20th Cyanophyte/Cyanobacteria Research Symposium

28th August to 2nd September 2016

Program & Abstracts

Institute of Botany

University of Innsbruck

AUSTRIA

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Program & abstracts

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Foreword

I wish to express my warm welcome to all participants, both those with a long-term involvement with the IAC and those new to this informal group of scientists.

At this 20th IAC we have tried to follow the tradition of earlier IAC Symposia by: keeping the group small, in contrast to large congresses. Everyone can then take part in the scientific program without any parallel sessions. It also permits hands-on activities together with discussion of fundamental problems and facilities for cyanobacteria / cyanophyte research. It should help to make clear and resolve any discrepancies between the rich knowledge that has come from studies of the organisms in their natural habitats versus the results from sophisticated modern methods. There will be many opportunities to discuss fundamental theories and particular topics and the classroom with 27 microscopes permits this be done for light microscopy.

The tradition of discussions stimulated by field excursions in overwhelming alpine landscapes goes back to the very roots of the IAC in 1959, when there was a field visit (linked to the SIL Congress in Vienna, Austria) to the Traunsee to collect samples from the littoral and plankton. The visit to this large peri-alpine lake in Upper Austria involved Prof. Otto Jaag and Dr. Edith Kann, both of whom went on to be a driving force for IAC’s future.

In the present meeting we will show you sites of special interest to us in N-Tyrol, where we have sampled over several years. These include central alpine high altitude streams and northern calcareous streams and springs. In the early days observations from the field were at the center of interest, though with a gradually increasing interest in cultures and life cycles. More recently many new and successful methods have been developed, especially biochemical, ultrastructural and molecular genetic analyses. However the multitude of these approaches sometimes tends to obscure the search for potential or missing phylogentic relationships. I suggest there is a risk overestimating the stability of conclusions from these studies and to approaches becoming somewhat fossilized. This meeting provides a good opportunity to bring together controversial views on the interpretation of genetic markers and their natural variability and evolutionary lineages in order to find solutions likely to help future progress.

My wish is that all participants will find the meeting a rewarding time, both scientifically and personally. Please let us know early in the meeting if you think there are ways the program could be made even more helpful.

Eugen Rott, August 2016

Program of the 20th IAC Symposium 2016

Sunday, 28th August 2016

17:00 – 19:30: REGISTRATION (lecture hall B, ground floor, main building) and MOUNTING OF POSTERS (2nd floor, new building)
17:00 – 20:00: ICEBREAKER for all (Botanical Garden near the IBI; drinks, snacks and jokes are served.

Monday, 29th August 2016

From 8:30: REGISTRATION of participants (lecture hall B, main building of IBI)
9:00 – 9:30: Welcome addresses by the Vice Rector of Research Univ. Prof. Sabine SCHINDLER, the Head of Institute of Botany Univ. Prof. Klaus OEGGL and the organizer.

Session 1: Functional molecular biology and phylogeny of cyanophytes / cyanobacteria

(Chair: TURNER Séan)

9:30 – 10:00: MAKOWER K., SCHUURMANS J. M., MATTHIJS H. C.P., GROTH D., **DITTMANN** E.: Plasticity and interaction of bloom-forming cyanobacteria of the genus *Microcystis*. (KEYNOTE)
10:00 – 10:20: KURMAYER R., HOLZINGER A., ROTT E: Single colony genetic analysis of epilithic stream algae of the genus *Chamaesiphon* sp.

10:20 – 10:50 COFFEE BREAK

10:50 – 11:20: **GOLUBIC** S., PALINSKA K., KLEINTEICH J., RADTKE G.: Nature and culture based sources in cyanobacterial diversity and phylogeny. (KEYNOTE)
11:20 – 11:40: McGREGOR G. B., SENDAL B. C.: Novel cyanobacterial lineages from crenic habitats of north-eastern Australia.
11:40 - 12:00: ADHIKARY S. P.: Diversity of cyanobacteria on stone monuments of cultural heritage in India and their molecular phylogeny.
12:00 – 12:20: Short 5 min. PRE-PRESENTATIONS OF POSTERS TO SESSION 1 (GENUARIO BONALDO, LORENZI, SAHU, SANT'ANNA), lecture hall A

12:20 – 14:30: LUNCH BREAK (on your own)

14:30 – 14:50 POSTER PRESENTATION of SESSION 1 on 2nd FLOOR, new building.

Session 2: Biogeography of cyanophytes / cyanobacteria

(Chair: HAUER Tomáš)

14:50 – 15:20: **JOHANSEN** J.R.: Do cyanobacteria have biogeography? Some observations on geographically restricted areas. (KEYNOTE)
15:20 – 15:40: BOHUNICKÁ M., MAREŠ J., HAUER T., KOMÁREK J., ŠTENCLOVÁ L., ZIMA J., BECERRA-ABSALÓN I., JOHANSEN J. R.: Biogeography of the recently described pantropical genus *Brasilonema* Fiore et al. (Nostocales, Cyanobacteria).
15:40 – 16:00: KAŠTOVSKÝ J.: The cyanobacterial flora from the Venezuelan Table Mountains.

16:00 – 16:20: SMIRNOVA S., BELJAKOVA R.: Species of the genus *Stichosiphon* (Cyanoprocaryota) from Russia.

16:20 – 16:50: COFFEE BREAK

16:50 – 17:20: D'ACQUI L. P., MASCALCHI C., SILI C., **VENTURA** S.: Cyanobacteria in polar habitats in the Arctic and Antarctic (KEYNOTE)

17:20 – 18:20: **ROUND TABLE 1**: Systematics and taxonomy of cyanobacteria in the light of new methodology (Moderator: GOLUBIC Stjepko)
With members of the scientific committee invited for statements and open discussion for all.

From 18:20 **OPTIONAL MICROSCOPY** (classroom 2, ground floor, new building)

Tuesday, 30th August 2016

Session 2: Biogeography (continued)

(Chair: WHITTON Brian)

9:00 – 9:30: **GUTOWSKI** A., FOERSTER J.: Cyanobacteria in running waters of Germany. (KEYNOTE)

9:30 – 9:50: WILLÉN E., ZANGA N., WILANDER A.: Lake Tumba and Mai Ndombe, two large, acid, blackwaters in DR Congo – pioneer phytoplankton studies with focus on small chroococcal cyanobacteria.

9:50 – 10:20: Short 5 min. PRE-PRESENTATIONS OF POSTERS TO SESSION 2 (CHATCHAWAN, DAVYDOV, GAYSINA, LEON-TEJERA, POPIN, VOGT) in lecture hall A

10:20 – 10:50: COFFEE BREAK

10:50 – 11:20: POSTER PRESENTATION of SESSION 2 on 2nd FLOOR, new building.

Session 3: Systematics and taxonomy of cyanobacteria / cyanophytes

(Chair: DITTMANN Elke)

11:20 – 11:50: **KOMÁREK** J.: Important taxonomic changes in the modern cyanobacterial system according to the polyphasic approach. (KEYNOTE)

11:50 – 12:10: BERRENDERO-GÓMEZ E., JOHANSEN J.R., BOHUNICKÁ M., KAŠTOVSKÝ J.: A taxonomic study of the *Calothrix*-group based on polyphasic approach.

12:10 – 12:30: MÜHLSTEINOVA R., HAUER T.: Seeking the true *Oscillatoria*.

12:30 – 14:30 LUNCH BREAK (on your own)

14:30 – 15:00: **MAREŠ** J.: Molecular taxonomy of cyanobacteria in the genomic aera (KEYNOTE)

15:00 – 15:20: PRÖSCHOLD T., ALBRECHT M.: IST/CBC approach for classification of cyanobacteria.

15:20 – 16:00: **TURNER** S., SKIPPINGTON E., PRYER K., PALMER J.: Large ribosomal subunit RNAs of cyanobacteria exist in two forms: implication for phylogenetic analysis. (KEYNOTE).

16:00 – 16:30 **KUSBER** WH., JAHN R.: Cyanophyta vs. cyanobacteria: how to deal with two different sets of nomenclatoric rules in taxonomy, biodiversity informatics and practice. (KEYNOTE)

16:30 – 17:00: COFFEE BREAK

17:00 – 18:00: **ROUND TABLE 2**: Systematics and taxonomy of cyanobacteria in the light of novel methodology (Moderator: GOLUBIC Stjepko)
With members of the scientific committee and open discussion for all.

From 18:00 **OPTIONAL MICROSCOPY** (classroom 2, ground floor, new building)

Wednesday, 31 August 2016:

ALL DAY EXCURSIONS 1 and 2 with CYANO-SAMPLING FACILITIES (see separate informations for equipment, departures etc.) LATEST RETURN 18 h

20.00 – 22:00: INVITATION TO CHAMBER MUSIC EVENING in the green house of the botanical garden featuring: **String Quartett of the Innsbruck Symphony Orchestra** (Snacks and drinks will be offered during the break - Please: Reserve seats for the elderly!)

Thursday, 1st September 2016:

Session 3: Systematics and taxonomy (continued)

(Chair: MAREŠ Jan)

9:00 – 9:25: Short 5 min. PRE-PRESENTATIONS OF POSTERS TO SESSION 3 (HAUER, HENTSCHKE, SABER, VONDRÁŠKOVÁ, WILMOTTE) in lecture hall A

9:25 – 9:50: POSTER PRESENTATION of SESSION 3 on 2nd FLOOR, new building.

Session 4: Biocalcification of cyanobacteria and related topics

(Chair: McGREGOR Glenn)

9:50 – 10:20: **PENTECOST** A.: Cyanobacteria phosphate-calcite interactions in freshwater. (KEYNOTE)

10:20 – 10:40: PALINSKA K. A., BRANDES M., ALBACH D. C., VOGT J. C., ABED R., RADTKE G., GOLUBIC S.: Microbial, marine eu-endoliths: morphological vs. molecular diversity.

10:40 – 11:10: COFFEE BREAK

11:10 – 11:40: **SANDERS** D.: Cyanobacterial colonization and desert stromatolites in cliffs of carbonate rocks: sedimentology calling for biology. (KEYNOTE)

11:40 – 12:00 ZAMMIT G.: New genera of sciaphilous cyanobacteria from the Maltese islands.

12:00 – 12:25: Short 5 min. PRE-PRESENTATIONS OF POSTERS TO SESSION 4 (HERBURGER, TRAN, PIETRASIAK, SCIUTO, VILLANUEVA) in lecture hall A

12:25 – 12:50 POSTER PRESENTATION of SESSION 4 on 2nd FLOOR, new building.

12:50 – 14:40 LUNCH BREAK (on your own)

Session 5: Functional ecology and biodiversity of cyanobacteria / cyanophytes and other microbes

(Chair: PALINSKA Katarzyna)

14:40 – 15:10: **SATTLER** B.: ICE & LIFE – living cryosphere. (KEYNOTE)

15:10 – 15:30: DEBNATH M.: Spatial distribution pattern of cyanobacteria along ambient to extreme biotopes: study from sea level to high mountain (West Bengal, India).

15:30 – 15:50: PERONA E., BENICHOU F., ÁLVAREZ C., MACIAS B., GONZÁLEZ L., MUÑOZ M. Á., MATEO P.: Effects of temperature on cyanobacterial growth.

15:50 – 16:10: PESSI I. S., PUSHKAREVA E., BORDERIE F., ELSTER J., WILMOTTE A.: Successional trajectories of cyanobacterial communities following glacier retreat in Svalbard (High Arctic).

16:10 – 16:40: COFFEE BREAK

16:40 – 17:00: BAUER F., FLEISCHMANN N., RAEDER U., GEIST J., ZWIRGLMAIER K.: Impact of global warming on freshwater cyanobacteria in Bavaria.

17:00 – 17:20: RUBER J., RAEDER U., GEIST J., ZWIRGLMAIER K.: Small but powerful: Distribution of *Synechococcus* in the Osterseen Lake District in Southern Germany.

17:20 – 18:20: **ROUND TABLE 3**: Systematics and taxonomy of cyanobacteria in the light of novel methodology (Moderator: GOLUBIC Stjepko)
With members of the scientific committee and open discussion for all.

18:20 – 19:20: **OPTIONAL MICROSCOPY** (demonstration of excursion field samples, classroom 2, ground floor, new building) and
optional **MOLDAENKE FLUORESCENCE PROBE demonstration**
(Fa. SCHOBER and organizer, classroom 1, basement floor, new building)

From 20:00: **EVENING GET TOGETHER at STIFTSKELLER** in town
(We invite you for a modest dinner and one beer or soft drink).

Friday, 2nd September 2016

Session 5: Functional ecology (continued)

(Chair: HOLZINGER Andreas)

9:00 – 9:20: **ROTT** E.: Diversity and niche differentiation of cyanobacteria across water and light gradients in cascades, springs and rivers of the Eastern Alps in Austria. (KEYNOTE)

9:20 – 9:40: ČAPKOVÁ K., ŘEHÁKOVÁ K., ČAPEK P., MAREŠ J., DOLEZAL J.: Biological soil crusts of W Himalaya – metabolic activity of microbial community.

9:40 – 10:15: Short 5 min. PRE-PRESENTATIONS OF POSTERS TO SESSION 5 (AIGNER, CORDEIRO-ARAUJO, KOMAREK O.; NIIYAMA, PATOVA, PEREZ, SAFIULINA) in lecture hall A

10:15 – 10:50: POSTER PRESENTATION of SESSION 5 on 2nd FLOOR, new building.

10:50 – 11:20: COFFEE BREAK

11:20 – 12:10: **2nd MICROSCOPY SESSION** (classroom 2, ground floor) and
optional second demonstration of **MOLDAENKE PROBES** (classroom 1, basement floor).

12:10 – 13:00: CLOSING SESSION including OBITUARIES, PLANNING of FUTURE MEETINGS and PUBLICATION of meeting contributions.

13:00: FAREWELL

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Numbers are poster numbers, underlined authors will give the poster pre-presentation

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2 LORENZI Adriana Sturion, SILVA Genivaldo Gueiros Z., LOPES Fabyano Alvares C., CHIA Mathias Ahii, EDWARDS Robert A., BITTENCOURT-OLIVEIRA Maria do Carmo
Cyanobacterial blooms in Brazilian semiarid reservoirs assessed via next-generation DNA sequencing technology

3 SAHU Jayanti K., KUMAR Dhanesh, KAŠTÁNEK Petr, ADHIKARY Siba P
Diversity of cyanobacteria in biological soil crusts on arid soils in the eastern region of India and their molecular phylogeny

4 WERNER Vera R., GAMA WATSON Arantes, RIGONATO Janaina, AZEVEDO M.Teresa P., FIORE Marli F., SANT’ANNA Célia L.
Sphaerocavum: a coccoid morpho-genus that showed to be identical to *Microcystis* in terms of 16S rDNA and ITS phylogeny

Session 2: Biogeography of cyanophytes / cyanobacteria

5 CHATCHAWAN Thomrat, INKHA WANNAWONG Sirisopha, SUSAWAENGSUP Chantana
Diversity and distribution of cyanobacteria from tropical paddy fields in some areas of Thailand.

6 DAVYDOV Denis, PATOVA Elena
The diversity of cyanoprokaryota from freshwater and terrestrial habitats in the Eurasian Arctic and Subarctic

7 GAYSINA Lira, BOHUNICKÁ Markéta, JOHANSEN Jeffrey R.
Biodiversity of terrestrial cyanobacteria of the South Ural region

8 LEÓN-TEJERA H., GONZÁLEZ-RESENDIZ L., JOHANSEN J.R.
Benthic marine heterocytous cyanoprokaryotes (cyanobacteria) from the coast of Mexico

9 POPIN Rafael Vicentini, ABREU Vinicius Augusto Carvalho de, RIGONATO Janaina, DÖRR Felipe Augusto, PINTO Ernani, FIORE Marli Fatima
Comparative genomics of toxigenic *Nodularia spumigena* strains from geographically distant origin

10 VOGT Janina C., ABED Raeid M., PALINSKA Katarzyna A., ALBACH Dirk C.
Microbial diversity in hypersaline Oman tidal flats

Session 3: Systematics and taxonomy of cyanobacteria / cyanophytes

11 HAUER Tomáš, MARES Jan, MÜHLSTEINOVÁ Radka, VONDRÁŠKOVÁ Alžběta
Phylogenetic position of the genus *Kyrtuthrix* Ercegović within the order Nostocales

12 HENTSCHKE Guilherme Scotta, JOHANSEN Jeffrey R., PIETRASIAK Nicole, RIGONATO Janaina, FIORE Marli F., SANT’ANNA Célia L.
Komarekiella atlantica gen. et sp. nov. (Nostocaceae, Cyanobacteria): a new subaerial taxon from the Tropics.

13 SABER Abdullah Antar, CANTONATI Marco, MAREŠ Jan, ANESI Andrea, GUELLA Graziano
Multifaceted characterization of *Westiellopsis prolifica* (Cyanobacteria) from the El-Farafra Oasis (Western Desert, Egypt)

14 VONDRÁŠKOVÁ Alžběta, HAUER Tomáš, MAREŠ Jan, JOHANSEN Jeffrey R.
Molecular characterization of four cyanobacterial genotypes from their type localities in Scandinavia

15 WILMOTTE Annick, RENARD Marine, LARA Yannick, DURIEU Benoit, SIMONS Véronique, LAUGHINGHOUSE Dail, CORNET Luc, BAURAIN Denis
The BCCM/ULC collection to conserve and study the biodiversity of polar cyanobacteria

Session 4: Biocalcification of cyanobacteria and related topics

16 HERBURGER Klaus, AIGNER Siegfried, ROTT Eugen, HOLZINGER Andreas
Pseudoscytonema sp., a calcite-precipitating macroscopic niche-forming cyanobacterium from a seepage spring in the Alps. Part 1: Ecophysiology and cell biology

17 TRAN Ha, ROTT Eugen, KOFLER Werner, SANDERS Diethard
Pseudoscytonema sp., a calcite-precipitating cyanobacterium forms macroscopic stromatolites in a seepage spring in the Alps. Part 2: Calcite sedimentology and environment

18 PIETRASIAK Nicole, STOVALL Megan, SHALYGIN Sergei, JOHANSEN Jeffrey
Subaerial epilithic cyanobacteria from Yosemite National Park, California, USA

19 SCIUTO Katia, MOSCHIN Emanuela, MORO Isabella
Polyphasic characterization of three *Leptolyngbya*-like strains from the Giant Cave (Trieste, Italy)

20 VILLANUEVA Chelsea, HÁSLER Petr, CASAMATTA Dale
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Session 5: Functional ecology and biodiversity of cyanobacteria / cyanophytes and other microbes

21 AIGNER Siegfried, HERBURGER Klaus, HOLZINGER Andreas, ROTT Eugen
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22 CORDEIRO-ARAÚJO Micheline K., CHIA Mathias A., BITTENCOURT-OLIVEIRA Maria do Carmo
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24 NIIYAMA Yuko, TUJI Akihiro
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25 PATOVA Elena, SIVKOV Michail
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26 PÉREZ M. C., BONILLA S., HAAKONSSON S., AROCENA R.
Dynamics of Chroococcales and Nostocales in a turbid subtropical estuary: Río de la Plata, South America

27 SAFIULLINA Liliya, ZAKIROVA Mariia
Cyanobacteria of some Arctic regions, and low temperature resistance of *Nostoc sp.*

ORAL CONTRIBUTIONS

Diversity of cyanobacteria on stone monuments of cultural heritage in India and their molecular phylogeny

ADHIKARY Siba Prasad

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Several stone temples and mortar monuments with artistic expression in almost all parts of India are now disfigured due to colonisation by cyanobacteria biofilms enhancing weathering processes. They are composed mainly of the cyanobacteria *Hassallia, Scytonema, Tolypothrix, Calothrix* and *Lyngbya*, with the relative abundance of these genera depending on substratum and exposure to solar irradiance. The organisms adhere tightly to the substratum and are difficult to remove during the hot summer months. However, renewed growth occurs soon after being wetted with monsoon rain. Several other species of other genera (*Nostoc, Gloeocapsa, Camptylonema, Chroococcidiopsis, Dichothrix, Chlorogloeopsis, Aulosira* and *Westiellopsis*) occurred as associated organisms as shown by their appearance upon prolonged culture of the biofilms. Molecular phylogenetic analysis based on 16SrRNA partial gene sequencing (PCR, 500 BP) of 24 of these cyanobacteria from 11 genera isolated from stone and mortar monuments from different regions of India along with those of other cyanobacteria isolated from similar substrata in other parts of the world showed that the tropical species clustered together differently from those in temperate regions. It was also observed that harsh conditions typical of the dry season in almost all regions of India significantly reduced the biodiversity of the phototrophic microflora on the surface of the monuments in comparison with the rainy season.

Impact of global warming on freshwater cyanobacteria in Bavaria

BAUER[1] Franziska R., FLEISCHMANN[1] Nadja, RAEDER[1] Uta, GEIST[1] Jürgen, ZWIRGLMAIER[1,2] Katrin

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Climate change and global warming have ecological consequences for cyanobacteria in marine environments and freshwater. Cyanobacterial dominance and the incidence of harmful algal blooms, as well as the spreading of invasive species such as *Cylindrospermopsis raciborskii* in temperate regions, is predicted. The aim of this study was to investigate the impact of climate change, particularly increasing temperatures, on the prevalent cyanobacterial community structures in selected Bavarian lakes. An innovative study design was used to gain more detailed information on that. We hypothesized (1) that the community structures of cyanobacteria in Bavarian lakes will shift towards bloom-forming species due to global warming and (2) that the intensity of these effects is dependent on the season, which is influenced the most by the increasing temperatures. We conducted eight-week aquarium experiments with water derived from two small lakes with different characteristics: Lake Ostersee (oligo-mesotrophic, clear) and Lake Bergknappweiher (eutrophic, turbid). Global warming was simulated by incubating the water in climate chambers with increased temperatures (initial temperature + 5°C/+ 10°C) compared to the controls at three time points in the annual cycle: in spring, summer and autumn. The changes in community structures were analyzed by PCR-ELISA. This test method was developed to identify bloom-forming genera (e. g. *Microcystis sp.*) based on reverse hybridization of 16S rRNA targeted probes. The results are complemented by Illumina MiSeq sequence data of the whole cyanobacterial community of the aquariums and the lakes. By the replacement of pure culture with open water aquarium experiments, the impact of global warming on cyanobacterial community structures could be analyzed directly in their natural composition.

A taxonomic study of the *Calothrix* group based on a polyphasic approach

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Heterocytous, tapering cyanobacteria have been shown in past studies and in the present one to be polyphyletic, forming many different clades. A clear example of this is the genus *Calothrix*. All noncolonial tapered heterocytous filaments would key to *Calothrix*, even though molecular data show that growth form types *Calothrix* are represented in several distinct clades. The type species of *Calothrix* is marine, and is characterized as having a single basal heterocyte, no akinetes, and distal ends tapering abruptly into a short hair. Unfortunately, there is not molecular data for this typical morphotype. Our main aim was to realize a taxonomic revision of the genus *Calothrix* in depth using a polyphasic approach, based on morphological evaluation, feature of habitat, biogeography and phylogenetic analysis of the sequences of the 16S rRNA gene and 16S–23S rRNA intergenic spacer regions. Besides the latter, the phylogenetic resolution was improved by sequencing of two more phylogenetic markers (*rpoC1*, *rbcLX*) on a smaller selection of representative strains. In this study, more than 80 tapering cyanobacteria, including freshwater and marine representatives, were analyzed. The marine *Calothrix* fell into two lineages, but we lack the generitype and so cannot identify the clade corresponding to the type species. The freshwater and soil *Calothrix* fell into the *C. parietina* clade and are characterized by having a basal heterocyte, no akinetes, and gradual tapering trichomes — but not extended into a long hyaline hair. Recently, we have described the new genus *Macrochaete*, a freshwater sister taxon to the *Calothrix* lineages. The species in this genus differ morphologically from *Calothrix* by the ability to produce two heteromorphic basal heterocytes, specific secondary structures of the 16S–23S ITS and the presence of a distal, long hyaline hair in most species. The taxonomic status of the above mentioned groups and their relationships to other *Calothrix*-like tapering genera are discussed in detail.

Biogeography of the recently described pantropical genus *Brasilonema* Fiore et al. (Nostocales, Cyanobacteria)

BOHUNICKÁ[1] Markéta, MAREŠ[1,2] Jan, HAUER[1,3] Tomáš, KOMÁREK[1,3] Jiří, ŠTENCLOVÁ[3] Lenka, ZIMA[2] Jan, BECERRA-ABSALÓN[4] Itzel, JOHANSEN[3,5] Jeffrey R.

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Brasilonema was separated from *Scytonema* only in 2007 (Fiore et al. 2007, J. Phycol. 43). Its diagnostic morphological characteristics include vacuole-like structures in older cells, frequent purple pigmentation of the cells, rare false branching and fasciculate growth of filaments. *Brasilonema* has so far always been found attached to the substrate in aerophytic habitats, exclusively in (sub)tropical countries (Brazil, Guadeloupe, Hawaii, Mexico). We have gathered around 70 new *Brasilonema* strains from North, Central and South America, central Africa, South and East Asia and Europe. We applied a polyphasic approach to their examination. All taxa were first examined morphologically and subsequently their relationships were tested using the 16S rRNA gene sequence together with three other phylogenetic markers (*nif*D, *rpo*C1, *rbc*LX). The results revealed close relationships between specimens obtained from very distant localities (different continents) as well as phylogenetic distance between single *Brasilonema* strains collected from the same biotope. Although largely overlooked (or incorrectly identified), our results provide evidence that *Brasilonema* is an easily morphologically distinguishable genus, common in all tropical and subtropical regions with humid climate and can be found also in tropical greenhouses, power-plant cooling towers and other suitable habitats in other climatic regions. Based on our results we conclude that *Brasilonema* is a pantropical genus, there are no geographical constraints in its dispersal. Its absence in natural habitats of the colder climatic zones may possibly be caused by intolerance to winter freezing.

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Biological soil crusts of W Himalaya – metabolic activity of microbial community

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Our study investigates biological soil crusts (BSCs) in the high mountain cold desert of Tibetan Plateau (W Himalaya, Ladakh). Biological soil crusts, which consist of communities of phototrophic and heterotrophic microorganisms, are an important component of the arid regions (West 1990). Through their ecosystem functions (soil fixation, decomposition, photosynthesis), BSCs affect physico-chemical properties of the soil. Cyanobacterial communities (as first colonizers of high-mountain soils) influence nutrient availability for vascular plants, and water and nutrient status of plants (Řeháková et al. 2011).

We have investigated the BSCs from many perspectives. We studied diversity and biomass of the heterotrophic and phototrophic part (Cyanobacteria) of their microbial community on the elevation gradient 4500 - 6000 m a.s.l., the influence of soil physico-chemical properties on biomass and composition of cyanobacterial community. The production of lipopeptides as a group of bioactive secondary metabolites typical for biofilm-associated cyanobacteria was investigated as well. The ability of BSCs to fix molecular nitrogen was determinate.

The aim of our present study is to quantify photosynthetic and heterotrophic activity of BSCs from the subnival zone of Tibetan Plateau. The presence of microbial crusts in extreme ecosystems promotes the development of higher plant vegetation (Schmidt et al. 2008). However, microbial communities in BSC can only supply the environment with nutrients when they are in an active state. We hypothesize that the most important factors which influenced the metabolic activity of BSCs are the combined effect of temperature and moisture. We measured BSC production and consumption rates of CO_2 /O_2 in situ and in the field under different temperatures and moisture levels and at light/dark conditions to separate metabolic activity of heterotrophs/autotrophs from each other. We measured significant environmental characteristics (soil temperature, moisture, amount and stoichiometry of soil nutrients) to propose a numerical model to estimate the overall metabolic activity of BSCs.

Cyanobacterial spatial distribution patterns along environmental gradients from the coastal areas to the high mountains including extreme biotopes of West Bengal (India)

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Cyanobacteria from all biogeographic regions of West Bengal State, India along a distance of 750 km from the southern coastal plains to the high mountains in the northern extremes (up to 3594.81 meters were surveyed. Species distribution in different environmental regime will be represented emphasizing temperature, moisture, salinity and trophic status. Cyanobacterial communities from coastal, estuarine, alluvial plain, lateritic soil, thermal spring, terai region and eastern Himalayan high-mountain habitats, were documented. Environmental variables of soil, water or subaerial habitats such as temperature, relative humidity, light intensity, pH, electrical conductivity, salinity, major ions, dissolved oxygen, nitrogen and phosphate were analysed either *in situ* or *ex situ* following standard protocols. Distinct cyanobacterial species compositionwas observed in the respective niches. A conservative enumeration revealed 57 cyanobacterial taxa: 13 Chroococcales, (5 genera), 27 Oscillatoriales (11 genera), and 15 Nostocales (6 genera). Taxa were identified by LM using morphology and morphometry assessments across habitats. All planktic cyanobacteria were non-heterocystous, except the bloom forming *Anabaenopsis* sp. and *Aphanizomenon* sp. in fresh water ponds. *Merismopedia* was dominant in fresh and *Synechococcus-Synechocystis* in brackish and thermal spring waters. *Coleofasciculus cthonoplastes* was the dominant on tidal mud flats, followed by *Geitlerinema* spp. Soil crusts from all biotopes surveyed, were dominated by simple trichal morphotypes (*Geitlerinema* spp., *Oscillatoria* spp. and *Phormidium* spp.) in early stage but successively replaced by sheathed morphotypes of *Lyngbya* spp.,*Scytonema* spp., and *Nostoc* sp. Species of *Nostoc* were well represented in rice fields. Lithophytic communities were characterized by species with thick sheath and mucilage such as *Petalonema* sp. and *Nostochopsis lobata*. In subaerial habitats, sheathed cyanobacteria such as *Lyngbya*, *Porphyrosiphon*, and *Scytonema* were prevalent. Seasonal variation and tree bark specificity was also noted along gradients of longitude and elevation. Unique species composition dominated by simple trichal Oscillatoriales was documented from the habitats that were thermally most extreme. True-branching morphotypes were rare in all habitats.

Plasticity and interaction of bloom-forming cyanobacteria of the genus *Microcystis*

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Microcystis is one of the most widespread bloom-forming cyanobacteria in freshwater ecosystems. Sequencing analyses have revealed a mosaic-like structure of *Microcystis* genomes consisting of a highly conserved core genome and a flexible genome portion. The different genotypes form heterogeneous populations comprising a large pan-genome. Flexible genome portions encode e.g. components of the cell surface, the carbon concentrating mechanism and variable secondary metabolite biosynthetic pathways (Humbert *et al*., PLoS One 2013). We have investigated the role of intercellular signals in the expression of genes in axenic laboratory strains as well as in field colonies additionally comprising heterotrophic bacteria using transcriptome and metabolome analyses. Our results reveal an intra- and interspecific cross talk of secondary metabolites among *Microcystis* strains (Makower et al., Appl. Environ. Microbiol. 2015). Co-cultivation of an axenic laboratory strain with exudate of a xenic non-toxic field strain led to a significant global response in the gene expression. Remarkably, the interaction mostly affected genes assigned to the flexible genome portion e.g. encoding components of the cell surface, the carbon concentrating mechanism and secondary metabolite pathways. Together, these data suggest a multi-faceted interaction and interdependence of *Microcystis* strains. *Microcystis* strains in lakes may represent a heterogeneous master community whose plasticity reflects the extent of competition and facilitation between individual genotypes.

(Keynote presentation)

Nature to culture sources in cyanobacterial diversity and phylogeny

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Microbial diversity analysis is based on two long-standing traditions. One is based on medical treatments of pathogenic microorganisms in humans and domestic animals, the other on biology of the environment. Both approaches have more than a century long tradition (Robert Koch – Ferdinand Cohn), but the approaches are still in the process of reconciliation. Molecular techniques of gene sequencing became the principal stimulus in this process, as were the culture-independent applications of molecular tools. The insights in microbial diversity that resulted from these developments represent the main task in the studies of the process of microbial speciation for which cyanobacteria serve as a useful model due to their distribution, relatively complex structure and ecological importance.

(Keynote contribution)

Cyanobacteria in running waters of Germany

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A method called ‘PHYLIB’ exists in Germany to assess the ecological status of running waters by means of the composition and abundance of the aquatic flora. It considers three components: aquatic macrophytes, benthic diatoms, and benthic non–diatomaceous algae (http://www.lfu.bayern.de/wasser/gewaesserqualitaet_seen/phylib_englisch/ index.htm). The assessment routine is based on the registration of morphospecies in their natural habitat linking these data to the knowledge about their ecological and physiological tolerances and preferences. After 15 years of application, data from more than 5.600 sampling events for benthic non–diatomaceous algae are now being analysed within a project financed by the German Environment Agency (UBA) in cooperation with the University Duisburg/Essen. Cyanobacteria constitute about 1/3 of all records, most taxa belonging to Chroococcales or Oscillatoriales. Most frequent is *Pleurocapsa minor* found in more than 20% of all sampling events in nearly all types of running waters. *Chamaesiphon incrustans*, *Phormidium incrustatum*, *Homoeothrix varians and H. janthina* occur in 10 to 14 % of all sampling events, but their occurrence differs considerably with respect to geochemistry and, hence, river type. As expected, *H. janthina* is recorded most frequent in siliceous types and *H. varians* and *Ph. incrustatum* in calcareous types, respectively. Among the rare cyanobacteria, e.g., *Nostoc parmelioides* was found only in siliceous streams. In addition, many species turned out to be very sensible indicators with regard to trophic and saprobic levels or otherwise disturbed conditions. Progress has been made with regard to our knowledge about the biodiversity of cyanobacteria in Germany and about the distribution, occurrence, and autecology of some species. However, gaps in the taxonomic descriptions and constraints of the methods have also become apparent.

(Keynote presentation)

Do cyanobacteria have biogeography? Some observations on geographically restricted taxa

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Baas-Becking's hypothesis, "Everything is everywhere, *but* the environment selects" was made following his studies of oceanic bacterioplankton. It has been widely applied to microbial species, and is still accepted as fact by many microbiologists. However, in recent years some workers have started to question whether this dictum applies to cyanobacterial taxa. There is considerable evidence that different habitats and climatic regions have specific cyanobacterial floras, and in an age of molecular characterization, we are finding that the evidence grows stronger that cyanobacteria are not so easily dispersed.

We have found geographically restricted taxa (identified using a polyphasic approach) in desert soils, tropical islands, wet rocks, and even lakes in our floristic surveys of cyanobacteria. Some restriction is due to habitat. *Microcoleus vaginatus* and *Trichocoleus desertorum* appear to have world-wide distributions, but only in arid soils. *Oculatella* species have been found in arid soils of North America, South America and Europe, and with more sampling in Africa and Asia they will likely be found to occur in arid-climate soils worldwide. However, there are some species and genera which seem very restricted, such as *Kastovskya adunca* in the Atacama Desert, and the putative new genus *Myxacorys*, which has two species represented by numerous isolates, one in the Northern hemisphere deserts, one in the Southern hemisphere. Our discovery of geographically restricted taxa in Hawaii was even more astounding. Of 20 taxa isolated from caves on Kauai, 12 were species new to science, including four new genera. Finally, we recently have sampled type localities in Europe. *Stigonema mammilosum, Pulvinularia suecica, Paracapsa siderophila, Borzinema rupicola*, and *Capsosira brebissonii* all have restricted distributions, but could still be found either in or near the type locality. The evidence at hand indicates that at least some taxa are restricted geographically, likely due to an inability to disperse effectively.

(Keynote contribution)

The cyanobacterial flora from the Venezuelan Table Mountains

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Table mountains – tepuis – from the northern part of South America represent a unique ecosystem, composed of mosaics of wet rock walls, temporary rock pools, shallow wetlands and streams. Approximately one-kilometer-high vertical rock walls cause considerable isolation of the upper plateau (meseta) of table mountains from surrounding biotas. This geomorphological character of the meseta makes it an “inland island”, with substantial levels of endemic species, as has been documented in the case of fungi, mosses, higher plants, invertebrates and vertebrates. Phycological studies from three tepuis (Roraima, Churí, Akopán) reached similar results also. In the last decade were described from these localities one new genus of desmid (*Vincularia*), one green alga (*Ekerewekia*), two new species of diatoms (*Eunotia churiensis* and *E. multirimoportulata*) and four Cyanobacteria (*Albrightia roraimeae, Entophysalis arboriformis*, *Porphyrosiphon latissimus* and *Schizothrix venezuelana*). Moreover, here occur numerous other algal organisms, which are probably new species (or genera), but because they are rare taxa we have not enough material for a reliable taxonomical description. Using a morphological approach we found 65 cyanobacterial taxa (27 coccal, 14 filamentous and 24 heterocytous), but despite exploation of all available literature, we were able to credibly determine only 31 cyanobacteria to species level. Preliminary metagenomics studies support the existence of unknown cyanobacterial taxa in these localities and indicate, that theory of moderate endemicity is probably true.

Important taxonomic changes in the modern cyanobacterial system according to the polyphasic approach

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This presentation will be publishe in full length in the Symposium volume (Rott, Mares & Pentecost Hydrobiologia in prep.)

(Keynote presentation)

Single colony genetic analysis of epilithic stream algae of the genus *Chamaesiphon* spp.

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The genus *Chamaesiphon* Braun ex Rabenhorst 1865 occurs with a dozen of morphospecies in habitats, stressed for example through mechanical abrasion (fluctuation in flow regime), or eutrophication. In order to understand *Chamaesiphon* niche diversification and adaptation processes we investigated the morphological differentiation in relation to 16S-ITS rDNA and 16S rDNA by means of single colony genetics. From a unique dataset on the occurrence of *Chamaesiphon* in Austria, a few representative sampling sites were selected. Individual colonies of cyanobacteria were isolated under the microscope directly from field sites and analyzed both morphologically and genetically. For a number of specimen the morphological description was supplemented by TEM analysis that revealed a variable thylakoid structure mostly not arranged in parallel to the cell wall. All obtained 16S rDNA sequences (1200 bp, n = 42) clustered most closely (97-99% identity) with *Chamaesiphon* strains deposited in the NCBI database. A phylogenetic tree comprising all major lineages of the phylum was suggesting that *Chamaesiphon* forms a monophyletic taxon. The colonies assigned to *Ch. geitleri* Luther 1954 isolated from one sampling site were comprised of closely related genotypes (sequence variation 0.1%, n = 6). In contrast genotypes obtained from *Ch. starmachii* Kann 1972 from two different sampling sites were more diverse (sequence variation 4.2%, n = 17) and either clustered with *Ch. geitleri* or formed another well supported branch. Similarly *Ch. polonicus* (Rostafinski) Hansgirg 1893 was found to reveal most diverse genotypes (sequence variation 4.4%, n = 5) that clustered with *Ch. starmachii*. Thus it is possible that the morphospecies *Ch. starmachii* and *Ch. polonicus* do not represent monophyletic morphospecies. In summary, the results imply that (i) the colony isolation technique is sufficiently pure, and (ii) the nucleotide diversity with the 16S rDNA gene is relatively high (max. 3.94%) implying high phylogenetic diversity within populations in the field.

Cyanophyta vs. cyanobacteria: How to deal with two different sets of nomenclatural rules in taxonomy, biodiversity informatics, and practice

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Blue green algae are phylogenetically bacteria and unique prokaryotes with oxygenic Chlorophyll a photosynthesis like all autotrophic plants. Taxa descriptions of the 19th and 20th centuries were predominantly based on morphological features. Phycological and ecological research have used these taxa to gain information for environmental studies and monitoring purposes. But for current and future research also molecular information is needed. This can be provided using cultured strains when new taxa are described or known taxa are epitypified. Nomenclaturally, blue greens are ambiregnal taxa, treated by the International Code of Nomenclature for algae, fungi, and plants (Melbourne Code) as well as by the International Code of Nomenclature of Prokaryotes (ICNP).

Both codes provide tool kits to link taxa with their morphological and molecular characters to scientific names. However, both codes are currently incompatible with each other in some points. Even though a unified nomenclatural code for all organisms has not been established yet, the BioCode (http://www.bionomenclature.net/) serves as a framework for over-arching practices of the current series of codes and in the long run for the harmonization of all codes. These initiatives are handled by the International Committee on Bionomenclature (ICB). A complete list of all known taxa cannot as yet be provided either under ICNP or under ICN. Thus, the first step to harmonization is to gather the knowledge of the scientific names and types of all known taxa.

Within the DFG funded “Global Registration and Index System for Scientific Names and Types of Algae” nomenclatural acts will be registered and provided according to the ICN to serve the phycological and ecological communities as well as all cross domain attempts to overcome the current nomenclatural shortcomings.

(Keynote presentation)

Molecular taxonomy of cyanobacteria in the genomic era

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Modern taxonomy of cyanobacteria combines data from a variety of sources including morphological, ultrastructural, (bio)chemical, ecological and molecular analyses. Nevertheless, the most widely used taxonomic concept is always based on monophyletic evolutionary units (species, genera, families, and orders), and thus requires a robust phylogeny as a starting point. Up to recently, the majority of cyanobacterial phylogenetic trees was inferred exclusively from 16S rRNA gene data, sometimes in a combination with the rRNA ITS region. Occasionally, studies have been published, which have compared or combined trees based on multiple genomic loci, although not many of them have specifically dealt with taxonomy. Reconstructions based on single or few loci suffer from a number of problems such as low statistical support of clades and horizontal gene transfer. In 2014, a review paper was published (Komárek et al., Preslia 85:295-335), which was first to introduce a phylogenetic tree based on a greater number of conserved loci mined from complete genomes, while linking it to the traditional botanical system of cyanobacteria. Here I present a more recent version of this tree, comparing it to the 16S rRNA tree of cyanobacteria. Specific problems of the currently used phylogenetic concepts and possible more extensive utilization of whole-genome data in future are further discussed.

(Keynote presentation)

Novel cyanobacterial lineages from crenic habitats of north-eastern Australia

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Due to their isolation and hydrogeology, crenic habitats or spring wetlands, in arid and semi-arid areas often support biotic assemblages that exhibit local specialization, high levels of endemism, are highly restricted, and have genetically structured distributions. In Australia, at least 26 macroinvertebrate species, four species of fish, and a number of aquatic macrophytes only inhabit thermal springs. Despite the microflora being conspicuous and potentially unique, there are few studies on their distribution and ecology. We studied material and isolated strains from two thermal spring systems of contrasting hydrogeology. Talaroo thermal springs comprises a thermogene travertine mound with six active vents discharging water high in fluoride and sodium chloride, at temperatures 48.5 – 62.7°C. Cyanobacteria colony forms included floating “lily-pads”, conical stromatolites, and unstructured microbial films and mats. The most conspicuous cyanobacteria formed dense blackish-green subaerophytic mats along minidam crests just above thermal water and along unconfined areas of the discharge apron. Filaments with tolypotrichoid and scytonematoid false-branching were densely arranged forming hemispherical cespitose mats beginning as 1–4 cm diameter circular tufts up to mats 4–6 cm wide by several metres long. Egbaston springs are a complex of approximately 100 shallow wetlands fed by the Great Artesian Basin, an aquifer system which underlies large areas of north-eastern Australia. They contain slightly saline water (ca. 1 mS/cm) that emerges from vents to form shallow pools < 10 cm deep, with water temperature 24 – 28°C. Cyanobacteria were conspicuous on the substratum as spherical to discoid, blue-green to olive-green colonies, 5–25 mm in diameter. Phylogenetic analyses based on partial sequences of the 16S rRNA and nifH genes indicated strains from both sites are related to members of the Scytonemataceae, however sufficiently distant to be considered novel genera. The Egbaston springs strain tested positive by HPLC-MS/MS for the cyanotoxin nodularin (800 µg/g dwt).

Seeking the true *Oscillatoria*

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Modern approaches to cyanobacterial taxonomy have provided a great deal of new information and lines of evidence in the past few years. By the means of electron microscopy, DNA sequencing of specific genes, as well as whole genomes, algologists have been able to obtain large amounts of data which help to reveal more realistic relationships among cyanobacteria. However, the taxonomic system cannot be rebuilt de novo after each new analysis; we need to relate current findings to the already existing traditional taxonomic system, despite its problems. The genus *Oscillatoria,* together with the whole family Oscillatoriaceae and the order Oscillatoriales defined around it, provides an excellent example of an organismal group in which new methods do not allow us to reliably revise the genus nor the higher ranks, unless we establish the reference phylogenetic position of the nomenclatural type - *Oscillatoria princeps* VAUCHER EX GOMONT. Here we show a connection between the original description of *O. princeps* collected in Switzerland in the 19th century with an organism isolated to culture last year from Austria and consequently analyzed by modern methods including TEM, and DNA sequencing. Since the holotype exists only in a form of an illustration, it cannot be subjected to any advanced methods. Here we would like to introduce our material as a candidate for an epitype of the genus *Oscillatoria,* and thus provide a phylogenetic reference point allowing further revisions.

Microbial, marine eu-endoliths: morphological vs. molecular diversity

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We provide a comparative analysis using pyrosequencing of the 16S rRNA gene combined with extensive microscopy of the endolithic microbial community on a profile along a wave-exposed limestone coast of the Croatian Adria. The results showed close correlation between taxonomic composition and local habitats, but no direct correlation between particular cyanobacterial taxa and salinity ranges within these habitats. Further, they indicate that the selective pressure in these extreme environments favours survival rather than growth under conditions of fluctuating salinity. Community composition and surviving depend on waves of settlement of populations during optimal conditions for particular organisms, which then tend to survive over unfavourable periods.

The analysis included molecular comparison of bacterial (phototrophic and heterotrophic) populations along the land-sea gradient, and showed that most pyrosequences were affiliated with Cyanobacteria (43%). Furthermore, the pyrosequencing clearly separated the subtidal communities from those of the intertidal and supratidal ranges, the latter characterized by clear prevalence of cyanobacteria. Other clearly expressed differences separated the intertidal from supratidal habitats, respectively, as well as habitats exposed to regular fluctuation of tides and waves in rock pools. We have used single-cell amplification to obtain sequences of endolithic species *Hormathonema* spp., *Hyella caespitosa, Scytonema endolithicum, Solentia paulocellulare* and *Kyrtuthrix dalmatica.* Molecular signatures of all these organisms were found in our profile and their specific placement confirmed morphological observations. The results show that the different methods produced consistent, reproducible patterns of distribution and diversity of forms and taxonomic units as constructed on the basis of the 16S rRNA gene fragments. The nomenclature employed in the morphological and molecular approaches, however, requires further reconciliation and future studies need to include application of molecular methods to field populations.

Cyanobacteria phosphate-calcite interactions in freshwater

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English headwater streams are often rich in dissolved calcium and frequently deposit calcium carbonate (calcite) associated with cyanobacteria. However, in some catchments, historic studies have shown that calcite deposition has ceased and this has been attributed to high levels of dissolved orthophosphate inhibiting calcite crystal growth. This article investigates two aspects of the problem.

1) Inhibitory levels of dissolved oxy-phosphorus compounds are reviewed and the proposed mechanisms described. Statistics will be presented illustrating the extent of inhibitory dissolved orthophosphate concentrations in English fresh waters. The study will be accompanied by analyses of dissolved orthophosphate from a range of calcite-depositing English headwaters and factors controlling these levels will be discussed. This will demonstrate the widespread occurrence of inhibitory levels of dissolved orthophosphate due to agricultural and urban pollution. A similar situation will occur in other densely populated regions worldwide.

2) The role of cyanobacteria in controlling phosphorus levels in the calcite deposits through their metabolic activities is investigated. Cyanobacteria remove phosphorus from the surrounding water during growth thus potentially reducing orthophosphate levels alleviating calcite growth inhibition. This is an hypothesis that will be tested using known growth rate parameters for the associated cyanobacteria plus analyses of total organic and inorganic phosphorus in the calcite crusts. The possible role of organic phosphates and their utilisation through alkaline phosphatase activity is also considered.

(Keynote presentation)

Effects of temperature changes on cyanobacteria

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Cyanobacteria are well distributed in rivers and soils crusts and are found under a range of ecological ranges including extreme environments such as arid deserts, hot springs and polar regions.Nevertheless, their ecological gradients and the influence of environmental conditions such as temperature are often unknown. Information on temperature gradients is important to explain biotic interactions and potential community composition changes associated with climate change. Studies on the influence of temperature on cyanobacterial growth and some ecophysiological processes will be presented. These were carried out on both natural populations collected from Spanish rivers and cultured strains of *Nostoc, Phormidium* and *Tolypothrix* isolated from different rivers. The experiments were done at temperatures of 4, 12, 18, 24, 30 ºC over periods of 10 and 20 days, with assays of growth, pigment concentrations, photosynthesis and nitrogen fixation. The results show clear differences depending on strain type and and its origin.

Successional trajectories of cyanobacterial communities following glacier retreat in Svalbard (High Arctic)

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The effects of global warming are pronounced at high northern latitudes, where the warming trend observed for the past decades is almost twice as the global average. Most glaciers in Svalbard (High Arctic) have been retreating and thinning since the end of the Little Ice Age in the late 19th century, and retreat rates have increased substantially in the last decades. As a glacier retreats, it systematically exposes new terrestrial habitats for the colonization by pioneering (micro) organisms. Distance from the glacier terminus can be used as a proxy for time since deglaciation, which makes glacier forefields well suited for the study of primary succession. In the present study, we investigated the successional trajectories of cyanobacterial communities along a 100-year deglaciation gradient in the forefield of two Svalbard glaciers (Ebba- and Hørbyebreen). Cyanobacterial abundance was assessed by epifluorescence microscopy and cyanobacterial diversity was investigated by pyrosequencing of partial 16S rRNA gene sequences. Filamentous cyanobacteria were more abundant than unicellular and heterocystous cyanobacteria in both forefields, and an increase in the abundance of cyanobacteria was observed along the deglaciation gradients. Pseudanabaenales was the most OTU-rich order, followed by Chroococcales, Oscillatoriales, Synechococcales, Nostocales and Gloeobacterales. At the genus level, classified phylotypes were assigned to *Leptolyngbya*, *Phormidium*, *Nostoc*, *Pseudanabaena*, *Chroococcidiopsis* and *Microcoleus*. Interestingly, OTU richness increased along the deglaciation gradient in Ebbabreen, but an inverse correlation was observed in Hørbyebreen. Beta diversity estimations indicated contrasting cyanobacterial phylogenetic structures along the temporal gradient, with a clear separation of initial (10-20 years), intermediate (30-50) and advanced (80-100) communities. Time since deglaciation accounted for around 25% of the phylogenetic variability in both forefields, with organic carbon content also explaining a significant proportion of community turnover along the deglaciation gradients. Taxonomic composition was somewhat constant along the deglaciation gradient, but OTUs associated with initial communities were related to sequences predominantely restricted to polar biotopes, while advanced communities included phylotypes related to cosmopolitan taxa.

ITS/CBC approach for classification of cyanobacteria

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The systematics of cyanobacteria have been revolutionized based on the molecular phylogeny using SSU rDNA sequences. Most of the traditional orders are polyphyletic and recently a new system has been proposed based on SSU and protein sequences. More than eight evolutionary lineages have been revealed, traditional orders have been revised and new clades were described. Whereas these lineages are highly supported in most of the phylogenetic analyses, the subdivision into families and genera is often unresolved and needs support by approaches such as the combination of morphological, molecular, physiological and ecological features. This integrative approach, which has been used for taxonomic revision of eukaryotic microalgae and protists, has also been introduced for cyanobacteria. For species delimitation the internal transcribed spacer region (ITS) between the small and large subunits of the ribosomal operon has been used. Secondary structures and the presence of compensatory base changes (CBCs) showa high significance of separation at the species/population level. The ITS region of cyanobacteria varies in length and structure and contains two tRNAs (tRNA-Ile and tRNA-Ala). Both tRNAs are separated by spacer regions, which form a secondary structure. We analyzed the secondary structures of ITS regions among representatives of all lineages revealed by phylogenetic analyses. Each lineage can be distinguished by a characteristic pattern of spacer regions, which differ in length and structure. This pattern can be used as a diagnostic feature at the generic level. The presence of CBCs in the secondary structure of the spacer regions seems to be characteristic for certain populations or species. For example, the *Synechococcus* / *Prochlorococcus* / *Cyanobium*-complex could be resolved using the ITS/CBC approach. The three genera can be clearly distinguished by the ITS spacer pattern and each genus has characteristic CBCs in the secondary structure to support the subdivision into species / populations.

Diversity and niche differentiation of cyanobacteria across water and light gradients in cascades, springs and rivers of the Eastern Alps (Austria)

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Springs and rivers of the Eastern Alps containing strong gradients of moisture and light were surveyed for cyanobacterial communities. Study sights included a wide range from periodically dry spray zones and endolithic cavities of spring rocks to permanently submerged areas of streams and rivers. Examples will be shown from (A) a dark blue-green endolithic layer growing in spring limestone cavities of a temporary cascade in a central alpine dry valley dominated by *Dichothrix*, *Gloeocapsa*, and *Nostoc*, (B) an almost monospecific leathery brown sligthly calcified layer dominated by a filamentous *Leptolyngbya* related taxon (*Pseudoscytonema* sp.), and (C) epilithic, small spot to extended vegetation-coloration forming cyanobacteria in streams from divergent phylogenetic affiliations. The cyanobacteria of the latter sites included some rarely recorded *Chamaesiphon*-like (e.g. epiphytic *Cyanophanon*) and *Pleurocapsa*-like taxa (*Siphononema*) to trichal Oscillatoriales (*Phormidium*-related genera) and Nostoccales (*Coleodesmium*). The integration of published and unpublished checklists will enable researchers to pinpoint rare or overlooked taxa and to study their specific habitats. A summary of ecophysiological studies of cyanobacteria dominated communities to key environmental variables will be combined with gene bank information of their respective communities. Information from environmental characters of the waters and rocks, photosynthetic light response (rETR) curves, the specific pigment spectrum along altitudinal and light (UV) gradients will be combined to identify potential drivers for habitat specifications. In addition problems with interpretation of specific phylogenetic methods (morphological vs. molecular phylogeny studies based on field samples and cultures) will be shown. Finally the potential biogeographic specificity of cyanobacterial communities for aquatic habitats of the Central Eastern Alps will be discussed.

(Keynote presentation)

Small, but powerful: Distribution of *Synechococcus* in the Osterseen Lake District in Southern Germany

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Cyanobacteria are important players in the global carbon cycle and as primary producers they can have a mitigating effect on climate change. The ecology and niche adaptation of cyanobacteria, especially of the autotrophic picoplankton (APP), have been studied very well in the oceans, but there are few studies about the diversity of freshwater picocyanobacteria (< 2 µm), with *Synechococcus* as the main representative.

The Osterseen Lake District, which is located 50 km South of Munich near Lake Starnberg in Bavaria, consists of a chain of 19 small lakes which exhibit a pronounced trophic gradient. *Synechococcus* has been identified as the dominant genus within the cyanobacteria community in several of these lakes. We present first results of the detailed phylogenetical study of this genus.

Four lakes of the Osterseen Lake District, which differ in their trophic states and physical parameters, were selected for this study. Water samples from each lake comprising the entire water column in 1 m steps from the surface to just above the ground were taken. The DNA was extracted and the 16S rRNA gene was amplified with universal bacterial primers. The PCR-product was sequenced via Illumina MiSeq, analysed and sequences (400 bp) were clustered phylogenetically. The total cyanobacteria composition of each studied lake could be detected with this method. *Synechococcus* was found even in a eutrophic lake, although it prefers meso- and oligotrophic conditions. On the one hand the analysed sequences clustered within clades which are already known from literature. On the other hand we detected new unknown groups.

Furthermore, a monitoring of the whole euphotic zone was carried out throughout the vegetation period from April to October. Samples were analysed with a flow cytometer to study the distribution of auto- and heterotrophic bacteria.

Cyanobacterial colonization and desert stromatolites in cliffs of carbonate rocks: sedimentology calling for biology

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Aside of rockfalls generating coarse-grained scree slopes, the biological contribution to cliff degradation and microgelivation is hardly known. Microgelivation is a process, presumed to be associated with freezing of water, whereby a portion of a cliff's rock volume weathers under production of ‚mud' of silt to clay-size grade.

Cliffs provide large colonization surfaces for epi- to endolithic communities mainly of (cyano-)lichens and non-lichenized cyanobacterial assemblages. These communities have to withstand a wide range of environmental conditions, e.g., with respect to cliff surface temperature, water availability, freezing, physical abrasion, and limitation of essential elements.

With respect to cliff erosion and stability, the communities may take a twofold role. Cave microstromatolites growing within joints, and desert stromatolites of calcified *tintenstriche* on the daylit surface, both tend to stabilize the cliff surface – a fact well-known to climbers. Colonization of rock by eu-endolithic (boring/microboring) assemblages, in contrast, may take a similar role as the process of biologically-induced ‚micritization' in the marine realm: Infestation weakens the rock surface and renders it susceptible to physical erosion such as, e.g., snow cascading/avalanching down the cliff, stone-laden rainwash and, perhaps, frost cracking on millimeter- to submillimeter-scale. The resulting sediment is a fine-grained mud. In contrast to the obvious fragments of scree, however, muddy sediments produced in rock-cliff degradation commonly are overgone because they infiltrate the large pore space within scree slopes.

To date, practically no data exist on the relative volume of fine-grained sediment produced by biological cliff degradation, and a similar gap exists with respect to the rock volume dissolved or altered by biochemical attack. Transdisciplinary integration of a sedimentological and a biological approach should help to better understand the problems of degradation and material flux – from micro- to macroscale – of cliffs of carbonate rocks.

(Keynote presentation)

ICE & LIFE - Living Cryosphere

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Once thought to be barren of life, icy environments of the cryosphere are home to rich microbial communities consisting of bacteria, algae, viruses and fungi which are capable of significantly altering the Earth's carbon budget by contributing significantly to the annual availability of new organic carbon, which in turn supports higher forms of life. These ecosystems are highly sensitive to temperate rise due to resulting enhanced availability of liquid water which is the prerequisite for life.

Melting of the ice surface promotes increased levels of microbial activity via the creation of unique and ideal life-habitats (e.g. cryoconite holes which are considered "hot spots" for primary productivity and biogeochemical cycling upon the surface of glaciers). Colonization of these niches subsequently leads to further darkening of the ice surface. The result is enhanced absorption of solar radiation, promoting further melt and providing yet more water for microorganisms, which are then dispersed to other parts of the ice surface and the glacier forefield. We hypothesize that glaciers become increasingly biological and "greener" as they decay, and that glacier wastage is, in part, a biologically-mediated process that initiates ecological succession long before the ice has disappeared. Microbial activity and depositions influence the albedo of the ice surface and thus contribute to the negative mass balance of retreating valley glaciers also due to climate change.

Glacial surfaces are also subject to atmospheric depositions such as manmade radionuclides deriving from Chernobyl and atomic bomb test – especially in the Alps. Since the various compartments of the cryosphere are climate-relevant there is an urgent need to understand the biogeochemical processes before some start to vanish as it is the case in the Alps.

(Key note presentation)

Species of the genus *Stichosiphon* (Cyanoprokaryota) from Russia

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The genus *Stichosiphon* Geitler 1932 (Chroococcales, Stichosiphonaceae Hoffmann, Komárek et Kaštovský) has been described on the basis of the freshwater species *S. regularis* Geitler 1932, and currently includes 12 species and one infraspecific taxon. Species of this genus inhabit mainly freshwater habitats. The only marine representatives are *S. mangle* Branco, Silva et Sant'Anna and *S. sansibaricus var. marinus* L. Hoffmann. Most members of the genus were recorded from tropical regions. Two species are found only in Europe: *S. hansgirgii* Geitler and *S. pseudopolymorphus* (Fritsch) Komárek. Two tropical species (*S. regularis* Geitler, *S. willei* (N.L. Gardner) Komárek et Anagnostidis) were also encountered in Europe, in reservoirs with warm water and tropical vegetation. One species – *S. himalayensis* C.C. Jao et H.Z. Zhu - was described from mountain streams of Tibet.

During the light microscope studies of samples, collected in N, NW and NE Russia in 1970–2015, several new representatives of this rare genus were found. From benthos and epiphyton in waterbodies of the NW European part of Russia three new species of *Stichosiphon* were described: *S. tenerum* S. V. Smirnova et Beljakova and *S. longus* S. V. Smirnova et Beljakova from rivers, streams and lakes of "Valdaysky" National Park (Novgorod region), and *S. borealis* Beljakova et S. V. Smirnova from springs and streams of the Leningrad region. One more new species was found in the White Sea littoral pools, living on planktic invertebrates. There is also a presumably new taxon that appears to be *Stichosiphon* from peaty waters of the Russian North and North-East.

The present study was carried out within the framework of the institutional research project (no. 0120125605) of the Komarov Botanical Institute of the Russian Academy of Sciences and partially supported by the Russian Foundation for Basic Research under Grant 16-04-00549.

Large ribosomal subunit RNAs of cyanobacteria exist in two forms: Implications for phylogenetic analysis

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A preliminary study in which genes of the large ribosomal subunit RNA (LSU rRNA) of over 20 strains of cyanobacteria were sequenced led to the surprising discovery that this rRNA exists in two distinct forms among cyanobacteria. Since then, the advent of rapid genome sequencing technology has greatly expanded the LSU rRNA dataset, allowing for a much more robust comparison of phylogenetic analyses of the LSU rRNA genes with the corresponding small subunit rRNA (SSU rRNA) genes from the same strains. Initial results with 124 strains of cyanobacteria showed the phylogenetic trees for the two genes to be in significant disagreement with each other. The source of this discrepancy is a region of the LSU rRNA gene of approximately 150 base positions in length. Exclusion of this region from analyses resulted in LSU rRNA trees in close agreement with those derived from both SSU rRNA analyses and mutli-locus protein gene analyses. Approximately half the cyanobacteria strains, covering the full breadth of cyanobacterial diversity, have the shortened form of this region that is radically different in sequence composition from the longer form present in the rest of the cyanobacteria strains. This difference is great enough to swamp the phylogenetic signal from other, more conserved, regions of the LSU rRNA gene, resulting in the discordance between LSU rRNA and SSU rRNA phylogenetic trees when the region is included in analyses. The most parsimonious explanation for the distribution of the short form LSU rRNA among cyanobacteria is rampant horizontal gene transfer of a gene of mixed ancestry constructed by homologous recombination, rather than divergence of an ancestor with both forms with multiple instances of independent secondary loss.

(Keynote presentation)

Cyanobacteria in polar terrestrial habitats in the Arctic and Antarctic

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Terrestrial habitats in Arctic and Antarctic regions are among the locations where it is easy to find many and diverse cyanobacteria, yet still need intensive surveying, sampling, isolation, and description to disclose the richness of new species and new genera. Among questions still pending are the extent of geographical isolation and the extent to which there are true cryophilic cyanobacteria in polar terrestrial habitats. The role of cyanobacterial populations in the primary colonization carried out by complex communities like biological soil crusts is still to be fully clarified. Are cyanobacteria of polar terrestrial habitats true extremophiles? What are the consequences of climate change on them?

A study of observations by the authors is presented here to help answer questions on diversity of cyanobacterial populations. It is based on visit to the High Arctic places over several years and Antarctica for a much shorter time. A molecular approach complemented by light microscopy and strain isolation and characterization has been used. A large part of the work has been done on recently deglaciated habitats on the forefront of receding glaciers, where biocrusts dominate.

An NGS study of biocrusts from around the Kongsfjorden (Spitsbergen, Svalbard) has been focused on the complex microbial association, including cyanobacteria, that carries out primary colonization on places recently deglaciated as a consequence of climate warming.

Laminar cyanobacterial macrocolonies developing on the ground surface from several locations around the Arctic have been characterized to investigate their species composition and geographic isolation.

From data presently available, the presence of true cyanobacterial extremophiles in polar terrestrial regions seems to be limited to few habitats like rock surfaces, icy habitats, and perhaps some more.

(Keynote presentation)

Lakes Tumba and Mai Ndombe, two large, acid, blackwaters in DR Congo – pioneer phytoplankton studies with focus on small chroococcal cyanobacteria

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The Lake Tumba landscape in DR Congo is the largest extent of swamp and flooded forest in the country, and it is included in Ramsar´s priority areas. The soils are extremely poor, and rich in humic acids that confer to the waters an acid and chemically impoverished character, with pH varying from 3.9 to 4.6 and a water colour in the range of 300–500 mg Pt L^{-1}.

Here we present pioneer phytoplankton studies of two large blackwater lakes, Mai Ndombe (area 2300 km^2) and Tumba (750 km^2), both located just south of the Equator. The lakes are shallow (mean depth 5 and 3 m respectively). DR Congo freshwaters are of paramount interest because they are expected to contain a great biodiversity and a high level of endemism of several groups of organisms. Special attention is given to the ichthyofauna due to its vital nutritional value for the local rural population and the threat for overfishing, while other aquatic groups of organisms are virtually unknown. Absence or poor conditions of roads can make a seemingly simple sampling expedition an adventure.

Phytoplankton was sampled during some occasions in 2011 (L. Tumba) and 2015 (L. Mai Ndombe) by N.Z., and analysed quantitatively and with a special focus on species identification by E.W. No earlier studies of the plankton flora in the lakes are known. The quantity of algae is very low, with biomasses well below 0.5 mg L^{-1} dominated by diatoms and green algae. The chroococcal cyanophytes are in minority but species of e.g. *Snowella*, *Gomphosphaeria*, *Woronichinia*, *Merismopedia*, *Radiocystis* and other small-celled colonial forms are common, although they build up small biomasses. Here the aim is a taxonomic discussion of these very small-celled chroococcal species.

New genera of sciaphilous cyanobacteria from the Maltese islands

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Ten years ago, a sampling campaign was initiated for cyanobacteria growing as phototrophic biofilms on different substrates in Maltese hypogea. Most belong to probable new species of the well-known genera *Leptolyngbya*, *Pseudanabaena*, *Nostoc*, *Fischerella*, *Chroococcidiopsis*, *Asterocapsa* and *Gloeocapsa* and are currently being described.

Two new genera are presented here on the basis of their cytomorphology, ecology and genetics; *Lanfrankia penumbrata* and *Albertania skiophila.* The 16S rRNA genes of both are sufficiently different from those of previously published taxa to justify the creation of new genera. Moreover, the strains fit a very particular ecological niche with the formation of stable ecotypes that are equipped with a number of morphological features designed to exploit it. Among the important adaptations to the hypogean environment are the filamentous mode of life, the production of a multi-layered sheath and a thick EPS to aid adherence to the substrate, the presence of heterocytes for nitrogen fixation and trichomes with frequent branches protruding from the substrate and growing towards a light source. In addition, *Oculatella subterranea* (described in 2012), exhibits phototaxis associated with the presence of a photosensitive apical cell containing a rhodopsin-like pigment. The strains possess phycoerythrin, phycocyanin and phycoerythrocyanin enabling absorption of light at very low intensities. *Albertana skiophila* and *Oculatella subterranea* were originally described from Maltese and Italian hypogea. *A. skiophila* has also been recorded from similar environments in Spain*,* while *O. subterranea* has recently been characterised from a Greek cave. These cyanobacteria seem to be restricted to a specific habitat and a distinct geographical region leading to a defined biogeographical pattern in hypogea and caves around the Mediterranean region. However, the problem of under-sampling in these environments has to be taken into consideration. There is an important need to continue understanding the evolutionary history and ecology of such new strains of cyanobacteria, especially because this is the key to the discovery of new biomolecules.

POSTER PRESENTATIONS

Photosynthetic performances and related UV-photoprotectants from epilithic stream algae of the genus *Chamaesiphon*

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Several *Chamaesiphon* species form visible colonies well known from calcareous and siliceous cobbles and boulders in lotic ecosystems of the Eastern Alps, characterized by mostly clear, unpolluted or moderately polluted waters. Seasonal fluctuations in water level and light conditions expose these immobile blue-green algae to harsh and strongly fluctuating conditions, often intense irradiation with high ultraviolet spectral components. However, data on their photoprotection ability are scarce.

To better understand species specific response to enhanced photon flux densities (PFDs) and strategies of photoprotection, we collected *Chamaesiphon geitleri, C. polonicus*, and *C. starmachii* from stones in subalpine rivers, and estimated their PFDs dependent relative electron transport rates (rETR) and synthesis and accumulation of UV-photoprotectants. Morphological diversity and variation in the colonial structure were studied with confocal microscopy (CLSM). Primary and accessory (phycobiliproteins) pigments as well as potential photoprotective compounds were identified spectrophotometrically and by High Performance Liquid Chromatography (HPLC).

We found different light responses (rETR) among *Chamaesiphon* species, depending on the qualitative and quantitative pigment composition, including mycosporine-like amino acids (MAAs) and carotenoids, which act as molecular sunscreens. *C. starmachii* showed the highest performances under increasing PFDs, followed by *C. geitleri* and *C. polonicus*. The latter species showed a different pigmentation and colonial organization when compared to *C. starmachii* (on silicate stones) and *C. geitleri* (on calcareous stones), which accumulated high amounts of a MAA (Porphyra 334).

These results demonstrate varying strategies in photoprotection among closely related morpho-species, indicated by the synthesis of different molecular sunscreens. We anticipate our findings to be a basis for further use in biotechnological applications and pharmaceutical products as well as marker compounds for chemotaxonomic studies.

Diversity and distribution of cyanobacteria from tropical paddy fields in some areas of Thailand

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Cyanobacteria play important roles as primary producers. They also provide large amounts of nitrogen to paddy fields by nitrogen-fixation. The research on cyanobacterial diversity in rice fields of Thailand is still limited. This study focuses on the diversity and distribution of cyanobacteria in some rice fields of Thailand. The cyanobacterial samples were collected from 14 rice fields in 5 provinces including Nan, Phitsanulok, Chiang Mai, Chiang Rai and Phrae during the summer season between February 2016 and May 2016. The pH and temperature of soil samples were recorded. The study showed that cyanobacteria were presented as different types of microbial mats and filaments which were tightly packed on the soil surfaces. Based on cyanobacterial morphology and ecology, the 46 species were identified: 24 species of Oscillatoriales, 14 species of heterocytous and 8 species of Chroococcales. The dominant species were *Microcoleus lacustris* (Raebenhorst) Farlow ex Gomont*, Nostoc* sp., and *Aphanothece stagnina* (Sprengel) A. Braun. The occurrence of cyanobacterial species in this study differs from what was found in other geographic areas.

Physiological effects of UV-B radiation and PAR on *Microcystis aeruginosa* BCCUSP232 and *Sphaerospermopsis aphanizomenoides* BCCUSP55: growth and toxin production

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Changing global climatic conditions such as elevated temperatures and UV radiation are expected to influence the ecophysiology of toxic cyanobacteria, bloom formation and cyanotoxin production. Microcystins (MCs), produced by several cyanobacteria, are hepatotoxins commonly found in drinking water sources worldwide. The toxins have been implicated in several cases of human intoxication and deaths. The aim of the present study was to evaluate the combined effect of photosynthetic active radiation (PAR) and ultraviolet (UV-B) radiation on MCs production and release, and growth of *Microcystis aeruginosa* BCCUSP232 and *Sphaerospermopsis aphanizomenoides* BCCUSP55. The strains were exposed to combined 30 µmol m^{-2} s^{-1} PAR and 0.8 W m^{-2} UV-B, and the treatment is hereafter abbreviated as PAR+UV-B. The controls were maintained under optimum light condition (30 µmol m^{-2} s^{-1}) for 10 days. Compared to the control, growth and pigment content of *M. aeruginosa* were slightly stimulated by the PAR+UV-B treatment. On the other hand, the growth and pigment content of *S. aphanizomenoides* were significantly ($p<0.05$) lowered by PAR+UV-B. Total intracellular MCs concentration (pg $cell^{-1}$) of *M. aeruginosa* was significantly lowered by PAR+UV-B, while that of *S. aphanizomenoides* was increased by the same treatment. Surprisingly, extracellular MCs content of both cyanobacterial species was higher in the PAR+UV-B treatment. Our results suggest that increasing UV-B radiation might not only affect growth and pigment content, but also cyanotoxin production and release by *M. aeruginosa* and *S. aphanizomenoides*. In addition, the response of the species to PAR+UV-B exposure was variable.

The diversity of cyanoprokaryota from freshwater and terrestrial habitats in the Eurasian Arctic and Subarctic

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The diversity and geographical distribution of cyanoprokaryotes in Eurasian Arctic and Subarctic were studied. The studies of cyanoprokaryotes in high latitudes are rare and heterogeneous due to the region location and accessibility. We have combined the literature data and our own research that was carried out for 11 years in various parts of the Spitzbergen (Svalbard) archipelago. Our own research was carried out in terrestrial and freshwater habitats, we collected and identified 514 samples (about 1500 specimens). Both original and published data on biodiversity were submitted into the CYANOpro database (http://kpabg.ru/cyanopro/) and used for the analysis.

A total of 583 species were detected. In the Arctic zone, 435 species were found. The Murmansk region (354 species), Spitzbergen archipelago (281) and Bolshezemelskaya tundra (191) have the highest number of species among the studied regions. Taimyr peninsula (125), Polar Urals (119), Chukotka (84), Franz Josef Land archipelago (68), Malozemelskaya tundra (67), Novaya Zemlya archipelago (54), Yamal peninsula (56) were studied partly and have a lower number of species. The smallest number of species were found in Chukotka (48), and in Severnaya Zemlya archipelago (41). Cyanoprokaryota are the third most biodiverse group of algae in the Arctic after diatoms and green algae. The Bolshezemelskaya tundra and the Polar Urals have the most similar floras with 78 species in common and the highest Sørensen index (47%). The flora is unevenly studied in different regions of the Arctic, thus it is too early to speak about significant specificity of algal flora of different areas. Typical terrestrial algal species of the Arctic are *Nostoc commune*, *Microcoleus autumnalis*, *Stigonema minutum*, *Stigonema ocellatum*, *Oscillatoria tenuis*, *Chroococcus turgidus*. In freshwater ecosystems, the most widespread species are *Dolichospermum lemmermannii*, *Dolichospermum flos-aquae*, *Tolypothrix tenuis*, *Aphanizomenon flos-aquae.*

Biodiversity of terrestrial cyanobacteria of the South Ural region

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South Ural is a territory with unique geographical position and diverse natural conditions. For these reasons we undertook a study of the terrestrial cyanobacteria of this region. A total of 56 cyanobacteria were identified during investigations of the terrestrial communities in boreal and broad-leaf forests, forest-steppe, and steppe regions (including salted soils and spoils of the Sibay branch of Uchalinsky mining). Study sites were situated in the Republic of Bashkortostan and the Bredinskiy district of the Chelyabinskaya region. *Phormidium*, *Leptolyngbya* and *Nostoc* were the most abundant genera with 12, 8 and 6 species respectively. *Leptolyngbya foveolarum*, *Microcoleus vaginatus*, cf. *Trichocoleus hospitus*, *Leptolyngbya voronichiniana*, *Pseudophormidium hollerbachianum, Phormidium dimorphum, Nostoc* cf*. punctiforme* and cf.*Chlorogloeoa purpurea* are the most frequent species. *Trichormus variabilis* and *Cylindrospermum michailovskoënse* were detected in the forest zone, characterized by more humid conditions. *Phormidium ambiguum* was typical for forest-steppe and steppe zones. *Pseudophormidium hollerbachianum* and *Nostoc* cf. *commune* were most abundant in steppe. During our investigations, several strains were identified as *Scytonema* and *Tolypothrix*. Detailed molecular studies of these strains supplemented by a polyphasic approach revealed that they belong to the new genus *Roholtiella,* which contained 4 new species, 3 of which were found in the territory of South Ural: *Roholtiella edaphica*, *Roholtiella bashkiriorum* and *Roholtiella fluviatilis* (Bohunická et al., 2015). Thus, for understanding the true biodiversity of cyanobacteria of South Ural, further molecular-genetic research is necessary.

Isolation and phylogenetic investigation of cyanobacteria from Amazonian rivers

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The Amazon River basin is the largest in the world comprising about 40% of the total area of South America. Its tributaries rivers are classified in three different types according to their color, which in turns is related to their substrate features and physical-chemical properties. The composition of microbial communities is scarcely investigated, especially the cyanobacterial one. Up to date only one study was dedicated to the isolation and characterization of cyanobacterial strains collected in sediments from the edge of Amazon and Solimões rivers (Fiore et al., 2005). In the present study, water samples were collected in four rivers differing in their water color (Negro, Solimões, Amazonas and Tapajós). Cyanobacterial strains were isolated and morphologically identified using an optical light microscopy. After total genomic DNA extraction, the 16-23S rRNA sequences of the isolated strains were obtained by PCR amplification, cloning and sequencing. Forty-seven, forty and six strains were isolated from Solimões, Amazon and Negro rivers, respectively, totalizing ninety-three isolates. Morphologically, these strains belong to the genera *Alkalinema, Calothrix*, *Chroococcidiopsis, Cyanospira*, *Leptolyngbya*, *Microchaete*, *Nostoc*, *Oscillatoria, Pantanalinema*, *Planktothrix*, *Pseudanabaena*, *Thrichocapitatum*, *Tolypothrix* and *Woronichinia*. Thirty-nine isolates had their 16-23S gene sequenced with identities of 16S partial sequences ranging from 92.0 to 99.9%, according to EzTaxon server. Based on these results and phylogenetic trees, at least three distinct evolutionary lineages were detected suggesting they may represent novel genera. These results highlight the importance of studying tropical and less accessed environments such as Amazonia, for a better understanding of cyanobacterial systematic.

Phylogenetic position of the genus *Kyrtuthrix* ERCEGOVIĆ within the order Nostocales

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The euendolithic genus *Kyrtuthrix* was originally described in 1929 by A. Ercegović from the Dalmatian coast. Due to its isopolar filaments *Kyrtuthrix* is classified within the latest cyanobacterial system as part of the family Scytonemataceae, even though trichomes tapering towards their ends represent a feature typical for the family Rivulariaceae. Until recently, only limited molecular data were available for this genus, and they did not allow a reliable assessment of its phylogenetic relations to other cyanobacterial genera. However, we were able to obtain sequences of the 16S rRNA gene in sufficient length for phylogenetic analyses for two species of *Kyrtuthrix* - the type *K. dalmatica* collected from the Dalmatian coast, and *K. maculans* collected from the Pacific coast of Peru. Our analyses revealed that both taxa are related to marine members of the genus *Rivularia*, and thus confirmed the importance of trichomes tapering towards their ends as a diacritical feature of this taxon. Consequently, the genus *Kyrtuthrix* should be re-classified into the family Rivulariaceae. Our results also showed that there are several strains under different generic assignments very closely related to our material in the main culture collections worldwide.

Komarekiella atlantica gen. et sp. nov. (Nostocaceae, Cyanobacteria): a new subaerial taxon from the Tropics

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Six strains of nostocacean Cyanobacteria sampled on tree bark from tropical and subtropical environments of the Atlantic Rainforest, São Paulo, Brazil (23º20'S and 45º09'W) and from a mat found in a rain-fed puddle on concrete in Hawaii (21.9156° N 59.51° W) were studied by morphological and molecular methods. In culture, their colonies present compact aggregations of cells. In juvenile stages filamentous cell arrangement is not visible, but in later growth phases aggregates become more diffuse with apparent trichomes, similar to *Nostoc*, *Desmonostoc*, *Mojavia* and *Halotia*. *Komarekiella* differs from them by unequal division of akinetes into a small heterocyte and a large vegetative cell. This character makes *Komarekiella* morphologically indistinguishable from *Chlorogloeopsis*, and consequently these genera can be considered to be cryptic taxa. Parsimony analyses of the 16S rDNA phylogeny shows *Chlorogloeopsis* in a basal position in a nostocacean tree (227 OTU's) and *Komarekiella* strains strongly supported in a sister clade to *Halotia* and *Goleter*. The last three genera are a sister clade to *Mojavia*. Primary sequences from the 16S-23S ITS D2, D3, Box A and D4 domains were conserved among *Komarekiella*, *Desmonostoc* and *N. commune* strains. Among the *Komarekiella* strains, the Box B, V2 and V3 helices were identical, but the D1-D1' helix presented three slightly different patterns in the central helix, specifically on the 3' side. The D1-D1' helix of all *Komarekiella* strains showed the basal unilateral bulge opposed by three unpaired nucleotides on the 5' side of the helix, a feature not observed in any cyanobacterial taxon to date. Due to its phylogenetic distance from morphologically similar taxa, its morphological distinctness from sister taxa, and its genetic distance from all taxa, *Komarekiella* is well supported as a new genus. The uniqueness of the D1-D1' helix secondary structure is the single diagnostic character separating it from other Nostocales.

Pseudoscytonema sp., a calcite-precipitating macroscopic niche-forming cyanobacterium from a seepage spring in the Alps.
Part 1: Ecophysiology and cell biology

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Pseudoscytonema sp., a filamentous cyanobacterium, calcifies in montane seepage springs of suitable water chemistry. In these habitats, seasonally changing temperature, light, and moisture regimes challenge organisms to maintain sufficient photosynthetic performance under a broad range of photon fluence rates and temperatures. However, information on the photosynthetic response of *Pseudoscytonema* sp. to temperature and light gradients is missing. Here we show by pulse amplitude modulation (PAM) fluorometry that fine mats of *Pseudoscytonema* sp. exhibit electron transport through PSII between 0 – ~600 µmol photons m^{-2} s^{-1} ($rETR_{max}$ ≈ 3.8 µmol electrons m^{-2} s^{-1}) and a strong temperature dependence of the maximum quantum yield of PSII (F_v/F_m) with the highest value (0.42) at 16 °C. Spectrophotometry and High Performance Liquid Chromatography (HPLC) revealed primary and accessory (phycobiliproteins) pigment composition. Furthermore, cell morphological and ultrastructural traits investigated by confocal laser scanning, scanning electron and transmission electron microscopy, respectively, will be discussed with respect to the calcification processes (see Abstract of Tran et al., this volume). Our results provide the first ecophysiological characterisation of a *Pseudoscytonema* species which shows high adaptability to light- and temperature gradients.

Morphological variability of Oscillatoriaceae in cross gradients of temperature and light intensity

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Species of the family Oscillatoriaceae are considered to be morphologically robust with respect to changing environmental conditions. This assumption is the basis of standard identifications used in both ecological and taxonomic studies. Characteristic features are described as stable or with limited variability according to literature. On the other hand, the morphological characters presented in many species descriptions show considerable overlap.

This study aims to clarify the morphological variability and extreme dimensions for filaments/trichomes for the most important genera of the family Oscillatoriaceae. We studied the influence of light and temperature (5-45°C) on morphological (cell dimensions, filament dimensions, sheets presence, hormogonia production and other structural features) and compare them with values originally cited in the taxonomic literature. Out of eleven genera of the Oscillatoriaceae we studied eight strains of the large genera *Oscillatoria*, *Lyngbya* and *Phormidium*. Most strains are from the CCALA collection of microorganisms held in Trebon, supplemented by 2 new isolated strains from nature.

Strains were cultivated in crossed gradients of temperature and light intensity. The morphological measurements were taken by optical microscope. The ranges of the morphological data were compared with the new information from the specimens under standard cultivation conditions and of eco-physiological measurements of photosynthetic activity by kinetic fluorescence methods. The morphological stability or large scale variability under limited growth and / or during hormogonia production vs. optimal conditions was determined. These data complete the morphological description of individual strains and allow for more reliable identification of several common species of the family Oscillatoriaceae.

Benthic marine heterocytous cyanoprokaryotes (cyanobacteria) from the coast of Mexico

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Recent surveys of México´s Pacific and Gulf of México supratidal and intertidal zones have shown several conspicuous photosynthetic mats or crusts of cyanoprokaryotes, frequently growing isolated, below or intermingled with macroalgae. Morphological characterization of these was obtained for ten localities along the coast of Jalisco, Guerrero and Oaxaca in the Pacific and Veracruz in the Gulf of México. At most of these localities the field sample analysis showed that heterocytous forms constitute the most abundant component and important structural element. Several different morphotypes of *Kyrtuthrix*, *Scytonematopsis* and *Rivularia* were common components, as well as others similar to "*Calothrix",* "*Microchaete"*, or "*Petalonema*", but some populations showed morphological traits that did not allowed easy taxonomic identification. For some of these populations the 16S rRNA gene sequence was obtained and compared with GenBank available sequences, mainly from the Nostocales. Phylogenetic analyses revealed that some of the strains obtained in this work fall within different clades of well known Rivulariaceae members.

Cyanobacterial blooms in Brazilian semiarid reservoirs assessed via next-generation DNA sequencing technology

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High-throughput sequencing was used to (1) characterize cyanobacterial communities, and (2) to identify species associated with cyanotoxin genes in two Brazilian semiarid reservoirs. Target sequences of 16S-23S rRNA ITS and *cpc*BA-IGS regions were used to reveal the taxonomic aspects of cyanobacterial blooms; and genes coding for cyanotoxin biosynthesis genes such as microcystin (*mcy*E), saxitoxin (*sxt*A) and cylindrospermopsin (*cyr*J) were investigated. Taxonomic analyses performed on DNA sequences showed the dominance of the genus *Microcystis* in the Mundaú reservoir. In Ingazeira reservoir, *Microcystis* was only dominant during the dry season, and was followed by *Planktothrix*. *Cylindrospermopsis* comprised 54% of the cyanobacterial community structure of Ingazeira reservoir in the rainy season based on the 16S-23S rRNA ITS sequences. Detection of the *sxtA* gene was mainly associated with the genus *Cylindrospermopsis*, while the *mcyE* gene was with *Microcystis* in both reservoirs. The *cyrJ* gene was not detected. Our results showed that cyanobacterial composition of Mundaú reservoir was highly conserved during the dry season, while it changed over time in Ingazeira reservoir. For the first time, we present results of high-throughput sequencing specific to cyanobacterial community analysis of Brazilian freshwater reservoirs. These results are important for better understanding of the cyanobacterial community structure and functions in aquatic ecosystems of semiarid regions.

Pseudanabaena species producing 2-methylisoborneol from Japan

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Several Japanese *Pseudanabaena* strains were compared on basis of morphological and genetical analyses (16srRNA, ITS and rbcL genes). Over many years thin filamentous planktonic cyanobacteria producing 2-methylisoborneol (2-MIB) in Japan were misidentified as *Phormidium tenue* (Menegh.) Gomont. We have now clarified identification to show that they belong into the genus *Pseudanabaena* based on typical morphological characteristics including the parietal arrangement of thylakoids and also the 16S rRNA gene sequence analysis. Two new species, *Pseudanabaena foetida* Niiyama, Tuji et Ichise and *P*. *subfoetida* Niiyama et Tuji (Niiyama et al. 2016) have been recognized. However, Tuji & Niiyama (2016) have shown that the cultured strain NIES-512 has intermediate characters between these two species.

We have now found another 2-MIB producing planktonic *Pseudanabaena* in other lakes in Japan. The trichome colour is blackish-purple in contrast with bright blue-green of *P*. *foetida*, *P*. *subfoetida* and NIES-512. The analysis of the 16S rRNA gene indicates that it belongs to a different clade.

Nitrogen-fixing cyanoprokaryota of soil crusts in tundra communities of European North-West Russia

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The present study aimed to collect information on species diversity and nitrogen-fixing activity in biological soil crust (BSC) in different types of lowland and mountain tundra. The studies were conducted in moss-shrub communities of lowland (Malozemelskaya, 68°25'N, 53°13'E) and mountain (Subpolar Urals, 65°11'N, 60°18'E) tundra. Two types of BSC common in European tundra were selected. The first taken from an area of low moisture, where *Stigonema (S.minutum* and *S.ocellatum)* were dominant. The second was taken from wet habitats, where *Nostoc commune* and *Scytonema* dominated. Nitrogenase activity was measured using the acetylene reduction method. The data were used to estimate seasonal accumulation of N, with temperature values.

At 15 °C value for nitrogenase activity in the Urals was 0.53 ± 0.21 mg C_2H_4 m^{-2} h^{-1} where *Stigonema* dominated, 1.76 ± 0.49 where *Scytonema* and *Nostoc* dominated. Nitrogenase activity of the Malozemelskaya tundra BSC dominated by *Stigonema* was 0.66 ± 0.09 mg C_2H_4 m^{-2} h^{-1}. The mean daily value for nitrogenase activity of Urals BSC with *Stigonema* was 12.3 ± 1.8 mg C_2H_4 m^{-2} h^{-1} and with *Scytonema* and *Nostoc*, 32.7 ± 6.2 mg C_2H_4 m^{-2} h^{-1}; the value for Malozemelskaya tundra BSC was 11.8 ± 2.1 mg C_2H_4 m^{-2} h^{-1}.

The values during the120-day vegetative period of Urals BSC were 1.10 mg C_2H_4 m^{-2} h^{-1} for soil crusts with *Stigonema* and 4.10 with *Nostoc* and *Scytonema*. Using a coefficient of 3:1 for conversion (Belnap, 2003; Zielke et al., 2005), the BSCs fix 0.3 and 1.3 g N m^{-2} (120-day) resp. In the case of the crusts of the Malozemelskaya tundra, the value was 0.3-0.4 g N m^{-2} over the same period.

Dynamics of Chroococcales and Nostocales in a turbid subtropical estuary: Río de la Plata, South America

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According to climate change scenarios, cyanobacterial blooms will increase in the future. Despite the relevance of these events, there is limited information from subtropical large rivers and estuaries. Here we analyzed the phytoplankton community from October 2014 to March 2016 in a bay with a highly variable fluvial and marine influence of the Río de la Plata estuary (34° 45´ S, 56° 32´ W). The phytoplankton composition and biovolume were evaluated from net and quantitative bottle samples. The chlorophyll *a* concentration, temperature and salinity were also determined. The water column was permanently mixed resulting in a shallow euphotic zone and a small Zeu/Zmix ratio. These conditions were more favorable for eukaryotic algae (diatoms) than for bloom forming cyanobacteria. Altogether 22 taxa of cyanobacteria were identified belonging to Chroococcales, Nostocales and Synechococcales. *Microcystis* and *Dolichospermum* were the dominant genera regarding total cyanobacterial biovolume. During summer the highest chlorophyll *a* concentrations (414 µg.L^{-1}) corresponded to high cyanobacterial biovolume (37.7 mm^3.L^{-1} in 2014 and 1.1 mm^3.L^{-1} in 2015) and to the highest cyanobacteria abundance (4.36x10^5 cell.mL^{-1} in summer 2014); all of them exceeded the World Health Organization guidance threshold for high exposition risk in recreational waters. *Dolichospermum uruguayense* co-dominated with *Microcystis aeruginosa* in summer 2014 and with *Microcystis protocystis* in summer 2015. Cyanobacteria biovolume was directly correlated with temperature and inversely correlated with salinity. Our results contribute to elucidate the environmental requirements of the recently described nostoccalean species *D. uruguayense*. Despite the dynamic conditions of the sampling sites, cyanobacteria typical from calm stratified waters were found in high proportion in the community. Finally, our results show that subtropical water bodies have been subjected to colonization and dominance by cyanobacteria that impair their ecosystem services.

Subaerial epilithic cyanobacteria from Yosemite National Park, California, USA.

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Subaerial epilithic cyanobacteria represent a large portion of known cyanobacterial diversity. However, floristic studies of such communities from North America are underrepresented. In an effort to improve our knowledge of subaerial cyanobacteria from this part of the world we studied the epilithic cyanobacterial flora from Vernal Falls, Yosemite National Park. Granitic rock fragments were used to inoculate Z8 medium agar plates with the algae. We obtained 104 isolates which we microscopically differentiated into 25 morphotypes. The initial classification of isolates resulted in eighteen genera and eleven families according to the newest taxonomic classification scheme proposed by Komárek et al. 2014, representing the orders Synechococcales, Chroococcales, Oscillatoriales, and Nostocales. Families include Synechococcaceae, Merismopediaceae, Leptolyngbyaceae, Heteroleibleiniaceae, Aphanothecaceae, Chroococcaceae, Coleofasciculaceae, Microcoleaceae, Scytonemataceae, Chlorogloeopsidaceae, and Capsosiraceae. Obtaining isolates from genera difficult to culture such as *Eucapsis*, *Asterocapsa*, and *Gloeocapsopsis* is an especially exciting outcome. We are currently in the process of characterizing all morphotypes by their DNA sequence data focusing on the 16S rRNA and 16S-23S ITS gene regions in order to accurately describe the cyanobacterial diversity. We show the first results on the diversity of these interesting cyanobacteria from this unique habitat.

Comparative genomics of toxigenic *Nodularia spumigena* strains from geographically distant origin

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A bloom of *Nodularia spumigena* was described for the first time in Brazil in 2011 in shrimp production ponds, causing the death of these crustaceans. These ponds contained estuary water pumped from the Cassino Beach (southernmost beach of the Atlantic Brazilian coast), Rio Grande, Rio Grande do Sul state. *N. spumigena* may have been introduced by natural ways such as migrating birds from Uruguay or ship ballast water. To gain insight into Brazilian *N. spumigena*, the isolated strain CENA596 was subjected to genome sequencing. The draft genome analysis yielded 291 contigs with a total size of 5,189,679 bp on which genes for 4,443 proteins were annotated. Secondary metabolite gene cluster prediction using antiSMASH algorithm recognized potential 12 gene clusters. Among the known peptides, gene clusters of nodularin, spumigin, and anabaenopeptin were predicted as well as geosmin, a terpene compound. With the exception of geosmin gene cluster, all the other gene clusters had already been identified in the genome of *N. spumigena* CCY9414. The production of the four metabolic compounds by the strain of *N. spumigena* CENA596 was confirmed by high performance liquid chromatography (HPLC) coupled to tandem mass spectrometry (LC–MS). The phylogenomic analysis of *N. spumigena* CENA596 based on 21 conserved protein sequences positioned this strain together in the same branch with *N. spumigena* CCY9414 isolated from the Baltic sea with 100% bootstrap value. The identities between the 16S rRNA gene sequences of both strains are high (99.2% identity, 100% coverage). Automatic annotation of the genomes using subsystems technology revealed a related number of coding sequences and functional roles. Analysis of orthologous groups identified a large number of shared genes between the two strains. The comparative analysis between CENA596 and CCY9414 strains showed that both genomes are considerably similar despite their geographically distant origin.

Multifaceted characterization of *Westiellopsis prolifica* (Cyanobacteria) from the El-Farafra oasis (Western Desert, Egypt)

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A multifaceted approach was used to investigate in depth the morphotaxonomic, phylogenetic (16S rRNA sequencing), bioorganic (pigments and lipidomics), ecological characteristics of the true-branching cyanobacterium *Westiellopsis prolifica* from the arid desert-soil habitats of El-Farafra Oasis (Western Desert of Egypt). The morphometric diagnostic features, including the uniseriate thallus structure and reproductive structures, such as pseudohormocytes and monocytes, besides the ecological preferences of the specimens studied, corresponded (with minor discrepancies in dimensions) to the descriptions in literature. Based on molecular data of the 16S rRNA gene, the strain formed a tight cluster with available strains of *Westiellopsis* and other genera of Hapalosiphonaceae, a family in need of polyphasic revision. Bioorganic screening showed the presence of thylakoid monogalactosyl-diacylglycerols (MGDG), digalactosyl-diacylglycerols (DGDG) and sulfolipid sulfoquinovosyl-diacylglycerols (SQDG), and membrane phospholipids phosphatidylcholine (PC) and phosphatidylglycerol (PG). Thylakoid lipids are characterized by low unsaturation index (UI) and short fatty acyl chains, a mechanism ensuring adequate membrane fluidity and preventing the inhibition of photosynthesis in harsh environmental conditions. Among carotenes and carotenoids, most abundant species are α/β carotene (38.1%), the cyanobacterial echinenone (14.3%), zeaxanthin (13.4%) and myxoxanthophyll (8.8%). From the ecological standpoint, the true T-branching cyanobacterium *W. prolifica* seems to be restricted in distribution to arid and hyper-arid subtropical and tropical environments. In conclusion, this study improved knowledge on the distribution, autecology, phylogenetic position, and bioorganic characteristics of *W. prolifica*. Moreover, this investigation confirmed that cyanobacterial polyphasic studies could be considered not only as an urgently-important pre-requisite for species delineation but also useful to characterize eco-physiological adaptive mechanisms to special habitats.

Diversity of cyanobacteria in biological soil crusts on arid soils in the eastern region of India and their molecular phylogeny

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This account of cyanobacteria in eastern India is from a region with a distinct tropical environment of rain during June-September following a prolonged dry spell almost 4 months) in March - June with high solar irradiance and air temperatures up to 45 °C. The biological crusts (BSCs) on lateritic soils, red soils and mine-waste burdened soils over a transect of about 800 km were composed mainly of sheathed cyanobacteria belonging to *Scytonema*, *Tolypothrix* and *Lyngbya* along with few species of *Cylindrospermum, Nostoc, Calothrix* and *Fischerella.* Molecular phylogeny based on 16S rRNA gene sequence (PCR, 500BP) of isolates from BSCs of India showed that these formed a separate clade from species of the same genera from other regions of the world. Species with a thick sheath around the trichome under the genera *Scytonema, Tolypothrix* and *Lyngbya* which were the dominant component in BSCs in India were clustered with filamentous species from all types of habitat elsewhere, but as a separate clade. This suggests that these were genetically distant, perhaps of being acclimatized to a tropical monsoon climate.

Sphaerocavum: a coccoid morpho-genus that showed to be identical to *Microcystis* in terms of 16S rDNA and ITS phylogeny.

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Sphaerocavum is a typical planktonic coccoid cyanobacterium which is constantly found in blooms co-occurring with *Microcystis* species. Morphologically described in 2003 by Azevedo and Sant'Anna, *Sphaerocavum* is a morpho-genus distinguishable from *Microcystis* by its hollow colonies and cell division in two planes. The cells are loosely placed on the colony surface and occupy the entire mucilaginous sheath. The type species, *Sphaerocavum brasiliense*, has CCIBt3094 designated as reference culture and the genus life cycle was determined based on this lineage. All these morphological features clearly separate *Sphaerocavum* from *Microcystis*, but its true phylogenetic position has never been established. Six *Sphaerocavum* strains isolated from eutrophic lakes in tropical and subtropical Brazilian regions, including the type strain CCIBt3094 (= SPC484), were herein studied by morphological and molecular methods. The 16S rDNA phylogeny based on maximum likelihood analyses reveals that *Sphaerocavum* and *Microcystis* are grouped together in a well-supported clade. All Brazilian strains from subtropical regions grouped with some *Microcystis* lineages from Asia and Europe with high identity. The type strain and the other lineages from Brazilian tropical regions positioned closer to a *Microcystis panniformis* strain from Vietnam. The secondary structure and phylogenetic tree of 16S-23S ITS confirmed that strains from the Brazilian subtropical regions grouped apart from those tropical ones. Species recognition inside *Microcystis* by molecular markers is still unclear and new markers must be found, but the position of Brazilian tropical lineages in 16S rDNA and ITS trees, the geographic origin and morphologic features suggest that these Brazilian lineages could be considered as a different species of *Microcystis*.

Polyphasic characterization of three *Leptolyngbya*-like strains from the Giant Cave (Trieste, Italy)

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Hypogean environments, like caves, present life-limiting conditions, of which light intensity is one of the most important factors. While at the cave threshold several organisms (e.g. microalgae, bryophytes, ferns) compete for sunlight, in the deepest recesses cyanobacteria are usually the unique phototrophs. In show caves, these prokaryotes constitute most of the microflora growing in proximity of artificial lighting (i.e., "Lampenflora"), representing both the base of several food chains and a possible threat to the cultural heritage. Investigations on cyanobacteria isolated from caves underlined that the particular conditions of these environments often lead to the selection of unusual taxa, apparently not reported from other habitats.

Many studies have been carried out on the hypogean flora worldwide, but caves of some areas were not or poorly investigated, like the Giant cave, a Karst show cave located in Trieste, Italy. The artificial lightening and, most likely, the flow of people in this tourist cave have favoured, during the years, the proliferation of "Lampenflora", largely represented by cyanobacteria.

In 2012 we started a survey on the microflora of the Giant Cave that led to the isolation of several cyanobacterial strains. Three of these isolates were non-heterocytous filamentous cyanobacteria and presented a very simple morphology, with thin trichomes, narrower than 3.5 µm; thus they were initially attributed to the heterogeneous genus *Leptolyngbya* Anagnostidis and Komárek.

Here we present the characterization of these *Leptolyngbya*-like strains using a polyphasic approach, which includes morphological, ultrastructural, biochemical, molecular, and phylogenetic analyses. These last were based on the 16S rRNA gene and the 16S-23S ITS region; moreover the analysis of 16S-23S ITS secondary structures was also performed.

Pseudoscytonema sp., a calcite-precipitating cyanobacterium forms macroscopic stromatolites in a seepage spring in the Alps. Part 2: Calcite sedimentology and environment.

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Rainwater and snowmelt seepages on a vertical canyon flank near Innsbruck support a calcifying assemblage comprised mainly of mosses, cyanobacteria and diatoms. The annual mean air temperature at the site is 6.5°C, with monthly averages ranging from 0°C (December–January) to 20°C (July–August). The winter cold spells lead to freezing and icicle formation on the calcifying surfaces. The spring water with a Mg/Ca ratio of ~0.9, is oversaturated for calcite (Langelier index LSI ~1.5), and precipitates low-magnesian calcite. Mosses (e.g., *Palustriella commutata*) calcify *in vivo* by encrustation with calcite crystals. Between moss. In addition, the mosses are covered by yellow–brown, friable calcite coatings and by mucus-rich biofilms of cyanobacteria (*Pseudoscytonema*) and diatoms.

Samples of the calcite coatings show high total water content (58-<u>65</u>-68 wt% of field-wet samples), and high content in organic matter (6–9% dry weight loss at 400°C). When dry, the calcified biofilms resemble styrofoam. In thin sections, the biofilms are seen to form tufa stromatolites with smoothly draped lamination. Tufa laminae consist of a loose aggregate of apparently free-floating rhombohedral calcites of microspar to micrite in size (10-1 microns); per lamina, these calcites can be surprisingly similar in size. Locally, thread-like structures of more densely-spaced microspar is identifiable. Electron microscopy underscores the close association of cyanobacterial filament meshworks with calcite crystals and crystal clusters.. In many cases, the crystals nucleated on the filament surface of and the clusters engulfed cyanobacterial filaments.

The loose aggregate of free-floating calcites of uniform microspar to micrite sizes imply crystal nucleation pulses and/or crystal growth limited by transport (most probably diffusion) of ions to crystallization sites, reminiscent of artificial crystal growth within gels. Compared to other types of tufa stromatolites, the stromatolites associated with *Pseudoscytonema* films comprise a peculiar type of extremely high intrinsic porosity and uniform size of idiomorphic calcite crystals.

Novel microaerophytic cyanobacteria isolated from cemetery headstones in northeastern Florida, USA

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Cyanobacteria are common constituents of lichen-dominated biocrusts throughout the world. However, the diversity of the cyanobacteria in such consortia has not been thoroughly examined, especially in subtropical habitats. As part of a survey of aerophytic cyanobacteria from lichen-dominated habitats we sampled biocrusts from granite and marble headstones of northeastern Florida. Epilithic crustose, leprose, and foliose lichens were collected from five vertical headstones oriented eastward, in a 128-year-old southern folk cemetery complex situated on a barrier island just half a mile from the Atlantic Ocean to the east and the Intracoastal Waterway to the west. Numerous morphotypes were recovered, most of which were filamentous and capable of nitrogen fixation as shown by heterocyte production. Modern cyanobacterial systematics employs a total evidence approach consisting of morphological, molecular, and ecological data sets. Based on these criteria, here we present two novel species from this survey: *Calothrix* sp. nov. and *Brasilonema* sp. nov., with analysis of 16S rDNA gene sequence data, ITS secondary folding structures, and ecological context providing evidence for the erection of new taxa. *Calothrix* sp. nov. was recovered from the cephalodia of a grey green shield lichen growing on the northern aspect of a 42 year old granite headstone. *Brasilonema* sp. nov. was isolated from a pinkish brown crustose lichen inhabiting the western aspect a 41 year old marble headstone. Many other putatively novel taxa were also recovered indicating a potentially rich source of cyanobacterial biodiversity.

Microbial diversity in hypersaline Oman tidal flats

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The molecular diversity of hypersaline microbial mats from Oman tidal flats (Arabian Sea) was investigated at two locations: Location 1 had laminated sandy sediment, high water availability and a salinity of 54‰. Location 2 included five sites within a 5.8 km intertidal gradient from terrestrial to marine with high salinity (180-190‰); the sites showed increasing water availability, decreasing thickness of the covering salt crust and increasing sediment stabilization towards the sea.

Bacterial, cyanobacterial and archaeal diversity was investigated using next generation sequencing (MiSeq) of the 16S rRNA gene. The microbial community (referred to relative sequence abundance) was dominated by halotolerant to extreme halophilic bacteria and archaea, but the composition differed between the two locations and along the gradient within location 2. The bacterial community of location 1 was dominated by aerobic heterotrophic *Gammaproteobacteria*, the cyanobacterial one by Pleurocapsales and Chroococcales and the archaeal one by halobacteria. At location 2 the bacterial community of the more terrestrial sites was dominated by phototrophs like *Salinibacter* (Bacteroidetes), *Lyngbya* (Cyanobacteria) and *Rhodovibrio* (Alphaproteobacteria) and that of the more marine sites by aerobic heterotrophs like *Salisaeta* (Bacteroidetes) and anaerobes like *Anaerolinaceae* (chloroflexi), *Spirochaetales* and *Deltaproteobacteria*. The cyanobacterial community along the gradient was characterized by decreasing abundance of Chroococcales and increasing abundance of Oscillatoriales. Halobacteria dominated the archaeal community and showed a hump-backed distribution along the gradient.

Richness and diversity was highest for Bacteria, lowest richness was found for Archaea and lowest diversity for Cyanobacteria. Beta diversity was clearly related to distance between the compared sites. Increase in distance led to higher dissimilarity and less shared richness.

Molecular characterization of four cyanobacterial genotypes from their type localities in Scandinavia

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More than three hundred cyanobacterial genera have been described up to the present. For every valid genus a type species must be specified at the time of description. Even though we have entered a time in which sequencing has become practical and widespread, the basic molecular characterization (e.g., 16S rRNA gene sequence) of most cyanobacterial type species is still lacking. About fifteen genera were described from Scandinavia. Following a field excursion in which the type localities for the type species of these genera were visited and sampled, we succeeded in finding four type species from (or very near) their type localities: *Capsosira brebissonii*, *Paracapsa siderophila*, *Pulvinularia suecica*, and *Stigonema mamillosum*. Cells or filaments of these species were isolated and used for single-cell/-filament PCR amplification of the 16S rRNA gene, and subsequent sequencing. This allows firm establishment of epitype sequences of these genera, to which morphologically similar taxa can now be compared.

The BCCM/ULC collection to conserve and study the biodiversity of polar cyanobacteria

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In polar regions cyanobacteria represent key primary producers and main drivers of the food webs in a wide range of aquatic to terrestrial habitats. For example, they build benthic microbial mats in lakes and soil crusts in terrestrial biotopes. They may present interesting features to survive freeze/thaw cycles, seasonally contrasted light intensities, high UV radiations, dessication and other stresses.

The BCCM/ULC public collection has been funded by the Belgian Science Policy Office since 2011 and an ISO9001 certificate was obtained for the public deposition and distribution of strains, as part of the multi-site certification for the BCCM consortium. The collection aims to gather a representative portion of the polar cyanobacterial diversity with different ecological habitats (limnetic mats, soil crusts, cryoconites, endoliths,….) and make it available for researchers to study the taxonomy, evolution, adaptations to harsh environmental conditions, and genomic make-up. It presently includes 226 cyanobacterial strains, with 119 being of Antarctic origin (catalogue: http://bccm.belspo.be/catalogues/ulc-catalogue-search).

The morphological identification shows that the strains belong to the orders Synechococcales, Oscillatoriales, Pleurocapsales, Chroococcidiopsidales and Nostocales. The 16S rRNA and ITS sequences of the strains are being characterized. Our first results show that the 85 Antarctic strains already studied are positioned into 25 OTUs (sequences with > 97,5% 16S rRNA similarity), and thus, represent a quite large diversity. Moreover, strains identified as members of the genera *Leptolyngbya* or *Phormidium* appear in several lineages. This supports the need to revise these polyphyletic genera with a simple filamentous morphology. To better understand the functioning, metabolism and adaptative strategies of cyanobacteria in the extreme Antarctic environment, the genome sequencing of a few strains has been started.

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Cyanobacteria of some Arctic regions, and low temperature resistance of *Nostoc sp.*

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Cyanobacteria are constituent elements in terrestrial ecocystems. These organisms are especially important in cold deserts, often being among the first colonizers of the bare ground exposed by retreating snow and ice cover. The purpose of the present research was to study the diversity of cyanobacteria in three geographically separated Arctic regions (Taimyr Peninsula (73°31'07.9"N, 80°41'08.3"E), Dickson Island (73°30'30.8"N, 80°24'48.9"E), and Hayes Island (80°36'41.2"N, 57°54'56.2"E), and to evaluate the resistance of some strains to extremely low temperatures. Frost resistance of selected clonal cultures across a gradient from above freezing to extremely low temperature (+4°, -10°, -18°, -50°, -80°, -100°, -120°, -140°, -160°C) was determined.

Twenty-one species and intraspecific taxa of Cyanobacteria from five families were detected. In all studied samples, *Trichocoleus* cf. *hospitus* (Hansgirg ex Forti) Anagnostidis and *Nostoc sp.* were observed. Several species of the polyphyletic genus *Leptolyngbya* were found. Among them, *Leptolyngbya woronichiniana* Anagnostidis et Komárek was the most frequently encountered species. This is the first report about cyanobacteria of Dickson and Hayes Islands. In experiments with freezing cultures, *Nostoc* sp. isolated from Hayes Island was used as the test organism. At temperatures from -18° to -140°C, the appearance of brownish cytoplasmic inclusions was detected. Possibly, these inclusions represent carotenoids. At -160°C the death of 65% vegetative cells was observed. About 50% of cyanobacteria experienced morphological disturbance in the form of thinning of trichomes as well as plasmolysis of vegetative cells and heterocysts. An increased amount of mucilage and increased presence of bacteria and fungi in the mucilage were found.

The study of cyanobacterial resistance to extremely low temperature could help us to understand the mechanisms of vitality in cyanobacteria as well as the distribution of these organisms in extreme climates.

(Poster)