climate constrains lake-internal mixing. In prealpine Lake Iseo (Italy), a monimolimnic water layer is currently decoupled from the seasonally mixed water body for already a whole decade. In a series of field campaigns we quantified pools and fluxes of water- and sediment-borne biogeochemical analytes throughout 250m deep Lake Iseo. The resulting balances revealed that the undisturbed monimolimnion acts as a temporary sink for the nutrient phosphorus that is recycled from the settling detritus. We show that a large part of the detrital phosphorus is not permanently buried in the sediments but rapidly redirected to the bottom water. Following a strong and stormy winter, the monimolimnic phosphorus can then induce a marked increase in phototrophic production when re-mixed into surficial waters.

As a warming climate extends the periods of accumulation, Lake Iseo is potentially threatened by more intensive yet episodic eutrophication. Deciphering the nutrient distribution through the benthic and pelagic compartments will help to identify the drivers that control the response of this and other deep lakes to a changing climate.

Disentangling the seasonal and depth-related long-term differential warming in a mountain lake

***Georg H. Niedrist*[1, 2]**, *Roland Psenner*[3*], *Ruben Sommaruga*[3]

[1]River Ecology and Conservation Research Group, Institute of Ecology, University of Innsbruck, Innsbruck, Austria
[2]Natur.Gewalt, Umweltanalyse und -service, Innsbruck, Austria
[3]Lake and Glacier Ecology Research Group, Institute of Ecology, University of Innsbruck, Innsbruck, Austria

[*]Present address: EURAC Research, Bozen/Bolzano, Italy

Abstract text:

Lakes around the world are warming, but not all water layers increase in temperature at the same rate. Here, we analysed a 44 year-long monthly temperature time-series obtained at 9 different depths from a small, 24.6 m deep mountain lake in the European Alps. While we observed a differential long-term warming in epi-, meta-, and hypolimnetic water layers corresponding to 0.36, 0.18 and 0.07°C per decade, respectively, a significant seasonal warming only occurred from August to December in all water layers. The warming of Lake Piburg occurred twice as fast (0.23°C per decade) as the air temperature (0.12°C per decade), but slowed down when reaching averaged local air temperature in 2004. This differential warming of lake water was accompanied with significant shifts of lake freezing and thawing dates, leading to shorter periods where lake water is shielded from atmospheric influences such as solar radiation and cold air during winter. Finally, the variance in water temperature increased significantly during the observation period, however only in the epilimnion. These results assume a winter-warming effect of lake water together with an increasing intensity of temperature fluctuations, especially in seasonally ice-covered small mountain lakes, suggesting that current broad scale estimates of climate change impacts on lakes, based on summer temperature measurements, require modification. Generally, our work demonstrates an elegant method to decompose time-series data and to extract temperature patterns not previously considered in freshwater ecology.

Searching for keystone species in aquatic food webs

***Anett Endrédi*[1]**, *Vera Senánszky*[1], *Ferenc Jordán*[1]

[1]Danube Research Institute, MTA Centre for Ecological Research, Budapest, Hungary

Abstract text:

Trophic relationships are of crucial importance in community organisation. The interactions of resources and consumers (preys and predators) are summarised in food web models, depicting who eats whom in ecosystems. Food web models represent a large amount of ecological data and are potentially applicable in many areas from system-based conservation to sustainable fisheries management. With network approach, for example, it is possible to find keystone species (species of extraordinary importance) or functional groups (e.g. benthic feeders) in these food webs or examine the spread of direct and indirect effects (e.g. trophic cascade) in the community as well. In this presentation, we would like to summarise the potential application of food web models in aquatic communities and present some (8) freshwater and marine examples for them.

Genomic causes of large intraspecific genome size variation in a species of rotifer

Julie Blommaert *[1], Riss S[1], Heacox-Lea B[2], Mark-Welch D[2], Stelzer CP[1]*

[1]Research Institute for Limnology, University of Innsbruck, Mondsee, Austria

[2]Josephine Bay Paul Centre, Marine Biological Laboratory, Woods Hole, USA

Abstract text:

Rotifers are an important part of freshwater ecosystems. The *Brachionus plicatilis* species complex inhabits a wide range of freshwater habitats worldwide. This complex of at least 15 species is morphologically diverse, both within and between species, and likely inhabits many different niches within these ecosystems. As well as this range of morphologies, *B. plicatilis* spp. exhibits genome size variations up to 8-fold. This dramatic change in genome size across the species complex is likely the largest observed in such closely related animals. The consequences of such variation, on both the structure and composition of genome, and the biology of the species complex is unknown. One species in this complex, *Brachionus asplanchnoidis*, has genome sizes ranging from 205Mbp to 271Mbp. Genome sequencing and analysis of different populations from this species are the first step in understanding such large genome size changes on short evolutionary time-scales. These data can then be related to biological and ecological outcomes. Often, in similar cases of genome size variation in plants, these changes are largely driven by non-coding DNA. Initial analyses of *B. asplanchnoidis* genomes indicate that repetitive DNA sequences are indeed responsible for a large part of the observed genome size variation. The identity and distribution of these repetitive sequences shed light on the influence of such sequences not only on genome size evolution, but also on rotifer biology.

When lumbriculids (Annelida: Clitellata: Lumbriculidae) have power: clitellate assemblages in some Carpathian spring fens

***Martina Bílková*[1]**, *Jana Schenková*[1]

[1]Department of Botany and Zoology, Masaryk University, Kotlářská 2, 602 00, Brno, Czech Republic

Abstract text:

Spring ecosystems are often neglected although they belong to the important part of streams. We studied 56 sites in the Western Carpathian Mountains and focused on one part of permanent fauna–on clitellates („Oligochaeta“ and leeches).

Spring fens are wetlands that are formed by one or more spring outflow, spring brook(s), small pools and places that are permanently or occasionally wet. Their stable water conditions (mainly in and near the outflow) provide optimal environment for aquatic macroinvertebrates. Individual spring fens differ in water chemistry (especially in mineral richness) that is forming species composition of fauna and flora.

In spring and autumn (2006–2012) we sampled macroinvertebrates at two contrasting mesohabitats in fens (flowing and standing water) using an iron frame (25x25 cm, 5 cm depth). Clitellates were manually sorted out and determined to the species or genus level.

We found over 24.000 individuals belonging to 55 taxa of clitellates. There were typically aquatic species (from families Naididae and Lumbriculidae) but also semiaquatic (e.g. Eiseniella tetraedra, Trocheta cylindrica or some enchytraeids) and rarely terrestrial species (from family Lumbricidae and Enchytraeidae).

In most of sites (52) there were always found individuals from family Lumbriculidae (Lumbriculus variegatus, Stylodrilus heringianus, Trichodrilus strandi and T. tatrensis). In 25 sites lumbriculids dominated in samples (their percentage in assemblage was equal to or higher than 50%). Cluster analysis divided those 25 sites into 3 groups. Although taxa richness was the same, average number of individuals was different. First group comprised of sites where only L. variegatus and S. heringianus were found, also naidids, enchytraeids and leeches were very frequent. By contrast, in second group’s sites only T. strandi was found and enchytraeids and leeches were rare. The third group can be characterized as a group with no S. heringianus and very little naidids dominated by lumbriculids T. strandi and/or L. variegatus.

These differences in clitellate assemblages are caused by changes in water chemistry, more details on symposium.

Growth and survival of pearl mussel (*Margaritifera margaritifera*) for bioindication

Eva Niedlová[1], *Irena Šetlíková*[1]

[1]University of South Bohemia in České Budějovice, Faculty of Agriculture, Departments of Biological Disciplines

Abstract text:

Growth and survival of juvenile pearl mussels (Margaritifera margaritifera Linnaeus, 1758) „in-situ“ indicates suitable habitats for their rearing and subsequent reintroduction. Six streams in Aš region (Rokytnice, Lužní potok, Pekelský potok, Újezdský potok, Perlový potok, Bockbach) including 15 profiles were evaluated throughout the season (1. 6. – 31. 8. 2015). One year old pearl mussels (n = 580) sized from 700 – 1400 µm. Mean survival of pearl mussels was 63 % in all streams. Mean absolute growth increment attained 755 µm throughout the season. Growth of pearl mussels (1+) was positively correlated with the water temperature (R2 = 0,1084). Both the highest survival (70 %) and the highest absolute growth (1027 µm and 997 µm) of pearl mussels was determined on localities in Bockbach (Bockbach 11 and 1). In contrast to Bockbach 11 and 1 mean survival (28%) and absolute growth (304 µm) was the lowest in Lužní potok 2. Survival rate of two years old pearl mussels was higher than that of one year old pearl mussels. Both of these age categories grew similarly.

Demographic differences in the *Keratella cochlearis* species complex

***Adam Cieplinski*[1, 2]**, *Ulrike Obertegger*[1], *Thomas Weisse*[2]

[1]Department of Sustainable Agro-ecosystems and Bioresources, Research and Innovation Centre, Fondazione Edmund Mach (FEM), Via E. Mach 1, 38010 San Michele all'Adige (TN), Italy
[2]Research Institute for Limnology, University of Innsbruck, Mondseestraße 9, 5310 Mondsee, Austria

Abstract text:

In microscopic species such as rotifers the existence ofcryptic species (morphologically indistinguishable species) has been revealed by DNA taxonomy. Coexistence of cryptic species that presumably share the same niche is difficult to explain. Small niche preferences and differences in life parameters seem to determine co-occurence of well-known cryptic species of *Brachinus plicatilis* complex.

Keratella cochlearis is a ubiquitous freshwater rotifer that shows wide phenotypic diversity and for which recently the presence of a cryptic species complex has been indicated. Here we investigated life parameters and population parameters of three different haplotypes of *K. cochlearis* corresponding to two different putative Evolutionary Significant Units (ESUs). Our results will be interpreted in the light of co-existence of cryptic ESUs of *K. cochlearis*.

We observed and recorded all life parameters of 96 amictic females from each of the three haplotypes using 96-well plates.

All population parameters such as instantaneous growth rate of the population (r), generation time (T), net reproduction rate (Ro) were significantly different between the three haplotypes as well as between the two ESUs. Also the number of male offspring, percent of rejected eggs and number of mutated offspring were significantly different between all haplotypes. Only average lifespan and a number of offspring were not significantly different or only slightly different between the two haplotypes that belonged to one ESU.

Our results confirmed that most life history and population parameters are different between different ESUs from the *K. cochlearis* cryptic species complex. This finding has important implications for the interpretation of co-existence of cryptic species.

How many ways can an aquatic beetle spend its time? Study on the movement and breathing behavior of *Cybister lateralimarginalis* De Geer, 1774

Péter Mauchart[1], *Bálint Pernecker*[1], *Estera Garajová*[1], *Eszter Sebestyén*[1], *Tomáš Ondáš*[2], *Joacim Näslund*[3], *David S. Boukal*[3, 4], *Zoltán Csabai*[1]

[1]Department of Hydrobiology, Institute of Biology, Faculty of Sciences, University of Pécs, Ifjúság útja 6, H-7624 Pécs, Hungary

[2]Department of Zoology, Faculty of Science, Charles University, Viničná 7, CZ-12844 Praha, Czech Republic

[3]Department of Ecosystem Biology, Faculty of Science, University of South Bohemia, Branišovská 31, CZ-37005 České Budějovice, Czech Republic

[4]Institute of Entomology, Biology Centre CAS, Branišovská 31, CZ-37005 České Budějovice, Czech Republic

Abstract text:

Aquatic invertebrates and their distributions are mostly studied via field surveys where the occurring species/individuals counted. However, learning more about the movement and activity patterns of benthic macroinvertebrates should get in to focus, because the success of these field surveys may depends on the behavior of each specimens. This is particularly true for large and mobile species such as the diving beetles from the Dytiscinae subfamily. To fill this gap, we studied the movement and air uptake behavior of male *Cybister lateralimarginalis* individuals in a pilot laboratory experiment focusing on their behavior near fishing traps baited with fresh chicken liver, which are now routinely used for the monitoring of large and mobile species. Observations were performed at 22°C (10D:14L photoperiod) in 2.4 m x 2.4 m square basins filled with 14 cm of aged tap water and provided with two bricks as resting places and a baited fishing trap. Individuals were acclimated in 600-L aquaria for several days before the experiment. We recorded their behavior continuously with high definition (2K) IR-sensitive cameras for 8 hours during the day and night conditions and subsequently scored the videos for the following types of behavior: resting, swimming (including swimming speed and direction), and breathing (timing and duration of air uptake). Our preliminary analyses identified highly contrasting behavior between day and night: the movement of the individuals were much more random at day and were more consistent at night when they were usually swimming around on almost the same route. Moreover, average speed and distance covered were also significantly higher at night because the individuals spent more time swimming. Additionally, air uptake duration were significantly longer at night, while the intervals were similar both at day and night.

Behavioural types in aquatic insects and their potential effects on the food web structure and stability

***Joacim Näslund*[1,2], *David S. Boukal*[1,2,3]

[1]Department of Ecosystem Biology, Faculty of Science, University of South Bohemia

[2]SoWa Research Infrastructure

[3]Department of Biosystematics and Ecology, Biology Centre AS CR, Institute of Entomology

Abstract text:

Animal personalities, or consistent individual differences in behaviour, is a hot topic in behavioural ecology. However, most research has focused on the evolutionary background for this variation, and its consequences for fitness within individuals. The field of investigation is now changing towards effects of different personality types on the ecosystem. In this presentation, we will show that personality traits are found also in aquatic insects. Using a standardized laboratory test measuring voluntary activity, we show that both trichopteran (*Limnephilus lunatus*) and odonate (*Aeshna cyanea*) larvae show consistent individual differences in their activity rates, after correcting for relevant influencing factors. In *A. cyanea* the activity rates were also correlated with temperature and routine metabolism (as measured in a closed respiration chamber). However, despite clear predictions about 1) a positive relationship between activity and metabolism, and 2) a positive effect of temperature on both these traits, preliminary results indicate complex relationships. Overall, the presence of consistent individual differences in behaviour suggests that different individuals in a population may have different functional roles in the ecosystem. This indicates that changes in the environment may favour certain behavioural types over others, which then may lead to ecological feedbacks (e.g. trophic cascades) with consequences for food web structure and stability.

Turbidity mediates the relative importance of herbivory and carnivory in a fairy shrimp

***Dunja Lukić*[1, 2]**, *Csaba F Vad*[1], *Robert Ptacnik*[1], *Zsófia Horváth*[1]

[1]WasserCluster Lunz, Lunz am See, Austria

[2]Department of Limnology and Bio-Oceanography, University of Vienna, Vienna, Austria

Abstract text:

Large branchiopods, a group including anostracans, are a flagship group of temporary ponds. Temporary waters are usually very shallow habitats, exposed to the mixing effect of wind, which may contribute to high levels of turbidity. There are many gaps in our knowledge about temporary ponds, and turbidity due to inorganic particles is largely understudied in particular. Our aim was to determine whether turbidity affects the feeding process of anostracans and if there is a difference in response between filter and predatory feeding. An anostracan species, *Branchinecta orientalis*, was cultured from sediment collected in Central European soda pans. Short-term feeding experiments were performed with several turbidity levels. For the turbidity treatment, we used sterilised fine sediment from a soda pan. As filter-feeding test, we used two unicellular green algal species: a relatively larger species and a picoplanktonic species, which are dominant members of soda pan phytoplankton throughout the year. In the predatory feeding test, a copepod and a rotifer co-occurring with *B. orientalis* were employed. There was a pronounced decrease in the clearance rates on algae with increasing turbidity. The effect of turbidity was significant for both algae. Conversely, predation efficiency was not significantly affected by turbidity. Our results therefore imply that the same anostracan species could feed omnivorously in transparent and more predatory in turbid waters, as turbidity only impairs the feeding rates on phytoplankton and not on zooplankton. It confirms our assumption that turbidity directly affects the feeding type of *B. orientalis*. Our study species, *B. orientalis*, exhibits high densities in its natural habitats and therefore might have a strong effect on the co-occurring planktonic species. According to our findings, turbidity may act as a switch on an intra-guild predation relationship, where fairy shrimps feed omnivorously on algae and their grazers at low turbidity, while they feed more exclusively on small zooplankton at high turbidity.

Unexpected nonlinear effect of habitat complexity on functional responses

Pavel R. Soukup ***[1, 2]***, *Julien Mocq*[1], *David S. Boukal*[1, 2]

[1]University of South Bohemia in České Budějovice, Branišovská 1645/31a, 370 05 České Budějovice, Czech Republic

[2]Institute of Entomology, Biology Centre CAS, Branišovská 1160/31, 370 05 České Budějovice, Czech Republic

Abstract text:

Habitat complexity features prominently among environmental factors that modify the strengths of consumer-resource interactions and thereby affect the structure and stability of food webs. In a variety of ways, it can influence the shape and magnitude of consumer functional responses. However, possible changes in functional responses along a gradient of habitat complexity are surprisingly little known. To fill these gaps, we conducted a laboratory experiment to estimate the functional response parameters of *Aeschna cyanea* feeding on *Chaoborus obscuripes* in seven densities (2, 4, 8, 16, 32, 64, 128 individuals) along a gradient of habitat complexity (0, 1, 2, 4, 8 artificial plants). Contrary to our expectations, our results revealed no refuge effect of habitat complexity that would lead to a change in the shape of the functional response. Furthermore, we found a unimodal dependence of handling time to habitat complexity with a maximum at intermediate levels. Our results challenge current theoretical and empirical evidence and show that future studies in the context of trophic interactions should carefully characterize habitat complexity beyond the commonly used presence-absence binary scale.

Multiple biotic influences on functional response in an intraguild predation system

***Julien Mocq*[1, 2, 3]**, *David S. Boukal*[1, 2, 3], *Julie Egon*[4]

[1]Department of Ecosystem Biology, Faculty of Science, University of South Bohemia, Branisovska 31, Ceske Budejovice, Czech Republic

[2]Biology Centre CAS, vvi, Institute of Entomology, Laboratory of Aquatic Insects and Relict Ecosystems

[3]SoWa Research Infrastructure, Biology Centre CAS, Na Sádkách 7, Ceske Budejovice, Czech Republic

[4]Département Biologie-Environnement, Faculté des sciences, Université Catholique de l'Ouest, 3 place André Leroy, F-49008 Angers, France

Abstract text:

Immature individuals have as purpose to grow and to stay alive, trying to eat as many as possible available preys while paying attention to competitors and predators. In this context, an individual has to deal simultaneously with the prey availability, the competition and interferences due to conspecifics and the presence of a potential intraguild predator through cues such as chemical or visual information. All of these variables may affect the functional response of the individual but their precise combined effects are unknown. We used 4 densities of *Chaoborus obscuripes* as intermediate predator, feeding on 7 densities of *Daphnia magna* as prey-resource, with the optional presence of chemical or visual cues of *Aeshna cyanea* without direct contact. *Chaoborus* systematically exhibits a functional type-II response. Then, the mutual interference had a medium magnitude, decreasing slightly the prey consumption per individual, even if *Chaoborus* can use a swarming strategy to protect against predators. However, neither the chemical cues, nor the visual cue or both simultaneously exhibited a clear influence on *Choaborus* predation. *Choaborus* may use another form of perception of the predator, or is unable to perceive these information, or behave boldly despite clear information about a threat.

Temperature, prey availability and predator diversity jointly influence surplus killing in a freshwater food web

***Lukáš Veselý*[1]**, *David Boukal*[2, 3], *Miloš Buřič*[1], *Irina Kuklina*[1], *Martin Fořt*[1], *Buket Yazicioglu*[1], *Martin Prchal*[1], *Pavel Kozák*[1], *Antonín Kouba*[1], *Arnaud Sentis*[2,3,4]

[1]University of South Bohemia in České Budějovice, Faculty of Fishery and Protection of Waters, South Bohemian Research Centre of Aquaculture and Biodiversity of Hydrocenoses, Zátiší 728/II, 389 25 Vodňany, Czech Republic

[2]University of South Bohemia, Faculty of Science, Department of Ecosystem Biology, Branišovská 1760, 370 05 České Budějovice, Czech Republic

[3]Biology Centre CAS, Institute of Entomology, Laboratory of Aquatic Insects and Relict Ecosystems, Branišovská 1160/31, 370 05 České Budějovice, Czech Republic

[4]Unité Mixte de Recherche 5174 'Evolution et Diversité Biologique', Université de Toulouse - École Nationale de Formation Agronomique- Centre National de la Recherche Scientifique, BP 22687, 31326 Castanet-Tolosan, France

Abstract text:

Surplus killing (i.e., killing of prey that are subsequently not completely eaten or abandoned by the predator) is a widespread behavior in vertebrate and invertebrate predators that has important implications for population dynamics and ecosystem functioning. However, factors influencing this behavior and its dependence on environmental conditions remain poorly understood, leaving a substantial gap in our knowledge of the impacts of environmental changes on ecological communities. Here we experimentally investigated the effects of temperature, prey density, and predator diversity on surplus killing in an aquatic food web composed of dragonfly larvae (*Aeshna cyanea*) and juvenile marbled crayfish (*Procambarus fallax* f. *virginalis*) preying on common carp (*Cyprinus carpio*) fry. We found that surplus killing, measured as the ratio of killed but not eaten prey over initial prey density, increased proportionally with prey density but varied strongly with predator diversity. Intraspecific predator assemblages left more uneaten prey than interspecific assemblages. Moreover, warming reduced surplus killing but the magnitude of the effect was species-specific. Our study provides new insights into how the joint effects of temperature, prey density and predator diversity influence surplus killing, which has implications for the stability of ecological communities under rapid environmental change.

Top, bottom or both? Management actions aimed at recovering salmonid populations may have unintended net detrimental effects

Joseph Huddart[1, 2], *Guy Woodward*[1], *Stephen Brooks*[2]

[1]Imperial College London

[2]The Natural History Museum

Abstract text:

Widespread declines in freshwater species populations have made river habitat restoration a widely accepted societal goal. Restoring instream hydromorphology and habitat quality using woody debris is a globally implemented measure, often targeting recovery of culturally significant species such as salmonid populations. Such large woody debris (LWD) additions are expected to provide flow and habitat diversity, enhanced food resources, and refugia from predation. However, restoration monitoring and assessment remain rare, and where it does take place, is often inadequate in terms of design and measures used, and so unable to isolate responses to restoration from wider environmental noise.

In this experiment, we used a robust multiple-before-after-control-impact (MBACI) design using quantitative and standardized measures to assess response of a diverse fish community to LWD restoration in a heavily modified (channelized) lowland chalk stream. The restorations improved habitat diversity in restored reaches, however, responses in target species trout (*Salmo trutta*) were limited, with the greatest responses in predatory fish at higher trophic levels. While from an ecological context increased abundance of top predators suggests a healthier functioning ecosystem, this increases top-down predation pressure on target trout species, so the benefits of restoration to trout may be outweighed, with a net-detrimental impact on their recovery. Additionally, efforts to control predator densities by removing pike similarly failed to assist trout recovery, but facilitated the emergence of its intraguild prey and competitor, *Perca fluviatilis*.

These findings have implications for the efficacy of species-led conservation management strategies aimed at either reducing top-down or enhancing bottom-up forces on species populations, as both had counterintuitive outcomes. Established practices often lack empirical support, and as highlighted in this study, outcomes are often less prosaic than expected. In order for the efficacy or appropriateness of conservation measures to be truly understood, an appreciation of the community, biotic interactions, as well as robust monitoring and assessment are required. As in the sea, in rivers, no fish is an island.

Do Great Cormorants *Phalacrocorax carbo* target fish of the same species and sizes as anglers?

Roman Lyach[1], *Martin Čech*[1, 2]

[1]Institute for Environmental Studies, Faculty of Science, Charles University in Prague

[2]Institute of Hydrobiology, Czech Academy of Sciences, České Budějovice

Abstract text:

The Great Cormorant *Phalacrocorax carbo* is a widespread piscivorous water bird. Cormorant predation on fish stocks has been causing widespread conflicts between recreational anglers and environmentalists. This study aimed to evaluate the difference in fish catches between anglers and overwintering cormorants. We collected and analysed cormorant pellets in North Bohemia (Czech Republic) during winter. We compared species composition and size of fish caught by cormorants to species composition and fish size in catches of anglers from the most important fishing grounds in the area, calculating a dietary overlap between cormorants and anglers. Roach *Rutilus rutilus* dominated in cormorant diet while common carp *Cyprinus carpio* dominated in catches of anglers. Cormorants targeted significantly different fish species of different sizes than anglers did. Cormorants mostly preyed upon small fish of lower angling value while anglers mostly took large fish of higher angling value. Dietary overlap between catches of cormorants and anglers was low. Cormorants mostly preyed upon fish species and sizes that are generally very abundant while anglers mostly selected rare stocked fish species and sizes with an addition of bream *Abramis brama*. In case of fish species with high angling value, cormorants took almost exclusively fish legally undersized for anglers.

Environmental DNA as a fish monitoring tool for Alpine rivers

***Dominik Kirschner*[1]**, *B. Thalinger*[1], *C. Moritz*[2], *R. Schwarzenberger*[2], *J. Wanzenböck*[1], *M. Traugott*[1]

[1]Institute of Ecology, University of Innsbruck, Technikerstr. 25, 6020 Innsbruck, Austria

[2]ARGE Limnologie GesmbH, Hunoldstr. 14, 6020 Innsbruck, Austria

Abstract text:

The EU Water Framework Directive has changed the ecological classification system for European rivers by including fish diversity as an important parameter besides invertebrates, aquatic plants and water chemistry. Along with invasive alien species, which can negatively impact the biodiversity found in fresh water ecosystems, this led to an increased need for reliable fish monitoring systems. At present, the fish status of European rivers is evaluated by electrofishing. However, this method is invasive, time consuming, expensive, and prone to miss benthic or rare fish species. Recently, environmental DNA (eDNA), which is DNA obtained from environmental samples not including the organism itself, has been evaluated as an alternative and/or complementary approach to traditional fish monitoring. So far most eDNA studies focused on fish identification in stagnant waterbodies or lowland rivers with low disturbances and comparably little is known about molecular detection of fish in turbid, fast flowing Alpine rivers. The FFG Project “eDNA-AlpFisch” addresses this knowledge gap by assessing the suitability of the eDNA approach for this environment via aquarium and field experiments.

Here, we present an optimized field sampling protocol including the use of glass fibre filters, non-destructive lysis of DNA, and the robotic Biosprint-96 platform for DNA extraction as well as first results of field experiments which took place in a fish-free river in Tyrol (Austria) during summer and winter discharge situations. Four different fish species were caged for these week-long experiments and water samples were taken daily from the cages up to two kilometres downstream.

Detection of fish eDNA was possible from samples taken at different distances to the cage both in the summer and winter experiment with variable detection success between species. Furthermore, the molecular fish detection patterns differed significantly between the discharge situations.

These results demonstrate the applicability of the eDNA approach to detect fish species in Alpine rivers. In a next step we will apply semi-quantitative analyses comparing fish eDNA signals with relative biomasses.

Grazing of Nuclearia thermophila and Nuclearia delicatula (Nucleariidae, Opisthokonta) on the toxic cyanobacterium Planktothrix rubescens

Sebastian Dirren* [1]*, *Pitsch, Ga1, Da Silva, Marisa O.1, Posch, Thomas1*

[1]Limnological Station, Department of Plant and Microbial Biology, University of Zurich, Switzerland

Abstract text:

During the last decades, the planktonic cyanobacterium Planktothrix rubescens became a dominant primary producer in many deep pre-alpine lakes. While altered physiochemical conditions (bottom up factors) seem to favour this cyanobacterial species, its dominance is partly attributed to factors conferring grazing resistance (top down factors). The rigid structure of the cyanobacterial filaments and toxic secondary metabolites (e.g. microcystins) protect against diverse grazers. Nonetheless, species of the protistan genus Nuclearia (Nucleariidae, Opisthokonta) are able to overcome this grazing protection. Time lapse video documentation served as tool to record slow feeding processes of N. thermophila and N. delicatula. Three different feeding strategies could be distinguished: i) Phagocytosis of small fragments, ii) serial break-ups of cyanobacterial cells and iii) bending and breaking of filaments. While observations revealed mechanical manipulation to be important for the efficient breakdown of P. rubescens filaments, the toxin microcystin had no pronounced negative effects on N. thermophila. Growth experiments with different accompanying bacterial assemblages pointed to a pivotal role of distinct prokaryotic species for toxin degradation and for the growth of N. thermophila. Bacterial degradation (e.g. by cyanobacteria-lysing factors) of cyanobacterial cells seemed to favour the breakdown of P. rubescens filaments by nucleariids. Taken together, under culture conditions the synergistic effect of N. thermophila and distinct prokaryotic species leads to efficient degradation of P. rubescens along with its toxin.

Common stress me out – how stressors affect freshwater communities

Julia Nuy, *[1], J. Manfred[1], R. Oliver[2], B. Dominik[2], L. Florian[3], B, Jens[1]*

[1]Department of Biodiversity, University of Duisburg – Essen, Germany

[2]Department of Geobotany, Ruhruniversity Bochum, Germany

[3]Department of Aquatic Ecosystem Research, University of Duisburg – Essen, Germany

Abstract text:

Freshwater ecosystems are affected by anthropogenic stressors worldwide. Understanding the direct effects of stressors such as increased salt concentrations, decreased flow velocity and fine sediment addition on community composition and structure is a highly relevant topic nowadays. However, stressors occur rather combined than in its pure form and the response of freshwater microbes is yet poorly understood. Here we analysed effects of single and multiple stressors to the eukaryotic and bacterial diversity of different microhabitats in a stream mesocosm experiment.

The above mentioned stressors were applied to mesocosms with pumped stream water in single stressor treatments and as well in a combined form in double and triple stressor treatments. The community effects were captured with the Illumina amplicon sequencing method targeting the sequences of the V9 rRNA gene and ITS1 rRNA molecule.

Surprisingly, especially the eukaryotic biofilm community responded strongly to the stressors. We could show that the control treatment had a similar OTU composition and relative abundance of reads compared to the triple stressor treatment. The core community of all treatments had a high read abundance, a comparably low proportion of OTUs and showed in general poor affection by the stressors on community level. The flexible community is composed of a high proportion of rather rare OTUs and is highly affected by especially sediment related stressors. Most OTUs affiliated to Gomphonema parvulum were strongly selected in the sediment-salt treatment, whereas many Chlorophyta OTUs appeared to benefit from the salt and low - flow treatment.

In summary, rare and abundant taxa are antagonistically affected by the stressors. Abundant OTUs show a subtractive response to triple stressors on community level. In comparison, rare OTUs show an additive response to multiple stressors. Finally, OTUs from the same taxon are selected under different stress conditions. The investigated patterns contribute to the growing field of molecular monitoring and with it to the conservation of freshwater biodiversity.

Diversification and coherence in a species of pelagic freshwater bacteria

Hoetzinger, Matthias[1], Hahn, Martin W.[1]

[1]Research Institute for Limnology, Mondsee, University of Innsbruck

Abstract text:

In many prokaryotic genera a clustered phylogeny is observed, comparably to the occurrence of species in sexually reproducing organisms. Yet, the diversity within bacterial species can be vast compared to what is known from macroorganisms, implying the coexistence of various closely related genotypes within a single habitat. Two major questions can be addressed. (i) What is the ecophysiological relevance of the diversity observed within lineages/species and (ii) what are the driving forces providing coherence within species?

Polynucleobacter is a particularly interesting taxon for studying these issues in freshwaters due to its cosmopolitan distribution and high global abundance. *Polynucleobacter asymbioticus*, prevalent in dystrophic ponds in the Austrian Alps, was selected for polyphasic investigations, including the targeted isolation of strains from different sites, genetic analysis (multi locus sequence typing and genome sequencing) in the context of geographic structure and physiological testing.

Overall, genetic variability occurs most notably in genomic islands, to some of which specific functions could be assigned and demonstrated in ecophysiological experiments. Interspecies genome comparisons provide evidence for recent exchanges of genomic islands across species boundaries. The variability resulting from the presence of different genomic islands might provide fine scale niche differentiation and thus, enable the coexistence of numerous closely related genotypes. On the other hand, analysis of the core genomes indicates high recombination rates between conspecific strains, not significantly reduced by the geographic separation of the respective habitats. This may indicate that homologous recombination is the main factor providing genetic coherence within the species.

Novel and abundant streamlined Synechococcus sp. genomes assembled from freshwater reservoirs

***Pedro José Cabello-Yeves*[1]*,** *José Manuel Haro-Moreno[1], Ana-Belen Martin-Cuadrado[1], Rohit Ghai[2], Antonio Picazo-Mozo[3], Antonio Camacho[3] and Francisco Rodriguez-Valera[1]*

[1]Department of Microbiology. Universidad Miguel Hernández, San Juan de Alicante, Spain.

[2]Department of Aquatic Microbial Ecology. Institute of Hydrobiology CAS. České Budějovice.

[3]Instituto Cavanilles - University of Valencia

Abstract text:

Freshwater picocyanobacteria including Synechococcus remain poorly studied at the genomic level, compared to their marine representatives. Here, using a metagenomic assembly approach we discovered two novel Synechococcus sp. genomes from freshwater reservoirs Tous and Lake Lanier, both sharing a 96% of average nucleotide identity (ANI) and displaying high abundance levels in these two lakes located at similar altitude and temperate latitude. Fluorescent in-situ hybridization (FISH) confirmed that this microbe consist of very small cells that amount to 90% of the picocyanobaceria in Tous. They appear together in a phylogenomic tree with the marine Synechococcus sp. RCC307 strain, the main representative of sub-cluster 5.3 that has itself one of the smallest marine Synechococcus genomes. We detected a type II PBS-gene cluster in both novel genomes, which indicates that they belong to a phycoerythrin-rich pink pigmentation and low-light ecotype. The remarkable decrease of acidic proteins and the higher content of basic transporters and membrane proteins in the novel Synechococcus genomes support their freshwater specialization. A sulphate Cys transporter which is absent in marine but has been identified in many freshwater cyanobacteria was also detected in Synechococcus sp. Tous. The RuBisCo subunits from this microbe are the phylogenetically closest to the freshwater Paulinella chromatophora symbiont, supporting a freshwater origin of its carboxysome operon. The novel genomes are streamlined, with the smallest estimated size and intergenic spacers ever seen in this genus, what could help explaining their success in oligotrophic freshwater systems.

Beta-diversity and the main drivers of benthic diatom communities in soda pans of the Carpathian Basin

Szabó, Beáta*[2]*, *Lengyel, Edina*[2]*, Padisák, Judit*[1,2]*, Stenger-Kovács, Csilla*[1]

[1]University of Pannonia, Department of Limnology, H-8200 Veszprém, Egyetem str. 10., Hungary

[2]MTA-PE, Limnoecology Research Group, H-8200 Veszprém, Egyetem str. 10., Hungary

Abstract text:

In the recent study, we aimed to determine the regional β-diversity and its components of benthic diatom communities in soda pans and to highlight the role of deterministic and stochastic processes in their assembly. Furthermore, we wanted to assess to what extent community variation is influenced by pure environmental factors and spatial and temporal distance or by their shared effects in such extremely stressed ecosystems. Benthic diatoms and a number of environmental variables were determined monthly in soda pans from two different parts of the Carpathian Basin: the Fertő-Hanság region (2013-2014) and the Danube-Tisza Interfluve (2014-2015). Following the multiple-site framework, regional β-diversity (βSOR) was calculated for both regions separately which was partitioned into turnover (βSIM) and nestedness (βNES) components. Then, their relationship to overall β-diversity values expected "under" and "beyond" random community assemblage given a null model was investigated by Mantel permutation tests. To reveal the importance of pure and shared effects of the environmental variables and spatial and temporal distance on the variance of diatom assemblages, variation partitioning was conducted. Prior to the final analysis, physical and chemical factors were selected using a model selection procedure of RDA, then only significant parameters were included in the group "environmental variables". To define "spatial distance" group, PCoA of the geographical distance matrix was carried out to compute dbMEM eigenvectors that were considered as explanatory variables. For "temporal distance", the days elapsed between two sampling were used as explanatory variables. In both areas, we found a quite high β-diversity (>90%) of diatom communities which was mainly driven by species turnover, while nestedness was negligible. Based on the results of null model analyses and variation partitioning, we conclude that diatom communities of both regions were most likely assembled by deterministic processes, primarily according to the environmental gradients, which comply with the species-sorting paradigm of the metacommunity concept. Additionally, temporal distance affected also significantly the community structure in the Fertő-Hanság region probably related to the water management conducted in this area.

The microbiology of cave water pools and dripping points – aspects from Romanian show caves

Silviu Bercea*[1]*, *Ruxandra Nastase-Bucur*[1]*, Marius Kenesz*[1]*, Silviu Constantin*[2]*, Oana Teodora Moldovan*[1]

[1] Department of Cluj, Emil Racoviţă Institute of Speleology, Cluj-Napoca, Romania

[2] Department of Geospeology and Palentology, Emil Racovitza Institute of Speleology, Bucuresti, Romania

Abstract text:

As tourism is on the rise in all the natural parks and objectives, robust tools are needed to evaluate the impact and establish various guidelines for each site. Microbial diversity is a key aspect of every environment and its monitoring is a good tool in assessing changes induced by anthropogenic factors. We studied 5 Romanian show caves: Urșilor, Muierilor, Meziad, Polovragi and Fundata, all located in the Carpathian Mountains. The cave water pools and drip points were sampled at different time intervals to obtain an overview of the changes that occur over a yearly cycle. The extensive microbial monitoring was done between March 2015 and March 2016, through the use of microbiological monitoring test kits (RIDA@Count, R-Biopharm AG, Germany). The test plates revealed the total bacterial count, yeasts and molds count, and clinically important, human-associated groups as Enterobacteriaceae and Coliform bacteria, with specific indicators for Escherichia coli. For 16S rRNA gene sequencing, agar based cultures were prepared and cultured ex situ. The overall number of colony-forming units (CFU) was lower in the winter months, although almost a permanent presence of microbes was found in the sampling sites. It was observed that CFU varied in all of the studied caves, with very few absences of CFU in the overall studied sites, bacterial median values were lower in the sampling locations situated outside off the tourist area, than those from the sites near tourist trails, the values of CFU/ml for human associated organisms were rarely positive in the sampling locations from the restricted areas, while in locations near the trails presence was registered, sometimes in significant numbers, fungi were lower, sometimes by an order of magnitude, and with more absences of colonies in the tested water, compared to bacteria. A rise of culturable microorganisms was observed in areas of the caves that were subject to intense human visitation, in contrast to unvisited parts of the systems.

Metagenomic analysis reveals the role of two submerged macrophyte species in shaping water column and sediment bacterial community

***Yanran Dai*[1,2]*,* *Juan Wu*[3], *Shuiping Cheng*[3]

[1] State Key Laboratory of Freshwater Ecology and Biotechnology, Institute of Hydrobiology, Chinese Academy of Sciences, Wuhan 430072, China

[2] WasserCluster Lunz GmbH, Dr. Carl Kupelwieser Promenade 5, 3293 Lunz am See, Austria

[3] Key Laboratory of Yangtze River Water Environment, Ministry of Education, Tongji University, Shanghai, 200092, China.

Abstract text:

Submerged macrophytes as the important component of aquatic ecosystems, occupy key interfaces and therefore has major effects on productivity and biogeochemical cycles. With the facilitation of culture-independent biology techniques, it has become a research hotspot how the macrophyte shapes the bacterial structure. Here, we assembled mesocosms and utilized the high-throughput sequencing to characterize the shifts of bacterial community in freshwaters driven by two contrasting submerged macrophyte species, Ceratophyllum demersum L. and Vallisneria spiralis L. Although the microflora in both the water column and sediment were largely modulated by the macrophyte, the effect varied considerably depending on bacterial locations and macrophyte species. There was a significantly larger shift in microflora of the water column, which can be derived from the phenomenon that the presence of macrophyte clearly enriched the bacterial abundance, significantly higher Shannon-Wiener diversity in the C. demersum group as well as high-dimensional biomarkers and significantly a higher frequency of OUTs were detected ($P<0.05$). Pronouncedly different performance between the two species was also observed. In the C. demersum system, water column bacteria in terms of both richness and alpha diversity increased more dramatically than those in the V. spiralis system. Additionally, the presence of C. demersum remarkably enriched the relative abundance of dominant taxa, Cytophagia and Sphingobacteriia, and the absolute abundance of Gammaproteobacteria, Mb-NB09, BS119, TM7-1, TM7 and OM190, while in the V. spiralis system they were Actinobacteria, Flavobacteriia and BSV26. Noticeably, the water column bacteria in the control showed striking variability among the parallel systems compared with the planted groups. Taken together, the findings from this study reveal the two species of submerged macrophyte modified the bacterial community in waters, despite the obvious interspecific performance differences.

Functional identity matters to ecosystem functioning in natural phytoplankton communities

Abonyi, András[1,2,3], *Horváth, Zsófia*[1], *Ptacnik, Robert*[1]

[1] WasserCluster Lunz, Biologische Station GmbH, Dr. Carl Kupelwieser Promenade 5, A-3293 Lunz am See, Austria

[2] MTA-PE Limnoecology Research Group, University of Pannonia, Egyetem u. 10, H-8200 Veszprém, Hungary

[3] MTA Centre for Ecological Research, Danube Research Institute, Karolina u. 29, H-1113 Budapest, Hungary

Abstract text:

Hutchinson asked how so many species coexist in phytoplankton. Since then, the question has been reversed to how many species are needed to ensure ecosystem functioning. Recent studies clearly support a positive biodiversity–ecosystem functioning relationship in phytoplankton. The relationship has never been tested based on functional richness of natural phytoplankton assemblages. Here, we analyzed the biodiversity–functioning relationship using taxonomic and functional (trait and group) approaches in a broad-scale phytoplankton dataset covering the Fennoscandian peninsula. First we analyzed how taxonomic and functional compositions were related to local environmental predictors. We then tested whether the relationship between ecosystem functioning and taxonomic richness is further enhanced once functional richness is also considered. We found that functional levels, especially using the functional trait approach lead to stronger correspondence between the phytoplankton composition and local environmental predictors. In the entire dataset, independently of taxonomic richness, residual variations in the functional trait and group richness increased our ability in predicting ecosystem functioning. In individual Fennoscandian countries, however, only the functional group richness enhanced the diversity-functioning relationship. Our results suggest that the functional group approach provides a reliable basis to represent environmental complexity, whereas higher complexity is responsible for assembling functionally more diverse phytoplankton communities. Higher functional group richness then predicts better functioning, which effect is not included in the taxonomic richness. Functional trait richness alone may not improve the diversity-functioning relationship on top of genus richness. We argue that dominance relationships among traits may be more important in shaping the relationship, than the functional trait richness alone.

Temperature- and light intensity preference of four freshwater green algae from different habitats

Pálmai, Tamás*[1]*, *Szabó, Beáta*[2]*, Hubai, Katalin Eszter*[1]*, Selmeczy, Géza Balázs*[1]*, Padisák, Judit*[1,2]

[1] Department of Limnology, University of Pannonia, Veszprém, Hungary

[2] MTA-PE Limnoecology Research Group, Veszprém, Hungary

Abstract text:

The term “green algae” comprises several algal divisions, among them chlorophytes and charophytes. Photosynthetic production of four freshwater green algae in a total of 65 combinations of the interaction of light and temperature conditions were examined, measurements of photosynthetic activity were carried out in a wide range of temperature (5-45°C) and light intensity (0-2200 µmol m-2 s-1) in a photosynthetron to determine the optimum and the tolerance ranges of the species. Three Chlorophyta (Coelastrum sp., Dictyosphaerium pulchellum, and Scenedesmus sp.) and one Charophyta (Cosmarium majae) species were studied. Both unialgal cultures (Scenedesmus sp., Coelastrum sp.) and closely monodominant field populations (Dictyosphaerium pulchellum, Cosmarium majae) were used for the experiments. Samples were taken from a deep and a shallow lake and from two small garden ponds. The biomass specific production maxima of all the four species were found at 30-35°C. Optimal light intensity for photosynthesis (Ik) increased with increased temperature and had maxima at 35-40°C. Maximal Ik values of the four species changed between 244 for Cosmarium majae and 434 µmol m-2 s-1 for Dictyosphaerium pulchellum. Efficient light utilization of Cosmarium majae and Coelastrum sp. were observed. Photoinhibition were obtained along the temperature gradient for Cosmarium majae and Coelastrum sp. but only at low temperatures (5-15°C) and for Dictyosphaerium pulchellum and Scenedesmus sp. at the highest irradiance used. Biomass specific respiration of all species increased along the temperature gradient. Remarkable differences between the photosynthetic parameters of the species were not found, physiological preferences of the species from different habitats were quite similar. The preference of high light intensities with good light utilization and the lack of photoinhibition may help the dominance of planktonic green algal species in small, shallow, temperate water bodies.

Burbot ecology in Central European reservoirs

Blabolil, Petr*[1,2]*, *Duras, Jindřich*[3]*, Jůza, Tomáš*[1]*, Matěna, Josef*[1]*, Muška, Milan*[1]*, Říha, Milan*[1]*, Vejřík, Lukáš* [1]*, Peterka, Jiří* [1]

[1]Biology Centre of the Czech Academy of Sciences, Institute of Hydrobiology, České Budějovice, Czech Republic
[2] University of South Bohemia, Faculty of Science, České Budějovice, Czech Republic
[3]Povodí Vltavy, State Enterprise, Holečkova 8, 150 00 Praha, Czech Republic

Abstract text:

Burbot is one of the most mysterious freshwater species, typically inhabiting cold and oligotrophic waters. Therefore, it is highly sensitive to anthropogenic changes (e.g., euthrophication, global warming) and hence protected in many areas. Monitoring of burbot populations is difficult because of rare catch in commonly used nets. Therefore, we developed a unique sampling scheme using considerate methods (visual exploration by SCUBA divers, two types of fyke nets, electrofishing) and long-lines simulating anglers practice. This scheme was tested in four Czech drinking-water reservoirs with burbot stocking for biomanipulative purposes to control planktivore species. Efficiency of the sampling methods was dependent on local conditions. Burbot were detected in all but one reservoirs. Juvenile burbot were captured in the inflowing streams or in littoral zone of reservoirs with rubbles. Bigger burbot inhabited deeper parts of reservoirs. A catch subsample was taken to laboratory to determine population characteristics and age, and to analyse digestive tract content. Most of the burbot were juveniles (up to 3 years old) and the age groups corresponded to stocked fish. The most common diet was found to be temporal insects, fish and microcrustaceans. The other food sources were permanent water invertebrates, beatles and crayfish. Our study is unique in complex conception, starting in development of sampling procedure and ending in discussion of burbot ecology.

The effects of different DOM-sources from agricultural catchments on microbial activity in stream sediments

Campostrini, Lena[1], *Weigelhofer, Gabriele[2], Hein, Thomas[1]*

[1] University of Natural Resources and Life Sciences, Vienna
[2] University of Natural Resources and Life Sciences, Vienna, WasserCluster Lunz

Abstract text:

Agriculture is the dominant land use form in Lower Austria, covering more than 46 % of the total area. Agriculture delivers significant amounts of dissolved organic matter (DOM) to streams, thereby changing basic processes at the water-sediment interface and affecting the ecological state of the stream ecosystem. The aim of the project is to investigate the influence of agricultural land use on the quantity and quality of DOM inputs to streams and to clarify the effects of these DOM inputs on the aquatic carbon cycling in stream ecosystems.

Via in-door flume experiments, we investigate the short-term effects of different DOM sources (amongst others, extracts from manure, leaves, and soil from pasture and crop fields) on the growth of benthic microorganisms, the benthic respiration and the activity of extracellular enzymes. The DOM sources are analyzed as to their fluorescence (Excitation-Emission-Matrices) and absorbance characteristics (e.g. SUVA254), as well as the concentrations of dissolved inorganic nutrients and DON. A field study in 2016 showed increasing DOC concentrations in streams with increasing land use intensity. DOC ranged from 1-1.5 mg L-1 in forests to about 2 mg L-1 in pastures and 2.5-6.5 mg L-1 in cropland. The humification index decreased with land use intensity, while the protein-like peak was highest in cropland streams.

Relative roles of environmental control and spatial structuring on different macroinvertebrate dispersal mode groups within a metacommunity in small streams and higher order rivers

András Csercsa **[1,2],** *Ildikó Szivák* [3], *Péter Mauchart* [4], *Gábor Várbíró* [2], *Eszter Á. Krasznai* [2], *Arnold Móra* [4], *Diána Árva* [3], *Mónika Tóth* [3], *Tibor Erős* [3], *Pál Boda*[2]

[1]University of South Bohemia, Faculty of Science, Department of Biology of Ecosystems, České Budějovice, Czech Republic

[2]MTA Centre for Ecological Research, Danube Research Institue, Department of Tisza Research, Debrecen, Hungary

[3]MTA Centre for Ecological Research, Balaton Limnological Institue, Tihany, Hungary

[4]Department of Hydrobiology, University of Pécs, Pécs, Hungary

Abstract text:

Environmental control, spatial structuring and dispersal are the most common key factors which regulate local community structure within a metacommunity. The effect of these factors is highly dependent on species traits and characteristics of the studied area. We investigated the importance of environmental and spatial factors on the temporal structuring of aquatic macroinvertebrate dispersal mode groups (aquatic passive dispersers, terrestrial active and terrestrial passive dispersers) within a metacommunity in small streams and higher order rivers using watercourse distances. We hypothesized that environmental control should have a strong influence on community composition in small streams and the combination of environmental and spatial factors should determine the community assembly in higher order rivers. We also expected that active dispersers are controlled by mostly the environment, while joint effects of environmental and spatial processes should determine the community composition of passively dispersing species. We predicted that the relative role of environmental control and spatial structuring on metacommunity dynamics should differ between seasons. We applied partial redundancy analysis based on quantitative abundance data from two seasons and Moran's eigenvector maps based on watercourse distances. We found that the role of environmental control has been more dominant than spatial structuring in almost all the cases. Results showed seasonal differences in the impact of environmental control and spatial structuring. The effects of these factors were detectable more clearly in summer than in spring. We found strong environmental control without spatial structuring on active dispersers in both seasons and passive dispersers were influenced by environmental factors with low spatial impact.

Spectroscopic and phylogenetic studies of the phototrophic microbial communities in a geothermal spring in Rupite, Bulgaria

***Dachev Marko*[1,2]*,** *Kaftan David[1,2], Selyanin Vadim[1], Goecke Franz[3], Kopejtka Karel[1,2], Strunecky Otakar[2], Kasia Piwosz[1], Koblížek Michal[1,2]*

[1]Institute of Microbiology CAS, Center Algatech, *Třeboň*, Czech Republic.

[2]Univ of South Bohemia, Faculty of Science, Č. *Budějovice*, Czech Rep.

[3]Norwegian university of life sciences, Oslo, Norway.

Abstract text:

Thermal springs are considered hotspots of diversity, with potential interest for evolution, biogeography, microbial ecology studies, as well as for biotechnology [1]. We studied photosynthetic bacterial communities in six connected ponds of the South-West Bulgarian hot spring, Rupite, using fluorescence emission and absorption spectroscopy. The water temperature ranged from 30 to 70°C, pH was from 6.5 to 8.5, and sulphate content was around 135 mg/ml. From the collected microbial mats, emission spectroscopy revealed abundance of anoxygenic phototrophic bacteria (green non-sulfur bacteria and purple bacteria). Oxygenic phototrophs (algae and cyanobacteria) dominated the signal of allophycocyanin and phycocyanin. Specific primers were used for amplification of 16S rRNA sequencing by Roche 454 and Illumina next generation sequencing. In addition, cyanobacteria predominated the microbial mats, therefore several cyanobacteria species were isolated and their pigments analyzed by HPLC.

Historical changes and phenotypic variation in Daphnia longispina species complex in Lago Maggiore

Faktorová, Zuzana*[1]*, *Piscia, Roberta*[2]*, Manca, Marina*[2]*, Petrusek, Adam* [1]

[1]Department of Ecology, Faculty of Science, Charles University, Prague, Czech Republic

[2]Institute of Ecosystem Study, Verbania Pallanza, Italy

Abstract text:

Hybridizing species of the Daphnia longispina complex are key taxa in plankton communities of many European lakes. In several of these lakes, it has been documented that taxonomic structure of the complex during the 20th century has substantially changed following human-mediated environmental changes, particularly eutrophication and re-oligotrophication and fish stock changes. Typical scenario, documented from analyses of dormant egg banks in, e.g., Lake Constance (Germany/Switzerland) and Greifensee (Switzerland), is as follows: D. longispina prevailed (or was the only taxon) in the oligotrophic period, D. galeata invaded with increasing phosphorus concentrations, hybridization between the two species occurred, and the genetic footprint of these events remains even after recent reductions of phosphorus levels. One of the aims is to test whether this scenario is alike in Lago Maggiore (Italy/Switzerland), southern prealpine lake, which also passed through the human-mediated environmental changes.

Lago Maggiore is one of best and longest studied European lakes so a large number of historical Daphnia samples from regular monitoring are available. Because local Daphnia do not form dormant egg banks suitable for genetic analysis (being able to overwinter in water column), we use combination of morphology and geometric morphometrics (elliptic Fourier analysis). We will evaluate the taxonomic changes in the Daphnia longispina complex in Lago Maggiore over the last decades (years 1948-2012) and want to detect the impact of environmental changes in the respective period on Daphnia body shapes and body size.

Processing of samples is still running but first findings indeed suggest the presence of interspecific hybrids in late 20th century samples. Geometric morphometrics indicate that longispina-like Daphnia from the 1950s are phenotypically similar to those from the 2000s and different body shapes in the peak of eutrophication in the 1970s. Thus, it appears that we will be able to track relationship between Daphnia body shapes and environmental changes but this still needs further testing.

Fish schooling behavior in the pelagic habitat of a freshwater temperate reservoir

Holubová, Michaela[1,2], *Blabolil, Petr[1,2], Čech, Martin[1], Vašek, Mojmír[1], Peterka, Jiří[1]*

[1]Biology Centre of the Czech Academy of Sciences, Institute of Hydrobiology, Na Sádkách 7, 370 05 České Budějovice, Czech Republic

[2]University of South Bohemia, Faculty of Science, Branišovská 31, 370 05 České Budějovice, Czech Republic

Abstract text:

Grouping and social living of animals is a broadly occurring phenomenon, particularly fish schooling behavior is an excellent example, although poorly studied in freshwater systems. School compositions and species-specific schooling tendencies and preferences of the adult fish were studied in pelagic habitat of Římov Reservoir, Czech Republic. Total number of 34 days (16 h per day) of video recordings captured during clear water period (May/June) of seasons 2005, 2012 and 2014 were analyzed. From four species identified as school-forming species – bream (Abramis brama), bleak (Alburnus alburnus), roach (Rutilus rutilus) and perch (Perca fluviatilis), 40 % of observed individuals formed schools. Schooling tendencies (proportion of individuals engaged in schools) differed among species. In the cyprinids the species averaged body mass (wet weight) negatively affected schooling tendency. Although the schools were predominantly composed of conspecific individuals, 20 % of individuals formed heterospecific schools except bleak that schooled strictly with the conspecifics. Heterospecific groups showed an uneven species proportion with one major species dominating numerically the other. Major species varied among schools, roach dominated numerically in the count of schools whereas bream dominated in the count of individuals in the school. Findings indicate that the anti-predator function of the schooling behavior is intensified with rising vulnerability of the species. This study represents a pilot attempt of monitoring schooling behavior in the temperate freshwater reservoir of the Czech Republic.

Mayflies of the Caucasus Mountains: diversity and perspectives

Hrivniak, Ľuboš **[1,2]*****,*** *Sroka. Pavel*[1], *Godunko. Roman* [1,3]

[1]Institute of Entomology, Biology Centre CAS, České Budějovice, Czech Republic

[2]Faculty of Sciences, University of South Bohemia, České Budějovice, Czech Republic

[3]State Museum of Natural History, National Academy of Sciences of Ukraine, Teatralna 18, 79008 Lviv, Ukraine, email: godunko@seznam.cz

Abstract text:

Caucasus represents a mountain region situated between the Black and Casiapan Seas. A unique topographic and climatic complexity of this region is leading to the high heterogeneity of environments, ecological stratification and endemism within small geographical area. Thus the Caucasus region is recognized as one of the Biodiversity hot spots of the world. Despite the fact that it is a scientifically supremely interesting area, it remains poorly investigated.

Mayflies of Caucasus are very diverse, with more than a hundred known species. Most of the mountain and submountain species are endemic to the region. However, our knowledge about the Caucasian mayflies is mostly limited to the alpha-taxonomic level (original species descriptions and territorially limited checklists), and more complex studies analyzing phylogeographic patterns or ecological requirements of individual species are still missing.

Our research aims to fill this gap in order to clarify the species diversification and distribution within Caucasus and adjacent areas. The model group in our study is represented by the genus Epeorus Eaton (1881) (s.l.), one of the most diversified genera in the Caucasus region, with ten species described so far. Our main goals are: i) analyze the morphological and molecular variation within populations of individual species to clarify their taxonomic status using integrative approach, ii) reconstruct phylogeographic pattern of the selected species to clarify the colonization of Caucasus by these headwater stream specialists, iii) provide a complex identification key for the genus, needed for future hydrobiological surveys. Investigated material at our disposal was obtained from all major regions of Caucasus (Turkey, Russia, Georgia, Armenia, Iran, Azerbaijan).

According to our preliminary results based on the morphology and mitochondrial gene (COI) sequence data, all previously described species were supported as monophyletic lineages. One new species was discovered is being described. Speciation events will be further tested by phylogenetic methods with addition of nuclear marker/s and a detailed comparative morphological study.

Populations of individual Epeorus species show high degree of geographical isolation. Detailed phylogeographic reconstructions unraveling the colonization patterns will be performed on larger datasets.

Shoreline morphology as a controlling factor for epilithic algal communities (Danube River, Austria)

Marina Ivanković*[1]*, *Elisabeth Bondar-Kunze*[1, 2], *Éva Ács*[3], *Zsuzsa Trábert*[3], *Thomas Hein*[1, 2]

[1]WasserCluster Lunz - Biologische Station GmbH, Lunz am See, Austria

[2]Institute of Hydrobiology and Aquatic Ecosystem Management, University of Natural Resources and Life Sciences, Vienna, Austria

[3]MTA Centre for Ecological Research, Danube Research Institute, Budapest, Hungary

Abstract text:

Throughout the world rivers are increasingly subjected to hydromorphological alterations due to human interventions. A wide range of studies focused on the ecological value of engineering and regulation measures within lotic systems, mostly focusing on disturbed lateral and longitudinal river connectivity, while studies which directly address the ecological effects of shoreline modifications are still scarce. Within large rivers, benthic algae as sessile autotrophic organisms are usually restricted to a narrow shoreline zone and should be especially sensitive to shoreline modifications. The aim of this study was to estimate the response of epilithic algal communities to different human modified riverbank structures within the Austrian Danube section during mean water level conditions.

The selected Danube section (east of Vienna, 1887.5-1885.4 rkm) represents a hot spot of engineering measures, which have the overall goal to stabilize fairway conditions and improve the ecological situation of this river section. The sampling was carried out when mean water level was reached after a flood event, whereby algae were given enough time to develop into mature communities. Sampling sites were placed on frequently used river engineering structures, including rip-rap embankments (RR), a groin filed (GF), a secondary flow channel (SFC) and a near-natural gravel bar (GB). From those sites the structure and physiology of epilithic algal communities was measured: algal biomass (via chlorophyll-a and fluorometry), species composition (light and electron microscopy), class composition (HPLC) and photosynthetic performance (PAM Fluorescence). Additionally, diatoms species were grouped into functional groups (ecological guilds). Biological data were supplemented with physico-chemical water properties and hydromorphological surveys.

RR, GB and sites within the SFC were characterized by a higher accumulation of epilithic algal biomass consisting of filamentous cyanobacteria and/or filamentous green algae combined with diatom guilds typical for more mature three-dimensional algal communities. Compared with these, the sites within the GF and on the Danube oriented side of the SFC island were characterized with a less efficient photosynthetic activity and lower algal biomass which mainly consisted of taxa typical for a recently disturbed or early successional stage.

Biodiversity of aerobic heterotrophic microorganisms of Caspian Sea

Farahani Homa*[1]*, *Amoozegar Mohammad Ali* [1,2], *Mehrshad Maliheh*[1,3], *Shahzadeh Fezeli Seyed Abolhassan*[2,4]

[1]Extremophiles Laboratory, Department of Microbiology, Faculty of Biology and Center of Excellence in Phylogeny of Living Organisms, College of Science, University of Tehran, Tehran, Iran.

[2]Microorganism Bank, Iranian Biological Resource Centre (IBRC), ACECR Tehran-Iran.

[3]Institute of Hydrobiology, Department of Aquatic Microbial Ecology, Biology Center of the Academy of Sciences of the Czech Republic, České Budějovice, Czech Republic

[4]Department of Molecular and Cellular Biology. Faculty of Basic Sciences and Advanced Technologies in Biology. University of Science and Culture, Tehran, Iran.

Abstract text:

Brackish water is a water with salinity value in between freshwater and seawater. Thus, brackish covers a range of salinity regimes and is not considered a precisely defined condition. Some seas and lakes around the world have brackish salinity including Baltic Sea, Caspian Sea, and Black Sea. Caspian Sea is the largest land-locked water body on Earth disconnected from the Ocean and it has a stable brackish salinity at around 1.1 to 1.2%. Very little is known about the microbial community of permanently brackish environments. Recent metagenomics studies on the microbial community structure and reconstructing genomes of the representative microbes of the Caspian Sea shows a remarkable difference from marine and freshwater typical temperate communities.

Detailed analysis of reconstructed genomes shows that most of them belong to hitherto unknown groups, although related to either marine or freshwater groups. In present study we tried to culture some representative microbes of the Caspian Sea microbial community. To aim this purpose, sample were taken from the photic zone (10 m depth) in winter (March, 2016). Part of sample has been collected on 0.22 µm filters to analyze the community structure via 16S rDNA amplicon sequencing. And for the culture campaign based on the basic sea water chemistry; several culture and enrichment media were designed to retrieve the aerobic heterotrophic microorganisms of this environment. A total of 170 isolates have been purified from one of the designed media (Modified Marine Agar medium) and isolates from other culture and enrichment media are in the process of being purified. Based on primarily morphological and physiological traits of so far purified isolates a total number of 40 isolates have been selected for molecular characterization via 16S rDNA sequence analysis.

Among the sequenced strains, representatives of phyla Bacteroidetes, Gamaproteobacteria, Alphaproteobacteria, and Actinobacteria were present. Some of these strains could be representatives of new taxa at genus and species level.

Microhabitat use of fishes in submontane streams – size matters

Maroda, Ágnes , *Sály, Péter*

[1]Department of Hydrobiology, Institute of Biology, Faculty of Sciences, University of Pécs, Ifjúság útja 6, H-7624 Pécs, Hungary

Abstract text:

Different aged and sized fish have different needs for survival. Partitioning niche within and between species is a general mechanism, which can mitigate unfavorable interactions. One of the ways of niche partitioning is using different habitats. Submontane streams offer heterogeneous habitats for fish at both meso- and micro spatial scales. Whereas habitat use of fish at meso scale is well known, we have less knowledge on microhabitat use of different sized fishes within a stream reach. Our objective was to yield a picture on the micro scale distributional pattern of size classified fishes within submontane fish assemblages. Fish sampling and abiotic survey were conducted at two stream reaches using point-abundance sampling in 1 m2 patches. Individuals of four fish species were size-classified on the basis of the length-frequency distribution of the species. Microhabitat use of the size-classified fish was evaluated by using constrained ordination. Differences in occurrence patterns of the conspecific size classes were tested by Fisher's exact tests. Results showed similar microhabitat use of juveniles of three species, and that of the adults of two species. Within species, there were significant differences in occurrence pattern between the juvenile and the adult conspecifics in case of two species. The most important environmental variables were the average depth, average velocity, percentage of sandy substratum, and the diversity of substrate. Our study highlights and reinforces the relevancy of considering the size of individual fish in understanding the habitat needs of fish species during their life cycle, and the importance of within-reach heterogeneity of the abiotic conditions in stream habitat rehabilitation projects.

Valuation of Ecosystem services at the Biharugra Fishponds.

Palásti, Peter*[1]*, *Kerepeczki, Eva* [2]

[1] NARIC-HAKI, Szarvas, Hungary

Abstract text:

Ecosystem services (ES) are benefits of natural and semi-natural systems, which can support the existence of human societies and their well-being. Interest for ES has been exponentially growing in the fields of environmental and social sciences, and policy making since Millenium Ecosystem Assessment (2005), where scientists revealed the essential role and vulnerability of ES. One of the key challenges for ES research is to develop a comprehensive methodological approach, which can evaluate these services in a multi-dimensional way, integrating summarized results into the decision making process. We would like to assess extensive fishponds' ES, and analyze their biophysical, socio-cultural and monetary values.

Our study area is the Biharugra Fishponds, the second biggest fishpond system of Hungary (1920 ha), located in the southeastern region of the country. Despite their artificial nature, these fishponds have a significant conservation value, providing services, just like habitats for endangered species - especially waterbirds -, water retention or food provision.

In our earlier studies we have already listed the 23 typical services for earthen fishponds. Recently, our main goal has been to assign biophysical indicators to ES, so we could define their trends and current state.

In the future we would like to identify fishponds' specific services by conducting face-to-face surveys at the nearby villages and cities, where respondents can choose from the 23 services above. Our plans concludes socio-cultural valuation for the services too, by analyzing the importance people allocate to them. Besides that, respondents' social conditions are going to be studied to select factors having a significant effect on people's preferences. Additionally, to support further research, habitat mapping and database building are planned.

Breeding site use of protected amphibian species in Hungary

Péntek, Attila László

[1]Department of Zoology and Animal Ecology, Szent István University, H-2100 Gödöllő, Páter Károly u. 1. Hungary

Abstract text:

In 2011 the Amphibian and Reptile Conservation Group of MME Birdlife Hungary started a website for online mapping of amphibians and reptiles in Hungary (hepterkep.mme.hu). Between 2011 and 2016, thousands of amphibian records were received from the volunteers. Based on this dataset, my aim was to study the breeding site use and habitat preference of different species. After the validation process, I used 1322 photo-documented amphibian records for the analysis. I included lakes, ponds, temporary pools, marshes as well as streams and considered all developmental stages of the inhabiting species. With Google Earth Pro, I measured the percentage of forested, agricultural, and populated areas within a radius of 1000 and 5000 m from each breeding site to study the relative importance of these landscape factors. I found considerable differences in the breeding site use of different species. While some species (Bombina variegata, Ichtyosaura alpestris, Rana temporaria) preferred smaller waterbodies at higher elevations in highly forested landscapes, others (Pelobates fuscus, Triturus dobrogicus) mostly related to semipermanent waterbodies in lowland areas. In large permanent lakes the amphibian communities were dominated by Bufo bufo and the Pelophylax esculentus complex which taxa can successfully breed in the presence of fish. Amphibians are pond-breeding animals, but their dispersal is strongly affected by the surrounding terrestrial habitat. Conserving a high diversity of aquatic and terrestrial habitats are essential for the long-term protection of amphibian communities.

Double origin of fairy shrimp Eubranchipus grubii in Central European vernal pools

***Pešek, Pavel*[1]*,** *Sacherová, Veronika*[1], *Hana Rychtrmocová* [2]

[1]Department of Ecology, Faculty of Science, Charles University in Prague

[2]1st Dep. of Medicine - Dep. of Hematology, First Faculty of Medicine, Charles University in Prague

Abstract text:

Fairy shrimps Eubranchipus grubii (Anostraca, Chirocephalidae) live in a specific habitat of temporary spring pools. At present it is distributed approximately between 45 and 55 degrees of latitude in Central Europe, almost entirely in lowland floodplains. Cold temporary pools similar to present day vernal pools likely existed in Central Europe throughout the whole Pleistocene including ice ages. Current distribution and ecological requirements of E. grubii and our understanding of Pleistocene environment imply that E. grubii had no southern glacial refugia.

Genetic relationships of E. grubii populations were studied by using two mitochondrial markers (16S and CO1). Study area was limited to Czech Republic and included three main European drainages of Black (Morava), Baltic (Oder) and North Sea (Elbe). Both molecular markers showed identical major division of populations: the first lineage inhabits Oder watershed, the second lineage inhabits Elbe and Morava watersheds. CO1 provided further insight into the second lineage. According to CO1, individuals were divided into three haplotype lineages (A, B, and C), with partially disjunct geographic distribution. Individuals of lineage A belong mostly to Elbe and Morava catchments. Lineage B comes mostly from populations of Thaya (tributary of the Morava River) catchment and confluence of Thaya and Morava. Lineage C is most divergent, individuals mostly origin from populations in Odra river catchment. Here we also discuss possible glacial refugia and propose Central European refugium for lineages A and B and East European refugium for lineage C.

During our sampling campaigns we found several populations outside the typical lowland floodplains, separated either by elevation or distance. Also, members of all lineages can rarely be found among populations of another lineage. Human and/or animal transport is discussed as most likely dispersal scenario.

The Green Tetrahymena utriculariae n. sp. (Ciliophora, Oligohymenophorea) with its Endosymbiotic Algae (Micractinium sp.), Living in Traps of a Carnivorous Aquatic Plant

Pitsch, Gianna* [1]*, *Adamec, Lubomír* [2]*, Dirren, Sebastian* [1]*, Nitsche, Frank* [3]*, Šimek, Karel* [4]*, Sirová, Dagmara* [4, 5]*, Posch, Thomas*[1]

[1]Limnological Station, Department of Plant and Microbial Biology, University of Zurich, 8802 Kilchberg, Switzerland

[2]Institute of Botany CAS, Section of Plant Ecology, 379 82 Třeboň, Czech Republic

[3]University of Cologne, Biocenter, Institute for Zoology, General Ecology, 50674 Cologne, Germany

[4]Biology Centre CAS, Institute of Hydrobiology, České Budějovice, Czech Republic

[5]University of South Bohemia, Faculty of Science, České Budějovice, Czech Republic

Abstract text:

The genus Tetrahymena (Ciliophora, Oligohymenophorea) probably represents the best studied ciliate genus. At present, more than forty species have been described. All are colorless, i.e. they do not harbor symbiotic algae, and as aerobes they need at least microaerobic habitats. Here we present the morphological and molecular description of the first green representative, Tetrahymena utriculariae n. sp., living in symbiosis with endosymbiotic algae identified as Micractinium sp. (Chlorophyta). The full life cycle of the ciliate species is documented, including trophonts and theronts, conjugating cells, resting cysts and dividers. This species has been discovered in an exotic habitat, namely in traps of the carnivorous aquatic plant Utricularia reflexa (originating from Okavango Delta, Botswana). Green ciliates live as commensals of the plant in this anoxic habitat. Ciliates are bacterivorous, however symbiosis with algae is needed to satisfy cell metabolism but also to gain oxygen from symbionts. When ciliates are cultivated outside their natural habitat under aerobic conditions and fed with saturating bacterial food, they gradually become aposymbiotic. Based on phylogenetic analyses of 18S rRNA and mitochondrial cox1 genes T. utriculariae forms a sister group to T. thermophila.

Assimilation of organic matter by natural microbial communities in light and dark

Piwosz Kasia, *Kaftan David, Kolesár Fecskeová Lívia, Selyanin Vadim, Kopejtka Karel, Dachev Marko, Hanusová Martina, Dean Jason, Koblížek Michal*

[1]Institute of b Microbiology CAS, Centre ALGATECH, Třeboň, Czech Republic

Abstract text:

Photoheterotrophic organisms can use light as an energy source and organic carbon as a carbon source. Photoheterotrophs are found among all domains of life: eukaryotes (osmotrophic and bacterivorous algae), bacteria (aerobic anoxygenic phototrophes (AAP), proteorhodopsin-containing bacteria, cyanobacteria) and bacteriorhodopsin containing archaea. Photoheterotrophs are abundant in most aquatic ecosystems, indicating possible differences in energy transfer and carbon turnover between light and dark conditions. Still, the ecology and importance for photoheterotrophy in aquatic ecosystems are poorly understood. Here, we compared uptake rates of four tritiated substrates: aminoacids (glutamic acid and leucine), pyrimidine (thymidine), and sugar (glucose), by natural microbial communities in an oligotrophic lake, in the light and the dark. Uptake of glutamic acid and glucose was substantially higher in the light than in the dark (up to 38 and 56%, respectively). Subsequent measurements of uptake of glucose at different light spectra indicated that the difference could be attributed to the activity of cyanobacteria. Our data show that the uptake of organic molecules by natural microbial communities may be substantially higher in the light than in the dark, indicating that estimates based only on dark measurements might underestimate real rates of energy transfer and carbon turnover in oligotrophic lakes.

Cryptic diversity of the Gammarus fossarum species complex (Amphipoda) across the Bohemian Massif and Western Carpathians: phylogeny and lineage distribution

***Rutová, Tereza*[1]*;** *Copilaș-Ciocianu, Denis*[1]*; Pařil, Petr*[2]*; Petrusek, Adam*[1]

[1]Charles University in Prague, Faculty of Science, Department of Ecology

[2]Masaryk University in Brno, Faculty of Science, Department of Botany and Zoology

Abstract text:

Freshwater amphipods are an ecologically important component of permanent benthic macrofauna in temperate freshwaters. They have poor dispersal abilities and lack dormant stages, and their phylogeographies often reflect old historical processes. Gammarus is the most common epigean amphipod genus throughout the Western Palearctic, with more than 200 described species, many of which actually comprise diverse species complexes. Gammarus fossarum, widespread across central and south-eastern Europe, is one of such complexes. Previous studies have uncovered numerous lineages both in Western Europe and northern Balkans, and southwestern Carpathians were recently pinpointed as a major diversity hotspot and Pleistocene refugium for this complex. However, virtually nothing was known about the phylogeographic patterns of this complex in the northeastern part of its range. The region of Czechia and Slovakia, which transitions from the Bohemian Massif to the Western Carpathians, is a biogeographical boundary for plants and both aquatic and terrestrial invertebrates. We analysed lineage diversity and distribution of G. fossarum samples collected from more than 170 localities across Czechia and Slovakia by molecular barcoding of two mitochondrial genes; their phylogeny was assessed from representative samples by sequencing three additional nuclear markers. Overall, we found eight divergent lineages of apparently Miocene age with contrasting patterns of distribution: most of the Bohemian Massif has been colonised by a single recently expanded western-European lineage, while all eight lineages are scattered in a mosaic fashion in the Western Carpathians. Two lineages found in this region but not known further south are very divergent and have no clear phylogenetic affinities. These observations are consistent with a scenario that Carpathians lineages survived the Pleistocene climatic oscillations in situ, possibly facilitated by thermally buffered mineral springs that may have provided suitable conditions even in dry cold periods of the glacials. Analyses of small-scale distribution of the Carpathian lineages in the Vsetín region confirms that they often penetrate in the same streams, and may coexist upon contact. This provides a suitable model system for studying their ecological interactions in the future.

Effects of the chrysophyte Uroglena americana on the zooplankton secondary production in the alpine Lake Lunz, Austria

Schneider, Claudia, *Ptacnik, Robert, Vad, Csaba*

[1]WasserCluster Lunz, Dr. Carl Kupelwieser Promenade 5, A-3293 Lunz am See, Austria

Abstract text:

Global change scenarios predict far-reaching consequences for freshwater lakes due to their high sensitivity to environmental changes. The global change-mediated processes of brownification and enhanced thermal stratification may have effects on the interaction between primary and secondary producers leading to shifts in aquatic trophic webs. Compared to eutrophic lakes, very little is known about how global change may affect interactions in plankton communities of oligotrophic lakes.

Mixotrophic chrysophyte algae are typical members of the plankton community of oligotrophic lakes. Through bacterivory chrysophytes have access to otherwise limiting nutrients, giving them a competitive advantage over photoautotrophic algae in oligotrophic systems. Their relative abundance is predicted to increase with global change. Current literature suggests possible negative effects of chrysophytes on zooplankton secondary production. Recently, high abundances of the colony-forming chrysophyte Uroglena americana have been observed during summer in the alpine Lake Lunz in Austria.

The aim of this study is to assess the implications of the recent Uroglena americana blooms in Lake Lunz on the pelagic food web focusing on the secondary production of zooplankton. To this end, a combination of laboratory feeding experiments, field observations and lipid analyses will be performed. This study will provide information on the nutritional effects of the chrysophyte Uroglena americana on zooplankton. This will contribute to the understanding of climate-related changes in the food web of alpine lakes and the implications of these changes on ecosystem functioning.

Potency of water bloom lipopolysaccharide (LPS) to induce pro-inflammatory effects in vitro

Lenka Švihálková Šindlerová **[1,2]**, *Ondřej Vašíček*[1,3], *Barbora Ambrůzová*[1,4], *Mirna Velki* [5], *Gabriela Ambrožová* [1,3], *Pavel Babica*[2], *Lukáš Kubala*[1,3]

[1]Department of Free Radical Pathophysiology, Institute of Biophysics, Academy of Sciences of the Czech Republic, v.v.i, Brno, Czech Republic, sindler@ibp.cz

[2]Research Centre for Toxic Compounds in the Environment, Faculty of Science, Masaryk University Brno, Czech Republic

[3]International Clinical Research Center, St. Anne's University Hospital Brno, Brno, Czech Republic

[4]Institute of Experimental Biology, Department of Physiology and Immunology of Animals, Faculty of Science, Masaryk University, Brno, Czech Republic

[5]Department of Biology, Josip Juraj Strossmayer University of Osijek, Cara Hadrijana, Osijek, Croatia.

Abstract text:

Cyanobacterial water blooms are known to be toxic and able to cause various and also severe disease. One of the acute clinically-relevant pathologies observed in people exposed to contaminated water is gastroenteritis. Interestingly, it can be caused not only by drinking contaminated water but also recreational exposure could be sufficient to cause gastroenteritis. It, generally, can be induced by pathological exposure of colon epithelial cells to pathogenic microorganisms or toxins, e.g. LPS of gram negative bacteria. We hypothesise that cyanobacterial LPS also has the potency to activate these inflammatory processes and plays an important role in activation in gastrointestinal disease. Therefore, environmental samples of cyanobacterial water bloom from the Czech Republic were extracted by hot phenol extraction and LPS fractions were obtained. Non-toxic concentrations were used to expose Caco-2 cells, a model of intestinal epithelial cells. After 24 hours, increased concentration of pro-inflammatory cytokine interleukin (IL) 8 was detected (ELISA). Whereas permeability of the epithelium is increased during intestinal inflammation and thus toxins could pervade the epithelium and get to the lamina propria and immune cells present there, water bloom LPS ability to activate polymorfonuclear leucocytes (PMNL) was studied. Exposure to LPS resulted in increased production of reactive oxygen species (luminol-enhanced chemiluminescence), surface expressions of CD11b and CD66, receptors specific for particular granules, after 6 hours of incubation (flow cytometry), as well as production of IL-6, tumour necrosis factor α, and IL-1β (ELISA) after 24 hours of exposure determined in whole blood. Further, increased phosphorylation of p38 and ERK as well as NF-κB (western blotting) in LPS treated isolated PMNL was observed.Taken together, LPS extracted from cyanobacterial water bloom was able to induce in vitro pro-inflammatory effects of cells derived from intestinal epithelium as well as PMNL from human whole blood. Potency of the cyanobacteria to induce inflammation of gastrointestinal tract was published and the study of its mechanism should not be underestimated due to cyanobacterial water bloom worldwide occurrence.

The effects of puwainaphycin F on Caco-2 cell line as a model of the intestinal barrier

***Vasicek, Ondrej* [1,2,3], *Hrouzek, Pavel*[4,5], *Kubala, Lukas* [1,2] *and Svihalkova Sindlerova Lenka* [1,6]**

[1]Institute of Biophysics, Academy of Sciences of the Czech Republic, v. v. i., Brno, Czech Republic

[2]International Clinical Research Center – Centre of Biomolecular and Cellular Engineering, St. Anne's University Hospital, Brno, Czech Republic

[3]Institute of Experimental Pharmacology and Toxicology, Slovak Academy of Sciences, Bratislava, Slovak Republic

[4]Institute of Microbiology, Centre Algatech, The Czech Academy of Sciences, Trebon, Czech Republic

[5]University of South Bohemia, Faculty of Science, Ceske Budejovice, Czech Republic

[6]Research Centre for Toxic Compounds in the Environment, Faculty of Science, Masaryk University Brno, Czech Republic

Abstract text:

Cyanobacteria are a prolific source of structurally diverse secondary metabolites with a wide spectrum of bioactivities. Hundreds of compounds have been identified in recent decades as a promising source of secondary metabolites and novel pharmaceutical compounds of a large structural diversity. Puwainaphycins are cyclic lipopeptides of cyanobacterial origin and are composed of nine amino acid units and a β-amino fatty acid. Current knowledge indicates that puwainaphycins F/G are able to induce necrosis, increased Ca2+ influx and relocate the actin filaments.In this study, we focused on effect of 4 nature modifications of puwainaphycin F – PUW1118, PUW1146, PUW1188 and PUW1190 (labeled on the basis of their molecular weight) on Caco-2 cell line as a model of the intestinal barrier. We measured their cytotoxicity by detection of lactate dehydrogenase released into the medium and total protein concentration. Concentration of interleukin 8 (IL-8), a pro-inflammatory cytokine, was measured by ELISA. Changes in permeability of differentiated Caco-2 layer were measured by Dextran-FITC trans-well assay. Level of ZO-1, a tight junction (TJ) protein, was measured by western blotting (WB) and finally its localization in cell was observed using confocal microscopy (CM). Our findings show that PUW1146 was the most cytotoxic metabolite, PUW1118 and PUW1188 were slightly cytotoxic and PUW1190 was very low cytotoxic in used concentrations. The nontoxic concentrations of all PUWs (except PUW1190) were able to increase IL-8 production after 24 hours of exposure in dose-dependent manner. The permeability of differentiated Caco-2 layer was increased after the addition of PUWs. The preliminary data from WB and CM did not show any changes in ZO-1 level as well as in its localization for all tested PUWs. It can be concluded, that the cyanobacterial secondary metabolite puwainaphycin F has a cytotoxic and pro-inflammatory effect dependent on its structural modifications. The underlying mechanism of the changes of Caco-2 layer permeability is not clear yet. Therefore, we would like to study other TJ proteins (e.g. occludin, claudin) and changes in fluidity of membrane.

A farewell to distance-based clustering: Accurate reconstruction of rRNA gene diversity in environmental samples by radical denoising

Villiger, Jörg*[1]*, *Salcher, Michaela*[1]*, Piwosz, Kasia*[2]*, Pernthaler, Jakob*[1]

[1]Limnological Station, University of Zurich (Switzerland),
[2]Centre Algatech, Institute of Microbiology, Academy of Sciences of the Czech Republic

Abstract text:

Operational taxonomic units (OTUs) are amongst the most elusive microbial creatures that ever inhabited our planet. To date, no two researchers of aquatic microbial ecology have encountered the same OTUs in their samples, which is in fact impossible due to the very nature of their generation. Even worse, the available approaches (and their variants) allow for the production of uncountable OTU sets from a single collection of microbial rRNA genes that substantially differ in numbers, size distributions and taxonomic affiliations. There is no rational argument other than by authority which of these OTUs are more 'true' than others. While it is increasingly realized that error is responsible for much of the diversity observed in OTU-based analysis, this insight is at best used for data quality assessment or the more or less effective removal of chimeric sequences. Here, we take the denoising concept to its extreme, in order to accurately reconstruct the original diversity of sequence types in a sample exclusively by modelling the probabilities of the various errors that confound this diversity. Three types of errors with specific propagation properties are assumed, related to PCR amplification, chimera formation, and sequencing. The final assignment of individual reads to OTUs is not based on clustering with an arbitrarily fixed distance threshold. Instead, all sequences are recursively grouped with their most likely 'ancestors', and thus eventually with those 'core' sequences in the sample that most probably gave rise to erroneous variants during PCR and sequencing. By this, it is possible to reliably distinguish between OTUs that only differ by a few (2-3) bases, and to more accurately detect spurious OTUs resulting from chimerization. The resolution of OTU distinction by our method is only limited by the actual information content of the data set, i.e., the sequence length, the combined error rates and the relative frequencies of sequences per OTU. We present examples for the superior accuracy of our diversity reconstruction approach both in defined mock communities and natural bacterioplankton assemblages.

Fish Behavior and Fish Color Monitoring

Urbanová, Pavla; *Bozhynov, Vladyslav; Bárta, Antonín; Souček, Pavel; Císař, Petr; Urban, Jan.*

Laboratory of Signal and Image Processing, Institute of Complex Systems, Faculty of Fisheries and Protection of Waters, University of South Bohemia in České Budějovice, Zamek 136, Nove Hrady, 37333, Czech republic.

Abstract text:

One of the parameters, which serve as a monitoring of water quality, is the fish welfare. Various examples of deviations in behavior were already observed for wide range of causes. We present the semi-automatic indoor system for the time-lapse observation of the fish shoal behavior and evaluation of the mandatory attributes. The statistical evaluation of the fish movements distinguishes the behavior changes with certain level of confidence. The system monitered data could be connected with the bioWes system, in-house developed protocol manager and metadata database, describing the experiments, and connected also with processing moduls.

Another parameter for the fish welfare is the fish skin colour, which could be automatically evaluated using calibrated RGB camera. The color distribution in main colour spaces (RGB, HSV, L*a*b*) for one image or whole set is again described via statistical parameters.

Unexpected and diverse lifestyles within the genus Limnohabitans

Kasalický Vojtěch, *Salcher Michaela, Šimek Karel, Kratochvilová Hana, Ghai Rohit*

Biology Centre CAS, Institute of Hydrobiology, Czech Republic

Abstract text:

The genus Limnohabitans is an ubiquitous, diverse and highly abundant group of freshwater Betaproteobacteria. They have been considered as typical fast growing heterotrophs, rapidly responding to fluctuating environmental conditions. While the vast majority of abundant planktonic microbes remain uncultured, Limnohabitans offer the advantage of being relatively easy to cultivate thus making both experimental and omics approaches feasible. We have the largest strain collection of Limnohabitans isolates collected from a wide variety of freshwaters from all over the world (65 strains). Five higher-level lineages (LimABCDE) are now recognized and four species have been described, however, species-level differentiation using rRNA sequences alone is insufficient to resolve the phylogeny. Taking advantage of the culture collection that contains all Limnohabitans lineages (except LimD), we have sequenced thirty isolates, and closed at least one genome per lineage. Phylogenomic analyses largely supported the rRNA based phylogenies but suggested merging two lineages. Comparative analysis of all 35 knownLimnohabitans genomes (including 5 previously sequenced) revealed a wide variation in genome sizes ranging from 2.6Mb to nearly 5Mb, and at least 30 putative species (ANI <95%). Recently, some Limnohabitans isolates have been shown to carry genes for aerobic anoxygenic phototrophy (bacteriochlorophyll) and carbon fixation (Rubisco I or Rubisco II), suggesting they may exist as autotrophs. Remarkably, genome analyses revealed that nearly two thirds of all genomes encode genes for aerobic anoxygenic photosynthesis. This unexpected diversity in metabolic potential and the ability to live as facultative autotrophs in large population sizes makes Limnohabitans spp. unique model organisms for freshwaters.

First record of a putative pederin-type gene cluster and its product in a free-living cyanobacterium Cuspidothrix issatschenkoi

Andreja Kust [1,2,3] ***,*** *Jan Mareš*[1,2] *, Petra Urajová*[3] *, Pavel Hrouzek*[3]

[1]Biology Centre of AV ČR, v. v. i, Institute of Hydrobiology, České Budějovice, CZ

2Centre Algatech, Institute of Microbiology, AV ČR, v. v. i, Opatovický mlýn, Třeboň, CZ

[3]University of South Bohemia, Faculty of Science, Branišovská 1760, České Budějovice, CZ

Secondary metabolites in cyanobacteria are frequently synthesized by non-ribosomal protein complexes – non-ribosomal peptide synthesases (NRPSs) and polyketide synthetases (PKSs), accompanied by accesory enzymes. They are responsible for the existence of many compounds important in human medicines. Until a recent discovery of bacterial trans-acetyl transferase PKS (trans-AT) pathways, the only available structural information for PKS gene clusters/enzymatic complexes was obtained from cis-AT system. The only report of this PKS class in cyanobacteria comes from nosperin, representative of the important pederin-type family of toxins, produced by lichen-associated Nostoc sp. cyanobacterium. This finding led to a speculation about possible specificity of pederin-type antibiotics for bacteria-eukaryote symbioses. Strikingly, we have found strong evidence for the presence of a compound related to pederin family antibiotics synthesized via trans-AT PKS in a free-living planktic bloom-forming cyanobacterium Cuspidothrix issatschenkoi from our laboratory. The respective trans-AT pederin-like gene cluster was recovered from a high-quality genome draf produced by a combination of Illumina and PacBio NGS analysis. An additional gene cluster encoding the synthetase of cyanobacterial neurotoxin – anatoxin-a was identified in the genome. The production of anatoxin-a and a novel pederin-type compound was confirmed using high-performance liquid chromatography and high-resolution mass spectrometry. The resulting data elucidate predicted biosynthesis of the first trans-AT-synthesized antibiotic compound from a free-living (cyano)bacterium and in addition to that, in the same strain, provides evidence on production of the hazardous neurotoxin anatoxin-a. Further investigation is planned to fully characterize the chemical structure and bioactivity of the novel pederin-type compound in this important bloom-forming cyanobacterial strain.

Metagenomic recovery of phage genomes of uncultured freshwater actinobacteria

***Rohit Ghai*[1]**, ***Maliheh Mehrshad*[2,3]** , *Carolina Megumi Mizuno*[2,4] *and Francisco Rodriguez-Valera*[2]

[1]Institute of Hydrobiology, Department of Aquatic Microbial Ecology, Biology Center of the Academy of Sciences of the Czech Republic, České Budějovice, Czech Republic

[2]Departamento de Producción Vegetal y Microbiología, Evolutionary Genomics Group, Universidad Miguel Hernandez, Alicante, Spain

[3]Extremophiles Laboratory, Department of Microbiology, Faculty of Biology and Center of Excellence in Phylogeny of Living Organisms, College of Science, University of Tehran, Tehran, Iran and

[4]Unit of Molecular Biology of the Gene in Extremophiles, Department of Microbiology, Institut Pasteur, Paris, France

Low-GC Actinobacteria are among the most abundant and widespread microbes in freshwaters and have largely resisted all cultivation efforts. Consequently, their phages have remained totally unknown. In this work, we have used deep metagenomic sequencing to assemble eight complete genomes of the first tailed phages that infect freshwater Actinobacteria. Their genomes encode the actinobacterial-specific transcription factor whiB, frequently found in mycobacteriophages and also in phages infecting marine pelagic Actinobacteria. Its presence suggests a common and widespread strategy of modulation of host transcriptional machinery upon infection via this transcriptional switch.We present evidence that some whiB-carrying phages infect the acI lineage of Actinobacteria. At least one of them encodes the ADP-ribosylating component of the widespread bacterial AB toxins family (for example, clostridial toxin). We posit that the presence of this toxin reflects a 'trojan horse' strategy, providing protection at the population level to the abundant host microbes against eukaryotic predators.

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