

# CEESME

Central and Eastern Europe Symposium  
on Microbial Ecology

12-15 September 2023

Budapest, Hungary



Book of Abstracts

# CEESME



# Program



**CEESME**

| <b>Tuesday (September 12)</b>   |   |
|---|---|
| <b>Venue: Eötvös Loránd University, Harmónia Hall (1117 Budapest, Pázmány Péter stny 1/A)</b> |   |
| <b>Soft Skill Workshop for Young Scientists - Career Opportunities and Networking</b>         |   |
| <b>9:00</b>   | <b>Michaela Salcher:</b> There and back again: Moving from Western to Eastern Central Europe in a scientific career |
| <b>9:45</b>   | <b>Anna Székely:</b> Experiences of surviving Western academia with an Eastern PhD                                  |
| <b>10:30</b>  | <b>Hans-Peter Grossart:</b> Global networking: benefits and excitement  |
| <b>11:15</b>  | <b>Coffee Break</b>   |
| <b>11:45</b>  | <b>Aleksandra Ziemińska-Buczyńska:</b> Science communication in environmental research – will, necessity or demand? |
| <b>13:15</b>  | <b>Lunch Break</b>  |
| <b>14:30</b>  | <b>Lisa Stein &amp; Colin Murrell:</b> Publishing with ISME Journals  |
| <b>18:00</b>  | <b>ISME Ambassadors Meeting</b>   |

| <b>Wednesday (September 13)</b>  |   |
|--|---|
| <b>Venue: Hungarian Academy of Sciences, Great Hall (1051 Budapest, Széchenyi István tér 9.)</b> |   |
| <b>Welcome and Opening Remarks</b>   |   |
| <b>9:15</b>  | <b>Attila Szabó</b>   |
| <b>Plenary Talks</b>   | <b><u>Microbes Beneath our Feet</u></b>   |
| <b>9:30</b>  | <b>Petr Baldrian:</b> Forest soil microbiome: who does what and when (and why)  |
| <b>10:00</b>   | <b>Colin Murrell:</b> Focussed and functional metagenomics; a case study of trace gas metabolism  |
| <b>10:30</b>   | <b>Coffee Break</b>   |
| <b>Oral Talks</b>  |   |
| <b>11:00</b>   | <b>Vendula Brabcová:</b> Microbiome of decomposing branches: Climate sensitive biodiversity source in managed forest  |
| <b>11:12</b>   | <b>Ovidiu Copot:</b> Usefulness of the environmental DNA for fungal Red Listing   |
| <b>11:24</b>   | <b>Ariel Marchlewicz:</b> Ecosystem Health Implications: Through the Microbial Breakdown and Environmental Destiny of Non-Steroidal Anti-Inflammatory Drugs |
| <b>11:36</b>   | <b>John Kupagme:</b> African soil fungi: Drivers of diversity and community composition   |
| <b>11:48</b>   | <b>Izabela Mujakić:</b> Multi-environment ecogenomics analysis of the cosmopolitan phylum Gemmatimonadota   |
| <b>12:00</b>   | <b>Balázs Vajna:</b> Effect of an extreme drought and rain manipulations on soil microbial communities in a sandy grassland                                 |
| <b>12:12</b>   | <b>Tijana Martinović:</b> Uncovering microbial carbon utilization in forest soil through stable isotope probing   |
| <b>12:24</b>   | <b>Jane Oja:</b> Never home alone: global diversity and distribution of indoor microbial communities  |
| <b>12:36</b>   | <b>József Geml:</b> Landscape ecology of arctic ectomycorrhizal fungi in tundra ecosystems of northern Alaska   |
| <b>12:48</b>   | <b>Lunch Break</b>  |
| <b>Plenary Talks</b>   | <b><u>Welcomed and Unwelcomed Residents: Insights into Interactions</u></b>   |
| <b>14:30</b>   | <b>Kostas Kormas:</b> Understanding fish microbiomes through ecological principles and concepts   |

|                   |   |
|-------------------|---|
| 15:00             | <b>Bogdan Druga:</b> The impact of climate change on microalgae and consequences for human society  |
| <b>Oral Talks</b> |   |
| 15:30             | <b>Michal Karlicki:</b> Plastid-genome resolved metagenomics reveals diversity of photosynthetic microbial eukaryotes in the long-term study of freshwater lakes        |
| 15:42             | <b>Adrienn Geiger:</b> Microhabitats show stronger impact on grapevine mycobiome than cultivar, season, or health state   |
| 15:54             | <b>Jason Bosch:</b> Decomposition of <i>Fomes fomentarius</i> fruiting bodies is primarily driven by Arthropoda   |
| 16:10             | <b>Coffee Break</b>   |
| 16:40             | <b>Roey Angel:</b> What do millipedes actually eat, and how is their microbiome involved?   |
| 16:52             | <b>Niloufar Hagh-Doust:</b> Global Diversity of Leaf-Associated Bacterial and Fungal Communities  |
| 17:04             | <b>Chetna Tyagi:</b> Bioactive peptaibols from clade Longibrachiatum of Trichoderma against phytopathogenic bacteria: combining experimental and theoretical approaches |
| 17:30             | <b>Poster Session</b> (Krúdy Hall)  |
| 19:00 - 21:30     | <b>Welcome reception</b> (Krúdy Hall)   |

|  |  |
|--|--|
| <b>Thursday (September 14)</b>   |  |
| <b>Venue: Hungarian Academy of Sciences, Great Hall (1051 Budapest, Széchenyi István tér 9.)</b> |  |
| <b>Plenary Talks</b>   | <b><u>Microbes Thriving in Extreme Environments</u></b>  |
| 9:00   | <b>Natalie Barteneva:</b> Beneath the surface: imaging and spectral cytometry combined with next-generation sequencing in analysis of algal-microbial communities              |
| 9:30   | <b>Hovik Panosyan:</b> Exploring of thermophiles of terrestrial geothermal springs in Lesser Caucasus  |
| <b>Oral Talks</b>  |  |
| 10:00  | <b>Nurgul Balci:</b> Microbial diversity of hydromagnesite microbialites in Lake Salda, A Mars Analog Lake   |
| 10:12  | <b>Zsuzsanna Márton:</b> Contrasting Response of Microeukaryotic and Bacterial Communities to the Interplay of Seasonality and Local Stressors in Shallow Soda Lakes           |
| 10:24  | <b>Peter Pristas:</b> Where to find halophilic bacteria in inland country  |
| 10:36  | <b>Munavvara Dzhuraeva:</b> Draft genome sequencing of the two thermophilic anaerobes feather-degrading bacterial isolates from high-altitude geothermal springs in Tajikistan |
| 10:48  | <b>David Kaftan:</b> Constitutive photosynthetic activity in arctic AAP <i>Sediminicoccus rosea</i> KRV36  |
| 11:00  | <b>Coffee Break</b>  |
| <b>Oral Talks</b>  | <b><u>Harnessing Microbial Power</u></b>   |
| 11:30  | <b>Marcell Nikolausz:</b> Anna Karenina ecological principle in biogas reactor microbiology: stochasticity under ammonia stress  |
| 11:42  | <b>Aleksandra Ziemińska-Buczyńska:</b> Nitrogen removal bacteria communities' characteristics in the lab-scale wastewater treatment systems                                    |
| 11:54  | <b>Zsuzsanna Nagymáté:</b> Effect of bioremediation techniques supplemented with a newly developed bioaugmentation agent on the organohalide-respiring microbial communities   |
| 12:06  | <b>Adela Teban-Man:</b> Tracking carbapenem resistance in municipal wastewater: spatio-temporal variation, bacterial diversity, and environmental impact                       |
| 12:18  | <b>Dóra Balázs:</b> Comprehensive examination of peptaibol compounds and preparation of their future agricultural application  |
| 12:30  | <b>Knisz Judit:</b> Microbially Influenced Corrosion – More than just Microbes   |

|                      |  |
|----------------------|--|
| <b>12:42</b>         | <b>Anna Dzionek:</b> Stenotrophomonas terrae BB3 – a new bacterial strain capable of degrade metoprolol  |
| <b>13:00 - 14:00</b> | <b>Lunch Break</b>   |
| <b>Plenary Talks</b> | <b><u>From Sassy Swimmers to Microscopic Mischief</u></b>  |
| <b>14:00</b>         | <b>Sandi Orlic:</b> Methane cycling bacteria in Croatian lakes   |
| <b>14:30</b>         | <b>Meryem Beklioglu:</b> The Microbial Loop in Lake Ecosystems: Structure and Control  |
| <b>Oral Talks</b>    |  |
| <b>15:00</b>         | <b>Cristian Villena Alemany:</b> Exploring the Ecological Significance of Aerobic Anoxygenic Photoheterotrophic Bacteria in Freshwater Ecosystems                                    |
| <b>15:12</b>         | <b>Agnieszka Nowak:</b> Iodinated contrast media in wastewater – occurrences and implications to activated sludge  |
| <b>15:24</b>         | <b>Anita Perkins:</b> Fungi increases kelp (Ecklonia radiata) remineralisation and dissolved organic carbon, alkalinity, and dimethyl sulfoniopropionate production                  |
| <b>15:36</b>         | <b>Boglárka Somogyi:</b> Diversity and ecological role of the smallest algae in turbid and saline lakes  |
| <b>15:48</b>         | <b>Edina Szekeres:</b> Diversity and core taxa of the karst spring microbiome and community response to pathogen and antibiotic resistance gene contamination                        |
| <b>16:00</b>         | <b>Indranil Mukherjee:</b> Reassembly of planktonic protistan community and modulation of microbial food web during the establishment of stratification in Řimov reservoir           |
| <b>16:12</b>         | <b>András Hidas:</b> Microbial community dynamics and interactions during the winter-spring transition in a large shallow lake   |
| <b>16:24</b>         | <b>Michal Koblížek:</b> Cold-loving bacterium from a mountain lake harvests light energy using both bacteriochlorophyll-containing photosystems as well as proton-pumping rhodopsins |
| <b>16:30</b>         | <b>Coffee Break</b>  |
| <b>17:00</b>         | <b>Round Table Discussion</b>  |
| <b>18:00 - 18:15</b> | <b>Closing remarks: Kasia Piwosz</b>   |
| <b>19:00</b>         | <b>Social gathering</b>  |

# Tuesday

12 September 2023



# CEESME

**There and back again: Moving from Western to Eastern Central Europe in a scientific career**

*Michaela M. Salcher*

Institute of Hydrobiology, Biology Centre CAS, Ceske Budejovice, Czechia

After finishing the PhD thesis, most young scientists are lost with the many options and opportunities that might (or might not) result in a scientific career. There is no universal guideline on how to pursue a scientific career, how to become a group leader or professor and how to deal with the many pitfalls that are on this way. Every scientist is different and so is every scientific career. In this workshop, I will share my personal experiences and discuss the opportunities for doing research in Czechia. I did my master's degree in Innsbruck (Austria) and moved to Zurich (Switzerland) for doing a PhD thesis, where I also stayed for six more years as a postdoc. I then received a mid-career fellowship and worked for three years in Ceske Budejovice (Czechia). After another 2-year stay as senior researcher in Zurich, I decided to move back to Czechia, as this was a perfect opportunity to start a research group. I will talk about the other options I had and why I chose this specific path. Further, there will be an open discussion about alternative career paths and individual experiences in science.

**Experiences of surviving Western academia with an Eastern PhD**

*Anna Székely*

Swedish University of Agricultural Sciences, Uppsala, Sweden

Fourteen years ago, after defending my PhD in Hungary, I decided to try life as a postdoc abroad. While I knew there would be differences, many were unexpected. In the session I will talk about these experiences and lessons. I will also share what it took for me to reach a slightly alternative academic career that I love.



**Global networking: benefits and excitement**

*Hans-Peter Grossart*

Leibniz Institute for Freshwater Ecology and Inland Fisheries, IGB

Modern microbial ecology is driven by large international and transdisciplinary networks of scientists around the globe. Many benchmarking articles in our field are only possible due to large collaborative networks. One of the best examples in aquatic ecology is GLEON (Global Lake Ecosystem Observatory Network), which has started as a NSF project and is now an independent and purely bottom up driven project. In this workshop, I will provide tips and advises how to best build your own network in your scientific field and get engaged or even lead big international initiatives, which is highly beneficial for your own scientific career, but also lots of fun and excitement. You can start early on in your career to network and bring in your scientific knowledge in scientific enterprises with larger outreach to the public, but also to stakeholders and politicians. There are many ways to achieve this goal, but it is advisable to plan it a bit to increase your success. This workshop will be held in an interactive manner, first I'll give an introduction into ways of networking, provide an overview of possibilities, and then we'll discuss questions from all of you. I hope to convince you about the value and excitement of being part of large and active scientific networks and the many possibilities how to make your own science more visible and also more important.

**Science communication in environmental research – will, necessity or demand?**

*Aleksandra Ziemińska-Buczyńska*

Silesian University of Technology, Gliwice, Poland

Environmental issues are the crucial concerns of modern world. Such problems' solution is brought by a wide variety of environmental sciences and biotechnology research. However, the voice of scientists is often not respected in the public debate over environmental topics. Usually because of the lack of scientific voice in this dialogue, but more often because of scientists' lack of proper communication skills reaching the wider audience. Scientific language differs heavily from non-scientific communication. That is why scientists are often not understood or misunderstood by non-scientific recipients. Moreover, scientists also serve as teachers for a variety of social groups to explain phenomena of their field of expertise. This part of scientists' work also requires tailor-made communication to reach the society effectively. Is science communication a will, necessity or demand for a modern scientist? How to talk about our research to non-scientific audience to be properly understood? What tools would be useful for effective science communication? Does the modern world bring innovation also in science communication field? And finally, how to find our own way to excite our audience with our scientific excitement? Join me for this lecture to search the answers together.

**Publishing with ISME Journals**

*Lisa Y. Stein*<sup>1</sup>, *Josh Neufeld*<sup>2</sup>, *Colin Murrell*<sup>3</sup>

<sup>1</sup> University of Alberta, Edmonton, Canada

<sup>2</sup> University of Waterloo, Waterloo, Canada

<sup>3</sup> University of East Anglia, United Kingdom

The ISME Journal is the premier publication venue of the International Society for Microbial Ecology. The aims of the ISME Journal are “to promote diverse and integrated areas of microbial ecology spanning the breadth of microbial life, including bacteria, archaea, microbial eukaryotes, and viruses.” The three Editors in Chief -- Josh Neufeld, Jillian Petersen, and Lisa Stein -- are committed to creating the best possible publishing experience for authors with fast turn-around times and high quality scrutiny of submissions. We pay close attention to detail and offer support to our senior editors, editorial board members, and reviewers who work closely with authors to improve their papers. Although our rejection rate for submissions is high, we provide guidance to authors for improving their work and many are recommended for submission to our partner journal, ISME Communications. In this session I will share our ongoing vision for the journals as we change publishers to Oxford University Press, provide tips and tools for authors in preparing their best work for submission to ISME J and ISME Communications, and demystify the review process. Interactive participation and questions from attendees is encouraged in this session.

# Wednesday

13 September 2023



# CEESME

**Forest soil microbiome: who does what and when (and why)***Petr Baldrian*

Laboratory of Environmental Microbiology, Institute of Microbiology of the Czech Academy of Sciences, Videnska 1083, 14220 Praha 4, Czech Republic

Forest soils are of global importance since they represent an important sink of carbon (C). In forest soils, bacteria and fungi are important drivers of soil processes, mediating both decomposition and nutrient transfer from and to trees, the main primary producers. While the roles of fungi, bacteria and the members of their guilds overlap to some extent, there is a certain level of specialization of fungal and bacterial groups with respect to C utilization and N cycling. Furthermore, it was demonstrated recently, that microbial activity varies among seasons. Here we have explored the contribution of bacteria and fungi to soil processes in a temperate coniferous forest in the context of the seasonal differences among metabolomes. The combination of metabolomics, metagenomics, metatranscriptomics and metaproteomics as well as microbial community sequencing was used to assess the seasonality of nutrient availability at the root/soil interface and its effects on the composition of the microbiomes and their contribution to C and N cycling in early and late vegetation season and early and late winter. Profound differences in metabolome profiles were found between periods of tree activity during the vegetation season and in summer. While the communities of bacteria and fungi were similar across all seasons, their activity and growth rates differed seasonally. The rhizosphere and root compartments were the most dynamic, but roots, comprising ectomycorrhizal symbionts of tree roots showed higher activity of fungi, especially in summer. The C-cycle processes were dominated by bacteria in soil and rhizosphere and by fungi in litter and roots. Profound seasonality was also detected in the expression of N-cycling genes. Interestingly, protein pools appeared to be less seasonally variable than microbial transcription. The results show that the understanding of soil microbiome functioning is impossible without considering plant activity, demonstrated by the seasonality of metabolomes of soil microhabitats. Forest soils represent highly complex systems where bacteria and fungi locally dominate and contribute together to the C and N cycling in the ecosystem.

**Focussed and functional metagenomics; a case study of trace gas metabolism**

*J. Colin Murrell*

School of Environmental Sciences, University of East Anglia, Norwich, UK

Isoprene is a climate-active, organic compound that is released into the atmosphere in similar quantities to that of methane, making it one of the most abundant trace volatiles. Large amounts of isoprene are produced by trees but also by microbes, including algae in the marine environment. We have been studying bacteria that grow on isoprene using a soluble diiron centre monooxygenase isoprene monooxygenase (IsoMO) an enzyme similar to the well-characterized soluble methane monooxygenase (sMMO). We have purified and characterized IsoMO and studied its regulation using transcriptomics and molecular genetics. IsoMO is inhibited by octyne but not acetylene which enables us to differentiate between isoprene metabolism and co-oxidation by sMMO in environmental samples. The pathways for degradation of isoprene have been elucidated using transcriptomics, proteomics and metabolomics, combined with mutagenesis studies, and these will be outlined. Our studies on the physiology, biochemistry and molecular biology of aerobic isoprene degrading bacteria have also enabled us to develop and use molecular ecology tools to examine these bacteria in the environment. Functional gene probing, DNA-stable isotope probing (DNA-SIP) and metagenomics experiments reveal that isoprene-degrading bacteria are widespread in soils, leaf surfaces and estuarine sediments and that they are likely to play a major role in the metabolism of isoprene before it escapes to the atmosphere.

**Microbiome of decomposing branches: Climate sensitive biodiversity source in managed forest**

*Vendula Brabcová*<sup>1</sup>, *Vojtěch Tláškal*<sup>2</sup>, *Clémentine Lepinay*<sup>1</sup>, *Petra Zrůstová*<sup>1</sup>, *Ivana Eichlerová*<sup>1</sup>, *Martina Štursová*<sup>1</sup>, *Jörg Müller*<sup>3,4</sup>, *Roland Brandl*<sup>5</sup>, *Claus Bässler*<sup>4,6</sup>, *Petr Baldrian*<sup>1</sup>

<sup>1</sup> Laboratory of Environmental Microbiology, Institute of Microbiology of the Czech Academy of Sciences, Praha, Czech Republic

<sup>2</sup> Institute of Soil Biology and Biogeochemistry, Biology Centre of the Czech Academy of Sciences, Ceske Budejovice, Czech Republic

<sup>3</sup> Department of Animal Ecology and Tropical Biology, University of Würzburg, Würzburg, Germany

<sup>4</sup> Bavarian Forest National Park, Grafenau, Germany

<sup>5</sup> Animal Ecology, Department of Ecology, Faculty of Biology, Philipps-Universität Marburg, Marburg, Germany

<sup>6</sup> Department of Conservation Biology, Faculty of Biological Sciences, Institute for Ecology, Evolution and Diversity, Goethe University Frankfurt, Frankfurt am Main, Germany

Fine woody debris (FWD) represents the majority of deadwood stock in managed forests and serves as an important biodiversity hotspot and refuge for many organisms, including deadwood fungi. Wood decomposition in forests, representing an important input of nutrients into forest soils, is mainly driven by fungal communities undergoing continuous changes. Deadwood bacteria are involved in C and N cycles and together with fungi facilitate deadwood decomposition. While the assembly processes of fungal communities in long-lasting coarse woody debris have been repeatedly explored, similar information for more ephemeral habitat of fine deadwood is missing. Here, we followed fate of FWD of *Fagus sylvatica* and *Abies alba* in a Central European forest over 6 years by amplicon sequencing (ITS and 16S). The effect of microclimate on deadwood properties and microbial communities was addressed by comparing FWD decomposition in closed forests and under open canopies, as the large FWD surface-to-volume ratio makes it highly sensitive to temperature and moisture fluctuations. Fungal biomass increases and pH decreases were significantly higher under closed canopy in initial stages of decomposition indicating higher fungal activity and hence decay processes. Assembly patterns of the fungal community were strongly affected by both tree species and microclimatic conditions. Communities in the open/closed canopies and in each tree species were different throughout the whole succession with only limited convergence in time in terms of both species and ecological guild composition. Decomposition under the open canopy was characterized by high sample-to-sample variability, showing the diversification of fungal resources. Bacterial community undergoes continuous development resulting in more diverse community under the open canopy. Decomposing FWD increases local microbial diversity along the increasing heterogeneity of forest with canopy openings and contributes to ecosystem stability.

**Usefulness of the environmental DNA for fungal Red Listing**

*Ovidiu Copot<sup>1</sup>, Asko Lohmus<sup>1</sup>, Kessy Abarenkov<sup>1</sup>, Leho Tedersoo<sup>1</sup>, Kadri Runnel<sup>1</sup>*

<sup>1</sup> University of Tartu, Tartu, Estonia

For navigating the biodiversity crisis, a major uncertainty is the conservation status of inconspicuous, but megadiverse and functionally crucial, soil microorganisms. Massive datasets on soil biota are accumulating through molecular sampling approaches, but with limited input into conservation planning and management. We investigated how environmental DNA data of soil fungi contribute to regional Red List assessments that are currently fruit-body based. In our test region, with ca. 15,000 fruit-body records of 1,583 species assessed, an average soil sample increased the range estimates of threatened and Near Threatened species by 0.18%. At 500 samples collected, their range estimates almost doubled and 45% previously unrecorded species were found. However, even after accumulating >1000 soil samples, about half of the fruit-body recorded species on the regional Red List remained undetected. Effective conservation assessment of soil biota requires both the fruit-body and environmental DNA data, and special efforts to make these usable to conservationists.



## Ecosystem Health Implications: Through the Microbial Breakdown and Environmental Destiny of Non-Steroidal Anti-Inflammatory Drugs

*Ariel Marchlewicz*<sup>1</sup>, *Danuta Wojcieszynska*<sup>1</sup>

<sup>1</sup> University of Silesia in Katowice, Faculty of Natural Sciences, Institute of Biology, Biotechnology and Environmental Protection, Katowice, Poland

The increasing concern over the environmental fate of non-steroidal anti-inflammatory drugs (NSAIDs) like ibuprofen, paracetamol, diclofenac, naproxen, and ketoprofen, and their possible adverse ecological consequences calls for immediate attention. As one of the most commonly used pharmaceutical groups, NSAIDs have consistently been detected in different environmental matrices. For instance, diclofenac concentrations at 200 ng/l have been observed in surface waters in Germany. Similarly, the effluents from WWTP have shown the presence of ibuprofen and naproxen at levels of 50 and 28 ng/l, respectively [1]. NSAIDs have been associated with negative ecological impacts, such as the decline in fish populations, the harmful effects on vulture populations in Asia, and the documented detrimental effects of ibuprofen on certain algae growth [2].

Furthermore, our research has identified bacterial species and metabolic pathways involved in the degradation of NSAIDs. These include the degradation of ibuprofen by *Sphingomonas* sp. Ibu1, diclofenac by *Bacillus thuringiensis* B1(2015b), and paracetamol by *Pseudomonas putida* KB4 [3]. This presentation by highlighting the critical need for comprehensive research into the long-term ecological impacts of NSAIDs and emphasizing the necessity for developing effective pollution reduction strategies in the usage and disposal of NSAIDs.

[1] Hughes et al 2013. Global synthesis and critical evaluation of pharmaceutical data sets collected from river systems. *Environ. Sci. Technol.* 5;47(2):661-77

[2] Pires, A., Granek E.F. 2016. Effects of pharmaceuticals and personal care products on marine organisms: From single-species studies to an ecosystem-based approach. *Environ. Pollut.* 23, 22365–22384

[4] Marchlewicz et al. 2017. Exploring the Degradation of Ibuprofen by *Bacillus thuringiensis* B1(2015b): The New Pathway and Factors Affecting Degradation. *Molecules*, 22:10

**African soil fungi: Drivers of diversity and community composition**

*J.Y. Kupagme*<sup>1</sup>, *L. Tedersoo*<sup>1</sup>, *S. Polme*<sup>1</sup>, *N. S. Yorou*<sup>2</sup>, *J. Kuma*<sup>3</sup>, *V. Mikryukov*<sup>1,4</sup>

<sup>1</sup> Mycology and Microbiology Center, University of Tartu, Tartu, Estonia

<sup>2</sup> Faculté d'Agronomie, Université de Parakou, Parakou, Benin

<sup>3</sup> Université Felix Houphouët-Boigny, Abidjan, Cote d'Ivoire

<sup>4</sup> Institute of Ecology and Earth Sciences, Tartu, Estonia

The role of fungi is crucial in the functioning and servicing of any given ecosystem, especially in ecologically diverse ecosystems on the continent of Africa. Soil fungi perform various ecological functions, including nutrient cycling, ameliorating nutrient uptake in plants, causing diseases as well as alleviating pathogenic attacks. Mycorrhizal fungi have received significant attention due to their inestimable value in biodiversity conservation, but there is a paucity of soil fungal data in Africa compared to other continents. To fill this knowledge gap, DNA metabarcoding data were obtained from 471 top soils from various terrestrial ecosystems of Africa covering 32 countries, and processed using Pacific Biosciences (PacBio) sequences platform. Alpha diversity (soil fungal species richness and diversity) are driven by environmental variables such as precipitation, distance from the equator, while temperature, soil pH,  $\delta^{13}\text{C}$  and C content were primary drivers of beta diversity (soil fungal community composition). Our analysis revealed that the diversity pattern of soil fungi across Africa does not differ significantly by regions but by the different terrestrial biomes within the continent. Dry tropical forests were seen to be the habitat of most diverse soil fungi in Africa, and also in richness. We also provide fine-resolution continental maps of soil fungal distributions that can enable the assessment of the current state and trends of African soil fungal biodiversity and functions, as well as provide a reference for policy making regarding biodiversity conservation in Africa.

**Multi-environment ecogenomics analysis of the cosmopolitan phylum Gemmatimonadota**

*Izabela Mujakić*<sup>1,2</sup>, *Pedro J. Cabello-Yeves*<sup>3,4,5</sup>, *Cristian Villena-Aleman*<sup>1,2</sup>, *Kasia Piwosz*<sup>6</sup>, *Francisco Rodriguez-Valera*<sup>4</sup>, *Antonio Picazo*<sup>3</sup>, *Antonio Camacho*<sup>3</sup>, *Michal Koblížek*<sup>1,2</sup>

<sup>1</sup> Lab. of Anoxygenic Phototrophs, Institute of Microbiology of the Czech Academy of Sciences, Třeboň, Czechia

<sup>2</sup> Department of Ecosystem Biology, Faculty of Science, University of South Bohemia, České Budějovice, Czechia

<sup>3</sup> Cavanilles Institute of Biodiversity and Evolutionary Biology, University of Valencia, Valencia, Spain

<sup>4</sup> Evolutionary Genomics Group, Departamento de Producción Vegetal y Microbiología, Universidad Miguel Hernández, Alicante, Spain

<sup>5</sup> School of Life Sciences, University of Warwick, Coventry, UK

<sup>6</sup> Department of Fisheries Oceanography and Marine Ecology, National Marine Fisheries Research Institute, Gdynia, Poland

Gemmatimonadota is a relatively new and highly diverse phylum found in a variety of environments. So far, there are 6 cultured species, two of which are capable of anoxygenic photosynthesis through Bchl-a reaction centers. For a long time most of the research concerning Gemmatimonadota was focused on soil environments where they are one of top 10 bacterial phyla, and it was unclear if their presence in freshwaters was due to passive transport from sediments and soil. Previously, using metagenomes from several European freshwater lakes, we found that they persist in the water column, and are present throughout different years, seasons and depths. We also documented presence of different photoheterotrophic Gemmatimonadota in lakes. Furthermore, we collected all publicly available genomes of Gemmatimonadota and applied a multi-environment comparison of over 400 genomes from various aquatic environments, soils, sediments or host-associated species (with marine sponges/corals) to study their metabolism and potential roles. We observed a smaller genomes size and lowest GC content in marine Gemmatimonadota pointing to an oligotrophic environment adaptation. The principal coordinate and phylogenomic analyses grouped the different genomes according to their environment, and several metabolic pathways were environment-specific. We showed that, while photoheterotrophy occurred in wastewater or soda lake sediments, it predominates in freshwater genomes. Their potential roles were highlighted in presence of RuBisCOs in genomes from soda lake sediments and wastewater and gene involved in reduction of N<sub>2</sub>O in genomes from most environments. This study provides a detailed global overview of Gemmatimonadota metabolism, which are chemoorganotrophic organisms with numerous adaptations to different environments that enlarge their metabolic versatility.

**Effect of an extreme drought and rain manipulations on soil microbial communities in a sandy grassland**

*Balázs Vajna*<sup>1</sup>, *Dániel G. Knapp*<sup>2</sup>, *Bálint Dima*<sup>2</sup>, *Zoltán Szalai*<sup>3,4</sup>, *Anna Nagy*<sup>4</sup>, *Péter Szávai*<sup>4</sup>, *György Kröel-Dulay*<sup>5</sup>, *Gábor M. Kovács*<sup>2</sup>

<sup>1</sup> Eötvös Loránd University, Department of Microbiology, Budapest, Hungary

<sup>2</sup> Eötvös Loránd University, Department of Plant Anatomy, Budapest, Hungary

<sup>3</sup> Eötvös Loránd University, Department of Environmental and Landscape Geography, Budapest, Hungary

<sup>4</sup> Research Centre for Astronomy and Earth Sciences, Budapest, Hungary

<sup>5</sup> Institute of Ecology and Botany, Centre for Ecological Research, Vácrátót, Hungary

A multiannual extreme drought and rain manipulations (ExDRain-project) have been running to study the effect of local climate change in a multidisciplinary way in a sandy grassland near Fülöpháza (Hungary). Microbial communities have important roles in ecosystem functioning; therefore, our aim was to reveal the effect of local climate change on soil microbial diversity and analyse relationship among them and other measured parameters.

The experimental site was sampled extensively exactly before the manipulations and thereafter in first, third and fifth year resulting in 156 composite soil samples from 48 experimental pots. Community DNA was extracted from every composite soil sample with Qiagen DNeasy® PowerMax® Soil Kit. Prokaryotic 16S rRNA gene was amplified by the Earth Microbiome primer pair, whereas fungal nuclear rRNA ITS2 region was amplified by the ITS3\_KYO2 - ITS4 primer pair. The products were analysed by Next Generation Sequencing on the Illumina platform. The raw sequences were processed and analysed using the pipeline of the SEED2 software. Soil parameters were also measured. Statistical analyses were carried out with the R software.

The 16S rRNA gene amplicon sequencing resulted in a total of 35,000 – 98,000 high-quality prokaryotic reads per sample. Whereas sequencing of fungal nuclear rRNA ITS2 region resulted in a total of 5,000 – 263,000 high-quality fungal reads per sample. The main finding was, that manipulations had a significant effect on fungal community composition, whereas bacterial communities were grouped according to geographical distances among the sampling sites. Details of microbial diversity and relationship among the different measured parameters will be presented.

This research was supported by the Hungarian Scientific Research Found (OTKA K 129068 and 139026). Balázs Vajna and Dániel Knapp were supported by the János Bolyai Research Scholarship of the Hungarian Academy of Sciences (Grant No. BO/00156/21/8 and BO/00727/19/8).

**Uncovering microbial carbon utilization in forest soil through stable isotope probing**

*Tijana Martinović<sup>1</sup>, Tereza Mašínová<sup>1</sup>, Rubén López-Mondéjar<sup>1</sup>, Jan Jansa<sup>1</sup>, Martina Štursová<sup>1</sup>, Robert Starke<sup>1</sup>, Petr Baldrian<sup>1</sup>*

<sup>1</sup> Institute of Microbiology of the Czech Academy of Sciences, Vídeňská 1083, 142 20 Praha 4, Czech Republic

Microorganisms play a crucial role in soil ecosystems by driving various ecological processes. However, there is limited research on the specific contributions of fungi and bacteria to these processes. Recent studies have revealed that bacteria possess the ability to break down complex plant polymers in soil, highlighting their significance in the carbon cycle, alongside fungi. This study aimed to investigate the assimilation of carbon from forest soils into the biomass of fungi and bacteria using stable isotope probing. Microcosms were incubated with <sup>13</sup>C-labeled substrates of varying complexity, and the rates of substrate respiration were measured. Phospholipid fatty acids were used as an indicator of microbial biomass. The microbial taxa that incorporated <sup>13</sup>C into their biomass were identified through <sup>13</sup>C-DNA separation and amplicon sequencing. Results showed that microcosms supplied with labeled citric acid and glucose exhibited the highest respiration rates after one week of incubation, while those supplied with chitin showed the lowest rates. However, after three weeks, a significant increase in chitin respiration rate was observed, along with an increase in total microbial biomass and <sup>13</sup>C-labeled microbial biomass. Notably, microcosms containing <sup>13</sup>C-labeled chitin displayed a distinct microbial community, indicating the involvement of both fungi and bacteria in chitin decomposition. The findings revealed the presence of specialized and generalist taxa in all microcosms, highlighting the capacity of numerous microbial taxa to utilize different carbon sources. Furthermore, low-molecular-mass compounds were more readily respired, whereas carbon from complex biopolymers was predominantly incorporated into the microbial biomass.

**Never home alone: global diversity and distribution of indoor microbial communities**

*Jane Oja<sup>1</sup>, Farah Shafiq<sup>1</sup>, Vladimir Mikryukov<sup>1</sup>, Sten Anslan<sup>1</sup>, Leho Tedersoo<sup>1</sup>*

<sup>1</sup> Department of Botany, University of Tartu, J. Liivi 2, 50409 Tartu, Estonia

Day by day we are spending majority of our time indoors. While operating in homes or other buildings, we are exposed to a wide array of microorganisms, of which can pose a serious risk to human, animal, and plant health. Our objective was to identify dust-associated bacteria, fungi, and arthropods in homes across the globe and characterize factors that shape their diversity and distribution by using citizen scientists help and high-throughput sequencing technologies. Our dataset is the largest yet assembled for indoor microbial, and arthropod communities, encompassing samples from 79 countries and 6 continents. Our findings shed new light on the global distribution of indoor unnoticeable organisms, and we show that several of them are geographically structured. In addition, we reveal that the diversity of dust-associated microbial, and arthropod communities is, to some degree, predictable from temperature and precipitation. In sum, we get a better understanding of the environment around us and how it may impact our well-being, our pets and plant health.

**Landscape ecology of arctic ectomycorrhizal fungi in tundra ecosystems of northern Alaska**

*József Geml*<sup>1,2,3</sup>, *Attila Lengyel*<sup>1,4</sup>, *Luis N. Morgado*<sup>3</sup>, *Tatiana Semenova-Nelsen*<sup>3</sup>, *Donald A. Walker*<sup>5</sup>

<sup>1</sup> ELKH-EKKE Lendület Environmental Microbiome Research Group, Eszterházy Károly Catholic University, Eger, Hungary

<sup>2</sup> Research and Development Centre, Eszterházy Károly Catholic University, Eger, Hungary

<sup>3</sup> Naturalis Biodiversity Center, Leiden, the Netherlands

<sup>4</sup> Institute of Ecology and Botany, Centre for Ecological Research, Vácrátót, Hungary

<sup>5</sup> Institute of Arctic Biology, University of Alaska Fairbanks, Fairbanks, AK, U.S.A.

Most arctic plants are highly dependent on mutualistic relationships with mycorrhizal fungi for survival in these nutrient-poor environments. Ectomycorrhizal (ECM) fungi comprise a dominant functional group of fungi in the arctic tundra. Several studies in the Arctic observed clear shifts in fungal composition across gradients of bioclimates, primary succession, and nitrogen deposition, but little is known about how ECM fungal communities change along mesotopographic and edaphic gradients at landscape scales in tundra ecosystems. We investigated soil fungal communities in contrasting tundra types that are primarily distributed according to differences in soil moisture and snow depth largely driven by mesotopographic gradients. We generated and analyzed DNA sequence data generated from soil sampled in permanent vegetation plots on acidic and non-acidic soils at the Arctic LTER site at Toolik Lake, Alaska. Our results show that the genera *Tomentella*, *Cortinarius* and *Inocybe* dominated ECM fungal communities at the sampled plots, with fewer species detected in *Hebeloma*, *Lactarius*, and *Russula*. Community composition of ECM fungi differed among coenological vegetation types and that these differences appeared to be driven primarily by soil moisture and pH, and secondarily by the distribution of ECM host plants. Because of the close proximity of sampled plots, spore dispersal likely is unrestricted among the sampled plots and niche-based processes, such as environmental filtering, likely contribute to the observed differences in ECM fungal communities along environmental gradients and among tundra types.

**Understanding fish microbiomes through ecological principles and concepts**

*Konstantinos Kormas*

Department of Ichthyology & Aquatic Environment, University of Thessaly, 38446 Volos, Greece

Fish are among the oldest animals on our planet and, along with other aquatic organisms, they live in an environment that resembles a microbial culture. Despite that considerable data and knowledge on fish microbiomes has accumulated the last few years, basic questions on how these microbiomes are shaped and regulated, remain elusive, while novel roles of these microbiomes are being revealed. Before moving to full exploitation of these microbiomes, mostly for aquaculture and -lately- for conservation purposes, a lookback on well established, and relevant to the fishes' ecophysiology, ecological principles and concepts can be highly insightful and helpful.



**The impact of climate change on microalgae and consequences for human society**

*Bogdan Druga*

Institute of Biological Research

Climate change has been widely predicted to impact on phytoplankton fitness, and this impact will most likely vary among different groups of microalgae. Considering the paramount importance of phytoplankton in aquatic ecosystems, as primary producers, it is vital to understand the magnitude of the impact that future conditions might have on these organisms. However, long-term (more relevant) studies targeting their adaptive potential to climate change conditions have only rarely been carried until recently.

We examined the effect of acclimating both freshwater and marine phytoplankton to increased temperature and CO<sub>2</sub> concentrations, for hundreds of generations. The competitive ability of the strains after heat acclimation was also evaluated, by analysing their impact on plankton community composition (in mesocosm experiments). In parallel, genomes were sequenced and the expression of several thermal-relevant genes was also measured. We found that higher temperature leads to plastic (rather than genomic) responses within heat-adapted microalgae, resulting in the upregulation of certain genes associated with thermal tolerance. In parallel, we observed the alteration of the fatty acid profile in several microalgae, with possible negative effects along the food chain, including on human society.

**Plastid-genome resolved metagenomics reveals diversity of photosynthetic microbial eukaryotes in the long-term study of freshwater lakes**

*Michał Karlicki*<sup>1</sup>, *Jason Woodhouse*<sup>2</sup>, *Hans-Peter Grossart*<sup>2</sup>, *Kasia Piwosz*<sup>3</sup>, *Anna Karnkowska*<sup>1</sup>

<sup>1</sup>Institute of Evolutionary Biology, Faculty of Biology, Biological and Chemical Research Centre, University of Warsaw, Żwirki i Wigury 101, 02-089 Warsaw, Poland

<sup>2</sup>Department of Plankton and Microbial Ecology, Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB), Zur alten Fischerhuetten 2, 14775 Stechlin, Germany

<sup>3</sup>National Marine Fisheries Research Institute, ul. Kołłątaja 1, 81-332, Gdynia, Poland

Microbial eukaryotes, play significant role in freshwater ecosystems. However, their diversity and functions in these environments have not been fully studied due to limited sequencing efforts. While metagenomics has revolutionized our understanding of prokaryotic diversity, the exploration of protist communities remains challenging. We propose that targeting plastid genomes, which are small and present in abundance, could be a valuable approach for the metagenomic analysis of photosynthetic protists in freshwater ecosystems.

Here, we present the findings of our investigation into phototrophic microbial eukaryotes using their plastid genomes, which were extracted from a metagenomic dataset comprising 1096 samples. These samples were collected over ten years from four lakes with distinct trophic statuses. We devised an efficient pipeline that minimizes computational resources to handle the immense amount of data. The pipeline includes steps such as contig screening using tiara, mmseq2 validation of potential plastid-like contigs, and manual binning in Anvi'O.

By implementing this protocol, we detected and reconstructed environmental plastid genomes (ptMags) from eight co-assemblies. Our efforts resulted in the recovery of over 200 plastid genomes, which represent groups of photosynthetic protists belonging to Chlorophyta, Stramenopila, Haptophyta, Cryptophyta, Alveolata, and Euglenophyta. Among those, we identified two almost complete ptMAGs belonging to the first-ever reported freshwater Pelagophyceae, dramatically changing our perception of the distribution of this group of Stramenopiles.

To sum up, we aimed to enhance our understanding of the genetic diversity of phototrophic protists in freshwater environments over ten years. Our findings provide valuable insights into the successful recovery of plastid genomes from metagenomic data. These recovered plastid genomes offer a wealth of information for future investigations into the ecology of microbial eukaryotes.

**Microhabitats show stronger impact on grapevine mycobiome than cultivar, season, or health state**

*Adrienn Geiger*<sup>2,3</sup>, *Carla Mota Leal*<sup>1,2</sup>, *Zoltán Karácsony*<sup>3</sup>, *Richárd Golen*<sup>3</sup>, *Kálmán Zoltán Váczy*<sup>3</sup>, *József Geml*<sup>1,3</sup>

<sup>1</sup> ELKH-EKKE Lendület Environmental Microbiome Research Group, Eszterházy Károly Catholic University, Leányka u. 6. Eger 3300, Hungary

<sup>2</sup> Doctoral School of Environmental Sciences, Péter K. u. 1., Gödöllő 2100, Hungary

<sup>3</sup> Food and Wine Research Centre, Eszterházy Károly Catholic University, Leányka u. 6., Eger 3300, Hungary

Grapevine is an important plant cultivated in more than 80 countries around the world. To date, it is still unclear how infectious diseases, such as grapevine trunk diseases (GTDs) modify the microbiome of grapevine. In this study, we examined the mycobiome of asymptomatic and GTD symptomatic grapevine to see how health state affects grapevine mycobiome. We also tested the influence of cultivar, season, vintage and microhabitats on the mycobiome. DNA metabarcoding data were generated from bark, soil and woody tissue from four different cultivars in 2020 February and August, and 2021 February and August. The most common mycobial functional groups were plant pathogens, wood saprotrophs, soil saprotrophs, litter saprotrophs and mycoparasites. Plant pathogens were dominant, this was driven by GTD pathogens in bark and wood, and non-GTD pathogens in soil. Wood saprotrophs were mainly in bark, while soil and litter saprotrophs occurred in soil, mycoparasites were present mostly in bark. Abundance and richness values differed across microhabitats but not among health states. Seasonality and cultivar did not affect the mycobiome. Richness values of 2021 were lower in case of plant pathogens, wood saprotrophs and mycoparasites, probably due to the drier vintage. This suggests that environmental factors could be particularly important shaping the fungal mycobiome of grapevine, and studies are needed to investigate the effect of abiotic conditions on fungal compositional dynamics.

**Decomposition of *Fomes fomentarius* fruiting bodies is primarily driven by Arthropoda**

Jason Bosch<sup>1</sup>, Priscila Thiago Dobbler<sup>1</sup>, Tomáš Větrovský<sup>1</sup>, Vojtěch Tláškal<sup>1,2</sup>, Petr Baldrian<sup>1</sup>, Vendula Brabcová<sup>1</sup>

<sup>1</sup> Institute of Microbiology of the Czech Academy of Sciences, Prague, Czechia

<sup>2</sup> The Biology Centre of the Czech Academy of Sciences, České Budějovice, Czechia

*Fomes fomentarius* is a white-rot fungus, with a long-lasting fruiting body, that plays a major role in the decomposition of deadwood in Northern Hemisphere forests. It is of scientific interest for its ecological role, potential as a structural material and use as a medicinal supplement. However, little is known about the associated microbial community of the actively-growing fungus and how this changes during decomposition.

We compared the metagenome and metatranscriptome of fresh and rotten *F. fomentarius* fruiting bodies, hypothesising that the rotten fruiting bodies would serve as a growth substrate for fungivorous fungi and bacteria.

Fresh and rotten fruiting bodies of *F. fomentarius* growing on beech trees (*Fagus sylvatica*) in the Žofínský Prales National Nature Reserve in the Czech Republic were harvested in 2017. DNA was extracted with the NucleoSpin Soil Kit, sequenced on an Illumina MiSeq and assembled with MEGAHIT. RNA was extracted with the NucleoSpin RNA plant kit, sequenced on an Illumina HiSeq 2500 and assembled with Trinity. Functional predictions were made using FragGeneScan and hmsearch using the KOfam database and dbCAN HMM database V6. All subsequent analyses were performed in R.

In fresh samples, the majority of sequences are derived from *F. fomentarius* but, in rotten samples, the community shifts so that *F. fomentarius* is replaced largely by bacteria. In contrast to the adjacent deadwood bacterial community, the bacteria in rotten samples lack the ability to fix nitrogen. The largest proportions of CAZymes were produced by Arthropoda, Actinobacteria, Eusebia and Proteobacteria but almost all CAZymes targeting chitin were produced by Arthropoda. While this study is preliminary, it suggests that Arthropoda are the primary decomposers of *F. fomentarius* fruiting bodies and that the decomposition of aerial or soil fungal material may be qualitatively different.

**What do millipedes actually eat, and how is their microbiome involved?**

*Roey Angel*<sup>1,2</sup>, *Julius Eyiuche Nweze*<sup>1,2</sup>, *Shruti Gupta*<sup>1</sup>, *Terézia Horváthová*<sup>2,3</sup>, *Eva Petrová*<sup>1</sup>, *Vladimír Šustr*<sup>1</sup>

<sup>1</sup> Institute of Soil Biology and Biogeochemistry, Biology Centre CAS, České Budějovice, Czechia

<sup>2</sup> University of South Bohemia, České Budějovice, Czechia

<sup>3</sup> Department of Aquatic Ecology, EAWAG, Dübendorf, Switzerland

Millipedes are an essential group of detritivores, eating voraciously to compensate for their poor diet. Millipedes are considered keystone macrodetritivores in many terrestrial ecosystems after termites and earthworms, devouring 10-36% of the annual litter. Therefore, they contribute to soil formation and are essential ecosystem engineers.

Despite their ecological importance, it remains unclear whether millipedes are cellulolytic and what is their microbiome's role in the diet.

We evaluated to what degree tropical and temperate millipedes depend on their gut microbiome. First, we charted the microbiome of 11 millipede species and measured their guts' redox potential. Then, further experimented with two model species using chemical suppressors and RNA-SIP in conjunction with metagenomics and metatranscriptomics to elucidate the metabolic potential of key bacterial players in the hindgut.

Bacterial and archaeal communities were phylogenetically conserved while the fungi matched the diet. Random forest analysis partitioned the microbiome into three distinct groups, closely matching the gut's redox conditions. Chemical suppressors dramatically affected microbial functions, but with only minimal effect on the millipedes.

In total, 305 high-quality MAGs consisting of 18 prokaryotic taxa were obtained, including various novel bacteria. The results from reconstructed metabolic pathways indicate, in addition to fermentation, ammonia oxidation and nitrogen fixation.

Our results suggest that while the microbiome benefits the millipedes and its composition reflects the prevailing conditions in the gut, it is not essential. As opposed to, e.g., termites or ruminants, millipedes seem to feed on microbial biomass instead of fermentation products.

**Global Diversity of Leaf-Associated Bacterial and Fungal Communities**

*Niloufar Hagh-Doust*<sup>1,2</sup>, *Leho Tedersoo*<sup>1,2</sup>

<sup>1</sup>Institute of Ecology and Earth Sciences, University of Tartu, Tartu, Estonia

<sup>2</sup>Mycology and Microbiology Center, University of Tartu, Tartu, Estonia

Plant individuals act as holobionts, offering multiple microhabitats for diverse endophytic and epiphytic microbial lineages that colonize belowground and aboveground plant surfaces as well as internal tissues. Interactions between plants and their microbiome are a fundamental part of the ecosystem functionality. The aboveground organs of plants host numerous ecologically important fungi and bacteria including pathogens, endophytes, and epiphytes. However, the diversity patterns and spatial distribution of these microbes remain unknown. The main objective of our project is to uncover the diversity of leaf-associated bacteria and fungi at a global scale and determine the most important factors shaping their communities. I will give an overview of the ongoing project and talk about our hypothesis and different aspects of our project. I will also go through the methods, challenges and progress of the project so far.

**Bioactive peptaibols from clade Longibrachiatum of Trichoderma against phytopathogenic bacteria: combining experimental and theoretical approaches**

Dóra Balázs<sup>1,2</sup>, Tamás Marik<sup>1</sup>, András Szekeres<sup>1</sup>, Csaba Vágvölgyi<sup>1</sup>, László Kredics<sup>1</sup>, Chetna Tyagi<sup>1</sup>

<sup>1</sup> Department of Microbiology, Faculty of Science and Informatics, University of Szeged, Szeged, Hungary

<sup>2</sup> Doctoral School of Biology, Faculty of Science and Informatics, University of Szeged, Szeged, Hungary

In the past decade or more, integrated disease management (IDM) has been an important topic of scientific curiosity due to the rising environmental concerns of using industrially produced chemical pesticides. Members of the genus *Trichoderma* have recently been in the limelight owing to several properties which make them excellent biocontrol agents. In our study, the peptaibol production of *Trichoderma longibrachiatum* SZMC 1775, *T. longibrachiatum* f. *bissettii* SZMC 12546, *T. reesei* SZMC 22616, *T. reesei* SZMC 22614, *T. saturnisporum* SZMC 22606 and *T. effusum* SZMC 22611 were investigated to elucidate structure-activity relationships (SARs) between the bioactivities of peptaibols and their three-dimensional structures. The effects of each peptaibol mixture, divided into groups A and B, were examined against nine commonly known plant-pathogenic bacteria. The highest bioactivity was exerted by *T. longibrachiatum* f. *bissettii* SZMC 12546 against Gram-positive bacteria, and it could also inhibit the plant pathogenic Gram-negative *Rhizobium radiobacter*. To draw correlation with experiment, accelerated molecular dynamics (aMD) simulations were performed in aqueous solvent to explore the folding dynamics of 12 selected peptaibols (most produced in each group and their isomer from the other group). The main difference between the peptaibols from group A and B lies in the 'Gly-Leu-Aib-Pro' and 'Gly-Aib-Aib-Pro' motifs ('Aib' stands for  $\alpha$ -aminoisobutyric acid), which significantly affected their folding dynamics and might explain the differences in their expressed bioactivity. Group A peptaibols showed more restricted folding dynamics with well-folded helical conformations as the most stable representative structures. This structural stability and dynamics might explain the higher observed bioactivity of Group A peptaibols against the selected bacterial species.

# Thursday

14 September 2023



# CEESME



**Beneath the surface: imaging and spectral cytometry combined with next-generation sequencing in analysis of algal-microbial communities**

*Natalie Barteneva*

Nazarbayev University, Astana, Kazakhstan

Algal blooms are accompanied by a diverse community of heterotrophic bacteria important in bloom development. Current analysis of microbiome composition and functions are mainly based on sequencing technologies that are still far from routine. The downside of traditional microscopic methods is also low temporal resolution. With a growing demand for monitoring the dynamic behavior of algal-microbial communities at high temporal resolution, alternative methods are required. Recent advancements in single-cell analysis, such as imaging and spectral cytometry, have aimed to overcome the limitations of microscopy. The spectral flow cytometers provide unparalleled resolution of algal autofluorescence due to 186 detectors (SONY Biologicals Inc., USA). The analysis strategy relies on the combination of morphological and spectral features in parallel with nanopore-based next-generation sequencing and reveals dynamics and complex structures of algal-microbial communities. We are now able to follow changes in the algal-microbial microbiomes over long periods of time in response to environmental parameters..

**Exploring of thermophiles of terrestrial geothermal springs in Lesser Caucasus***Hovik Panosyan*

Yerevan State University, Yerevan, Armenia

The microbial diversity of high-altitude geothermal springs has been recently assessed to explore their biotechnological potential. However, little is known regarding the microbiota of similar ecosystems located in Lesser Caucasus Mountains. Here the information on the microbiota of high-altitude (960–2090 m above sea level) geothermal springs (temperature range 25.8–70 °C and pH range 6.0–7.5) in Armenia and Nagorno-Karabakh located on the Alpide (Alpine–Himalayan) orogenic belt, a seismically active region is summarized. The taxonomic diversity of hot spring microbiomes has been examined using culture-independent approaches, including 16S rRNA gene library construction, 454 pyrosequencing and Illumina HiSeq technics. The predominance of phylotypes of Proteobacteria, Firmicutes, Nitrospiraea and Deinococcus–Thermus bacterial and Euryarchaeota, Crenarchaeota and Thaumarchaeota archaeal phyla, in prokaryotic microbiota of studied springs has been shown. The obtained phylotypes shared <97% similarity with uncultured microbes in the Genbank indicating their novelty and uniqueness. The role of different microbes in biogeochemical cycle of biogenic elements, as well as the inverse relationship between microbial diversity and temperature of the geothermal springs has been revealed. Temperature seems to be an important factor in shaping the microbial communities of these springs. Overall, the diversity and richness of the microbiota are negatively affected by increasing temperature. Other abiotic factors, including pH, mineralization, and geological history, also impact the structure and function of the microbial community.

In total 114 strains belonging to 28 different species of genera *Bacillus*, *Geobacillus*, *Parageobacillus*, *Anoxybacillus*, *Paenibacillus*, *Brevibacillus*, *Aeribacillus*, *Ureibacillus*, *Thermoactinomyces*, *Thermus*, *Methylocaldum*, *Arcobacter* and *Methanoculleus* have been isolated and identified by polyphasic approaches and served as a base to create valuable culture collection of thermophilic microbes. A new species of thermophilic bacterium belonging to the genus *Anoxybacillus* named *Anoxybacillus karvacharensis* sp. nov. (= DSM 106524T = KCTC 15807T) and a new species of eurytherm aerobic metanotrophic bacterium belonging to the genus *Methylocaldum* have been discovered. Whole-genome shotgun sequencing of *Thermus scotoductus* K1, as well as of the potentially new *Treponema* sp. J25, were performed.

Detailed characterization of thermophilic isolates indicate the potential of the studied springs as a source of biotechnologically valuable microbes and biomolecules. Active producers of heat-resistant proteases, lipases and amylases, as well as exopolysaccharide producers have been described and characterized.

**Microbial diversity of hydromagnesite microbialites in Lake Salda, A Mars Analog Lake***Nurgul Balci*<sup>1</sup><sup>1</sup> Istanbul Technical University, Geomicrobiology-Biogeochemistry Laboratory

Lacustrine carbonates are the center of exobiology studies upon discovery of hydrated Mg-carbonates - hydromagnesite- $[\text{Mg}_5(\text{CO}_3)_4(\text{OH})_2 \cdot 4\text{H}_2\text{O}]$ -, in the marginal deposits of the paleolake in Jezero crater, Mars. As well documented on Earth carbonates within lacustrine systems have high biosignature preservation potential and can be biologically mediated. Thus, the Mg-carbonate bearing deposits in Jezero may also have high biosignature preservation potential as those on Earth. However, our ability to identify and characterize facies with high biosignature preservation potential in a microbially-dominated, mafic, and alkaline lacustrine system hosting hydrated Mg carbonates is limited due to the rarity of these types of systems on Earth. Lake Salda, located in the Southwestern of Turkey within the ultramafic terrains, is the best modern terrestrial analogs of martian lacustrine carbonates. A comprehensive molecular analysis using Illumina sequencing of different microbial layers of the microbialites identified at least 12 dominant bacterial phyla. Cyanobacteria were generally low in abundance and ranged from 1 % in the deeper carbonates mounds to 37 % in the shallow microbialites. Other photosynthetic members included green non-sulfur bacteria of the phylum Chloroflexi dominated by the genera of Ab4 and BR1031 in all microbial layers in the lake. Surprisingly, in contrast to the shallow growing microbialites, the deeply growing microbialites contained significant amounts of Firmicutes phylum, the genus of Exiguobacterium spp, In contrast to the deeper ones, Cyanobacteria and Chloroflexi dominated the microbial community of the shallow growing microbialites. Despite the sufficient light intensity reaching the deeper microbialites, the lack of dominant cyanobacteria, and the abundance of Firmicutes and Chloroflexi collectively suggest that heterotrophic metabolisms and anoxygenic photosynthetic processes influence carbonate precipitation process in the lake.

**Contrasting Response of Microeukaryotic and Bacterial Communities to the Interplay of Seasonality and Local Stressors in Shallow Soda Lakes**

*Zsuzsanna Márton*<sup>1,2,3</sup>, *Bianka Csitári*<sup>3,6,8</sup>, *Tamás Felföldi*<sup>1,4</sup>, *András Hidas*<sup>1,3</sup>, *Ferenc Jordán*<sup>7</sup>, *Attila Szabó*<sup>1,5</sup>, *Anna J Székely*<sup>5,8</sup>

<sup>1</sup> Institute of Aquatic Ecology, Centre for Ecological Research, Budapest, Hungary

<sup>2</sup> National Multidisciplinary Laboratory for Climate Change, Centre for Ecological Research, Budapest, Hungary

<sup>3</sup> Doctoral School of Environmental Sciences, ELTE Eötvös Loránd University, Budapest, Hungary

<sup>4</sup> ELTE Eötvös Loránd University, Budapest, Hungary

<sup>5</sup> Swedish University of Agricultural Sciences, Uppsala, Sweden

<sup>6</sup> Karolinska Institutet, Stockholm, Sweden

<sup>7</sup> Department of Chemistry, Life Sciences and Environmental Sustainability, University of Parma, Parma, Italy

<sup>8</sup> Uppsala University, Uppsala, Sweden

Seasonal environmental variation is a leading driver of microbial planktonic community assembly and interactions. Departures from general seasonal successional trends are often reported. To understand the role of local s in modifying seasonal succession, we sampled fortnightly throughout three seasons (spring, summer, and autumn) five nearby shallow soda lakes exposed to the same seasonal meteorological changes. We characterised their microeukaryotic and bacterial communities by amplicon sequencing. Biological interactions were revealed by the analyses of synchronous and time-shifted interaction networks, and the keystone taxa were topologically identified. The pans showed similar succession patterns during the study period with spring being characterised by high relevance of trophic interactions and certain level of community stability followed by a more dynamic and variable summer-autumn period. Adaptation to general seasonal changes happened through shared core microbiome of the pans. Stochastic events such as desiccation disrupted common network attributes and introduced shifts from the prevalent seasonal trajectory. Our results demonstrated that despite being extreme and highly variable habitats, shallow soda lakes exhibit certain similarities in the seasonality of their planktonic communities, yet random stochastic events such as droughts can instigate substantial deviations from prevalent trends for the microeukaryotic but not bacterial communities.

**Where to find halophilic bacteria in inland country**

*Peter Pristas*<sup>1</sup>, *Lea Nosalova*<sup>1</sup>, *Shivani Adhvaryu*<sup>1</sup>, *Jana Kiskova*<sup>1</sup>, *Mariana Kolesarova*<sup>1</sup>, *Lenka Malinovicova*<sup>1</sup>, *Maria Piknova*<sup>1</sup>

<sup>1</sup> Pavol Jozef Safarik University in Kosice, Slovakia

Halophiles are the rising stars of modern (next generation) biotechnologies due to their special characteristics and potential for a range of biotechnological applications. They can produce variety of products such as salt (and temperature) tolerant enzymes, osmoprotectors (ectoine, glycine, betaine), biopolymers (polyhydroxyalkanoates - PHA), and biosurfactants. Other biotechnological applications include bioremediation of saline soils and degradation of toxic compounds.

In the search for halophilic bacteria multiple natural saline and hypersaline environments in Slovakia and Ukraine were analysed. No true halophilic bacteria were detected in mineral and travertine springs or in relict sea water with total dissolved salts (TDS) content lower than 10 g/L.

Halophilic bacteria were detected in Slana voda (Salt water) natural spring in Northern Slovakia with mineralization level as high as 50 g/L and in two salt brines from former salt mines in Solivar (eastern Slovakia) and Solotvino (western Ukraine) with TDS more than 300 g/L. Cultivable bacterial community in all three hypersaline habitats was dominated by Proteobacteria - mainly by *Halomonas* spp. which was detected in all 3 habitats, *Idiomarina* spp. were detected in brines only. Other species - *Halovibrio* spp., *Shewanella* spp., *Pseudoalteromonas* spp., *Salinivibrio* spp., *Pseudoceanicola* spp., and *Alteromonas* spp. were locality specific. Phylogenetic analyses indicate that at least 10% of cultivable bacteria obtained are the representatives of new species. Biochemical and genomic analyses confirmed that isolated strains are promising source of salt-tolerant hydrolases (amylases, cellulases, proteinases etc.) and high level of PHA production was detected in *Halomonas* spp. In the members of this genus the highest ability to decolorize synthetic azo dyes was observed. Our data indicate that natural salt springs could be an unique source of new species of halophilic bacteria with valuable properties.

**Draft genome sequencing of the two thermophilic anaerobes feather-degrading bacterial isolates from high-altitude geothermal springs in Tajikistan**

*Munavvara Dzhuraeva*<sup>1,2</sup>, *Khursheda Bobodzhanova*<sup>1</sup>, *Nils-Kåre Birkeland*<sup>2</sup>

<sup>1</sup> Center of Biotechnology of the Tajik National University, Dushanbe, Tajikistan

<sup>2</sup> Department of Biological Sciences, University of Bergen, Bergen, Norway

Chicken feather, a major by-product of the poultry industry, represents a potentially high-quality protein source due to its high protein content of more than 85%. However, is currently mostly discharged into the environment or burned. Some microorganisms have keratinolytic enzymes that convert keratin to peptides.

The purpose of this study was to recover feather-degrading keratinolytic thermophilic anaerobic bacteria from hot springs in Tajikistan. Studies of feather- degrading microorganisms are mainly limited to cases of animal diseases and biotechnology purposes for processing large amounts of waste by-products in poultry processing plants.

Two bacterial isolates that degrade feather at 50 – 80°C were recovered from the Tamdykul geothermal spring using a nutrient-rich proteinaceous anaerobic medium. At 80°C, complete degradation of feathers could be seen after four days. Based on the sequence of the 16S rRNA gene, the isolates were identified as members of the genus *Fervidobacterium* and *Caldanaerobacter*. Draft genome sequencing of the *Fervidobacterium* and *Caldanaerobacter* strains yielded 2,115,188 bp and 2,516,960 bp of unique sequence data distributed over 57 and 547 contigs with an average guanosine + cytosine content of 39.61% and 37.37%, respectively. The values for average nucleotide identity (ANI) and digital DNA: DNA hybridization (dDDH) when compared to their closest relatives, *F. riparium* and *C. subterraneus* subsp. *tengcongensis* were 98.67% and 85,2%, and 97.13% and 82.6% respectively. These isolates represent the first recorded thermophiles from Tajikistan. Strains have potential for applications in agrobiotechnology for converting feather biowaste to higher value products like peptides and amino acids.

**Constitutive photosynthetic activity in arctic AAP *Sediminicoccus rosea* KRV36**

David Kaftan<sup>1</sup>, Jürgen Tomasch<sup>1</sup>, Karel Kopejtko<sup>1</sup>, Tomáš Bílý<sup>2</sup>, Alastair T. Gardiner<sup>1</sup>, Zdenko Gardian<sup>2</sup>, Sahana Shivaramu<sup>1</sup>, Michal Koblížek<sup>1</sup>

<sup>1</sup>Laboratory of Anoxygenic Phototrophs, Institute of Microbiology of the Czech Academy of Sciences, 37981 Třeboň, Czechia

<sup>2</sup>Institute of Parasitology, Biology Centre, Czech Academy of Sciences, 37005 České Budějovice, Czechia

*Sediminicoccus* (*S.*) *rosea* (Alphaproteobacteria, Rhodospirillales) formerly described from eutrophic tropical Lake Taihu (Qu et al., J. Gen. Appl. Microbiol. 59, 463–468, 2013) was isolated from an oligotrophic stream near Raufarhöfn in north-western Iceland, 30 km south of the northern Polar Circle. Conventional gene expression regulation with photosynthetic genes only expressed in the dark for later usage in the light, would pose severe drawbacks for all aerobic anoxygenic phototrophs (AAPs) due to the arctic summer and winter representing substantially prolonged light and dark periods, respectively. The cells of the arctic strain *S. rosea* KRV36 remain fully pigmented with unchanged content of BChl and perpetual presence of chromatophores during growth under continuous light, due to a constitutive expression of the photosynthetic genes. Here we describe ultrastructure, genome structure and provide details on transcriptional and metabolic response to the changing light conditions of an arctic AAP *S. rosea* KRV36 that successfully adapted to the light condition of a polar summer, challenging the universal validity of the current model of photosynthetic gene expression in AAPs.

**Anna Karenina ecological principle in biogas reactor microbiology: stochasticity under ammonia stress**

*Marcell Nikolausz*<sup>1</sup>, *Bogdan Rusu*<sup>1</sup>, *Washington Logroño*<sup>1</sup>, *Nafi'u Abdulkadir*<sup>1</sup>, *Ulisses Nunes da Rocha*<sup>1</sup>

<sup>1</sup> Helmholtz Centre for Environmental Research - UFZ, Leipzig, Germany

Microbial ecology of process inhibition in bioreactor systems with complex microbiota, such as biogas reactors, is an important topic. However, according to the Anna Karenina ecological principle, stressors have stochastic rather than deterministic effects on microbial community compositions, which can only be investigated by a large number of parallel reactor samples. Ammonia inhibition of anaerobic digestion was investigated by using small-scale semi-continuous reactors (7 controls, 7 treatments) in this study. Microbial community structures were monitored by amplicon sequencing of the 16S rRNA and *mcrA* genes before and after urea addition at 10 time points. A strong inhibition of methane production and accumulation of volatile fatty acids were observed in the treatment reactors. Ammonia stress initiated quick changes in the community structure of both Bacteria and methanogenic Archaea. The relative abundance of the genus *Methanotherix* decreased, while either *Methanobacterium* or *Methanosarcina* became predominant in a random way under ammonia inhibition. Along with separating the community structures of the inhibited reactors from the controls, a larger dispersion of the samples was observed, indicating that inhibited reactors varied more in composition than stable reactors. Such elevated  $\beta$ -diversity in samples suggests the validity of the Anna Karenina principle. It can be concluded that process inhibition studies require a better experimental design with a larger number of parallel reactors. Another implication of these results is that process control should focus on the stable communities instead of searching for indicator species of an inhibited state, which is mainly driven by stochastic effects.



**Nitrogen removal bacteria communities' characteristics in the lab-scale wastewater treatment systems**

*Aleksandra Ziemińska-Buczyńska*<sup>1</sup>, *Anna Banach-Wisniewska*<sup>2</sup>, *Mariusz Tomaszewski*<sup>3</sup>, *Filip Gamoń*<sup>1</sup>, *Magdalena Ćwiertniewicz-Wojciechowska*<sup>1</sup>, *Sebastian Żabczyński*<sup>1</sup>, *Sławomir Ciesielski*<sup>4</sup>, *Grzegorz Cema*<sup>1</sup>

<sup>1</sup> Environmental Biotechnology Department, Silesian University of Technology, Gliwice, Poland

<sup>2</sup> Regional Center for Water and Wastewater Management, Tychy, Poland

<sup>3</sup> TKS, Katowice, Poland

<sup>4</sup> Department of Environmental Biotechnology, University of Warmia and Mazury in Olsztyn, Poland

Biological wastewater treatment is based on microbial activity in activated sludge or biofilm-based systems. Communal wastewater treatment plants work usually with nitrification-denitrification, which is the most commonly used processes' combination for nitrogen removal from wastewater. However, since anaerobic ammonia oxidation (anammox) bacteria discovery in 1990s, also anammox process gains increasing attention, especially for nitrogen-rich wastewater treatment. Moreover, all nitrogen removal bacteria are detected in wastewater treatment systems communities according to the well-known environmental ecology rule: "everything is everywhere, but the environment selects". This work presents microbial community studies of lab-scale technological experiments: on activated sludge of sequencing batch reactors and biofilm of rotating biological contactor. The technological systems were influenced with a medium change: from artificial to real wastewater. The metataxonomic community analysis was performed with next generation sequencing on 16S rRNA partial gene. In all experiments nitrifiers, denitrifiers and anammox bacteria co-existed and cooperated. The particular functional groups' proportion was changed after real wastewater introduction, which was a result of community adaptation and functionality restoration in both, activated sludge and biofilm-based systems. These communities were usually dominated with Proteobacteria, and larger structure differences are visible already at the lower taxonomic levels. In researched communities unidentified bacteria were a large sequences' group. These results underline that there is still a wide group of unidentified bacteria in environmental communities which could be functionally relevant for wastewater treatment.

Authors are grateful for support of MEiN projects no.: BK-253/RIE7/2023, NN523562138 and NCN projects no: UMO-2016/N/NZ9/02147, UMO-2017/25/N/NZ9/01159, UMO-2013/09/D/NZ9/02438.

**Effect of bioremediation techniques supplemented with a newly developed bioaugmentation agent on the organohalide-respiring microbial communities**

*Zsuzsanna Nagymáté*<sup>1,2</sup>, *Gergely Krett*<sup>1</sup>, *Csaba Romsics*<sup>1</sup>, *Laura Jurecska*<sup>1</sup>, *Viktória Bódai*<sup>2</sup>, *Péter Szijjártó*<sup>2</sup>, *Tamás Farkas*<sup>2</sup>, *Balázs Erdélyi*<sup>2</sup>, *Károly Márialigeti*<sup>1</sup>

<sup>1</sup> Eötvös Loránd University, Microbiology Department, Budapest, Hungary

<sup>2</sup> Fermentia Ltd., Budapest, Hungary

Bioaugmentation inoculants containing *Dehalococcoides* sp. are capable of complete reductive dechlorination of short-chain chlorinated aliphatic hydrocarbons, providing feasible bioremediation. Our team developed a dechlorinating microbial culture maintained in anaerobic three-phase fermenters (up to 1000 L). To monitor the effectiveness of the inoculum in laboratory and on field polyphasic approach was applied. The inoculant was tested at pilot-scale with two different injection methods: gravity and closed-circuit based. According to the metabolic characteristic, the enrichments were characterized by fermentation, acetogenesis, sulphate reduction and methanogenesis, supporting the growth of organohalide-respiring bacteria with reductive dehalogenase <107 genes copy ml<sup>-1</sup>. At natural conditions cometabolic dechlorination by autochthonous ammonia-oxidizing Archaea was observed. During the pilot-test, highly reducing condition with pH <7 was developed and maintained independently of the technologies applied. After biostimulation elevated but stalled dechlorination activity was detected suggesting maintained cometabolic activity. After bioaugmentation, the contamination disappeared from the injection wells by the activity of the organohalide-respiring bacteria but owing to the slow flow of the groundwater the remediated area was limited. Considering the effect of the closed circuit system, the dispersion of the substances was enhanced, but the induced groundwater movement led to increased contaminant concentrations and the disturbance effect caused a decrease in microbial activity. After system shutdown, increased microbial activity was observed contributing to the reduction of contaminants. Addition of the bioaugmentation agent contributed to the increased diversity of the organohalide-respiring bacteria. The activity of the bacteria originated from the culture and the hydrogen generated enhanced the dechlorination of TCE regardless of the technology used.

**Tracking carbapenem resistance in municipal wastewater: spatio-temporal variation, bacterial diversity, and environmental impact**

*Adela Teban-Man*<sup>1</sup>, *Edina Szekeres*<sup>1</sup>, *Adriana Hegedus*<sup>1</sup>, *Andreea Baricz*<sup>2</sup>, *Marcel Pârvu*<sup>3</sup>, *Cristian Coman*<sup>1</sup>

<sup>1</sup> Institute of Biological Research Cluj, National Institute for Research and Development for Biological Sciences, 48 Republicii Street, 400015 Cluj-Napoca, Romania

<sup>2</sup> Department of Molecular Biology and Biotechnology, Faculty of Biology and Geology, Babes, -Bolyai University, 400084 Cluj-Napoca, Romania

<sup>3</sup> Department of Taxonomy and Ecology, Faculty of Biology and Geology, Babes-Bolyai University, 400084 Cluj-Napoca, Romania

The presence of carbapenem-resistant bacteria and carbapenem resistance genes (CRGs) in municipal wastewater is both a sanitary concern and a threat to natural ecosystems and public health. Nonetheless, to the best of our knowledge, no comprehensive studies have exploited the true potential of municipal wastewater in tracking circulating CRGs that correlate with microbial diversity. In this context, we conducted an investigation into the spatio-temporal variation of CRGs within the influent and effluent of municipal wastewater treatment plants, both with and without the presence of hospital sewage input. Correlations between gene abundances, bacterial community composition, and wastewater quality parameters were examined in order to identify potential indicators of CRG presence. As a result, the distribution of taxonomic groups and gene abundances showed a balanced distribution across different wastewater types, indicating that hospital sewage does not significantly influence microbial diversity and the pool of CRGs. The predominant bacterial taxa comprised *Proteobacteria*, *Firmicutes*, *Actinobacteria*, with *Acinetobacter* spp. being the most abundant group. In influent samples, the blaKPC gene was dominant, whereas blaIMP prevailed in the effluent. Bacterial load, along with abundances of blaNDM, blaKPC, and blaOXA-48, showed positive correlations with parameters such as biochemical oxygen demand, total suspended solids, oil and grease, chromium, copper, and iron concentrations in wastewaters. When converting gene abundance values in the influent to population equivalents (PE), the highest copies per 1 PE were observed for blaKPC and blaOXA-48, consistent with previous studies on clinical isolates. The data collected in this study is a valuable source of information that can serve as a foundation for future research aimed at mitigating the discharge of CRGs from wastewater into the natural environment.

**Comprehensive examination of peptaibol compounds and preparation of their future agricultural application**

Dóra Balázs<sup>1</sup>, Ákos Rozsnyói<sup>1</sup>, Tamás Marik<sup>1</sup>, András Szekeres<sup>1</sup>, Csaba Vágvölgyi<sup>1</sup>, Chetna Tyagi<sup>1</sup>, László Kredics<sup>1</sup>

<sup>1</sup> Department of Microbiology, Faculty of Science and Informatics, University of Szeged, Hungary

The increasingly frequent extreme weather conditions and problems of plant pathogenic microorganisms in the agriculture emphasize the use of new biological control methods. Filamentous fungal species from the genus *Trichoderma* may provide a possible solution in the future, due to their powerful biological activity, which is expressed through their secondary metabolic products. One of these important metabolites are the peptaibols, which have characteristic properties, such as a high amount of non-proteinogenic amino acids in the sequences and ion channel forming ability in the cell membrane. Peptaibols are mainly effective against Gram-positive bacterial and several fungal species, however in a few cases they may also inhibit Gram-negative bacteria. In addition to their inhibitory ability, peptaibols also affect plants by inducing systemic resistance and increasing auxin production.

In the case of our current research, two *Trichoderma rossicum* strains from the clade Stromaticum were studied and a comprehensive investigation of the peptaibols produced by them was carried out: the peptaibol compositions were determined by HPLC-ESI-MS method, then the minimum inhibitory concentration (MIC, mg ml<sup>-1</sup>) and effective concentration (EC, mg ml<sup>-1</sup>) values were determined against phitopathogenic bacterial and fungal strains. In parallel with the laboratory test, the folding mechanisms of the sequences were investigated with modern computational modeling techniques, such as accelerated molecular dynamics (aMD) simulations. By comparing the results, the structure-activity relationships (SARs) of peptaibols can be examined. We found correlations between the characteristic properties of sequences, such as amino acid motifs and sequence length, and their expressed bioactivity. With the knowledge of SARs, in the future we can promote the selection and further use of *Trichoderma* strains producing biologically active peptaibols for agricultural purposes.

**Microbially Influenced Corrosion – More than just Microbes***Judit Knisz*<sup>1</sup><sup>1</sup> Faculty of Water Sciences, University of Public Service, Baja, Hungary

Microbiologically influenced corrosion (MIC) is a phenomenon of increasing concern affecting a variety of industrial sectors, including but not limited to the oil and gas industry, utilities, industrial cooling water systems, the maritime industry, etc. MIC is defined as corrosion affected by the presence and/or activity of microorganisms. Our understanding about the microorganisms involved in, the mechanisms related to and factors influencing MIC has grown significantly in the past decades. Advanced tools are increasingly being used for detection and monitoring including molecular microbiological methods, and new approaches of mitigation have also emerged. However, there is still a long way to go in MIC research. Research fields associated with MIC are highly siloed, where scientists from different disciplines such as chemistry, electrochemistry, metallurgy and microbiology do not speak the same language preventing true collaborations and hindering further developments. In addition, collaborations between industry and academia are quite rare, the lack of information exchange means that scientists are not aware of the actual needs of the industry, thus, academic research can lack practical relevance. A recent initiative has aimed to overcome these challenges. The Euro-MIC COST Action aims to develop an interdisciplinary and intersectoral network that will encourage synergistic communication and collaboration between microbiologists, material scientists, corrosion engineers, chemists and integrity managers.

The presentation aims to provide microbiologists with background information on the various aspects of MIC and highlight areas where the insights and expertise of microbiologists are needed to help this field forward. Field examples will be presented to underline the importance of using the multiple lines of evidence approach in MIC studies both in the field as well as in the laboratory.

**Stenotrophomonas terrae BB3 – a new bacterial strain capable of degrade metoprolol**

*Anna Dzionek*<sup>1</sup>, *Cansel Taskin*<sup>1</sup>

<sup>1</sup> University of Silesia in Katowice, Katowice, Poland

Pharmaceuticals in surface and drinking waters are becoming a growing concern.  $\beta$ -blockers deserve special attention, the consumption of which increases year by year. Humans or activated sludge in wastewater treatment plants do not fully metabolize these drugs. As a result, they migrate into the environment in a slightly changed form. The non-degraded  $\beta$ -blockers in the environment may pose a severe threat to fauna and human health. Effects of these drugs on aquatic organisms include reduced reproductive rates and fertility and causing abnormal behavior. Since the most economical and eco-friendly method for drugs utilization is biodegradation, screening for microorganisms capable of degrading  $\beta$ -blockers is essential. In the literature, there is no report about the single-strain biodegradation of metoprolol.

In this study, we isolate, identify and characterize bacterial strains able to degrade one of the most popular  $\beta$ -blocker in Europe – metoprolol. Among a few isolated bacteria from activated sludge, strain BB3 identified as *Stenotrophomonas terrae* showed the most promising potential for metoprolol biodegradation. Various additional carbon and nitrogen sources were tested to support culture growth during the drug biodegradation and their influence on the metoprolol degradation was evaluated. It was observed that only the addition of glucose significantly accelerated metoprolol degradation.

This study revealed the potential of isolated from activated sludge bacterial strain *Stenotrophomonas terrae* BB3 in the cometabolic degradation of metoprolol. Further analysis of the factors influencing the dynamics of metoprolol degradation will provide the knowledge necessary to use this strain in bioremediation and bioaugmentation studies.

**Methane cycling bacteria in Croatian lakes***Sandi Orlic*

Ruder Bošković Institute

Lake ecosystems are centres of carbon circulation and transformation, controlled in large part by microbial populations. Methane is an important component of the carbon cycling in lakes and lakes represent the largest emission point from freshwater ecosystems. Methane production in lakes mainly occurs from anoxic sediment. Freshwater lakes significantly add to the natural global methane emission and on the other hand methane-oxidizing bacteria greatly reduce methane emissions from lakes to the atmosphere. The emissions are highest from well-mixed lakes, whereas release of methane from seasonally or permanently stratified lakes with anoxic bottom waters is greatly reduced.

We will present our data on the largest polymictic lake in Croatia (lake Vrana) and the differences in two ecological ecosystems (continental and Mediterranean) which exhibit seasonal anoxia in their hypolimnion. Using novel approaches (SIP, genomics and BONCAT) we will give our understanding which microorganisms contribute to methane cycling in these systems.

**The Microbial Loop in Lake Ecosystems: Structure and Control***Meryem Beklioğlu*

Biological Science Department and Ecosystem Research and Implementation Centre, Middle East Technical University, 06800, Ankara, Turkey

The typical microbial food web consists of viruses, heterotrophic bacteria, autotrophic picoplankton (0.2–2µm), and auto- and heterotrophic protists, emphasizing the transfer of energy and matter from primary producers up to secondary consumers and beyond. The typical microbial food web can be represented by functional units for simplicity and to avoid the complexity of taxonomic diversity. The two largest functional units in terms of biomass and elemental cycling or processing include heterotrophic bacteria and phytoplankton (mainly phototrophic picoplankton), which are interconnected through the provision of nutrients by the former to the latter, and the phytoplankton provide DOM to heterotrophic bacteria through excretion and lysis. However, the extent of this coupling varies depending on the trophic status of the lakes, climate (temperature), and the top-down control imposed by the micro to large grazers, which form the third functional unit of the microbial food web. In this way, the different compartments of the microbial food web are integrated into the “Microbial loop” as it is connected to the classical grazer food web. Several studies have presented data that the coupling between heterotrophic bacteria and phytoplankton appeared to be weaker in warm and eutrophic -hypertrophic lakes. The structure of the grazers community (micro, HNF, ciliates, metazooplankton) has a strong shaping effect on heterotrophic bacteria and phytoplankton through top-down control. The domination of the metazooplankton community, particularly large Cladocera, daphnids, has a strong control over the whole microbial community, whereas the effects of small-sized grazers, e.g., rotifers and copepods, which largely dominate in warm and eutrophic lakes, are limited. In this presentation, we will thoroughly discuss how the structure and biomass of the components of the microbial loop change and how they interact with the grazing food chain, as well as the control by bottom-up and top-down factors.



**Exploring the Ecological Significance of Aerobic Anoxygenic Photoheterotrophic Bacteria in Freshwater Ecosystems**

*Cristian Villena-Aleman*<sup>1,2</sup>, *Kasia Piwosz*<sup>3</sup>, *Izabela Mujakic*<sup>1,2</sup>, *Michal Koblížek*<sup>1</sup>

<sup>1</sup>Laboratory of Anoxygenic Phototrophs, Institute of Microbiology of the Czech Academy of Sciences, Třebon, Czechia.

<sup>2</sup>Department of Ecosystem Biology, Faculty of Science, University of South Bohemia, České Budějovice, Czechia.

<sup>3</sup>Department of Fisheries Oceanography and Marine Ecology, National Marine Fisheries Research Institute, Gdynia, Poland.

Aerobic anoxygenic photoheterotrophic (AAP) bacteria represent from 1-23% of aquatic bacteria. This functional group are characterized by large cell size, high activity and fast growth rates, which can be partially attributed to their ability to harvest additional energy from light through bacteriochlorophyll-a type-II reaction centres. Despite their ubiquitous existence little was known about their diversity dynamics and their role in the carbon cycle in freshwater environments. We found that their presence in freshwater environments decreased the overall bacterial respiration while increased organic carbon incorporation in the presence of light. Together with the AAP abundance and AAP community composition data, we pointed out their impact on the recycling of organic matter from phytoplankton blooms by enhancing the bacterial secondary production for the upper trophic levels. We also showed that AAPs, despite sharing the functional trait of anoxygenic photosynthesis, are a heterogenic ecological group with different seasonal behaviours, even within the confines of the same genus. Additionally, we demonstrated a yearly ecological succession pattern in the AAP freshwater community, which has persisted for three years and identified the key AAPs that make important contributions every year. Overall, the unique characteristics and the unveiled ecological traits of aerobic anoxygenic phototrophic bacteria make them an important subject of study to comprehend microbial community and its contribution to the aquatic ecosystems and to the global carbon cycle.

**Iodinated contrast media in wastewater – occurrences and implications to activated sludge**

*Agnieszka Nowak<sup>1</sup>, Danuta Wojcieszynska<sup>1</sup>*

<sup>1</sup> Institute of Biology Biotechnology and Environmental Protection, University of Silesia, Katowice, Poland

Iodinated contrast media are used in medical diagnostics for imaging anatomic structures in computed tomography and magnetic resonance, and their consumption is constantly growing annually. Their very stable structure cause them to be not effectively removed when they reach the wastewater treatment plant and are continuously detected in effluents. It is known that they are not completely degraded, but they can undergo biotransformation. There is a lack of information on whether these compounds affect the biodiversity of the ecosystems into which they enter.

The study aimed to determine the effect of diatrizoate on the functional diversity of activated sludge microorganisms. This analysis allowed us to obtain preliminary information on whether the increasingly commonly used contrast agents, although they are only slightly toxic to humans, do not have a negative impact on microorganisms in sewage treatment plants.

The experiment was conducted in flasks with activated sludge and diatrizoate for four months. Biological activity was assessed by measuring the activity of dehydrogenases, non-specific esterases and based on the results from 96-well Eco plates (BIOLOG). The analysis of the functional diversity of activated sludge indicated that long-term exposure to diatrizoate caused a decrease in the activity of microorganisms and their functional diversity. These parameters were the lowest for the highest concentrations of diatrizoate (20 mg/L). Differences in the oxidation profiles of the distinguished groups of substrates were also found. The presented results allow assuming that long-term exposure of the activated sludge microflora to diatrizoate caused significant, unfavourable changes in its metabolism.

The research was funded by the National Science Center under the MINIATURA 5 (2021-2022) for the project “Effect of selected iodine contrast agents on the activity and diversity of activated sludge microorganisms” (no. 021/05/X/NZ9/00457).

**Fungi increases kelp (*Ecklonia radiata*) remineralisation and dissolved organic carbon, alkalinity, and dimethyl sulfoniopropionate production**

*Anita K Perkins*<sup>1,2,3</sup>, *Andrew L Rose*<sup>2</sup>, *Hans-Peter Grossart*<sup>4,5</sup>, *Kai G Schulz*<sup>1</sup>, *Darshan Neubauer*<sup>4,5,6</sup>, *Matthew P Tonge*<sup>2</sup>, *Judith A Rosentreter*<sup>1</sup>, *Bradley D Eyre*<sup>1</sup>, *Keilor Rojas-Jimenez*<sup>7</sup>, *Elisabeth Deschaseaux*<sup>1</sup>, *Joanne A Oakes*<sup>1</sup>

<sup>1</sup> Centre for Coastal Biogeochemistry, Faculty of Science and Engineering, Southern Cross University, Lismore, NSW, Australia

<sup>2</sup> Southern Cross Geoscience, Faculty of Science and Engineering, Southern Cross University, Lismore, NSW, Australia

<sup>3</sup> Present address: Aquatic Botany and Microbial Ecology Research Group, National Laboratory for Water Science and Water Security, Balaton Limnological Research Institute, Tihany, Hungary

<sup>4</sup> Leibniz Institute for Freshwater Ecology and Inland Fisheries (IGB), Experimental Limnology, Neuglobsow, Germany

<sup>5</sup> University of Potsdam, Institute of Biochemistry and Biology, Potsdam, Germany

<sup>6</sup> Present address: Landesamt für Umwelt Brandenburg (LFU), Potsdam, Germany

<sup>7</sup> Escuela de Biología, Universidad de Costa Rica, San Jose, Costa Rica

Fungi are key players in terrestrial organic matter degradation, but little is known about their role in marine environments. Here we compared the degradation of kelp (*Ecklonia radiata*) detritus in mesocosms with and without fungi over 45 days to improve our understanding of the role of fungal organic matter degradation in marine systems. When fungi were inhibited via fungicides, the sediment bacterial community was less diverse and the extent and pathways of *E. radiata* detritus degradation changed; less detritus was degraded overall (25% degraded over 45 days compared to 68% with fungi present). With fungi, remineralisation of detritus to dissolved inorganic carbon, total alkalinity, dimethyl sulfide, dimethyl sulfoniopropionate and methanethiol has significantly increased. These substantial changes in sediment chemistry highlight the important biogeochemical role of fungal remineralisation and likely plays a crucial role in defining coastal biogeochemical cycling and sequestration for Blue Carbon.

**Diversity and ecological role of the smallest algae in turbid and saline lakes**

*Boglárka Somogyi*<sup>1</sup>, *Tamás Felföldi*<sup>2,3</sup>, *Attila Szabó*<sup>3,4</sup>, *Lajos Vörös*<sup>1</sup>

<sup>1</sup>National Laboratory for Water Science and Water Security, Balaton Limnological Research Institute, Tihany, Hungary

<sup>2</sup>Department of Microbiology, ELTE Eötvös Loránd University, Budapest, Hungary

<sup>3</sup>CER Institute of Aquatic Ecology, Budapest, Hungary

<sup>4</sup>Department of Aquatic Sciences and Assessment, Uppsala, Sweden

The energetic basis of the microbial loop is formed by the smallest algae of our lakes, the so-called picoalgae. We investigated the diversity and ecological role of these small algae in turbid and saline lakes of the Carpathian Basin, with a special focus on soda and saline lakes, that are rare within the European Union. Our results indicated that the increase in turbidity and salinity both promote the proliferation of picoalgae over larger phytoplankton. Picocyanobacteria were only detected with high abundance ( $>10^6$ – $10^7$  cells/ml) in turbid soda lakes, while picoeukaryotes were occurred in high numbers both in turbid and hypersaline lakes. Despite the extreme environmental conditions of these lakes, we observed remarkable diversity among picophytoplankton communities. In soda lakes, non-marine *Synechococcus*/*Cyanobium*, *Choricystis*, *Chloroparva* and uncultured trebouxioephycean green algae dominated in the picoalgae community, whereas marine *Synechococcus* and *Picochlorum* were prevalent in hypersaline lakes. Financial support: RRF-2.3.1-21-2022-00008 project and Sustainable Development and Technologies National Programme of the Hungarian Academy of Sciences (FFT NP FTA).

**Diversity and core taxa of the karst spring microbiome and community response to pathogen and antibiotic resistance gene contamination**

Edina Szekeres<sup>1,2,3</sup>, Andreea Baricz<sup>1,2</sup>, Erika Andrea Levei<sup>4</sup>, Oana Teodora Moldovan<sup>5</sup>, Horia Leonard Banciu<sup>1,2</sup>

<sup>1</sup> Department of Molecular Biology and Biotechnology, Babeş-Bolyai University, Cluj-Napoca, Romania

<sup>2</sup> Centre for Systems Biology, Biodiversity and Bioresources, Babeş-Bolyai University, Cluj-Napoca, Romania

<sup>3</sup> National Institute of Research and Development for Biological Sciences, Institute of Biological Research, Cluj-Napoca, Romania

<sup>4</sup> INCDO-INOE 2000, Research Institute for Analytical Instrumentation, Cluj-Napoca, Romania

<sup>5</sup> Cluj-Napoca Department, Emil Racoviţă Institute of Speleology, Cluj-Napoca, Romania

Karst aquifers play a crucial role in providing drinking water worldwide; however, their vulnerability to human-induced contamination necessitates a comprehensive understanding of their stable core microbiome and the impact of contamination on these communities. To address this knowledge gap, we conducted a year-long seasonal sampling of eight karst springs located in three regions of Romania. The core microbiota was analyzed using 16S rRNA gene amplicon sequencing. Additionally, we employed an innovative approach combining high-throughput quantification of antibiotic resistance genes and cultivation of potential pathogen colonies on Compact Dry plates to identify bacteria carrying antibiotic resistance genes and mobile genetic elements. The results revealed a taxonomically stable bacterial community predominantly composed of *Pseudomonadota*, *Bacteroidota*, and *Actinomycetota*. Core analysis confirmed the dominance of freshwater-dwelling, psychrophilic/psychrotolerant species affiliated with the *Rhodospirillum rubrum*, *Flavobacterium*, and *Pseudomonas* genera. Notably, over half of the studied springs were contaminated with fecal bacteria and pathogens. These samples exhibited elevated levels of resistance genes against sulfonamides, macrolides, lincosamides, streptogramins B, and trimethoprim, primarily disseminated by transposase and insertion sequences. Additionally, the differential abundance analysis identified *Synergistota*, *Mycoplasmata*, and *Chlamydia* as potential pollution indicators in karst springs. This study introduces a combined approach utilizing high-throughput quantification of antibiotic resistance genes and pathogen cultivation for estimating microbial contaminants in challenging low biomass environments like karst springs. The findings advance our understanding of karst spring microbiomes and provide insights for developing strategies to safeguard these vital water resources.

**Reassembly of planktonic protistan community and modulation of microbial food web during the establishment of stratification in Řimov reservoir**

*Indranil Mukherjee*<sup>1</sup>, *Vesna Grujić*<sup>2</sup>, *Michaela Maria Salcher*<sup>1</sup>, *Petr Znachor*<sup>1</sup>, *Jaromír Sed'a*<sup>1</sup>, *Miloslav Devetter*<sup>1</sup>, *Pavel Rychtecký*<sup>1</sup>, *Karel Šimek*<sup>1,3</sup>, *Tanja Shabarova*<sup>1</sup>

<sup>1</sup> Biology Centre of the Czech Academy of Sciences, Institute of Hydrobiology, České Budějovice, Czech Republic

<sup>2</sup> Department of Ecology, Environment and Plant Sciences, Stockholm University, Stockholm, Sweden

<sup>3</sup> Faculty of Science, University of South Bohemia, České Budějovice, Czech Republic

Freshwater protistan communities are phylogenetically and functionally highly diverse, with distinct groups inhabiting different depths of freshwater lakes. In deep freshwater lakes, the water column gradually separates from the mixed phase due to the establishment of thermal stratification during spring, where significant modulation of microbial food web occurs, which leads to the assembly of distinct microbial communities in different strata. To examine understudied protistan community assembly processes during spring and the responsible biotic and abiotic factors, we collected water samples from three depths representing the epilimnion, metalimnion and hypolimnion of Řimov reservoir, Czech Republic. Samples were collected 2-3 times a week to obtain high temporal resolution data corresponding to typical doubling time of microbes, starting just after the spring mixing during late March till May 2016, covering the transition to stratification phases. Microbial eukaryotic and prokaryotic communities were analysed using 18S and 16S rRNA gene amplicon sequencing, respectively. Furthermore, the dynamics of individual group of protists were analysed by Catalysed Reporter Deposition-Fluorescence in situ Hybridization (CARD-FISH). The epilimnion protistan community, which was dominated by cryptophytes, was associated with spring algal-bloom specialists within bacterioplankton groups. In contrast, the metalimnion and hypolimnion communities were dominated by putative parasitic group like perkinsozoa, detritus or particle-associated ciliates, cercozoans and excavate protists, co-occurring with the bacteria associated with lake snow and ammonia and methane oxidizers. Overall, our study revealed highly interconnected, depth-specific shifts in major players in both prokaryotic and eukaryotic communities driven by onset of stratification processes in a deep lake-like ecosystem.

**Microbial community dynamics and interactions during the winter-spring transition in a large shallow lake**

*András Hidas*<sup>1,2</sup>, *Boglárka Somogyi*<sup>3</sup>, *Attila Szabó*<sup>1,4</sup>, *Dóra Fehér*<sup>1,5</sup>, *Lajos Vörös*<sup>3</sup>, *Tamás Felföldi*<sup>1,5</sup>

<sup>1</sup> Institute of Aquatic Ecology, Centre for Ecological Research, Budapest, Hungary

<sup>2</sup> Eötvös Loránd University, Doctoral School of Environmental Sciences, Budapest, Hungary

<sup>3</sup> Balaton Limnological Research Institute, Tihany, Hungary

<sup>4</sup> Department of Aquatic Sciences and Assessment, Swedish University of Agricultural Sciences, Uppsala, Sweden

<sup>5</sup> National Multidisciplinary Laboratory for Climate Change, Centre for Ecological Research, Budapest, Hungary

Shallow lakes are delicate ecosystems that are vulnerable to changes in their physical, chemical, and biological properties. In this study, we used a multi-approach investigation to examine the changes in the phytoplankton and bacterioplankton communities from January to early April in Lake Balaton, Central Europe's largest shallow lake.

We collected weekly samples from three distinct sites in the lake. The composition and quantity of phytoplankton were determined using light microscopy, while 16S and 18S eDNA amplicon sequencing were used to identify planktonic bacteria, archaea, and eukaryotic phytoplankton. We applied co-occurrence network analysis to assess time-shifted interactions at each site.

Our results revealed significant changes in the phytoplankton and bacterioplankton communities in the lake over the study period. Topological importance indexes identified the key players in the communities. The most important keystone species were heterotrophs, mainly ciliates, which were unique to each location. One of the three sites was eutrophic, while the other two were oligotrophic. The community composition varied considerably among the locations.

In conclusion, our study demonstrated the potential of a multi-approach method that combines high-throughput sequencing, microscopy, and network analysis to better understand the dynamics of phytoplankton and bacterioplankton communities in shallow lakes. The rising water temperature during the study allowed us to analyze the temperature dependence of microbes. The identified keystone species revealed the most important interactions in the communities.

**Cold-loving bacterium from a mountain lake harvests light energy using both bacteriochlorophyll-containing photosystems as well as proton-pumping rhodopsins**

*Michal Koblížek*<sup>1</sup>, *Karel Kopejtko*<sup>1</sup>, *Juergen Tomasch*<sup>1</sup>, *Alastair Gardiner*<sup>1</sup>, *David Kaftan*<sup>1</sup>, *David Bina*<sup>2</sup>, *Zdeno Gardian*<sup>3</sup>, *Ruben Sommaruga*<sup>4</sup>

<sup>1</sup> Institute of Microbiology, Czech Academy of Sciences, 37981 Třeboň, Czechia

<sup>2</sup> Faculty of Science, University of South Bohemia, 37005 České Budějovice, Czechia

<sup>3</sup> Institute of Plant Molecular Biology, Biology Centre CAS, 37005 České Budějovice, Czechia

<sup>4</sup> Department of Ecology, University of Innsbruck, Innsbruck, Austria

Bacterium *Sphingomonas glacialis* AAP5 isolated from the alpine lake Gossenköllesee contains genes for anoxygenic phototrophy as well as proton-pumping xanthorhodopsin. However, these genes are not expressed in standard laboratory conditions.

In order to find under which conditions the organisms expresses its light harvesting apparatus we conducted a larger investigation employing RNA sequencing, RTqPCR, metabolic assays and biochemical and biophysical investigation of its photosynthetic complexes. We found out that our strain readily express xanthorhodopsin when illuminated at temperatures below 14°C. In contrast bacteriochlorophyll-containing reaction centers are expressed between 4 and 23°C in the dark. Thus, cells grown at low temperature under natural light-dark cycle produced both photosystems. The photosynthetic complexes contain circular light harvesting complex 1 surrounding the type-2 bacterial reaction center. The light harvesting complex is composed from 16 homodimeric subunits. Each subunit binds one bacteriochlorophyll-a pair and one spirilloxanthin molecule. The purified xanthorhodopsin contains carotenoid nostoxanthin serving as an auxiliary antenna and performs the standard photocycle. The xanthorhodopsin-producing cells reduced upon illumination their respiration by 70%. This documents that the harvested light energy was utilized in the metabolism, which can represent a large benefit under carbon-limiting conditions.

The presence of two different photosystems may represent a metabolic advantage in alpine lakes where photoheterotrophic organisms face large changes in irradiance, limited organic substrates and low temperature.

References:

Kopejtko et al (2022) A bacterium from a mountain lake harvests light using both proton-pumping xanthorhodopsins and bacteriochlorophyll-based photosystems. PNAS 119(50), e2211018119. <https://doi.org/10.1073/pnas.2211018119>



# Posters



**CEESME**

### Unravelling connections among grapevine chemical and physiological parameters and mycobiome composition under drought stress

*Anna Molnár*<sup>1,2</sup>, *József Geml*<sup>1,2</sup>, *Adrienn Geiger*<sup>1,2,3</sup>, *Carla Mota Lea*<sup>2,3</sup>, *Glodia Kgobe*<sup>2,3</sup>, *Adrienn Mária Tóth*<sup>4</sup>, *Szabolcs Villangó*<sup>4</sup>, *Miklós Lovas*<sup>1</sup>, *Nóra Bakos-Barczi*<sup>1</sup>, *Kálmán Zoltán Váczy*<sup>1,2</sup>, *György Lőrincz*<sup>4</sup>, *Zsolt Zsófi*<sup>4</sup>

<sup>1</sup> Food and Wine Research Institute, Research and Development Center, Eszterházy Károly Catholic University, Hungary

<sup>2</sup> ELKH–EKKE Lendület Environmental Microbiome Research Group, Eszterházy Károly Catholic University, Hungary

<sup>3</sup> Doctoral School of Environmental Sciences, Hungarian University of Agricultural and Life Sciences, Hungary

<sup>4</sup> Institute for Viticulture and Enology, Faculty of Natural Sciences, Eszterházy Károly Catholic University, Hungary

Improving our knowledge on biotic and abiotic factors that influence the composition of the grapevine mycobiome is of great agricultural significance, due to potential effects on plant health, productivity, and wine characteristics. Among the various environmental factors affecting the morphological, physiological, biochemical and molecular attributes of grapevine, drought stress is one of the most severe, becoming increasingly an issue worldwide.

In the present study we assessed the influence of water deficit and scion cultivar on the diversity and composition of fungal communities and chemical characteristics of the berries and leaves. Based on physiological parameters (pre-dawn water potential and gas-exchange) a sampling area was designed in the Eger Wine Region, Hungary, affected by moderate drought stress. We generated DNA metabarcoding data, and statistically compared the richness, relative abundance, and composition of several functional groups of fungi in two cultivars (*Vitis vinifera* cv. Furmint, and cv. Kadarka), which are partly explained by measured differences in chemical composition of leaves and berries and physiological traits of leaves. The richness and relative abundance of fungal functional groups statistically differ among berry and leaf, and control samples compared to those under drought stress, but less so among cultivars. We also detected cultivar-level and stress-related differences in the macro- and microelement content of the leaves, and in acidity and sugar concentration of berries. Finally, the correlation between fungal community composition and physiological variables in leaves is noteworthy, and merits further research to explore causality. Our findings offer novel insights into the microbial dynamics of grapevine considering drought stress, plant chemistry and physiology, with implications for viticulture.

### **A microbiological preparation to solve the problem of NSAID contamination in sewage treatment plants**

*Danuta Wojcieszńska<sup>1</sup>, Ariel Marchlewicz<sup>1</sup>, Katarzyna Hupert-Kocurek<sup>1</sup>, Urszula Guzik<sup>1</sup>*

<sup>1</sup> Institute of Biology, Biotechnology and Environmental Protection, University of Silesia in Katowice, Katowice, Poland

The increasing pollution of wastewater with non-steroidal anti-inflammatory drugs forces wastewater treatment plants to support the biodegradation of these compounds. The solution may be the construction of bacterial preparations containing strains with increased degradative abilities. Therefore, the work aimed to develop a bacterial preparation and to characterize the boundary conditions for the degradation process of paracetamol, ibuprofen, naproxen and diclofenac. The formed consortium includes *Bacillus thuringiensis* B1(2015b) and *Pseudomonas moorei* KB4 strains in a 1:2 ratio. The product has been shown to work in the pH range of 5.5 to 9 and a temperature of 15-35°C, as well as resistance to the toxic effects of ethanol, lead and chromium. The degradation rate in the batch sequencing reactor (SBR) was 4.88 mg/day, 10 mg/day, 0.1 mg/day and 0.05 mg/day for ibuprofen, paracetamol, naproxen and diclofenac, respectively. In addition, studies of the preparation composition after the experiment's end showed the survival of both strains in bioreactor conditions with activated sludge. This indicates resistance to the antagonistic effect of the activated sludge microbiome, which allows the preparation to be used in sewage treatment plants. This work was funded by the National Centre for Research and Development, Poland (grant number TANGO-IV-A/0050/2019-00).

**The use of immobilized strains in the breakdown of NSAIDs**

*Urszula Guzik<sup>1</sup>, Anna Dzionek<sup>1</sup>, Agnieszka Nowak<sup>1</sup>, Danuta Wojcieszewska<sup>1</sup>*

<sup>1</sup> Institute of Biology, Biotechnology and Environmental Protection, University of Silesia in Katowice, Katowice, Poland

Non-steroidal anti-inflammatory drugs (NSAIDs) are among the most commonly used drugs and therefore represent a significant burden in wastewater treatment plants. Immobilization of bacterial strains with increased decomposition capabilities of these compounds makes it possible to construct preparations for use in sewage treatment plants. The described NSAID-degrading strains include *Pseudomonas moorei* KB4, *Bacillus thuringiensis* B1(2015b), *Stenotrophomonas maltophilia* KB2, and *Planococcus* sp. S5. A plant sponge from *Luffa cylindrica* was used as a carrier for immobilizing the bacteria. After optimizing the conditions of immobilization of individual strains, the construction of a preparation supporting wastewater treatment plants in the direction of NSAIDs degradation was proposed. It has been shown that the optimal species composition of the proposed preparation includes all tested strains immobilized on a carrier with a mass of 1.2 g/l. In addition, no inhibition of the NSAIDs degradation process in the presence of phenol was demonstrated, which indicates that such a preparation can be successfully used in wastewater treatment plants loaded with aromatic compounds. This work was funded by the National Centre for Research and Development, Poland (grant number TANGO-IV-A/0049/2019-00) and the National Science Centre, Poland (grant number 2018/29/B/NZ9/00424).

**Methylotrophic methanogenesis in anoxic sediments from the Medway Estuary (UK)**

*Alejandro Huerta-Hurtado*<sup>1</sup>, *Mark Trimmer*<sup>1</sup>, *Özge Eyice*<sup>1</sup>

<sup>1</sup> Queen Mary University of London, United Kingdom

Methane, a potent greenhouse gas, plays a crucial role in the global carbon cycle. Among natural sources, wetlands, such as estuaries and saltmarshes, are the primary contributors to methane emissions. The biotic process responsible for methane production, known as methanogenesis, is exclusively carried out by archaea called methanogens. In anoxic saline sediments, methylotrophic methanogenesis is the dominant pathway for methane production. The key substrates driving this pathway are methanol, and trimethylamine (TMA). However, our understanding of the specific contribution of these substrates to total methane production in anoxic coastal sediments remains limited. Additionally, there is a significant knowledge gap regarding the diversity of microorganisms involved in the degradation of these compounds and their metabolic pathways. In this research, we aimed to quantify the extent of methylotrophic methanogenesis in anoxic sediments from Medway Estuary (UK) to characterise the diversity of microorganisms driving this process. We selected three sampling sites: marine, saltmarsh, and brackish. We conducted anoxic incubations using TMA and methanol as carbon and energy sources. We monitored the methane production in the incubations to derive the methanogenesis yields. We also performed molecular analyses to identify methanogens in our samples. Our findings revealed that the saltmarsh site exhibited the highest methane yield, reaching 47% and 27% of the theoretical yield in TMA and methanol respectively. The marine site incubations with methanol did not produce any detectable methane. These results suggest that methanogenesis occurs via the breakdown of particular compounds in different Medway Estuary and saltmarsh sediments and likely limited due to environmental factors within these sampling.

### **Improving the productivity of legume-rhizobial symbiosis for its maximum realization of nitrogen-fixing potential and soil restoration**

*Tetiana Nyzhnyk<sup>1,2</sup>, Sergii Kots<sup>1</sup>, Edyta Kiedrzyńska<sup>2</sup>*

<sup>1</sup> Institute of Plant Physiology and Genetics of the National Academy of Sciences of Ukraine, Kyiv, Ukraine

<sup>2</sup> European Regional Center of Ecohydrology of the Polish Academy of Sciences, Lodz, Poland

The formation of high productivity of most cultivated plants, is largely determined by the presence of nutrients available by the special nitrogen compounds in soil. However, due to the high cost of energy resources and the low commodity producers paying capacity, the use of mineral nitrogen has decreased sharply in recent years. An alternative way of solving this problem is the application of economically justified and ecologically safe methods in the technologies of growing promising crops. The process of biological fixation of molecular nitrogen by nitrogen-fixing microorganisms belongs to the only natural source of providing plants with nitrogen, which does not disturb the ecology of the environment. Therefore, this research related to the process of biological transformation of molecular nitrogen carried out by nitrogen-fixing microorganisms in associations with plants in natural ecosystems and agrophytocenoses is currently relevant and forward-looking. By the growing needs of modern agricultural producing and their transition to ecologically safe technologies for plants cultivating, it is prospective to use of bacterial preparations to increase the nitrogen-fixing activity and productivity of perspective legume crops. The purpose of research is to develop effective solutions for increasing the productivity of prospective legumes due to the maximum realization of their nitrogen-fixing potential and restoration of soil fertility when using ecologically safe bacterial compositions based on nitrogen-fixing microorganisms. This research involves the development and implementation a system of necessary agrarian methods for the environmental safe microbial preparations using. The necessity of biologicalization the agrotechnologies for crops cultivating and the conditions for the natural processes implementation in the soil-plant-atmosphere system has been proven.

**Recovery of eukaryotic metagenome assembled genomes from decade long metagenomic time-series in freshwater lakes.**

*Roudaina Boukheloua*<sup>1</sup>, *Paul-Adrian Bulzu*<sup>1</sup>, *Jason Nicholas Woodhouse*<sup>2</sup>, *Hans-Joachim Ruscheweyh*<sup>3</sup>, *Shinichi Sunagawa*<sup>3</sup>, *Hans-Peter Grossart*<sup>2,4</sup>, *Rohit Ghai*<sup>1</sup>

<sup>1</sup> Department of Aquatic Microbial Ecology, Institute of Hydrobiology, Biology Center CAS, České Budějovice, Czech Republic

<sup>2</sup> Department of Plankton and Microbial Diversity, Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB), Stechlin, Germany

<sup>3</sup> Department of Biology, Institute of Microbiology and Swiss Institute of Bioinformatics, ETH Zurich, Zurich, Switzerland

<sup>4</sup> Institute of Biochemistry and Biology, Potsdam University, Potsdam, Germany

Most freshwater protists remain uncultured and genomic information from the few cultures is also scarce. Metagenomics offers a culture-free alternative towards the recovery of genomes from the vast amounts of metagenomic sequence data that is becoming available and has been transformative for understanding prokaryotic diversity. Efforts to recover eukaryotic protist genomes, that may be hundreds of times larger than prokaryotic genomes, have remained limited due absence of long time series datasets with sufficient sequencing depth. In effect, genomes of abundant protists in freshwater habitats remain largely unknown. Here we assembled and binned 1096 metagenomes from decade long time series from four lakes (Lake Stechlin, Grosse Fuchskuhle, Breiter Luzin and Tiefwareensee) and assessed the recovery of eukaryotic metagenome assembled genomes (MAGs). Close examination of over 1000 putative eukaryotic MAGs - indicated several types of contaminations, from prokaryotes, viruses and even multiple, taxonomically distinct eukaryotes within these metagenomic bins. Using conservative filtration thresholds and manual curation we reconstructed 280 taxonomically coherent high-quality eukaryotic MAGs that ranged from 5-50 MB in size. These MAGs belong to most abundant eukaryotic groups in our dataset: *Daphnia* (n=74), *Chlorophyta* (n=54), *Ochrophyta* (n=41), *Cryptophyta* (n=26), *Prymnesiales* (n=20), *Euglenozoa* (n=5), *Fungi* (n=2), *Ciliates* (n=58). Some of these MAGs are as complete as genomes sequenced from isolates.

### **Bacterial communities of Hungarian soda pans and their growth on ammonium enriched media**

*Sofia Abad-Sojos*<sup>1,2</sup>, *Attila Szabó*<sup>1,3</sup>, *Tamás Felföldi*<sup>1,2</sup>

<sup>1</sup> Institute of Aquatic Ecology, Centre for Ecological Research, Budapest, Hungary

<sup>2</sup> Department of Microbiology, ELTE Eötvös Loránd University, Budapest, Hungary

<sup>3</sup> Department of Aquatic Sciences and Assessment, Swedish University of Agricultural Sciences, Uppsala, Sweden

The soda pans of the Carpathian Basin present unique physico-chemical properties which settle them as multiple extreme environments. These sites are characterized by permanent high pH, high turbidity, and (hydrogen) carbonate-dominated ionic composition. Their high carbon and phosphorus content originates from bird feces, groundwater inflow and decaying macrophytes, however the fate and effect of nitrogen compounds on aquatic microbes is currently not well-known. The present study provides information about the planktonic bacterial community composition in eight soda pans located in the Kiskunság National Park, which was supplemented with a cultivation-based experiment to test the relation of bacteria to selected nitrogen compounds. Environmental DNA-based analysis (Illumina amplicon sequencing of the 16S rRNA gene) confirmed previous studies that Actinobacteria, Cyclobacteriaceae and Flavobacteriaceae bacteria are dominant members of the planktonic community. The bacterial growth of the isolated strains were tested with three ammonium-containing compounds using nine different treatments containing ammonium chloride, ammonium sulfate, and ammonium carbonate in the concentrations 5 mM, 10 mM, and 20 mM. The isolates showed preference for ammonium chloride, while the two other tested compounds (ammonium sulfate and ammonium bicarbonate) resulted in lower bacterial growth values. The amount of nitrogenous compounds in these environments could be remarkably affected with nitrogen loss (volatilization) related to the chemical shift from ammonium to ammonia depending on the pH and temperature. Similarly, anion preference was observed in a previous research of our group when testing the relation of bacterial strains to different sodium compounds.



**Construction of an endophytic bacteria consortium against *Sclerotinia sclerotiorum* – a soil-borne pathogen of oilseed rape (*Brassica napus* L.)**

Sharon Lelo<sup>1,2</sup>, Bożena Nowak<sup>1</sup>, Katarzyna Hupert-Kocurek<sup>1</sup>

<sup>1</sup> Institute of Biology, Biotechnology and Environmental Protection, University of Silesia, Katowice, Poland

<sup>2</sup> Faculty of Nature and Technology, Bremen University of Applied Sciences, Bremen, Germany

Fungi are responsible for a range of severe crop diseases. For example, *Sclerotinia sclerotiorum* is a pathogen of over 400 plants, including rapeseed and sunflower. As a result of infection, plants have limited assimilation processes and reduced ability to conduct nutrients and water. A common practice of fighting phytopathogens is the use of chemical fungicides. However, growing concerns about their environmental effects contribute to the search for alternative plant protection methods, e.g. those based on biological control. Using microorganisms with antagonistic effects against phytopathogens is based mainly on single strains. However, a modern trend is the use of so-called consortia, increasing the effectiveness of protection. The conducted research aimed to develop a consortium of endophytic bacteria, which can be used to eliminate the negative impact of fungal pathogens and promote plant growth. Three bacterial strains: *Pseudomonas fluorescens* BRZ63 (B), *Serratia quinivorans* KP32 (P) and *Priestia megaterium* KW16 (K), with antifungal activity were used in the study. No antagonistic interaction between the tested strains was found (ladder test), which allows their use in constructing a consortium. Three different consortia (BP, BK and PK) of two strains each were prepared. The consortia were screened for their antifungal activity through a dual-culture antagonism assay. Four different pot experiments were set up to test the efficiency of each consortium in oilseed rape plants. It was found that the BK consortium, showing the highest antifungal activity in vitro, could not overcome the fungus's adverse effects on oilseed rape. In contrast, plant weight and length growth stimulation were observed in systems with PK or BP consortia in the presence of *S. sclerotiorum*. These consortia can be used for further research on the formulation for sustainable agriculture. Funding source MEiN, Innovation Incubator 4.0; US/5/II 4.0/2021.

### Impact of long-term agricultural management on Glomalin-Related Soil Protein

*Tünde Takács<sup>1</sup>, Péter Juhász<sup>1</sup>, Sándor Pabar<sup>1</sup>, Katica Kocsis<sup>1</sup>, András Makó<sup>1</sup>, Ambrus Rév<sup>1</sup>, Anna Füzy<sup>1</sup>*

<sup>1</sup> Institute for Soil Sciences, Centre for Agricultural Research, Budapest, Hungary

Agricultural land use optimization contributes to yield and soil security. Soil organic matter is crucial for soil fertility, it affects the stability of aggregates, water storage, chemical properties, and protective functions of soil and it has an important role in the regulation of many atmospheric constituents. Glomalin produced by arbuscular mycorrhizal (AM) fungi forms a significant part of soil organic carbon. Glomalin has an essential role in building the soil structure and protecting soil carbon in soil aggregates. However, intensive fertilization and tillage harm AMF diversity and functions just like glomalin production.

The effect of soil management on glomalin (Easily Extracted Glomalin-Related Soil Protein; EE-GRSP) has been examined at sites of three long-term field experiments: (1) NPK fertilization experiment with and without farmyard manure treatments; (2) conventional and organic farming fields (Martonvásár; Hungary) and (3) no-tillage, mouldboard ploughing and deep cultivation (Józsefmajor; Hungary) treatments were tested.

The soil disturbance had the most significant effect on topsoil EE-GRSP. Highly positive correlations were detected between various physicochemical soil properties (humus and nitrogen content, dissolved organic carbon and macroaggregate stability) and the EE-GRSP. The EE-GRSP was inversely related with pH. The topsoil glomalin ranged from 0.2 mg/g soil to 0.77 mg/g soil in different long-term experiments. The highest soil glomalin contents were found in the no-tillage system and N-fertilized plots.

The synthesis of our data could result in a land use effect assessment considering the quantity of soil glomalin. Glomalin is not just a C storage, but it is also a universal indicator of land use change effects on soil C and soil health.

The research was funded by the Eötvös Loránd Research Network (SA-26/2021) and the Sustainable Development and Technologies National Programme of the Hungarian Academy of Sciences (FFT NP FTA).

## The effect of vegetation shifts on carbon process rates and soil biodiversity in sub-Arctic region

*Liina Soonvald<sup>1</sup>, Sophia Zielosko<sup>1</sup>, Kari Anne Bråthen<sup>1</sup>*

<sup>1</sup> University of Tromsø, Tromsø, Norway

Climate change can lead to shifts in vegetation cover patterns, which, in turn, can impact the soil microbiome and related ecosystem processes. The alteration in vegetation patterns also has a significant impact on mycorrhizal fungi due to their strong dependence on plant type. These mycorrhizal associations, in turn, play an important role in nutrient cycling processes by enhancing nutrient uptake and carbon allocation in ecosystems. The aim of the experiment was to examine the effects of vegetation type shifts on the soil microbiome and soil carbon storage in sub-Arctic regions. To achieve this, soil samples representing arbuscular mycorrhizal, ectomycorrhizal, and ericoid mycorrhizal habitats were collected for a greenhouse experiment. Seedlings from different mycorrhizal types were planted in their respective habitat soils as well as in soils from the other habitats. Throughout the season, soil samples were collected along with measurements of CO<sub>2</sub>.

We hypothesized that soil communities would remain stable over time in soils grown with their respective plants, while changes would occur in soils exposed to new vegetation cover. Furthermore, we hypothesize that soil carbon content is linked to the dominant type of mycorrhizal associations. The presence of mycorrhizal associations is expected to enhance soil carbon storage compared to non-mycorrhizal conditions.

The initial results showed that the flux patterns for plant types are consistent across all soil types throughout the season. Therefore, the initial results indicate that CO<sub>2</sub> fluxes are primarily influenced by plant type rather than the soil in which they are planted. Interestingly, all treatment combinations acted as carbon sources at the beginning and middle of the season, only transitioning to carbon sinks at the end of the season. Plant type emerged as the primary factor in explaining both aboveground and belowground biomass, independent of soil type. The analysis of microbial data is still ongoing.

### **Antimicrobial resistance of fecal bacteria in recreational aquatic environments: a phenotypic and molecular approach**

*Łukasz Kubera<sup>1</sup>, Monika Harnisz<sup>2</sup>, Damian Rolbiecki<sup>2</sup>*

<sup>1</sup> Kazimierz Wielki University, Faculty of Biological Sciences, Department of Microbiology and Immunobiology, Bydgoszcz, Poland

<sup>2</sup> University of Warmia and Mazury, Faculty of Geoengineering, Department of Water Protection Engineering and Environmental Microbiology, Olsztyn, Poland

One of the major public health concerns today is the increased antimicrobial resistance of bacteria. Widespread use of antibiotics in healthcare and agriculture has led to an increase in the number of drug-resistant bacteria also in natural environments. The aim of this study was therefore to assess the distribution and drug resistance of fecal bacterial strains isolated from the bacterioplankton layer of three lakes used for recreational purposes, located in the Zaborski Landscape Park. The study involved 20 isolates of *Escherichia coli* and 26 isolates of fecal streptococci, four of which were represented by *Enterococcus faecalis*, and 17, by *Enterococcus faecium*. The resistance of fecal bacteria to selected antibiotics was determined using the disc diffusion method in accordance with the EUCAST (The European Committee on Antimicrobial Susceptibility Testing) recommendations. Antibiotics of different classes, including ampicillin, piperacillin, imipenem, levofloxacin, vancomycin, tigecycline, gentamicin and cefepime were used in the study. Additionally, specific drug resistance genes (*vanA*, *tetA*, *qepA*, *aadA9* and *CTX*, *TEM*, *OXA-51* and *bla SHV*) were amplified in the PCR reaction, where strains isolated from municipal wastewater were used as control. The phenotypic analysis proved that the isolates of fecal bacteria were resistant to all applied antibiotics but to varying degrees. Only *Escherichia coli* showed 100% sensitivity to tigecycline. However, none of the amplified resistance genes was found in either *Escherichia coli* or fecal streptococci. Our results indicate that drug resistance of strains isolated from natural environments might be induced by different genes than the resistance of strains found in the municipal wastewater. They also suggest the need for further research aimed at detecting resistance mechanisms of environmental bacteria.

### **Unveiling the influence of inorganic nanoparticles on bacterial cell membrane: structure, properties, and functionality**

*Daniel Wasilkowski<sup>1</sup>, Oliwia Metryka<sup>2</sup>, Małgorzata Adamczyk-Habrajska<sup>3</sup>, Agnieszka Mrozik<sup>1</sup>*

<sup>1</sup> Institute of Biology, Biotechnology and Environmental Protection, University of Silesia, Katowice, Poland

<sup>2</sup> Doctoral School, University of Silesia, Katowice, Poland

<sup>3</sup> Institute of Materials Engineering, University of Silesia, Sosnowiec, Poland

The unique physicochemical and biological properties of nanomaterials have garnered significant attention in the contemporary world. The dynamic development of nanotechnology has revolutionised every dimension of life, giving new technological and industrial applications. The increasing use of engineering nanomaterials, particularly metallic nanoparticles (NMs), serves various advantageous purposes, notably their antibacterial properties. On the other hand, there is a concern regarding the potential uncontrolled release of these NMs into the environment, which could lead to the exposure of microbial populations and subsequent risks of their potentially toxic effects. Nowadays, despite the extensive research conducted to comprehend the impact of NPs on bacterial cells and their effects on the membrane properties and functioning, many issues remain unexplained.

Hence, the objective of this study was to investigate the multifaceted effects of commonly used Ag-NPs, Cu-NPs, TiO<sub>2</sub>-NPs, and ZnO-NPs on the structure and functionality of cell membranes in representative bacterial species, including *Escherichia coli*, *Bacillus cereus* and *Staphylococcus epidermidis*. The proposed experiments assessed the permeability of outer cell layers, cytoplasmic leakage, fatty acid profiling and SEM analysis to elucidate the interactions of individual NPs with bacterial cells upon NPs exposure. The results clearly showed differences in the impact of individual NPs on the measured parameters. The enhanced membrane permeability exhibited a strong correlation with increased cytoplasmic leakage. The fatty acid profile demonstrated strain-specific characteristics for each bacterial strain, highlighting significant changes in the proportions of hydroxyl, cyclopropane, branched, and unsaturated fatty acids. Conclusively, *E. coli* exhibited higher susceptibility to alterations than *B. cereus* and *S. epidermidis*.

**Thiothrix and Sulfurovum genera are key players in cold sulfur springs**

*Lea Nosalova*<sup>1</sup>, *Maria Píknova*<sup>1</sup>, *Peter Pristas*<sup>1,2</sup>

<sup>1</sup> Institute of Biology and Ecology, Pavol Jozef Šafárik University in Košice, Košice, Slovakia

<sup>2</sup> Institute of Animal Physiology, Slovak Academy of Sciences, Košice, Slovakia

Since the study of the bacterial genus *Beggiatoa* and the discovery of chemolithoautotrophy by Winogradsky, sulfur-oxidizing bacteria have attracted the attention of microbiologists for more than a hundred years. They are characterized by enormous phylogenetic, physiological, and ecological diversity, and in recent years, the microbiota of sulfur-rich environments has been extensively studied mainly due to their biotechnological potential or as a model of ancient life. Studies have been focused on thermal environments, and from this point of view, cold sulfur springs represent underexplored ecosystems. Despite that, it was suggested that sulfur springs harbor diverse microbial communities influenced by the unique geochemical conditions of the waters. There are only a few publications from Central Europe, and our recent works are the first on the cold sulfur springs microbiota in Slovakia. The microbiota of several sulfur springs was examined using a metagenomic approach, and the vast majority of sequences obtained belonged to the sulfur-oxidizing genera. The functional prediction analysis confirmed sulfur metabolism as a dominant energy-gaining process; moreover, the main metabolic sulfur oxidation pathways were identified. The clear dominance of the Proteobacteria and Epsilonbacteraeota phyla was observed, and sulfur-oxidizing genera constituted a dominant part of the microbial populations, with the *Thiothrix* and *Sulfurovum* genera identified as the core microbiota of cold sulfur terrestrial springs in Slovakia. Conversely, the cultivation analyses provided a completely different view on the diversity of cold sulfur springs microbiota with *Halothiobacillus* spp. been dominant cultivable species among 22 isolates of sulfur-oxidizing bacteria and no cultivable *Thiothrix* or *Sulfurovum* representative. Additionally, the study emphasizes that sulfur springs in Slovakia support unique, poorly characterized bacterial communities of sulfur-oxidizing bacteria.

### **The response of ectomycorrhizal, arbuscular mycorrhizal and nonsymbiotic fungi to tree diversity in a temperate forest**

*Sandra Awokunle Hollá<sup>1,2</sup>, Lukáš Vlk<sup>1,2,3</sup>, Petr Kohout<sup>1,2,3</sup>, Petr Baldrian<sup>1</sup>*

<sup>1</sup> Institute of Microbiology of the Czech Academy of Sciences, Prague, Czech Republic

<sup>2</sup> Charles University, Prague, Czech Republic

<sup>3</sup> Institute of Botany of the Czech Academy of Sciences, Průhonice, Czech Republic

Biodiversity-ecosystem functioning studies have been found in connection with plant diversity. However, the importance of biotic interactions between plants and mycorrhizal fungi as drivers of ecosystem processes is understudied. Even those studies trying to find link between trees and soil microbes almost exclusively focused on ectomycorrhizal (ECM) trees, while much less is known about tree interaction with arbuscular mycorrhizal (AM) fungi and information from stands where AM and ECM trees are both present are virtually missing. Here, we investigated the effect of a temperate forest with a variable share of AM/ECM trees and a wide range of plot-level tree diversity on fungal abundance, guild composition, and diversity. We characterized soil properties, the biomass of AM and non-AM fungi, and the community composition of AM and non-AM fungi across 59 plots of a temperate mixed AM/ECM forest in Germany with a wide gradient of tree species diversity. The botanical survey of tree species within an entire plot, including tree diameter at breast height (DBH), and ground vegetation survey with close proximity to soil sampling were recorded. Our results revealed that vegetation (proportion of mycorrhizal type volume, species richness, and composition) plays an important but minor role in comparison with soil properties (e.g. pH, moisture, and phosphor) to shape the community composition of AM and non-AM fungi and their biomass. Furthermore, we found increased fungal biomass at plots with intermediate proportions of AM/ECM trees and biomass decline towards purely AM as well as purely ECM stands. Our results answer some basic questions about the interactions of fungi of various guilds, but also inform forest management decisions indicating that a balanced proportion of AM and ECM trees may lead to highest fungal productivity.

### Functionality and genetic diversity of AM fungal community in a long-term fertilization field experiment

*Anna Füzy<sup>1</sup>, Péter Juhász<sup>1</sup>, Sándor Pabar<sup>1</sup>, Katica Molnár-Kocsis<sup>1</sup>, Ambrus Rév<sup>1</sup>, Tünde Takács<sup>1</sup>*

<sup>1</sup> Institute for Soil Sciences, Centre for Agricultural Research, ELKH, Budapest, Hungary

The long-term effects of fertilization practices on the functionality and diversity of symbiotic endomycorrhizal communities were studied. A 60-year fertilization experiment with mineral fertilizers, farmyard manure and combined treatments was sampled in 2021 with maize and in 2022 with wheat. Soil chemical properties were measured, the arbuscular mycorrhizal fungal (AMF) colonization of the roots was determined and metagenomic analysis of AMF community was performed to identify the fungi taxa and the relative and absolute abundance of the AMF species in the soil samples. Soil and root samples were taken at flowering stage of the crop plants. The measured parameters were analysed using ANOVA to determine treatment effects. The non-metric multidimensional scaling technique was applied to reveal the shifts in mycorrhizal communities in treated and non treated plots. The rate of AMF colonization responded mainly to plant nutrition status and plant requirements, so a plant-mediated effect appears to be present in the case of functionality of AMF, while metagenomic analysis pointed out, that this shift not only functional or quantitative, but also changes in taxonomic composition. Mineral nitrogen fertilization reduces drastically the abundance of *Funneliformis mosseae*, which species otherwise dominant in control plots. *Rhizophagus intraradices* also abundant in the samples, strong reduction effect was detected in case of NPK treated plots. *Septoglomus* species looks like good indicator species, as they disappear in case of long-term nitrogen fertilization.

This research was funded by the Eötvös Loránd Research Network (ELKH grant no. SA-26/2021) and the Sustainable Development and Technologies National Programme of the Hungarian Academy of Sciences (FFT NP FTA).



**Changes of microbial plankton along a river-reservoir-lake system**

*Diána Lázár<sup>1</sup>, Kálmán Tapolczai<sup>1</sup>, Lajos Vörös<sup>1</sup>, Anita Perkins<sup>1</sup>, Boglárka Somogyi<sup>1</sup>*

<sup>1</sup>National Laboratory for Water Science and Water Security, Balaton Limnological Research Institute, Tihany, Hungary

The Zala River (average discharge 7 m<sup>3</sup> s<sup>-1</sup>) and the Kis-Balaton reservoir system (72 km<sup>2</sup>) together with Lake Balaton (596 km<sup>2</sup>) cover a wide range of habitats from running water to algae-rich and algae-poor lentic water types, interspersed with aquatic vegetation of different densities and types (submerged, floating, emerged). Since algae and aquatic plants fundamentally determine the physical and chemical environment and the substrate supply for the bacterioplankton, the aim of our study was to determine the abundance and activity of bacterioplankton in this complex system. In addition to the environmental parameters, we determined the biomass and ATP production of bacterioplankton. Particular attention was paid to the spectral composition of underwater light and bacterial communities containing bacteriochlorophyll. Financial support: RRF-2.3.1-21-2022-00008 project and Sustainable Development and Technologies National Programme of the Hungarian Academy of Sciences (FFT NP FTA).

**Soil fertility and rhizospheric activity of giant reed (*Arundo donax* L.) grown in acidic sandy soil treated by wastewater sludge compost and AM fungi**

*Ambrus Rév*<sup>1</sup>, *István Parádi*<sup>2</sup>, *Anna Füzzy*<sup>1</sup>, *Péter Juhász*<sup>1</sup>, *Katica Kocsis*<sup>1</sup>, *Imre Cseresnyés*<sup>1</sup>, *Tünde Takács*<sup>1</sup>

<sup>1</sup> Institute for Soil Sciences, Centre for Agricultural Research, ELKH, Budapest, Hungary

<sup>2</sup> Eötvös Loránd University, Faculty of Natural Sciences, Institute of Biology, Department of Plant Physiology and Molecular Plant Biology, Budapest, Hungary

We examined the effect of low-dose, commercially available wastewater sludge compost (WSC; 15 t ha<sup>-1</sup>) treatment with or without arbuscular mycorrhizal fungal (AMF) inoculation on the nutritional status, heavy metal (HM) concentration and the rhizosphere enzymatic activity of giant reed (*Arundo donax* L. var. BL clon (Blossom)) plants in a short-term pot experiment. *Funneliformis mosseae* (BEG12; AMF1), *F. geosporum* (BEG11; AMF2), or their combination (AMFmix) were applied as AMF inoculation treatments. We supposed, this combined treatment enhances the fertility of a basically low fertility soil. The physiological and growth parameters of the host plants, the AMF root colonization, and the microbiological enzyme activity of the mycorrhizosphere were examined. Neither the WSC treatment nor the AMF inoculations changed the extent of root colonization. Based on the results of root electrical capacitance and the phosphorus uptake, plant nutritional status was improved by WSC addition, without any negative impacts. AMF treatments increased soil enzyme activities (dehydrogenase, phosphatase) and decreased the concentration of the potentially toxic HMs (Cu, Mn, Pb, Zn) in the roots, but the difference of Cu and Zn was compensated in the shoots. According to the results of substrate-induced respiration using the MicroResp™ measurement, the pattern of the microbial community changed by the type of AMF inoculation, Giant reed's efficient regulatory mechanism to adjust optimal/maximal colonization rate, and to select for preferential AMF partners might be responsible of its invasiveness and tolerance to a wide range of environmental conditions.

This research was funded by the Eötvös Loránd Research Network (ELKH grant no. SA-26/2021).

**Effect of microplastics on microbial communities from the coastal Baltic Sea**

*Uroosa<sup>1</sup>, Sohrab khan<sup>1</sup>, Marcin Białowqs<sup>1</sup>, Magdalena Jakubowska-Lehrmann<sup>1</sup>, Kasia Piwosz<sup>1</sup>*

<sup>1</sup> National Marine Fisheries Research Institute, ul. Kołłątaja 1, 81-332 Gdynia, Poland

Increasing microplastic (MP) pollution is greatly affecting the aquatic environment. Thus, it is vital to know its effects on the ecosystem. The current studies focus mostly on its toxicity in marine organisms, mostly animals such as fish, but little information is available regarding microbial communities. This study was designed to find out the effects of Polystyrene (PS) and Polyethylene (PE), which are of smaller size and commonly found pollutants. The natural microbial community was collected from the coastal Baltic Sea and exposed to bacteria-sized PS, PE and glass microspheres. Two experiments were designed. In the first experiment, we studied the effect of PS concentrations on the abundance and activity of heterotrophic nanoflagellates (HNF) and prokaryotes over five days, while in the second experiment, we compared the effects of PS and PE. We observed a consistent negative effect of PS (that was more conspicuous at higher concentrations) and PE on HNF abundance, while for bacteria the effect was negligible or, in the case of PS, even positive. Moreover, the presence of glass and MPs particles lowered the respiration rate of the microbial community, indicating the importance of the physical effects of increased particle concentrations in the water. These results indicate the complex nature the presence of MPs may have on microbial communities. The combined effect of toxicity and the physical presence of inedible particles may alter the primary microbial consumers and cause a disturbance in microbial aquatic food webs. Further experiments are planned to understand the observed patterns.

### High frequency dynamics of heterotrophic flagellates in coastal waters of Baltic Sea in early Spring

*Sohrab Khan*<sup>1</sup>, *Anetta Ameryk*<sup>1</sup>, *Aneta Jakubowska*<sup>1</sup>, *Mariusz Zalewski*<sup>1</sup>, *Uroosa Uroosa*<sup>1</sup>, *Bartosz Witalis*<sup>1</sup>, *Kasia Piwosz*<sup>1</sup>

<sup>1</sup> National Marine Fisheries Research Institute, ul. Kołłątaja 1, 81-332 Gdynia, Poland

The global nutrient cycle and the continual production of organic matter depend heavily on oceanic phytoplankton. Seasonal variations in phytoplankton biomass and total primary production are observed in temperate climates. According to aquatic microbial food webs, energy is transferred from prokaryotes to heterotrophic nanoflagellates, then to ciliates, and then to zooplankton. The fact that the key categories of freshwater bacterioplankton and planktonic bacterivorous HNF grow at similar rates indicates the importance of this trophic interaction and its fluctuation in the overall rates of both energy and carbon transfer to greater trophic levels.

Much less is known about the trophic role of the omnivorous/predatory HNF (usually 5-20 m). In the spring, we perform extensive sampling campaign (thrice a week) for over a period of more than six weeks in the Baltic Sea water (March-May 2023). The overall goal was to clarify the function of omnivorous/predatory protists, with an emphasis on middle-sized (5-20 m) HNF that inhabit freshwater, and improve our understanding of the complexity of microbial food webs. We measured Temperature, Salinity, nutrients, chlorophyll, microbial abundance, grazing rates and phylogenetic diversity of HNF. Bacterial abundance characteristically increased from low levels to a first peak around mid-April subsequent to phytoplankton spring blooms and followed by HNF peak. However, the grazing rates on bacteria were below the detection limits most of the time. Our findings contribute to our understanding of microbial food webs in coastal marine environments, pointing to the importance of HNF in the early spring time.

### Detection and molecular characterization of antibiotic resistant Enterobacteriaceae from hospital effluents and wastewater treatment plant

*Réka Héninger*<sup>1</sup>, *Christopher Mutuku*<sup>1</sup>, *Szilvia Melegh*<sup>2</sup>, *Krisztina Kovács*<sup>2</sup>, *Péter Urbán*<sup>3</sup>, *Eszter Virág*<sup>4,5</sup>, *Róbert Herczeg*<sup>3</sup>, *Ágnes Sonnevend*<sup>2</sup>, *Attila Gyenesei*<sup>3</sup>, *Csaba Fekete*<sup>1</sup>, *Zoltán Gazdag*<sup>1</sup>

<sup>1</sup> Department of Molecular Biology and Microbiology, Faculty of Sciences, University of Pécs, Pécs, Hungary

<sup>2</sup> Department of Medical Microbiology and Immunology, Medical School, University of Pécs, Pécs, Hungary

<sup>3</sup> Bioinformatics Research Group, Szentágotthai Research Centre, Pécs, Hungary

<sup>4</sup> Educomat Ltd., Keszthely, Hungary

<sup>5</sup> Department of Molecular Biotechnology and Microbiology, Institute of Biotechnology, Faculty of Science and Technology, University of Debrecen, Debrecen, Hungary

Wastewater treatment plants have been reported as hot spots for emergence of antibiotic resistance. The widespread use of antimicrobials in human and veterinary medicine results in selective pressure which is associated with the emergence of antibiotic resistant bacteria. The purpose of our study was to isolate extended-spectrum  $\beta$ -lactamase (ESBL) producing pathogens from the order Enterobacteriales from wastewater and to investigate the antimicrobial resistance profiles. The targeted bacteria were isolated from the wastewater treatment plant samples and identified by Matrix assisted laser desorption ionization-time of flight mass spectrometer MALDI-TOF/MS. The drug susceptibility of 126 identified enteric bacteria belonging to species *Escherichia coli*, *Klebsiella pneumoniae*, *Klebsiella oxytoca*, *Enterobacter cloacae* and *Citrobacter freundii* were investigated to four antimicrobial classes. The proportion of isolated antibiotic-resistant bacteria in relation to the total aerobic colony forming unit (cfu) count ranged between 36,9% and 49%. The proportion of multiple antibiotic resistant (MAR) enteric bacteria was high, *E. coli* demonstrated the highest MAR index (0.65) among the four genera. A high prevalence of resistance (>80%) was observed for the third generation cephalosporins (3GCs) ceftriaxone (CRO), ceftazidime (CAZ), cefotaxime (CTX), and cefpodoxime (CPD), while significantly lower resistance rates were measured for carbapenems, imipenem, and meropenem (IMP and MEM) compared to the other antibiotics. Wastewater from human sources may serve as an important reservoir of multiresistant Enterobacteriales. Monitoring wastewater from human sources for acquired resistance in clinically important bacteria may provide a cheaper alternative in regions facing challenges that limit clinical surveillance.

**Bacteria from extreme environment as inoculants for sustainable agriculture.**

*Igor Królikiewicz<sup>1</sup>, Agnieszka Kalwasińska<sup>1</sup>*

<sup>1</sup>Nicolaus Copernicus University, Toruń, Poland

Wheat is one of the most important crops in the world and a fundamental cereal in the human diet. The high salinity of soils negatively affects the development of wheat. It disrupts enzymatic processes by altering the osmotic potential, resulting in reduced yields, germination, and biomass production. Nitrogen is essential for growth and development of plants and its deficiency often is a major limiting factor of growth. Given the challenges posed by climate change and soil degradation, it becomes crucial to identify and describe bacteria from extreme environments that promote plant growth. This knowledge can help increase yields under unfavorable conditions and protect the population from hunger. Plant Growth Promoting Bacteria (PGPB) derived from these environments play a vital role in agriculture, particularly in adverse regions, where they can be utilized as bioinoculants or biofertilizers. Thus, the objective of this research was to investigate the nitrogen-fixing ability of bacteria isolated from alkaline lime, a by-product in the Solvay process of soda production. The aim was to enhance the growth of wheat (*Triticum aestivum* L.) in saline soil. The study employed various methods, including classic microbiology and molecular biology techniques, to confirm the Nitrogen-fixing ability of the bacteria and identify the query strain. Additionally, cultivation methods were utilized to demonstrate significant changes in wheat length after seed inoculation with beneficial bacteria, such as *Klebsiella michiganensis* isolated from alkaline lime. These results provide promising insights for further research on biopreparations for wheat cultivation under salinity conditions.

### Impact of different Plant Growth-Promoting Microbes on the rhizosphere enzymatic activities and the plant growth parameters

*Sándor Attila Pabar*<sup>1,2</sup>, *Tünde Takács*<sup>1</sup>, *Nándor Prettl*<sup>2</sup>, *Zsolt Kotroczó*<sup>2</sup>, *Borbála Biró*<sup>2</sup>

<sup>1</sup> Institute for Soil Sciences, Centre for Agricultural Research, Budapest, Hungary

<sup>2</sup> Department of Agro-environmental Studies, Hungarian University of Agriculture and Life Sciences, Budapest, Hungary

The effects of different Plant Growth-Promoting Microbes (PGRM) on the seed germination and development of white mustard (*Sinapis alba*) and perennial ryegrass (*Lolium perenne*) were examined in a short-term experiment. The model-experiment was conducted in a cell tray filled with a mixture of arenosol soil and compost. The plants were treated with inoculum of *Enterobacter ludwigii*, *Bacillus megaterium*, *Bacillus subtilis*, *Kosakonia cowanii*, *Pseudomonas fluorescens* Hx1, and a *Trichoderma harzianum* T-22 fungal strain. Aim of the experiment was to compare the biofertilizer effect of used strains in two different model-plants and selecting appropriate soil-biological parameters of their functioning.

For the test of PGPM functionality, the shoot length, fresh and dry weight of the plants, and also the germinated mustard seeds were examined. The total, non-specific enzyme activity of the rhizosphere microbes was measured by the fluorescein diacetate (FDA) hydrolysis analysis.

The results showed that almost all strains increased the yield of the biomass (especially the fresh) in both plant species, but in the case of mustard greater results were shown. Germination rate increase was observed at the mustard due to the treatments.

The greatest biomass increase was given by the *Enterobacter ludwigii*, *Bacillus megaterium* and the *Pseudomonas fluorescens* strains.

The FDA showed generally positive correlation with other parameters. The strongest correlation was with the shoot length data.

It was concluded that the PGPM treatments generally had a positive effect on the examined parameters. The used cell-tray experiment provided proper methodology of modelling and preselecting best microbial inoculums.

The research was funded by the Eötvös Loránd Research Network (SA-26/2021) and the Sustainable Development and Technologies National Programme of the Hungarian Academy of Sciences (FFT NP FTA).

**Marine, endolithic and epilithic cyanobacteria from Sweden**

*Wiktoria Chudzik<sup>1</sup>, Ilona Zloch<sup>1</sup>, Katarzyna Palińska<sup>1</sup>*

<sup>1</sup> University of Gdansk, Faculty of Oceanography and Geography, Gdynia, Poland

Organisms that colonize the interior of rocks, shell hash and other skeletal fragments are known as endoliths. The endolithic mode of life includes several different ecological niches: chasmoendoliths and cryptoendoliths occupy preexisting fissures and structural cavities in the rocks, whereas euendoliths actively penetrate soluble carbonatic and phosphatic substrates (Golubic et al. 1981). Tropical and Mediterranean endoliths were studied phenotypically since early 1900th, however endolithic microorganisms from cold and polar regions were not subject of any detailed investigations.

Here we show first diversity study on cyanobacterial endoliths from Sweden. The coastal profiles selected for this study represent ecotones between the sea and land, which express gradients of water supply and retention, solar illumination, and salinity. Microbial phenotypes and genotypes along the vertical coastal profile across the subtidal, intertidal and supratidal ranges showed large differences in dominance of taxa, but less in their diversity.

According to our results vertical gradient is clearly the most powerful explanatory variable for species composition. However, there are probably no distinct and sharp zones present, instead a continuous gradient was observed. The species composition of particular zones is similar to previous studies conducted e.g. in Adria. The presence of epilithic and endolithic organisms on the seashore causes very characteristic colouration of the rocks. However the majority of cyanobacterial species are not restricted to one zone and there are no well-distinguished zones, just a continuous compositional gradient.

The results of our investigation underline the importance of a combined approach in comparing the molecular data with microscopic observations in all phases of the study. Further RNA studies are needed to identify the actively growing parts of the endolithic community.



### The potential of *Chlorella* strain R-117 for municipal wastewater remediation

*Barbara Lucrezia Lezzi*<sup>1</sup>, *João Artur Câmara Manoel*<sup>2</sup>, *Karolína Štěrbová*<sup>2</sup>, *Jiří Masojídek*<sup>2,3</sup>

<sup>1</sup> University of Salento, Lecce, Italy

<sup>2</sup> Institute of Microbiology of the Czech Academy of Sciences, Centre Algatech, Laboratory of Algal Biotechnology, Třeboň, Czech Republic

<sup>3</sup> Faculty of Science, University of South Bohemia, České Budějovice, Czech Republic

Microalgae (including eukaryotic microalgae, prokaryotic cyanobacteria, and photosynthetic bacteria) are considered potential next-generation resources as they produce a variety of valuable bioproducts applicable in nutrition, agriculture, and industrial applications. They can also serve as environment-friendly solutions in CO<sub>2</sub> mitigation, wastewater treatment and biofuel production. Since the 1970s microalgae applications in wastewater remediation have been gaining increasing interest.

In this work, the robust, fast-growing microalga *Chlorella sorokiniana*, strain R-117 was tested in laboratory cultivations as concerns its ability to grow in urban wastewater obtained from a municipal wastewater treatment plant in Třeboň, South Bohemia. This strain was selected as it can grow well in outdoor large-scale open units. Changes in growth kinetics (biomass production), physiology, and photosynthesis were monitored in cultures grown in centrate from municipal wastewater compared to those grown in rich inorganic medium BG-11.

The results showed that the *Chlorella* culture can grow in the centrate of municipal WW although its growth was slower as compared to the culture in the rich inorganic medium used in outdoor production cultures. It was reflected in lower photosynthetic activity.

It can be concluded that *Chlorella* R-117 can grow in the centrate of municipal wastewater and might be potentially used in large-scale continuous cultivation (dilution = harvesting) in the centrate of municipal wastewater for nutrient remediation as described previously for other strains.

**On the origin of toxicity: what are the drivers of microcystin concentration in plankton biomass?**

*Martyna Budziak<sup>1</sup>, Wojciech Krztoń<sup>1</sup>, Edward Walusiak<sup>1</sup>, Małgorzata Łaciak<sup>1</sup>, Elżbieta Wilk-Woźniak<sup>1</sup>*

<sup>1</sup> Institute of Nature Conservation, Polish Academy of Sciences, Kraków, Poland

Microcystins, toxins produced by various species of cyanobacteria, have become one of the most concerning environmental problems. Their presence in the environment due to their detrimental effects, is recognized as a threat for biota dwelling aquatic ecosystems. As a consequence of climatic changes and increasing anthropogenic disturbances, microcystins presence is predicted to be more frequent in freshwaters, due to more intense and longer lasting cyanobacterial blooms. Although the factors that regulate microcystin synthesis remain unclear, some premises suggest that increased N availability as well as atmospheric conditions may lead to short-term boosts in toxin production. Here, we analysed whether the total concentration of microcystins (hepatotoxins) is correlated with nitrogen and carbon content in plankton biomass and with seasonal temperature, wind speed, cloud cover and precipitation. Results of our studies, showed a steady decrease in concentration of microcystins in subsequent years with highest records observed in 2019 and lowest in 2022. Similarly, we observed a decrease in N and C concentration in planktonic biomass (mg/kg). Moreover, total concentration of microcystins was significantly correlated with C and N ( $p < 0.05$ ) content in the planktonic biomass. The temperature was observed to be positively correlated with content of C and N in plankton biomass ( $p < 0.05$ ) but only in the pre-bloom part of the season. On the contrary, we observed that wind speed was negatively impacting N and C content in plankton biomass ( $p < 0.05$ ) during the bloom period. Whilst it is intuitive that nutrient availability is essential, regarding its impact on cyanobacterial blooms and the release of toxic compounds, our results suggest that it is also of high importance to track and understand the relationship between climate change and cyanobacterial blooms as the initial circumstances in pre-blooming period may be crucial for the microcystins production.

### Observation of the effect of different agents on mycotoxin producing *Aspergillus* and *Fusarium* species

*Enikő Makkai*<sup>1,2</sup>, *Tibor Bartók*<sup>3</sup>, *Zoltán Gazdag*<sup>1</sup>, *Árpád Czéh*<sup>2</sup>

<sup>1</sup> University of Pécs, Faculty of Sciences, Department of Molecular Biology and Microbiology, Pécs, Hungary

<sup>2</sup> University of Pécs, Faculty of Sciences, External Department of Applied Molecular Sciences, Pécs, Hungary

<sup>3</sup> Fumizol Kft., Szeged, Hungary

Mycotoxins are hazardous to human and animal health and are extremely stable against heat, physical and chemical treatment resulting difficulties in eliminating them during food processing procedures. Furthermore, animal-derived products are also dangerous due to carry-over to products such as milk, eggs or meat. Worldwide, approximately 25% of the harvested crops are contaminated with mycotoxins above regulatory limits. Chlorine has been the most common sanitizer. The main mycotoxin-producing fungi are among others the *Fusarium* and *Aspergillus* species. The aim of the study was to investigate the antifungal effect of chlorine-containing liquid and gel substances compared to voriconazole (VOR) as standard in case of the above-mentioned species. We observed 6 mycotoxin-producing species: *A. nomius* (SZMC 22273), *A. parasiticus* (SZMC 2473) as aflatoxin producers from the Szeged Microbiology Collection, and *F. culmorum*, *F. graminearum*, *F. proliferatum* and *F. verticillioides* as fumonisin producers from Fumizol Kft., Szeged. Minimum inhibitory concentration (MIC<sub>80</sub>) of the liquid and gel substances and voriconazole have been defined using microdilution method according to CLSI with some adjustments in case of the chlorine-containing substances. MIC<sub>80</sub> for both state of chlorine-containing substances were 1 µg/ml in case of *F. proliferatum* and *F. verticillioides*, which is less than the 2 and 4 µg/ml VOR. In case of *F. graminearum*, we observed 1 µg/ml MIC<sub>80</sub> both in liquid substance and VOR, but 2 µg/ml for the gel. The MIC<sub>80</sub> values were higher for the *A. nomius*, 4 µg/ml for the chlorine-containing substances. However, further examination is needed to more precisely understand the effectiveness of the substances. We plan to observe their possible alteration on the diameter of the colonies and also the mycotoxin-producing ability of the fungi.

### **The effect of *T.harzianum* on micronutrient content of tomato cultivars grown under conventional and organic farming**

*Gordana Racić<sup>1</sup>, Igor Vukelić<sup>1</sup>, Mirjana Bojović<sup>1</sup>, Zorana Srećkov<sup>1</sup>, Zorica Mrkonjić<sup>1</sup>, Milana Lazović<sup>2</sup>, Dejana Panković<sup>1</sup>*

<sup>1</sup> Faculty of ecological agriculture, Educons University, Sremska Kamenica, Serbia

<sup>2</sup> A Bio Tech Lab, Sremska Kamenica, Serbia

Positive influence of *Trichoderma* spp. on plants is recognized as stimulation of plant growth, induction of plant defence mechanisms and improvement of plant fruit quality. In terms of sustaining healthy and nutritional value diet, importance of micro and macronutrients contents in vegetables is highly important factor. Tomato as one of the most consumed vegetables is important source of vitamins, minerals, dietary fibers and bioactive compounds in human nutrition.

Aim of this research was to study micronutrient concentration of two tomato genotypes, Narvik and Gružanski zlatni in presence of *T.harzianum* SZMC22660. Plants were grown under 3 different growing conditions: conventional farming in greenhouse, organic farming in greenhouse and organic farming in the field. The concentration of As, Cd, Co, Cu, Cr, Fe, Mn, Ni, Pb and Zn in red ripe tomato fruits was determined by ICP-OES method.

Results showed that among different treatments the highest contents of Cd, Cu and Fe were found in fruits of both tomato cultivars grown under organic farming system in the greenhouse. In the same farming conditions, *Trichoderma* presence affected content of Fe and Zn. The content of Fe in the fruit increased by almost 50 %, whereas the content of Zn decreased also for 50 % in both tomato cultivars. Content of As, Cd, Co and Pb was below the detection limit, for all three treatments.

Our results suggest that *Trichoderma* application improves the quality of tomato fruits in both types of farming systems, conventional and organic. Further examinations on a larger scale of tomato cultivars are necessary.

**Bacterial community dynamics of Lake Balaton and Kis-Balaton Water Protection System**

*Milán Farkas*<sup>1</sup>, *Sándor Szoboszlai*<sup>1</sup>, *Lajos Vörös*<sup>2</sup>, *Zsófia Lovász*<sup>3</sup>, *Nikoletta Méhes*<sup>3</sup>, *Kálmán Mátyás*<sup>3</sup>, *Edit Kaszab*<sup>1</sup>, *Judit Háhn*<sup>1</sup>, *Gergő Tóth*<sup>1</sup>, *Péter Harkai*<sup>1</sup>, *Árpád Ferincz*<sup>1</sup>, *András Táncsics*<sup>1</sup>, *Balázs Kriszt*<sup>1</sup>

<sup>1</sup> Hungarian University of Agriculture and Life Sciences, Gödöllő, Hungary

<sup>2</sup> Balaton Limnological Research Institute, Tihany, Hungary

<sup>3</sup> Department Kis-Balaton, West-Transdanubian Water Directorate, Keszthely, Hungary

The Lake Balaton with surface area of 594 km<sup>2</sup> and 3,2 m average depth is the largest central European shallow lake. As a result of high external nutrient loads the lake became hypertrophic in the 70's, therefore strict regulations were introduced. To ameliorate the water quality and retain the nutrients from the lake the Kis-Balaton Water Protection System (KBWPS) was constructed.

After several decades of operation and multiple transformations, an attempt was made to explore the microbial community of the water reservoir and its relationship with algal groups and environmental parameters. To discover the spatial and the seasonal heterogeneity of planktonic bacterial community four sampling areas and seven time points were set based on the physicochemical and algae distribution parameters. Illumina 16S rDNA amplicon sequencing was used to assess precisely the bacterial community composition of the chosen samples.

In the main inflow Zala river, floods had the greatest effect on the microbial community composition, while in the open water areas of the KBWPS, the algae production that develops due to external nutrient load was the main driver of the bacterial community. In the high-macrophyte-covered areas, the decomposition processes of the dying algae biomass were the most decisive. Finally, in the large open water areas of Lake Balaton, the external and internal nutrient loads together determined the algal production and thus the bacterial community composition.

Acknowledgement:

Supported by the ÚNKP-21-4. New National Excellence Program of the Ministry for Innovation and Technology from the source of the National Research;

Development and Innovation Fund, Thematic Excellence Programme 2020, National Challenges Subprogramme (TKP2020-NKA-16) and GINOP-2.3.2-15-2016-00004

### **Assessing the effectiveness of a Dehalococcoides-containing bioremediation product for the remediation of a pilot area contaminated by chlorinated ethenes**

*Péter Szijjártó<sup>1</sup>, Tamás Farkas<sup>1</sup>, Zsuzsanna Nagymáté<sup>1,2</sup>, Gergely Krett<sup>2</sup>, Csaba Romsics<sup>2</sup>, Laura Jurecska<sup>2</sup>, Károly Márialigeti<sup>2</sup>, Viktória Bódai<sup>1</sup>, Balázs Erdélyi<sup>1</sup>*

<sup>1</sup>Fermentia Ltd., Budapest, Hungary

<sup>2</sup>Eötvös Loránd University, Department of Microbiology, Budapest, Hungary

According to our current scientific knowledge, members of the Dehalococcoides genus are the only organisms capable of complete reductive dehalogenation chlorinated ethenes like tetrachloroethylene (PCE) and trichloroethylene (TCE) to the benign end product, ethylene. Hence, the presence of Dehalococcoides on contaminated sites is considered essential for effective bioremediation. Fermentia Ltd. and ELTE's Department of Microbiology developed a dechlorinating microbial culture: Ferm&Go1V, that contains a high number of Dehalococcoides (at least 10<sup>7</sup> reductive dehalogenase gene copies ml<sup>-1</sup>) and can be manufactured on industrial scale. This microbial inoculant was used to treat wells on a pilot area contaminated by chlorinated ethenes. Effects of the bioaugmentation(s) were monitored both chemically and microbiologically, by qPCR measurements of Bacteria 16S rRNA genes, and Dehalococcoides-specific reductive dehalogenase genes TceA and VcrA. Copy number of these specific genes have increased in the ground water of the treated site, while the concentrations of the contaminants have severely decreased, these results clearly show the effectiveness of this bioaugmentation product.

**Global diversity and distribution of dust associated arthropods communities in homes**

*Farah Shafiq*<sup>1</sup>, *Jane Oja*<sup>2</sup>, *Sten Anslan*<sup>1,2</sup>, *Vladimir Mikryukov*<sup>1</sup>, *Daniyal Gohar*<sup>2</sup>, *Leho Tedersoo*<sup>1,2</sup>

<sup>1</sup> Institute of Ecology and Earth Sciences, University of Tartu, Tartu, Estonia

<sup>2</sup> Mycology and Microbiology Center, University of Tartu, Tartu, Estonia

The indoor environment serves as a habitat for a wide array of microorganisms, with dust acting as a favorable medium for their survival. Among indoor organisms, arthropods represent one of the least studied groups, despite the possibility of symbiotic or antagonistic relationships with indoor bacteria and fungi. As previous work has been in limited scale, we conducted a comprehensive analysis of 660 dust samples collected from various locations worldwide to investigate the presence of arthropod communities. Samples were collected from four different locations from each house with the help of citizen scientists. We used a DNA-based method for investigating arthropod diversity in homes via high-throughput sequencing by which various taxonomic groups were identified. Within the arthropod phylum, seven classes were represented in the dust samples, with insects (Insecta), springtails (Collembola), and arachnids (Arachnida) being the most diverse and abundant. Arthropods mites (Sarcoptiformes), true flies (Diptera) and booklice (Psocoptera) were the most species rich and frequent orders that were found in more than 50% of house dust samples. Dust associated arthropods tend to be geographically restricted and their diversity distribution was best predicted by temperature fluctuation and precipitation. Factors such as temperature, humidity, and the presence of specific microhabitats within the indoor setting appeared to influence the arthropod community structure. Within homes, floor was the most arthropods richer surface, however their community composition did not significantly differ among sampling points. However, our findings not only provide first continental-scale maps of household arthropod diversity, but we were able to document previously unknown geographic distributions of diverse arthropods. This emphasizes the necessity for future research to unravel the intricate relationship between arthropods and other microbial inhabitants within indoor environments.

### **Taxonomic diversity of planktonic and biofilm bacterial communities in different Danube water body types in Hungary**

*Kinga Julianna Lennert*<sup>1</sup>, *Attila Engloner*<sup>2</sup>, *Andrea K. Borsodi*<sup>1,2</sup>

<sup>1</sup> Eötvös Loránd University, Budapest, Hungary

<sup>2</sup> Centre for Ecological Research, Eötvös Loránd Research Network, Budapest, Hungary

Rivers play a fundamental role in providing drinking water and ecosystem services in urbanised regions. The water quality of the different water bodies is influenced by municipal, industrial, and agricultural human activities. Planktonic microbial communities also contribute to the self-purification processes by transforming and degrading organic pollutants. Managing water quality of rivers requires exploring and comparing the composition of microbiota in different and interrelated water types and habitats and environmental factors that influence them. For research, water and biofilm samples were collected at the beginning of the vegetation period (May) from (a) the main branch upstream (north) and downstream (south) of the capital, (b) a regulated side arm, (c) an oxbow, and (d) a separated oxbow lake. Among physical and chemical parameters, temperature, pH, electrical conductivity, dissolved oxygen, orthophosphate, total organic carbon, and nitrate of the water samples were measured. The taxonomic diversity of bacterial communities was determined using 16s rRNA gene-based amplicon sequencing method on Illumina MiSeq platform. Both water and biofilm samples were dominated by representatives of the phyla Proteobacteria and Bacteroidota, while the phylum Actinobacteriota was abundant only in the water samples. Additional characteristic community members included the phyla Verrucomicrobiota, Acidobacteria and Cyanobacteria. Based on the taxonomic diversity and composition of the microbiota, habitat types were more separated from each other than the different types of water bodies. The differences in the composition of planktonic microbial communities increased parallelly with the degree of separation of the water bodies from the main branch. Some taxonomic groups and physico-chemical parameters were well correlated with each other. This research was funded by the National Research, Development and Innovation Fund of Hungary, grant number 2018-1.2.1-NKP-2018-00011.



**Diversity and distribution of plant pathogenic fungi in Pannonian forests**

*József Geml*<sup>1,2</sup>, *Carla Mota Leal*<sup>1</sup>, *Richárd Nagy*<sup>2</sup>, *József Sulyok*<sup>3</sup>

<sup>1</sup> ELKH-EKKE Lendület Environmental Microbiome Research Group, Eszterházy Károly Catholic University, Eger, Hungary

<sup>2</sup> Research and Development Centre, Eszterházy Károly Catholic University, Eger, Hungary

<sup>3</sup> Bükk National Park Directorate, Eger, Hungary

Plant pathogenic fungi are diverse and contribute maintaining high plant diversity in forest ecosystems. We carried out DNA metabarcoding of fungi from soil samples taken at 62 sites in the Bükk Mountains in northern Hungary. The selected sampling sites represent the characteristic Pannonian forest types distributed along elevation (i.e. temperature), pH and slope aspect gradients. We compared richness and community composition of plant pathogenic fungi among forest types and explored relationships among environmental variables and fungal alpha and beta diversity. The DNA sequence data generated in this study indicated correlations between plant pathogenic fungal community composition and environmental variables, and resulting compositional differences among zonal, topographic or edaphic forest types. Despite the relatively high proportions of compositional variance explained by the tested environmental variables, a large proportion of the compositional variance remained unexplained, indicating that both niche (environmental filtering) and neutral (stochastic) processes shape fungal community composition at landscape level. Our work provides unprecedented insights into the diversity, landscape-level distribution, and habitat preferences of plant pathogenic fungi in the Pannonian forests of Northern Hungary.

### Application of QS signaling molecules and essential oil components against food spoilage yeasts

*Erika Beáta Kerekes*<sup>1</sup>, *Mariana Magalhães*<sup>1</sup>, *Miklós Takó*<sup>1</sup>, *Ilona Pfeiffer*<sup>1</sup>, *Csaba Vágvölgyi*<sup>1</sup>

<sup>1</sup> University of Szeged, Szeged, Hungary

Prevention of food contamination and spoilage require novel applications to avoid food waste. The quorum sensing (QS) system regulates life-processes in bacteria with accumulation of N-acyl homoserine lactones (AHL) while farnesol and tyrosol are used in yeasts. Studies highlight that essential oils (EOs), EO components, and QS signal molecules can be potential inhibitors of the QS system. These natural molecules may represent a new opportunity to extend shelf-life of foods. In the present study, signal molecules C4-AHL and C12-AHL in 4  $\mu$ M concentration as well as EO components thymol, trans-cinnamaldehyde and limonene were tested as potential inhibitory agents against yeast growth and biofilm formation. Also, supernatants of 48 h old yeast cultures were tested for their possible anti-QS effect using the model organism *Chromobacterium violaceum*. Ten yeasts serving as type strains were selected from a culture collection and ten yeasts were isolated from meat samples. Type strains were sensitive to C4 signal molecules; biofilm formation of most isolates was reduced by more than 50%. C12 inhibited biofilm formation most effectively in *Saccharomyces ludwigii* resulting in a 44% biofilm compared to control. Yeasts from meat samples were quite resistant; four strains showed biofilm inhibition after treatment with C4 and results for C12 were strain dependent. Cinnamaldehyde was the best inhibitor with minimal inhibitory concentration between 0.4-6.2 mg/ml. Cinnamaldehyde and thymol were significant biofilm inhibitors in most strains. Production of *C. violaceum* violacein pigment, that is regulated by the QS system, was reduced by about 40% in the presence of culture supernatants. Our results indicate that AHL molecules and EO components can affect growth activities in yeasts. The effective compounds can serve as a basis for the selection of potential food preservatives to be used in future studies. This research was supported by the NKFI grants PD 142122 and FK 134886.

## Dynamics of Cryptophyta and Chlorophyta during AU LMWE experiment using Nanopore-based next generation sequencing and imaging flow cytometry analyses

*Ayagoz Meirkhanova*<sup>1</sup>, *Adina Zhumakhanova*<sup>1</sup>, *Polina Len*<sup>1</sup>, *Eti Levi*<sup>2</sup>, *Erik Jeppesen*<sup>2</sup>, *Christian Schoenbach*<sup>1</sup>, *Thomas Davidson*<sup>2</sup>, *Natasha Barteneva*<sup>1</sup>

<sup>1</sup>Nazarbayev University, School of Sciences and Humanities, Astana, Kazakhstan

<sup>2</sup>Aarhus University, Department of Bioscience and Center for Water Technology (WATEC), Aarhus, Denmark

Freshwater ecosystems are highly heterogeneous, and the response mechanisms of such communities are diverse. The complex spatial and temporal dynamics are not only shaped by abiotic factors like temperature and nutrients. Still, they can also be influenced by interactions between phytoplankton and the associated microbial communities. Microbial and phytoplankton communities, bacterial-phytoplankton interactions, and overall ecosystem community dynamics, were monitored using outdoor mesocosms. Parallel analysis using Nanopore-based sequencing and imaging flow cytometry was applied. In total, 46 samples were collected in the period from July to August 2021 from 3 mesocosms, with varying temperature regimes and at two sampling depths.

16S-based sequencing was successfully applied to classify over 200 microbial species, while imaging cytometry-based analysis revealed dynamic changes in the phytoplankton composition. Nonmetric multidimensional scaling analysis revealed that both microbial and phytoplankton communities formed significantly different clusters based on a temperature regime. A large proportion of Cyanobacteria was present at mesocosm with ambient temperature, while tanks with an IPCC A2 and IPCC A2+50% regimes were dominated by Cryptophyta and Chlorophyta, respectively. In addition, microbial clusters were identified, with bacterial species co-occurring throughout the experiment (Pearson's coefficient > 0.75). Specifically, a positive correlation between the abundance of Cryptophyta and *Massilia aurea* (Betaproteobacteria) was identified.

The obtained results indicate successful application of the integrative approach of optical- and molecular-based methods for the comprehensive analysis of freshwater communities and provide insights into ecosystem dynamics at the mesocosm scale.

### Exploring the Structure of Spatial Heterogeneity in Microbial Communities of Tengiz-Korgalzhyn Lakes System

*Polina Len*<sup>1</sup>, *Ayagoz Meirkhanova*<sup>1</sup>, *Galina Nugumanova*<sup>1</sup>, *Erik Jeppesen*<sup>2</sup>, *Ivan A Vorobjev*<sup>1</sup>, *Alessandro Cestaro*<sup>3</sup>, *Claudio Donati*<sup>3</sup>, *Natasha S Barteneva*<sup>1</sup>

<sup>1</sup> Department of Biology, School of Sciences and Humanities, Nazarbayev University, Astana, Kazakhstan

<sup>2</sup> Department of Ecoscience, Aarhus University Center for Water Technology (WATEC), Aarhus, Denmark

<sup>3</sup> Unit of Computational Biology, Research and Innovation Centre, Fondazione Edmund Mach, San Michele all'Adige, Italy

One of the UNESCO World Heritage Sites, the Tengiz-Korgalzhyn Lakes system represents a remarkable wetland ecosystem harboring numerous protected and endemic species. Given the ongoing ecological pressures and the escalating impact of global climate change, it becomes imperative to assess the ecological condition of these vulnerable areas.

This study aims to investigate the role of spatial autocorrelation in the biodiversity of bacterioplankton based on the example of the lakes of Northern Kazakhstan, as well as to explore functional dependency between physico-chemical parameters and microbiome composition.

Microbial community data were obtained using full-length 16S amplicons generated by the MinION mk1c. Species-level classification and analysis were conducted in Emu, R, and R Studio, utilizing the phyloseq and vegan packages.

Our investigation has substantiated the crucial role of the salinity gradient in shaping the composition of microbiomes within the lakes. Notably, we have demonstrated that salinity, among all abiotic factors, exerts the most pronounced influence on the microbial communities' composition. Across all sampling sites, the abundance of Beta- and Gammaproteobacteria classes exhibited parallel changes with increasing salinity levels, displaying a decrease and increase, respectively. Nevertheless, we have found out that spatial autocorrelation in the structure of the microbial communities across different water bodies surpasses functional dependency on environmental descriptors, such as salinity, and that the main portion of similarity (or dissimilarity) among lakes is attributed to level geographical separation.

### Effect of *Lactobacillus* inoculation on the diversity of yeast communities in the experimentally *Aspergillus flavus* contaminated corn silages

*Dorottya Sárkány*<sup>1</sup>, *Csaba Dobolyi*<sup>2</sup>, *József Kukolya*<sup>3</sup>

<sup>1</sup> Eötvös Loránd University, Budapest, Hungary

<sup>2</sup> Hungarian University of Agriculture and Life Sciences, Gödöllő, Hungary

<sup>3</sup> Eszterházy Károly Catholic University, Eger, Hungary

Development of silages is performed by anaerobic fermentation catalysed mainly by different *Lactobacillus* species.

In our research, we investigated the effect of the high dose of *Lactobacillus* treatment on the population and diversity of yeasts communities in whole crop corn silage contaminated with an aflatoxin-producing *Aspergillus flavus* preparate (CSCA).

The amount of  $4.8 \times 10^7$  yeast CFU/g wet mass cultured from the initial mixture of chopped whole crop corn, while only  $2.4 \times 10^6$  CFU/g did from the uninoculated control CSCA, and only  $7.1 \times 10^5$  CFU/g from the lactobacillus-inoculated CSCA. Based on 144 randomly isolated strains, the yeast community of the initial mixture composed of 8 species. In contrast, the yeast community of uninoculated control CSCA composed only of 4 species determined by isolation of 132 randomly selected strains. Furthermore, lactobacillus-inoculated CSCA composed of only 3 species based on 158 randomly isolated strains. *Saccharomyces cerevisiae* and *Pichia kudrjavzevii* proved to be predominant in the uninoculated CSCA, while *Saccharomyces cerevisiae* and *Meyerozyma guilliermondii* were the most numerous in the *Lactobacillus* -inoculated CSCA. The species richnesses were also confirmed by alpha diversity values (1.828, 1.309, 0.935 as Shannon's indices). In response to *Lactobacillus* inoculation, species the diversity decreased considerably (from 1.309 to 0.953).

Based on our results we can conclude that the *Lactobacillus* treatment, which is widespread in silage practice, has a moderate effect on yeasts considered as autochthon microorganisms in silages.

#### *Acknowledgements*

*This work was supported by the NVKP- 16-1-2016-0009 project. Dorottya Sárkány was supported by the "FM Kutatói Utánpótlás Segítő Program."*

**Effect of phenological growth phase on microbiome diversity in oilseed rape (*Brassica napus* L.), maize (*Zea mays*) and sunflower (*Helianthus annuus*).**

*Renata Artimová*<sup>1</sup>, *Nikola Lipková*<sup>2</sup>, *Jana Maková*<sup>2</sup>, *Soňa Javoreková*<sup>2</sup>, *Juraj Medo*<sup>2</sup>

<sup>1</sup> Research Centre AgroBioTech, Slovak University of Agriculture in Nitra, Slovakia

<sup>2</sup> Institute of Biotechnology, Slovak University of Agriculture in Nitra, Slovakia

The plant microbiome plays a crucial role in plant health and productivity. The interaction between plants, soil and microorganisms is a major driver of ecosystem function, and any changes to the plant surface or soil properties can affect the microbial structure, which in turn affects ecological processes. Bacterial communities inhabit different plant organs, such as leaves or roots, either internally or on their surfaces. This study focuses on the metagenomic analysis of bacterial diversity in non-rhizosphere soil, rhizosphere, rhizoplane and internal plant tissues (roots, stems and leaves) of three crops: oilseed rape (*Brassica napus* L.), maize (*Zea mays*) and sunflower (*Helianthus annuus*). The analysis takes into account different phenological growth stages: BBCH 15, BBCH 55 and BBCH 85. The microbial composition was assessed by amplicon sequencing of the V4 region of the 16S rRNA gene using the Illumina MiSeq platform. Our results show that sample origin (soil, rhizosphere, rhizoplane, root, stem, leaf) significantly influences bacterial diversity, with a substantial part of the variation explained by the interaction between sample origin and phenological growth phase (BBCH). Shannon's diversity index showed similar bacterial diversity in all three crops at BBCH 15 and BBCH 55. However, bacterial diversity was different at BBCH 85, with a decrease compared to BBCH 15 and BBCH 55. The most abundant bacterial classes in all samples were Actinobacteria, Alphaproteobacteria, Betaproteobacteria, Gammaproteobacteria, Sphingobacteria and Spartobacteria. Non-rhizosphere soil, rhizosphere and rhizoplane samples showed a different taxonomic composition compared to internal plant tissues (roots, stems and leaves). Understanding the composition of the microbiome has important implications for agriculture, including improving crop production and reducing the use of chemicals.

**Microbial communities of publicly consumed mineral springs in Transylvania (Romania)**

*István Máthé*<sup>1</sup>, *Zsuzsanna Márton*<sup>2,3</sup>, *Attila Szabó*<sup>3,4</sup>, *Károly Márialigeti*<sup>2</sup>, *Andreea-Rebeka Zsigmond*<sup>5</sup>, *Tamás Felföldi*<sup>2,3</sup>

<sup>1</sup> Department of Bioengineering, Sapientia Hungarian University of Transylvania, Miercurea Ciuc, Romania

<sup>2</sup> Department of Microbiology, ELTE Eötvös Loránd University, Budapest, Hungary

<sup>3</sup> Institute of Aquatic Ecology, Centre for Ecological Research, Budapest, Hungary

<sup>4</sup> Department of Aquatic Sciences and Assessment, Swedish University of Agricultural Sciences, Uppsala, Sweden

<sup>5</sup> Department of Environmental Science, Sapientia Hungarian University of Transylvania, Faculty of Sciences and Arts, Calea Turzii 4, 4400193 Cluj-Napoca, Romania

Spring waters are consumed publicly in many regions around the globe, and their chemical and microbiological quality is determined mainly by the geological, meteorological conditions and by the human activities performed in the surrounding area. This study aimed to reveal the prokaryotic community composition of spring waters in Transylvania in different seasons, which was achieved by Illumina amplicon sequencing targeting the 16S rRNA gene.

The high values of estimated species numbers (~400 for Archaea and ~1000 in the case of Bacteria) indicated that natural mineral waters of Transylvania have a remarkable hidden bacterial diversity. It is important to note that the detected bacteria were mainly not pathogenic but natural (autochthonous) members of mineral waters. The chemolithotrophic iron-oxidizing genus *Gallionella* was detected in the largest amount, while the chemolithoautotrophic *Sulphurimonas*, which is capable of oxidizing sulfur and hydrogen, was also contributed to the prokaryotic community at high relative abundance. The iron-oxidizing *Sideroxydans*, the iron-reducing genus *Rhodoferax*, and the sulfur-oxidizing *Sulfuricurvum* and *Thiotrix* were also important community members. This corresponds well with the chemical results, according to which these waters contain organic matter at very low concentration, therefore bacteria mainly rely on the oxidation and reduction of inorganic compounds. Interestingly, magnetotactic bacteria ('*Candidatus Omnitrophus*') were also important community members. It was observed that several of the studied spring waters were very sensitive to environmental effects, therefore it is important to pay special attention to the preservation of the quality of these springs.

**Disentangling pelagic microbial food web structure in the Baltic Sea**

*Jared Vincent Lacaran*<sup>1,2</sup>, *Anetta Ameryk*<sup>1</sup>, *Janina Kownacka*<sup>1</sup>, *Krzysztof Rychert*<sup>3</sup>, *Vojtech Kasalicky*<sup>4</sup>, *Indranil Mukherjee*<sup>4</sup>, *Usman Asghar*<sup>4</sup>, *Tanja Shabarova*<sup>4</sup>, *Paul-Adrian Bulzu*<sup>4</sup>, *Karel Simek*<sup>4,5</sup>, *Kasia Piwosz*<sup>1</sup>

<sup>1</sup> Department of Fisheries Oceanography and Marine Ecology, National Marine Fisheries Research Institute, ul. Kołłątaja 1, 81-332 Gdynia, Poland

<sup>2</sup> Faculty of Chemistry, Gdańsk University of Technology, ul. Gabriela Narutowicza 11/12, 80-233 Gdańsk, Poland

<sup>3</sup> Pomeranian University in Słupsk, ul. Arciszewskiego 22a, 76-200 Słupsk, Poland

<sup>4</sup> Biology Centre of the Czech Academy of Sciences, Institute of Hydrobiology, Na Sádkách 7, 37005, České Budějovice, Czech Republic

<sup>5</sup> Faculty of Science, University of South Bohemia, 37005, České Budějovice, Czech Republic

Heterotrophic nanoflagellates (HNF) are a polyphyletic protistan group that serve fundamental roles in the carbon flow of pelagic ecosystems through prey-predator interactions. Despite the functional diversity of HNFs being widely recognized, the trophic roles of ecologically relevant groups are far less understood. The current marine microbial food web assumes an almost linear flow of carbon and energy from bacteria via bacterivorous nanoflagellates (NF) to microzooplankton and higher trophic levels. Interestingly, recent studies have shown experimental evidence that NF also feed on other eukaryotes. However, the extent to which NF communities are bottom-up or top-down controlled is still relatively unknown. In this study, we conducted a size fractionation experiment using a native microbial consortium from the Baltic Sea collected during the spring bloom. Our results demonstrated strong top-down control in the Baltic Sea, mostly by ciliates. Addition of the bacteria *Limnohabitans* as bacterial prey induced rapid growth of bacterivores (cryptomonads, *Paraphysomonas*) followed by an increase in predatory and omnivory NF (MAST-2, *Mataza* and *kathablepharids*) in the Baltic Sea. Using catalyzed reporter deposition – fluorescence in situ hybridization (CARD-FISH), we were able to identify different NF phylogenetic groups with *kathablepharids* being the most abundant NF. Our results enhance the understanding of marine microbial food webs, allowing for the fine-tuning of the novel model of marine pelagic processes.



**The impact of long-term adaptation to climate change on marine diatom *Skeletonema marinoi***

Charlotte L. Briddon<sup>1</sup>, Maria Nicoară<sup>1</sup>, Adriana Hegedüs<sup>1</sup>, Adina Niculea<sup>2</sup>, Richard Bellerby<sup>3,4,5</sup>, Wenche Eikrem<sup>3,6</sup>, Bibiana G. Crespo<sup>3</sup>, Sam Dupont<sup>7,8</sup>, Bogdan Drugă<sup>1</sup>

<sup>1</sup> Institute of Biological Research (NIRDBS), Cluj-Napoca, Romania

<sup>2</sup> Taxonomy and Ecology, Faculty of Biology and Geology, Babeş-Bolyai University, Cluj-Napoca, Romania

<sup>3</sup> Norwegian Institute for Water Research, Oslo, Norway

<sup>4</sup> State Key Laboratory of Estuarine and Coastal Research, East China Normal University, Shanghai, China

<sup>5</sup> Faculty of Applied Sciences, UCSI University, Kuala Lumpur, Malaysia

<sup>6</sup> Natural History Museum, University of Oslo, Oslo, Norway

<sup>7</sup> Department of Biological & Environmental Sciences, Kristineberg, Fiskebäckskil, Sweden

<sup>8</sup> Radioecology Laboratory, International Atomic Energy Agency (IAEA), Monaco

Ocean acidification is characterized by the enrichment of seawater with carbon dioxide resulting from fossil fuel burning. This phenomenon, alongside other climatic changes, is affecting marine organisms. Phytoplankton, comprising microalgae, plays a major role in biogeochemical cycles and as the base of aquatic food webs. It is still unclear how diatoms, one of the main groups of marine phytoplankton, will adapt to future challenges.

In this study, we analyzed whether long-term adaptation to ocean acidification and warming would bring *Skeletonema marinoi* an advantage when tested in natural communities and exposed to acidification conditions. We adapted *S. marinoi* for one year to two different temperatures (7, 19°C) and three pCO<sub>2</sub> concentrations (400, 600 and 1000 ppm), which cover the current and the predicted conditions for the middle and the end of the century. Then, we tested the adapted strains in natural communities while exposing them to different scenarios of acidification, by using land-based mesocosms and dialysis bags.

Results showed a high plasticity of *S. marinoi* related to temperature. The growth rates of the strains adapted to a higher temperature showed a higher or similar growth rate with the strains adapted to a lower temperature in the high temperature test condition, excepting the strain adapted to 600 ppm, which showed a higher growth rate in the case of the strain adapted to a lower temperature. In terms of pCO<sub>2</sub>, diatoms showed a lower chlorophyll a concentration and a higher growth rate when exposed to acidification conditions (600 and 1000 ppm). *S. marinoi* also showed a negative response to intense light exposure, as all the strains died shortly after they were exposed to direct sunlight.

Future studies should focus on the effects of climate change upon phytoplankton and consider the adaptation of microalgae to multiple physicochemical factors, while using an environmentally realistic experimental design.

### High herbicide concentration tolerant bacteria in plant growth promotion

Ivana Galic<sup>1</sup>, Iris Bertani<sup>2</sup>, Cristina Bez<sup>2</sup>, Nada Stankovic<sup>1</sup>, Vittorio Venturi<sup>2</sup>

<sup>1</sup> Institute of Molecular Genetics and Genetic Engineering, University of Belgrade, Belgrade, Serbia

<sup>2</sup> International Centre for Genetic Engineering and Biotechnology, Trieste, Italy

Modern agriculture still relies heavily on the use of agrochemicals that are harmful to non-target organisms, including microorganisms. In the global effort to increase agriculture sustainability, there is an emerging need for herbicide-resilient plant growth-promoting (PGP) bacteria that improve essential crops yield. From S-metolachlor-contaminated soils, we isolated 122 strains of high herbicide concentration tolerant (HHCT) bacteria capable of growing on or using herbicide as their sole carbon source. The aim of our study was to identify HHCT bacteria with the highest PGP potential, soil quality improvement ability, biocontrol activity, and plant colonization capability; then combine them into consortia that include all these traits, and test them *in planta*. PGP property evaluation included assays for nitrogen fixation, phosphate solubilization, IAA, siderophore, and exopolysaccharide production, detection of extracellular enzymatic activities, and motility. Strains were identified through 16S rDNA sequencing. Biocontrol potential was evaluated against plant pathogens such as *Fusarium sp.*, and *P. fuscovaginae*. The most promising candidates were combined in three consortia for growth-chamber experiments to investigate the promotion of maize seed germination, early-stage plant development, and root colonization evaluated by metagenomic analysis. The HHCT bacteria showed promising PGP potential. 32% of the collection exhibited 3-4 of four tested direct PGP mechanisms. 22 isolates had antifungal, and 13 had antibacterial activity. The strains with the highest *in vitro* PGP activity predominantly belonged to *Serratia*, *Pseudomonas*, and *Sphingobacterium* genera. These strains formed the most effective consortium that promoted seed germination and increased shoot and root dry weight at the early-stage development.



# Fermentia



**Fermentia Ltd. is an expert in fermentation technology.**

## We have extensive experience in:

- **aerobic** and **anaerobic** fermentation technologies
- **submerged** and **solid-state** fermentation technologies
- working with **bacteria, yeast, algae** and **mammalian** cell cultures

## Our services include:

- **contract fermentation** services
- **downstream processing**
- **development** of new microbial products
- **scale-up** from laboratory-scale to pilot-scale production (10l→100l→1000l fermenters)
- **molecular biological and analytical** monitoring and support of the processes

**Fermentia also has a strong focus on R&D:** our developed microbial products include mainly agricultural and bioaugmentation products. We actively welcome opportunities for research collaborations and joint participation in tenders. Eötvös Loránd University (ELTE) and Technical University of Budapest (BME) are already strategic partners of Fermentia Ltd.

## Three bioaugmentation agents are currently available to our Customers:

- **Ferm&Go 1V:** For chlorinated ethene (tetrachloroethylene/PCE, trichloroethylene/TCE, dichloroethylene/DCE, vinyl-chloride/VC) pollutions
- **Ferm&Go 2PT:** For total petroleum hydrocarbon (TPH) and polycyclic aromatic hydrocarbon (PAH) pollutions
- **Ferm&Go 3P:** For polycyclic aromatic hydrocarbon (PAH) pollutions



**Fermentia Ltd.**

**E-mail:** [info@fermentia.hu](mailto:info@fermentia.hu)

**Web:** [www.fermentia.eu](http://www.fermentia.eu); [www.fermandgo.hu](http://www.fermandgo.hu)

**Address:** Hungary, H-1045 Budapest, Berlini utca 47-49.

**Mobile:** +36 30 350 2847; **Phone:** +36 1 369 6024

The logo for TargetEx Biosciences features the word "TargetEx" in a red, lowercase, sans-serif font, followed by "BIOSCIENCES" in a black, uppercase, sans-serif font. To the right of the text is a stylized graphic consisting of a central red dot with four black arrows pointing towards it from the top, bottom, left, and right. Above the logo, there are several concentric circles of varying shades of gray, and a large, light gray arrow points downwards from the top left towards the center of the page.

# TargetEx

## BIOSCIENCES

TargetEx Ltd is a leading service provider and product manufacturer with over 20 years of collaborative R&D experience, integrating capabilities in protein expression & purification, cell line generation and target-based assay development.

Our protein production services include recombinant DNA work, protein expression, refolding, purification, analytics and activity determination. We have a proven track record in recombinant protein generation for nucleic acid-based diagnostics, for various formulations of vaccine antigens, for therapeutic antibodies, and for models of drug targets.

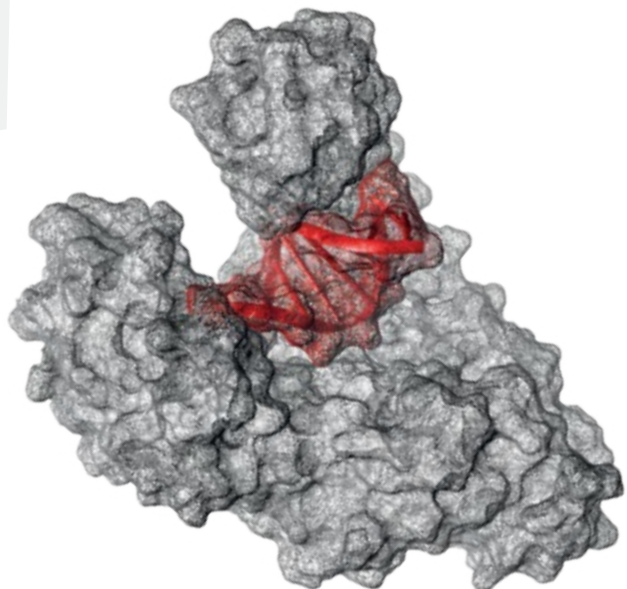
We strive to deliver high quality but cost-effective solutions throughout your R&D efforts with our suite of advanced protein engineering, manufacturing and screening capabilities. Our efforts have recently been rewarded with the 2022 'From Basic Research to Market' Innovation Award from the National Research, Development and Innovation Office of Hungary.



website



linkedin





# Rethink what is possible

## Orbitrap Astral mass spectrometer

Realize the promise of proteomics at scale to better understand biology and disease mechanisms with the novel technology of the Thermo Scientific™ Orbitrap™ Astral™ mass spectrometer. Powered by the synergy of the high resolution quadrupole mass filter, Thermo Scientific™ Orbitrap™ mass analyzer and the novel Thermo Scientific™ Astral™ mass analyzer, this revolutionary new instrument achieves unsurpassed performance with industry leading usability. The combination of these three mass analyzers enables the rapid acquisition of exceptional quality high resolution accurate mass (HRAM) data with high sensitivity and dynamic range. Expect whole proteome coverage at a depth of 12,000 proteins in an hour, the sensitivity to accurately and precisely quantify over 3,000 proteins from 80 single cells in a day and the throughput to analyze over a million protein groups across 180 samples in a day.

- **Faster throughput** – identify over 8,000 proteins with an 8-minute injection-to-injection cycle
- **Deeper coverage** – unlock near whole-proteome depth of coverage with the identification of 12,000 proteins in 1 hour from a single-shot experiment
- **Higher sensitivity** – increase throughput and depth of coverage with higher sensitivity by identifying over 5,000 proteins from 130 pg of HeLa at a rate of 80 samples per day
- **Accurate and precise quantitation** – achieve accurate and precise quantitation with a large dynamic range for label-free Quantitation (LFQ) using Data Independent Acquisition (DIA) and achieve faster throughput and deeper coverage with multiple quantitation using Tandem Mass Tags (TMT)

These ground-breaking capabilities empower you to comprehend the dynamic, temporal and spatial complexity of biology.



## **Thermo Fisher és Zymo Research termékek széles választéka a Biocenternél!**

Laboratóriumi fogyóeszközök és reagensek

Szekvencia-specifikus nukleinsav termékek

Sejtkultúra

Fehérje és sejt analízis

Laboratóriumi műszerek

Mintavételi eszközök nukleinsav izoláláshoz

Molekuláris biológia és nukleinsav analízis

Mikrobiális és DNS Standardok

Mikrobiom és metagenom analízis



Aktuális akcióinkért olvassa be a QR kódokat:

**Thermo Fisher akciók:**

**Zymo Research akciók:**



További információ:

[info@biocenter.hu](mailto:info@biocenter.hu)

+36/62-599-750

# Partners and Sponsors

