

Forschungsinstitut für
Limnologie



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1. Mission Statement

Our mission is to investigate and advance scientific understanding of freshwater ecosystems, and to disseminate this knowledge through scholarly publication and education. As an ecological discipline, limnology is the comprehensive science of the biological properties of inland waters in their physical-chemical environment. We use aquatic model organisms, reaching from bacteria to fish species, to investigate patterns and processes of general ecological and evolutionary relevance. We are especially interested in understanding the proximate and ultimate factors responsible for the distribution, interactions, and specific adaptations of freshwater organisms. Our emphasis is on process oriented basic research, but our research results are also used for consulting and in the search for solutions in the management and protection of inland waters. Our present research provides the basis for the sustainable use and protection of the water quality of our fresh waters. We provide training for national and international graduate students and post-doctoral fellows within various research projects. Our current research focuses on investigating the origin and maintenance of diversity of aquatic organisms and communities at various levels, ranging from molecules (genes and proteins) over organisms and populations to communities.

2. Scientific Activity 2012

2.1 . Zusammenfassung des wissenschaftlichen Berichts 2012

Während des letzten Jahres war das Institut für Limnologie (ILIM) mit den größten strukturellen Veränderungen seit seinem Bestehen konfrontiert. Fast 40 Jahre nach seiner Gründung wurde das Institut von der Österreichischen Akademie der Wissenschaften (ÖAW) an die Universität Innsbruck transferiert (mit Stichtag 1. September 2012) und ist nun das Forschungsinstitut für Limnologie, Mondsee der Fakultät für Biologie. Dieser Transfer verlangte große administrative Veränderungen und stellte für die involvierten Entscheidungsträger eine große Herausforderung dar. Das Institut möchte seinen Dank an die verantwortlichen Personen des Österreichischen Bundesministeriums für Wissenschaft und Forschung, der Oberösterreichischen Landesregierung, der Österreichischen Akademie der Wissenschaften und der Universität Innsbruck ausdrücken, die alle diese Angliederung stark unterstützten und ermöglichten. Besonderer Dank gilt Rektor T. Märk und seinem Rektoratsteam für die Bereitschaft und das entschlossene Handeln, das Institut, in so kurzer Zeit und unter schwierigen Bedingungen, in die Universität Innsbruck zu integrieren.

Ebenso wie das Institut wurden auch die "International Training Programmes in Limnology" (IPGL) im letzten Jahr an eine Universität übertragen. IPGL diene als zentrale Stelle für die Ausbildung internationaler Postgraduierter und war seit 1975 am ILIM beheimatet. Seit Oktober 2012 ist IPGL vollständig in die Universität für Bodenkultur Wien integriert. Obwohl der Weggang von IPGL nach Wien einen großen Verlust für die Ausbildungs- und Forschungskapazitäten des Instituts bedeutet, begrüßen wir, dass die vielfältigen Aktivitäten von IPGL nunmehr unter anderer Schirmherrschaft fortgeführt werden können.

Die zahlreichen administrativen und organisatorischen Veränderungen, die durch die Übertragung am ILIM hervorgerufen wurden, hatten gewisse Auswirkungen auf die Forschungsaktivitäten während des letzten Jahres. Die Forschungsarbeit unter dem aktuellen Thema *"Untersuchung des Ausmaßes, der Herkunft und der ökologischen Bedeutung innerartlicher Vielfalt von aquatischen Mikro- und Makroorganismen"* wurde fortgeführt. Der gemeinsame Nenner aller Forschungsgruppen am ILIM ist die Untersuchung von mikroevo-lutionärer (d.h. unterhalb des Art-niveaus) Anpassung an bestimmte, wechselnde Umweltbedingungen. Dazu dienen ausgewählte Modellorganismen aus Organismengruppen von Bakterien bis hin zu Fischen. Das bedeutet auch, die daraus resultierenden Entwicklungen dieser Änderungen auf die Organismen, die z. B. durch den Klimawandel hervorgerufen werden, auf Ökosystemebene zu berücksichtigen. Während des Berichtszeitraums konnte auf allen Ebenen, von Genen und Molekülen bis hin zu ökosystemaren Veränderungen in der Diversität, maßgeblicher Fortschritt erzielt werden.

Die Tatsache, dass die Zahl der anonym begutachteten Publikationen (16) im Jahr 2012 ungewöhnlich niedrig war, ist in erster Linie auf zufällige Schwankungen zurückzuführen. Dabei muss berücksichtigt werden, dass die Forschungsleistung hinsichtlich

begutachteter Publikationen im Vorjahr (2011) einen Höchststand erreicht hatte (36). Der Berichtszeitraum stellt das fünfte Jahr dar, indem die Aktivitäten des ILIM massiv infolge der Ausgliederung der Einrichtung auf fünf verstreute Standorte mit unzureichender Infrastruktur behindert wurden. Auch das Fehlen von adäquaten Arbeitsplätzen für Gastforscher beeinträchtigte die Forschungsleistung während der letzten Jahre. Die Zahl an 'senior scientists' wurde auf acht reduziert, im Vergleich zu 13 in den Jahren 2007/08. Es war daher von größter Wichtigkeit, dass die problematischen letzten Jahre an der ÖAW nun durch eine langfristige Perspektive an der Universität Innsbruck abgelöst wurden. Im laufenden Jahr hat ILIM zum ersten Mal eine finanziell stabile Situation mit Planungssicherheit für die nächsten drei Jahre erreicht. Der Umbau der Büro- und Laboreinrichtungen des Institutsgebäudes am Mondseeufer wird nun zügig vorangetrieben. Die Eingliederung der senior scientists des Instituts in die Lehraktivitäten der Fakultät für Biologie hat bereits begonnen und wird 2013 fortgeführt. Im Gegensatz zu den letzten Jahren ist das Institut nun wieder optimistisch hinsichtlich seiner nahen und mittelfristigen Zukunft und begrüßt die neuen Herausforderungen unter der Schirmherrschaft der Universität Innsbruck.

2.2. Summary of the scientific report 2012

During the past year, the reporting institute was confronted with the greatest structural changes during its existence. Almost 40 years after its foundation, the Institute for Limnology (ILIM) was transferred from the Austrian Academy of Sciences (AAS) to the University of Innsbruck (effective September 1st, 2012) and is now the Research Institute for Limnology, Mondsee, of the Faculty of Biology. This transfer required major administrative changes and provided a challenge for the decision makers at the various levels involved. The Institute expresses its gratitude to the responsible persons at the Austrian Federal Ministry for Science and Research, the Provincial Government of Upper Austria, the Austrian Academy of Sciences, and the University of Innsbruck, who all strongly supported and enabled this move. In particular, ILIM wants to thank Rector T. Märk and his rectorate team for their willingness and resolute acting to incorporate ILIM into the University of Innsbruck at a short notice and in difficult times.

Similar to the Institute, the long-term International Training Programmes in Limnology (IPGL), which served as a hub for international post-graduated training and were hosted by ILIM since 1975, were transferred to an Austrian university during the past year. Since October 2012, IPGL has been fully integrated into the University of Natural Resources and Life Sciences, Vienna. Although IPGL's move to Vienna represents a major loss for ILIM's training and research capacities, the Institute appreciates that IPGL's varied activities can be continued under a different umbrella.

The various administrative and organisational steps involved in ILIM'S move had some impact on its research activities during the past year. Research was continued in several projects within the current focus, i.e. investigating the *"extent, origin and ecological*

significance of intraspecific diversity of aquatic micro- and macroorganisms". The common denominator of all working groups at ILIM is to investigate microevolutionary (i.e., at the subspecies level) response to particular and changing environmental conditions, using selected model organisms ranging from bacteria to fish. This also implies to consider feedback emerging from changes at the ecosystem level to the organisms, which may be caused, for instance, by climate change. During the reporting period, significant progress was made at all levels, reaching from genes and molecules to ecosystem changes in the diversity.

The fact that the number of peer-reviewed publications (16) was unusually low during 2012 reflects primarily accidental fluctuations, considering that the research output of peer-reviewed publications had peaked in the previous year (36). However, the reporting period comprises the fifth year in which the activity of ILIM was significantly hindered due to the relocation of its facilities to five dispersed locations with inadequate infrastructure. The lack to offer guest researchers adequate work space compromised ILIM's research output during the past years. The staff of senior scientists was further reduced to only eight, compared to 13 in 2007/08. It is therefore of utmost importance that the agonising final years at the AAS were replaced by a long-term perspective at the University of Innsbruck. Beginning in 2013, ILIM had, for the first time, received a financial stable situation with planning certainty for the next three years. Rebuilding of ILIM's main office and laboratory facilities at the shore of Lake Mondsee will progress at a fast pace. Integration of ILIM's senior scientists into the teaching activities of the Faculty of Biology have already begun and will be continued in 2013. In short, in sharp contrast to the previous years, ILIM is optimistic about its own near and mid-term future and welcomes the new challenges under the umbrella of the University of Innsbruck.

2.3 Report on the scientific activity during 2012

The following pages report the results of ILIM's individual working groups. The principal investigators are listed in bold face.

Molecular ecology and physiology of cyanobacteria

(**R. Kurmayer**, S. Blank, Q. Chen, G. Christiansen, M. Frei, K. Moosbrugger, V. Ostermaier, P. Trummer, A. Wiedlroither)

Genotype determined toxin content in the cyanobacterium *Planktothrix* (FWF-P20231)

Single isolates of the genera *Microcystis* and *Planktothrix* differ consistently in the production rate of the hepatotoxin microcystin (MC) when grown under controlled and identical conditions in the laboratory (Fig. 1). The causes for these differences are not known. For the *mcy* gene cluster of *Microcystis* sp., a bi-directional promoter has been described and putative intercistronic transcription start sites have been suggested. In *Planktothrix* sp., *mcyT* located at the 5' end of the *mcy* gene cluster is transcribed in the opposite direction compared to the other *mcy* genes. We hypothesized that insertions/deletions within the putative promoter region(s) resulted in a change in the *mcy* transcription rate.

Thirteen strains were grown semi-continuously under maximum growth rate conditions at 20°C under relatively high irradiance ($50 \mu\text{mol m}^{-2} \text{s}^{-1}$); cells were extracted for both MC and mRNA to quantify the transcript amount of each of the nine *mcy* genes in relation to two housekeeping genes: phycocyanin (*cpcBA*), DNA dependent RNA polymerase (*rpoC*).

For the whole *mcy* gene cluster there was little variation in transcript amount between individual *mcy* genes. There was a statistically significant difference in the *mcyG* transcript amount between low and high MC producers. For *mcyH* and *mcyA* the difference in transcript amount between low and high MC producers was marginally significant. In contrast for all other genes no difference was observed. Linear regression analysis revealed a significant dependence of MC content on *mcyG* transcript amount (Fig. 2).

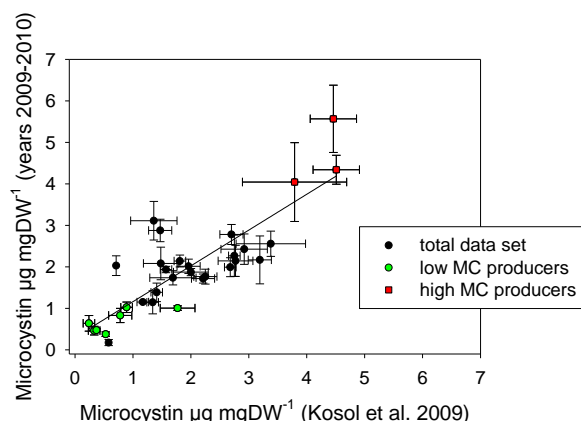


Fig. 1. Relationship between MC contents ($\mu\text{g MC-LR equiv. mg dry weight (DW)}^{-1}$) as determined from single isolates in the course of two consecutive experiments performed during years 2003-2004 and 2009-2010.

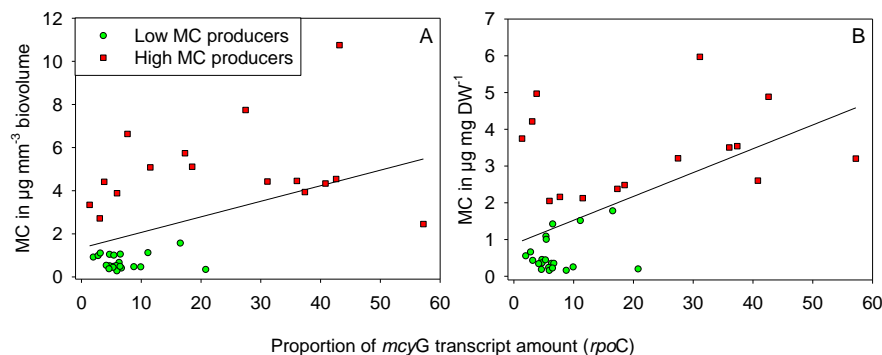


Fig. 2. Linear relationship between *mcyG* transcript amount and MC content per dry weight (A) and biovolume (B).

These results show, for the first time, that *mcy* genotypes differ in the *mcy* transcript amount which can explain a significant part of the variation of the MC content among isolates. Only the transcript amount of genes located downstream of the longest intergenic spacer *mcyEG* (274 bp), i.e. *mcyG*, H, A were significantly correlated with the MC content. Notably, two strains carrying a 128bp deletion within this longest intergenic spacer region (*mcyEG*) showed a high MC content and a weaker relationship between the transcript amount and MC content.

Genetic population structure, evolutionary loss of toxin synthesis genes and secondary metabolite synthesis in *Planktothrix* (FWF-P24070),

It is intriguing to note that toxins produced by cyanobacteria show a patchy distribution, i.e. within a species both strains able to produce a certain toxin as well as nontoxic strains exist. Green or red pigmented strains of the genus *Planktothrix* differ in the presence/absence of MC and numerous additional (non-)ribosomally produced bioactive peptides. The factors influencing this patchy distribution are not understood.

In this project 62 strains analysed previously for the presence/absence of the *mcy* synthesis gene cluster were supplemented by 76 strains isolated from Europe (Finland, Portugal, Italy/Sicily), Russia, North America (Alberta, Maine) and East Africa (Uganda). In total, we analyzed 138 strains for (i) the presence of remnants of the *mcy* gene cluster in non-toxic strains, (ii) for their phylogenetic relation from the genetic variation within seven housekeeping gene loci, (iii) the occurrence of MC and additional bioactive peptide families as revealed by LC-MS (J. Blom, Limnological Station, University of Zurich).

The phylogenetic analysis of the 138 strains revealed a trichotomy consisting basically of a non-toxic lineage 1 (n = 55) and a toxic lineage 2 (n = 73) occurring in both continents (Europe and North-America) as well as one non-toxic tropical lineage 3 (n = 7). Notably, all 56 strains that did not contain the full *mcy* gene cluster contained remnants of it.

In general, the peptide family called anabaenopeptins ($n = 100$) occurred most frequently. Further putative cyanopeptolins ($n = 102$), and MCs ($n = 64$) occurred in lineages 1, 2. The ribosomally produced planktocyclusins occurred with two variants and were the least abundant ($n = 23$). Using direct gradient analysis (CCA) the dependence of peptide occurrence on phylogenetic, ecophysiological (e.g. pigmentation) and environmental (water depth, geographical distance) parameters was determined. The two abundant groups MCs and anabaenopeptins showed little correlation with the phylogenetic, geographical or ecophysiological parameters. In contrast among the aeruginosins and cyanopeptolins many peptides had their optimum frequency within strains assigned to a specific phylogenetic lineage (Fig. 3).

Thus comparing peptide occurrence quantitatively between lineages can elucidate correlations between particular peptide abundance and the speciation of the respective lineages.

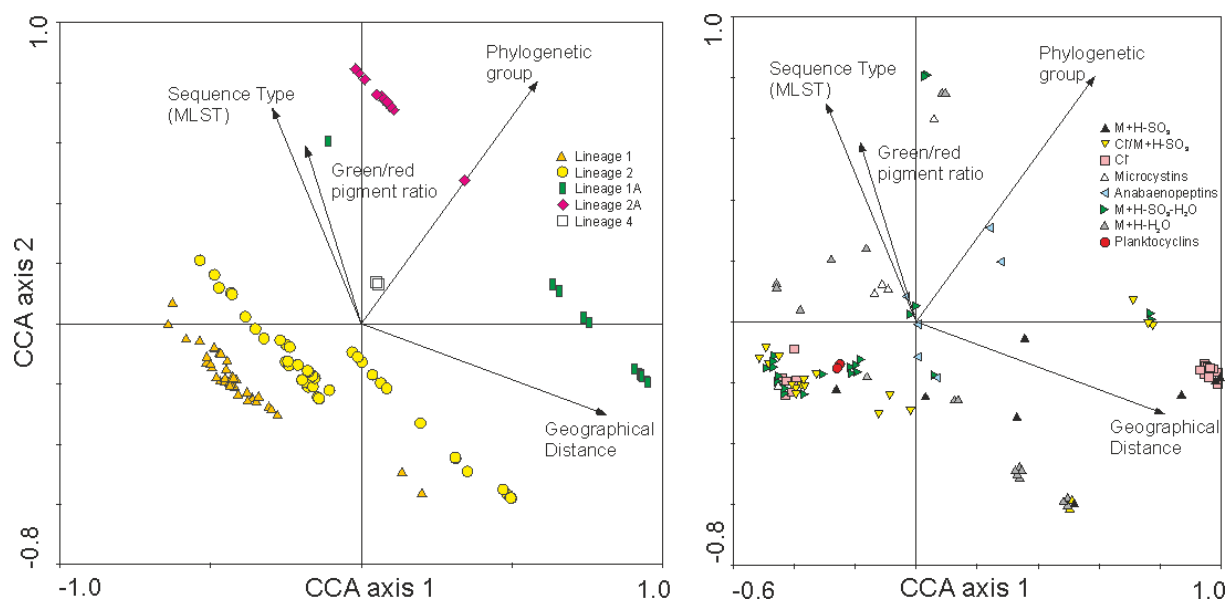


Fig. 3. CCA of bioactive peptide occurrence ($n = 95$) recorded among 134 *Planktothrix* strains in dependence on the parameters geographical distance, phylogenetic lineage, sequence type and pigmentation. A) strains vs parameters plot, B) peptides vs parameters plot. Peptides that occurred only once were omitted. Rare peptides were down weighed. The influence of CCA axis 1 and 2 was highly significant ($p < 0.002$). Legend: A) Orange triangle = non-toxic lineage 1, Green box = non-toxic lineage 1A, Yellow circle = toxic lineage 2, Pink diamond = toxic lineage 2A, white square = lineage 4. B) black triangle, yellow triangle-down, pink square = different aeruginosins, white triangle = MCs, blue triangle-left = anabaenopeptins, green triangle-right, grey triangle= different cyanopeptolins, red circle = planktocyclusins.

Characterization of microbial biodiversity in the pelagic zone of alpine lakes using high throughput sequencing (project DETECTIVE)

The influence of rising air temperature is expected to be particularly pronounced in alpine ecosystems as they are typically inhabited by cold-adapted stenothermic species which would become extinct. It has been suggested that alpine lakes with a low average water

temperature during summer are most vulnerable to a warmer climate, as a sudden rise in temperature would significantly shift species occurrence towards more opportunistic species such as bloom-forming cyanobacteria.

In order to characterize pelagic bacterial community composition in relation to average water temperature we used ultra-deep sequencing of the 16S rRNA gene amplified from five alpine lakes of the Niedere Tauern region (1700-2118 m a.s.l.) during the years 2009-2011. The lakes differed significantly in summer mean water temperature by approx. 4°C, which reflected rather local effects than the influence of the altitude. In general, the lakes were of oligotrophic state and the absolute bacterial numbers were correlated with phytoplankton biomass as indicated by chlorophyll a. Maximum Chlorophyll a values coincided with highest phototrophic cyanobacterial abundance.

The sequences were processed and analysed using the QIIME pipeline. A total of 272,571 sequences including the hypervariable region V3 and 594,260 sequences including V6 (average length 534 bp) were obtained, resulting in 9,366 OTUs and 16,751 OTUs, respectively (97% similarity). The most important phyla comprised proteobacteria (52% (V3); 56% (V6)), bacteroidetes (22%, 18%), actinobacteria (9%, 9%) and (non-chloroplast) cyanobacteria (5%, 4%). The highest cyanobacterial abundance in more productive lakes was confirmed and within cyanobacteria the genera *Cyanobium* (0-76%) and *Synechococcus* (24-63%) were identified most frequently. Other cyanobacteria such as *Limnothrix* and *Anabaena* occurred specifically in some lakes.

The lowest species diversity was observed in the lake with the lowest summer mean temperature (~8°C) implying that specific cold-adapted species might competitively exclude bacterial species occurring in warmer lakes (Fig. 4 and Fig. 5). Indeed the respective communities differed significantly and consistently in bacterial community composition suggesting that the annual variation in growth period (e.g. influenced by changing ice cover duration) within lakes did not lead to pronounced seasonal variation in bacterial community composition (data not shown).

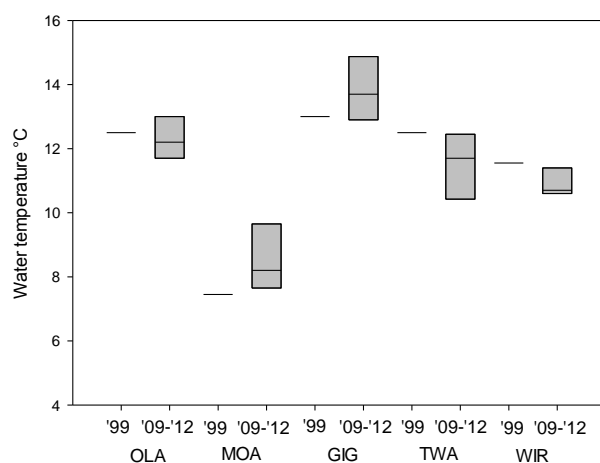


Fig. 4. Median (25-75% quartiles) water temperature in August (2.5 m depth) of five alpine lakes in the Niedere Tauern (during 1999 and 2009-2012).

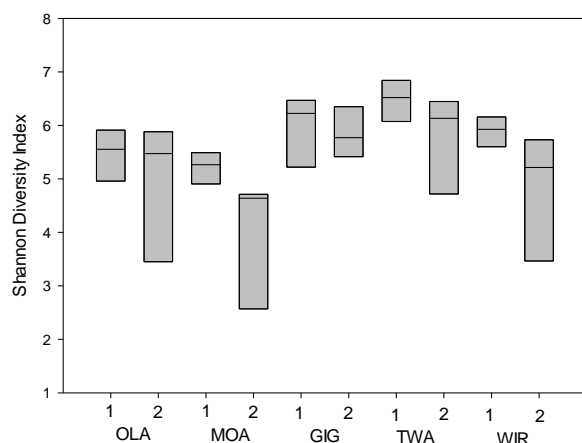


Fig. 5. Median (25-75% quartiles) alpha diversity of bacterial communities in two size fractions (1:>1.2 µm, 2:1.2-0.2 µm) in the same lakes (2009-2011)

Legend: OLA = Ob. Landschitzsee, MOA = Moaralmsee, GIG = Unt. Giglachsee, TWA = Twenger Almsee, WIR = Unt. Wirpitschsee.

Functional genetics of cyanobacteria

(G. Christiansen, S. Ullrich, R. Kurmayer)

This research was performed in the course of FWF project P20231 (Genotype determined toxin content in cyanobacteria).

For cyanobacteria the genetic regulation mechanisms in secondary metabolite synthesis are poorly understood. This work focused on genetic/enzymatic factors that control the rates of biosynthesis of the toxic metabolite microcystin in the cyanobacterium *Planktothrix agardhii* NIVA-CYA 126/8. Microcystins are toxic secondary metabolites that are synthesized by non-ribosomal peptide synthetases (NRPS). We have specifically investigated the influence of a tailoring enzyme (McyT) on microcystin production. Tailoring enzymes catalyze chemical reactions that are not essential for the production of secondary metabolites; instead they have decorating functions like the transfer of side groups such as methyl groups onto the final product. In previous experiments we have shown that McyT (a type II thioesterase) is involved in microcystin production as the CYA126/8 mutant with an inactivated *mcyT* gene showed a decreased microcystin content (minus 94% when compared to the wild type). In other organisms (*Bacillus subtilis*) the type II thioesterase associated with NRPS has been shown to have a cleaving function, regenerating the misloaded phosphopanthoine (PP)-cofactor from peptidyl carrier proteins (PCPs) since the PP-transferases are not able to distinguish between acetylated and free CoA. A misloaded PP-cofactor has the consequence that the biosynthesis is blocked until a type II cleaves the acetyl residue making the biosynthesis again possible. It was hypothesized that McyT also is positively influencing the synthesis rate of microcystin in *Planktothrix*.

We were interested in a CYA126/8 mutant that over expresses McyT and analyzed the consequences on microcystin production. Therefore we synthesized a second gene copy by means of synthetic biology (*mcyTsyn*) which was designed by back translation of McyT using the codon usage of *Planktothrix* and put this under the control of two differently active

promoters and terminator sequences. These two constructs were introduced into *Planktothrix agardhii* CYA 126/8 by electroporation. The two resulting mutants were cultivated under defined conditions and harvested three times when reaching OD880= 0.1. RNA was extracted and transcribed into cDNA and subsequently used for quantitative PCR. A specific antibody against McyT was raised and used to determine the abundance of McyT protein in the different transformants. Microcystin contents were determined by HPLC-DAD.

We could show that the second gene copy *mcyTsyn* is efficiently transcribed and translated into McyT enzyme in both mutants1, 2. Contrary to expectation, both mutants which overexpressed the McyT enzyme showed a negative correlation between additional McyT enzyme and microcystin content. One working hypothesis is that if too much McyT is expressed, then also a correctly loaded PP-cofactor would be cleaved, therefore resulting in a contraproductive function of McyT. If this is true, then this experiment would highlight the physiological fine-tuning of the microcystin biosynthesis pathway, for example by the evolution of the bi-directional promoter region in the microcystin biosynthetic gene cluster resulting in the same transcriptional rate of both the *mcy* gene cluster and *mcyT*. Investigations of the biochemical mechanisms of the role of McyT are underway and will include cross-linking experiments to identify the protein-protein interactions connected to McyT enzyme.

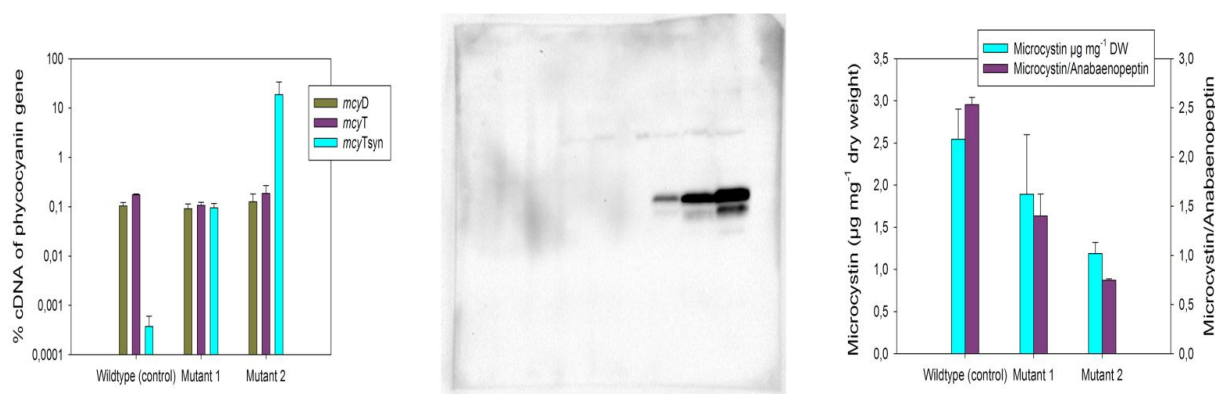


Fig. 6 (left): Quantification of cDNA abundance, indicating a moderate level of *mcyTsyn* (mutant1) and a high level of *mcyTsyn* transcription in mutant2, while other genes (*mcyD* and *T*) were unaffected.

Fig. 7 (middle): Immunohistochemical analysis of whole protein extracts of wild type (lanes 1-3), mutant1 (lanes 4-6) and mutant2 (lanes 7-9) with a specific antibody against McyT showing a clear signal in the high level of *mcyTsyn* transcription mutant 2 (lanes 7-9).

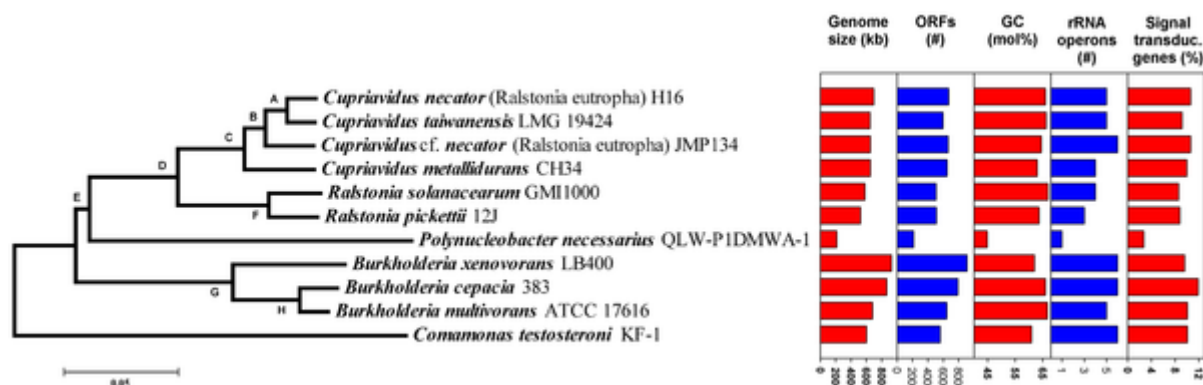
Fig. 8 (right): Microcystin content of wild type, mutant1 and mutant2 in relation to dry weight or another related but independently synthesized peptide Anabaenopeptin.

The work within the DETECTIVE project (PhD thesis S. Blank) was dealing with sample preparation optimization. We became aware that specific sequences of 5'-extensions ("barcodes") of oligonucleotides used for amplification of environmental DNA samples for ultra-deep amplicon sequencing can have significant effects on the efficiency of the DNA dependent DNA polymerase. We tested several PCR ingredients/conditions and different DNA dependent DNA polymerases until we found a blend which showed optimal amplicon yields.

Our research on genetic analyses of single cells/filaments (PhD thesis Chen Q.) showed that single filaments of *Planktothrix* spp. isolated from lake Mondsee and other lakes of central Europe contain sufficient amounts of chromosomal DNA for up to fifty different single PCRs. Using our established protocols we analyzed several hundreds of *Planktothrix* filaments directly isolated from the ecosystem and analyzed a large secondary metabolite gene cluster (*mcyT-J*) for genetic recombination events.

(M. Hahn, J. Schmidt, M. Gadermaier)

Fig. 9. **Phylogenetic position of the genome-sequenced *Polynucleobacter* strain.** Reconstruction of the phylogenetic position of the genome-sequenced strain *P.n. ssp. asymbioticus* QLV-P1DMWA-1 and genome characteristics of the strains used for the phylogenetic analysis. The presented tree is based on concatenated alignments of amino acid sequences of proteins encoded by eight housekeeping genes and was constructed using the NJ method. Letters A to H refer to bootstrap values obtained for the respective nodes by three different treeing methods in analyses of nucleotide and amino acid sequence data sets.



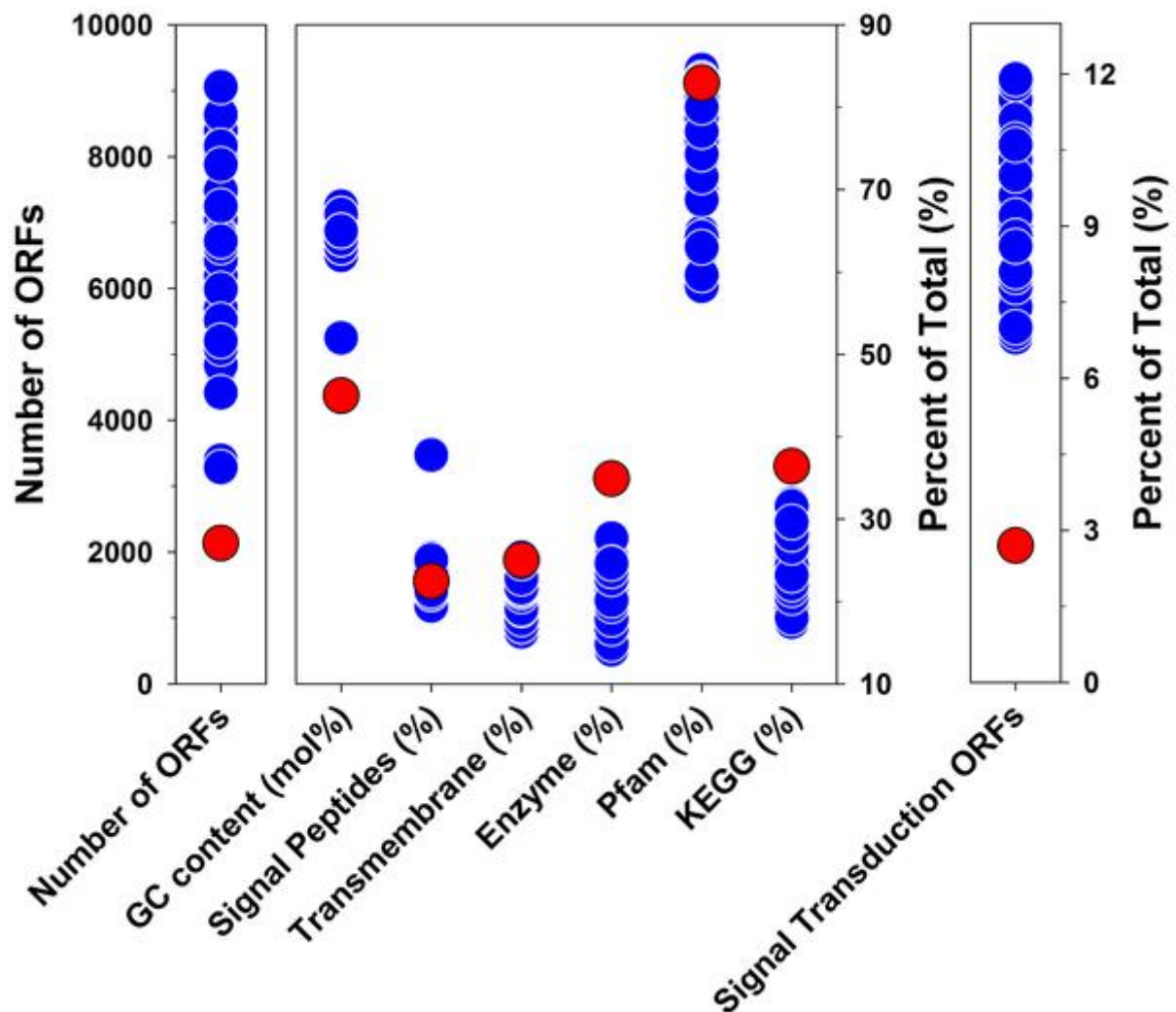


Fig. 10. **Variability of genomic traits among genome-sequenced members of the family *Burkholderiaceae*.** The depicted traits are the total number of ORFs, G+C content of the genomes, percentage of CDS encoding signal peptides, transmembrane domains, genes assigned to Enzyme Commission (EC) number classes, proteins assigned to protein families (Pfam), proteins assigned to KEGG categories, and proteins involved in signal transduction. For most traits, 78 genomes of strains affiliated with the family were analyzed using the Integrated Microbial Genomes (IMG) system. The sole exception is the analysis of signal transduction genes, which was performed using the MIST2 database, which provided data on 37 strains affiliated with the Burkholderiaceae. For all depicted parameters, all available genomes of family members were considered but not the genome of the endosymbiotic *Polynucleobacter* strain STIR1. Data of strain QLV-P1DMWA-1 are indicated as red dots.

Another important step performed during the reporting period was the description of the new species *Polynucleobacter difficilis* representing an important part of the *Polynucleobacter* cluster, i.e. the subgroup PnecB1 (Hahn et al., 2012a). This species description completes the description of at least one species representing one of the five *Polynucleobacter* subclusters PnecA, PnecB1, PnecB2, PnecC, and PnecD (Fig. 11). All these species descriptions performed over the last past years provide microbial ecologists with a sound taxonomic framework for investigations on the ecological significance and function of this important group of freshwater bacteria (Jezbera et al., 2012).

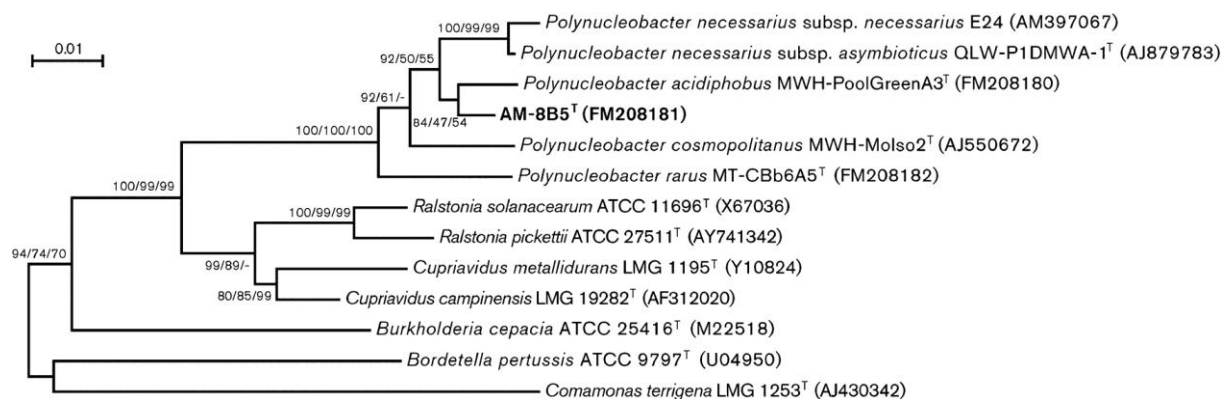


Fig. 11. **Phylogeny and taxonomy of the genus *Polynucleobacter* (*Burkholderiaceae*, *Betaproteobacteria*)**. The tree represents the currently taxonomically described *Polynucleobacter* taxa. All but the species *P. necessarius* were recently described by the Hahn group. The latest described species *P. difficilis* is represented in the tree by strain AM-8B5^T.

Plankton ecology and ecophysiology

(T. Weisse, P. Stadler, U. Scheffel, B. Gröschl)

Continuing previous research of ILIM, a new project investigates the **Effects of short-term climate fluctuations on phytoplankton in Lake Mondsee** (Master thesis B. Gröschl). This project encompasses field and laboratory work. Analyses of samples that had been taken from several stations in Lake Mondsee in the summer of 2011 in relation to meteorological extreme events (floodings, heat waves) are under way. Laboratory experiments investigating the response of an artificial, 'Mondsee-like' phytoplankton community to short-term temperature fluctuations (6°C change over three weeks) were begun at the end of the reporting period. Temperature variations spanning 6°C within a period of several weeks had been observed in the epilimnion of Lake Mondsee in recent years. The experimental work that will be continued in the current year will also include phytoplankton response to nutrient changes. Considering that, e.g., many chrysophytes species have lower nutrient (phosphorus) requirements than diatoms and are more sensitive to elevated water temperatures than most cyanobacteria, we expect significant changes in the phytoplankton community in response to temperature and nutrient fluctuations in L. Mondsee. Accordingly, the laboratory experiments are designed in a way that specific hypotheses can be tested.

We have continued the successful cooperation with the Helmholtz Centre Potsdam - German Research Centre for Geosciences (GFZ), Germany, with respect to assessing the environmental responses to late glacial and more recent climatic fluctuations recorded in the sediments of Lake Mondsee. We have assisted GFZ with the sampling program, deploying of moorings and buoys, etc. during the reporting period. Results from two ongoing dissertations supervised by GFZ, recent research conducted by the Department of Geoinformatics - Z_GIS of the University of Salzburg in the catchment area of L. Mondsee and ILIM's work shall lead to a joint research project between GFZ, ILIM and Z_GIS. As a first step for the

project application, a meeting was held at Mondsee in October 2012. We intend to submit a joint project application on the impact of flood events on the physical-biological coupling in Lake Mondsee and its catchment in 2013.

The focus of last year's work was on investigating the **Ecology of endemic ciliates from bromeliads** (FWF project P20360-B17, Morphology and ecology of endemic ciliates from bromeliads; in cooperation with W. Foissner, Univ. Salzburg, PI of the morphological part and leader of the joint project).

Our laboratory experiments on the ecology of the colpodid ciliate *Bromeliothrix metopoides* Foissner, 2010 were described in detail in ILIM's Annual Report 2011; the respective paper was submitted in the reporting period and is now in press (Weisse et al. 2013b). In 2012, we finished the experimental work on the ecology of the sympatric, recently described species *Glaucomides bromelicola* Foissner, 2013. We assessed the response of the ciliates to food, pH, and competition. Although these two species are the most common ciliates in tank bromeliads, their life strategies are clearly different. In contrast to the coexisting *B. metopoides* and many other colpodean ciliates, *G. bromelicola* does not form resting cysts, which jeopardizes this ciliate when its small aquatic habitats dry out. Both ciliates form bacterivorous microstomes and flagellate-feeding macrostomes. However, only *G. bromelicola* has a low feeding threshold and is able to adapt to different protist food. The higher affinity to the local bacterial and flagellate food renders it the superior competitor relative to *B. metopoides*. Continuous encystment and excystment of the latter enable stable coexistence of both species in their natural habitat (Fig. 12). Both species are tolerant to a wide range of pH (4-9). These ciliates appear to be limited to tank bromeliads because they either lack resting cysts (*G. bromelicola*) or have highly specific food requirements (*B. metopoides*).

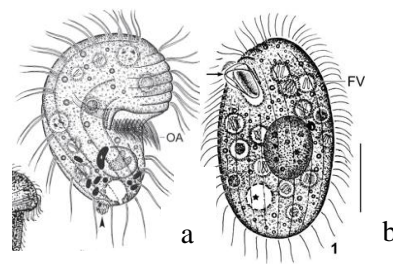
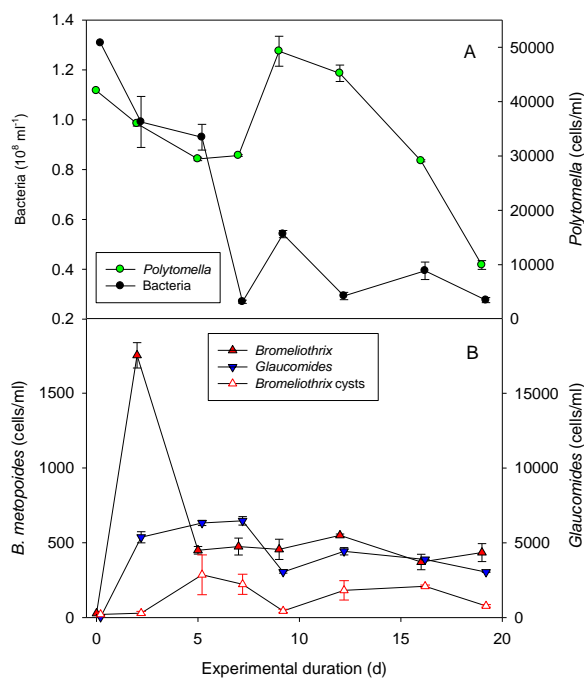


Fig. 12. Competition experiments with the ciliates *Bromeliothrix metopoides* (a; Foissner 2010) and *Glaucomides bromelicola* (b; Foissner 2013) fed with bacteria and the flagellate *Polytomella* sp. (A) revealed stable coexistence of both species over several weeks (B). Symbols are means of three replicates each, error bars denote 1 SD (Weisse et al., subm.).

Investigations on the adaptation of planktonic species (flagellates, ciliates, and rotifers) to extremely acidic mining lakes (former FWF project P20118-B17) were completed by submitting two papers to international journals. The article 'Multiple environmental stressors confine the ecological niche of the rotifer *Cephalodella acidophila*' (Weisse et al. 2013) analyzed the life history response of the recently described rotifer species *C. acidophila* Jersabek, Weithoff & Weisse 2011 to three environmental key factors, pH, temperature and food concentration, in a full factorial design. Using life-table experiments, we demonstrated that *C. acidophila* is a stenoeccious species with a pH-optimum in the range 3-4 and a comparably high food threshold. Combining the laboratory results with field data, we concluded that *C. acidophila* is severely growth limited in its natural habitat (Lake Langau, Lower Austria) and nonviable in circumneutral lakes. In extremely acidic Lake Langau (pH ~2.6), *C. acidophila* occurs at low abundance throughout the year, benefitting from release from competitors and predators.

The new ciliate species *Oxytricha acidotolerans* that was also isolated from Lake Langau in the course of this FWF project was formally described and its response to pH analyzed in comparison to the species *Urosomoida* sp. isolated from an acidic mining lake in Lusatia, Germany (Weisse et al. 2013). Although both ciliates are closely related and dwell in similar habitats, their maximum growth rates and pH optima were significantly different (Fig. 13). These results corroborate the significance of local adaptation that we had recently reported for flagellates (Moser & Weisse 2011a, b; Weisse et al. 2011) for ciliates.

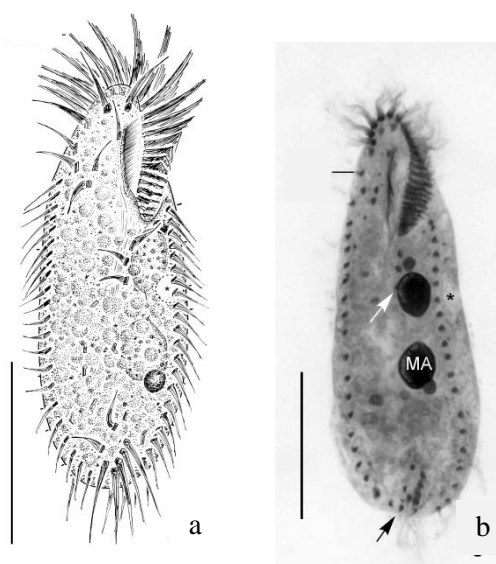
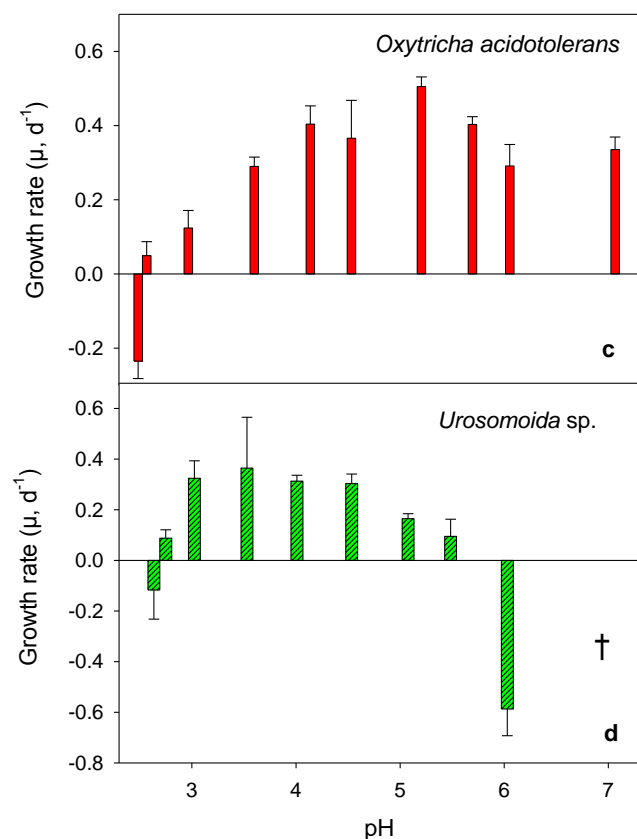


Fig. 13. Left: the ciliate *Oxytricha acidotolerans* in vivo (a) and after protargol impregnation (b). Right: pH response of *O. acidotolerans* (c) and the closely related species *Urosomoida* sp. MA=Macronuclear node; scale bars 30 μ m (modified from Weisse et al. 2012).



Ecology and taxonomy of planktonic ciliates

(B. Sonntag, B. Kammerlander, G. Ong'ondo, D. Pöll, C. Grubbauer, V. Ostermaier, U. Scheffel)

In the year 2012, we theoretically and practically deepened our knowledge on molecular analyses from sequencing individual ciliate species up to pyrosequencing approaches together with our cooperation partners Michaela Strüder-Kypke (University of Guelph, Canada) and the group of Thorsten Stoeck (University of Kaiserslautern, Germany). In the course of her Ph.D. studies, Barbara Kammerlander visited both groups to acquire and finally apply the necessary 'tools' in present and future studies in our working group. Our team was further supported by Veronika Ostermaier who contributes to further understanding of molecular workflows and data evaluation. Regarding this highly interesting morphological-molecular context, we are currently preparing three manuscripts for publication. In detail, i) biogeographic aspects on protists from two distant lake areas including transparent and turbid alpine lakes were investigated and ii) morphological and molecular ciliate data adjusted in samples from one lake. Further, in the ongoing project 'DETECTIVE', samples were taken for biogeographic aspects on the molecular level regarding one ciliate morpho-species from different lakes.

In autumn 2012, we carried out a series of experiments on the photoprotective role of mycosporine-like amino acids, i.e. natural sunscreen compounds present in some planktonic ciliates. This work was done in the course of the ongoing project funded by the Austrian Science Fund (FWF) on 'Ultraviolet radiation (UVR) effects on planktonic freshwater ciliates: an assessment of photoprotection and repair strategies'. Based on the results from the preceding year, important further aspects on the direct photoprotective function of the MAAs in the mixotrophic ciliate species *Pelagodileptus trachelioides* were tested. In detail, the sensitivity of different doses of UVR was carried out experimentally by applying a series of long-pass cut-off filters (Fig. 14). The results showed that the shortest wavelengths appeared to be the most damaging ones to the ciliates when UVR level exceeded 'natural' doses. Because the interim laboratory in Mondsee did not provide any possibility to conduct the necessary experiments, they were again carried out at the Institute of Ecology at the University of Innsbruck.

In the course of his Ph.D. study, Geoffrey Ong'ondo (Egerton University, Kenya) at the University of Duisburg-Essen (supervisor: Jens Boenigk) visited our lab in Mondsee and was trained in the methodology necessary to morphologically describe new ciliate species. Further, we successfully submitted a joint manuscript: Ong'ondo GO, Yasindi AW, Oduor SO, Jost S, Schagerl M, Sonntag B, Boenigk J: "Ecology and community structure of ciliated protists in two alkaline-saline Rift Valley lakes in Kenya with special emphasis on *Frontonia*" to the Journal of Plankton Research.

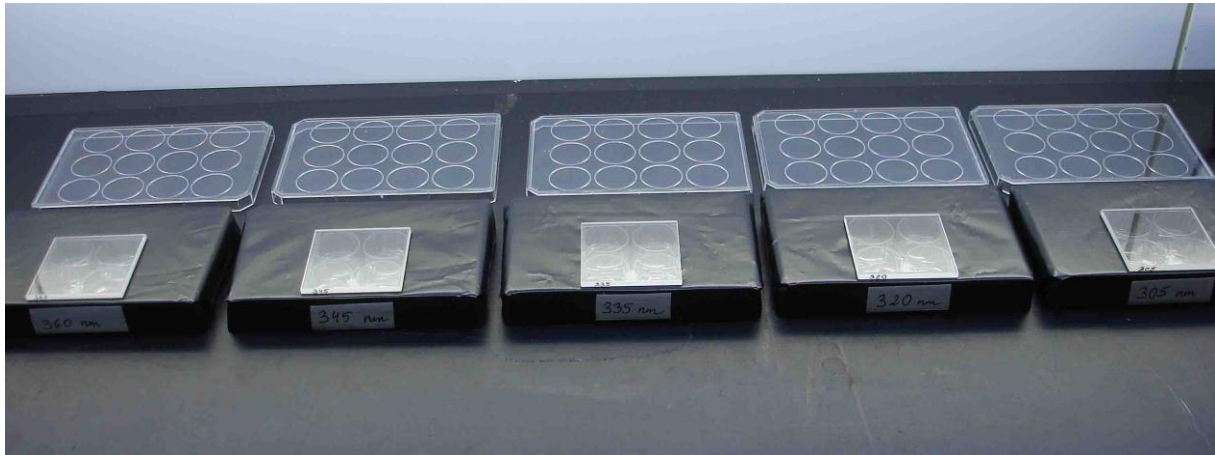


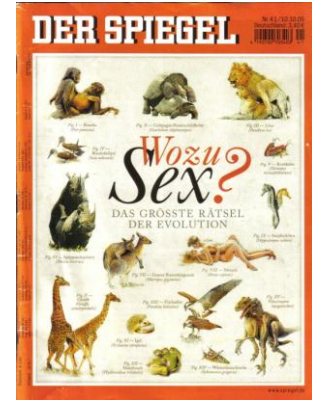
Fig. 14. Experimental setup to test for potentially damaging effects of different wavelengths of the ultraviolet irradiation spectrum on planktonic ciliates. 12-well plates were covered with different long-pass cut-off filters (4 wells each) and dark plastic foil to avoid side-irradiation.

In a cooperation with R. Schabetsberger (University of Salzburg) and U. Sichrowsky (University of Innsbruck), we observed ciliates from three lakes on a South Pacific Island. The ciliate assemblages in these lake are quite different from what has been found so far in temperate freshwater lakes. A detailed manuscript on the ciliate species in these lakes is in preparation.

Molecular & Cytogenetic Evolution of Asexual Aquatic Organisms

(D. Lamatsch, M. Pichler, with students and cooperation partners)

The paradox of sex remains the queen of problems in evolutionary biology and receives wide attention by the general public (right). Sexual reproduction is widespread throughout the animal and plant kingdoms, but under certain conditions remains costly compared to asexual reproduction. Sex creates a wide variety of genotypes on which natural selection can act, but it also breaks up favourable gene combinations. Asexuals have the ability to preserve their genome and to propagate genotypes that have a previous history of success. In addition, asexuals can reproduce twice as fast as sexuals, because all, rather than half, of their offspring are themselves capable of reproduction (=females). Although asexual reproduction offers several clear short-term advantages, ruling evolutionary theory dictates that the absence of a mechanism for rapid genetic change will direct clones persisting over long time frames into evolutionary dead ends. Several animal and plant groups nevertheless show a large incidence of asexual reproduction and some lineages might have been fully asexual for many millions of years.



Undergraduate students as well as interested pupils financed by the Austrian Research Promotion Agency (FFG) were integrated in ongoing research projects offering practical courses ("basic molecular laboratory techniques" and "basic cytogenetic techniques").

Phylogeny and biogeographic history of the cyprinid fish genus *Carassius* (Teleostei: Cyprinidae) with focus on natural and anthropogenic arrivals in Europe

Freshwater fishes of the genus *Carassius*, widespread throughout Europe and Asia, are important aquaculture fishes and include the world's most important pet fish, the goldfish. The high morphologic similarity between the species, however, has up to now prevented reliable conclusions on their taxonomy, biogeography and introduction history. A phylogeny of the fish genus *Carassius* based on the cytochrome b sequence of 404 specimens collected from aquaculture and open water localities across Eurasia identifies most of the presently recognised species as monophyletic lineages, but also that at least one lineage exists that does not correspond to any described species (Fig. 15). Within Europe, feral populations of *Carassius auratus* occur mainly in the Mediterranean area and Great Britain, while *Carassius gibelio* is found in most of non-Mediterranean Europe and some localities in Italy. *Carassius langsdorfii* has very scattered points of occurrence in at least six European countries. *C. auratus* and *C. langsdorfii* are not native to Europe. The populations of *C. gibelio* in eastern Central Europe and parts of Eastern Europe are considered as resulting from a natural postglacial range expansion, while the rest of Europe was colonised due to anthropogenic impact. The presence of diploid ($2n=100$) as well as triploid ($3n=150$) specimens in the three most widespread species indicates that ploidy level is not a character to identify the species of *Carassius*. A remarkably low genetic divergence in *C. gibelio* can be the result of clone selection in the gynogenetic populations. In general, our data present the

first comprehensive overview about the genus *Carassius* in Europe based on genetic data (Rylková, Kalous, Bohlen, Lamatsch, Petrýl 2013 *Aquaculture* 380–383:13–20).

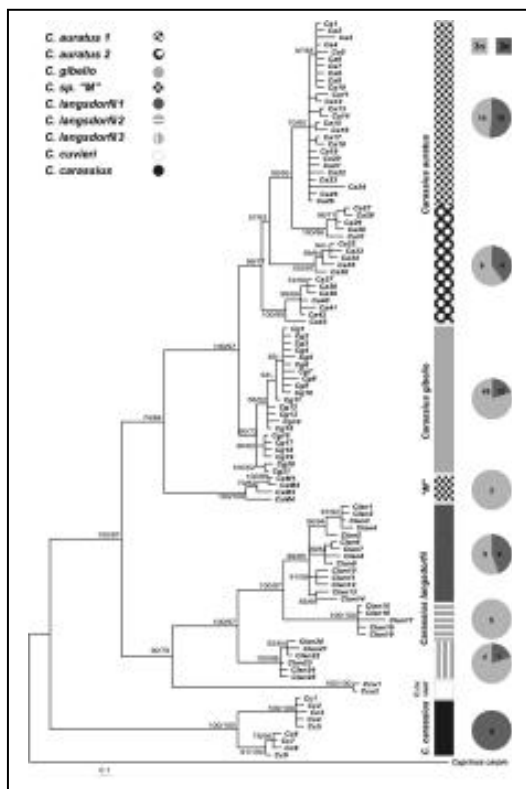


Fig. 15. Reconstructed phylogeny of the Cyt b sequences of *Carassius*. The numbers at the nodes represent statistical supports for BAY and MP analyses respectively. Pie charts indicate proportion (and actual numbers) of diploid and triploid individuals within each group.

The invasive potential of Prussian carp in Finland under the light of a novel semi-clonal reproductive mechanism

When invading European waters, Prussian carp had a strong impact on the ecosystems, but especially on the only European carassiid, the Crucian carp (*Carassius carassius*). In a breeding experiment (Fig. 16) the potential sexual hosts of Prussian carp in Finland and their genetic interactions were assessed. Based on the results the invasive potential and possible consequences of Prussian carp in Finland were evaluated. The studied complex was found to be highly diverse and capable of receiving introgressions from various sexual hosts regardless of genus. This might explain the Prussian carp's extreme success and its threat to the European crucian (Master thesis M. Deinhardt; supervised by J. Taskinen & D. K. Lamatsch).



Fig. 16. Aquaculture conditions for fish larvae from breeding experiment

A transcriptome derived sex –specific marker in the invasive Western mosquitofish *Gambusia affinis*

Sex-specific markers are a prerequisite for understanding the reproductive biology, the genetic factors involved in sex differences, the mechanisms of sex determination and the evolution of sex chromosomes. The Western mosquitofish, *Gambusia affinis* (Fig. 17) is of particular interest as a model for sex chromosome evolution due to its female heterogamety (ZW/ZZ), but also because of its ecological relevance as world-wide invasive species. Here, deep-sequencing transcriptomes were used to identify sequences that were highly transcribed in females but not in males. 179 primer pairs spanning 105 sequences were tested by PCR to identify sex-specific amplification products. From those one female-specific DNA marker was developed and validated in 115 fishes.



Fig. 17. The invasive Western mosquitofish, *Gambusia affinis*.

Sequence analyses revealed a high similarity to the 3' UTR of the aminomethyl transferase (AMT) gene of the relatively closely related platyfish (*Xiphophorus maculatus*). This is the first time that such a methodological approach was successfully used in a fish species, and the identified sex-specific marker represents one of a handful of such markers in fish species (Grant of the Marsden Fund, New Zealand 2010-2012; D. K. Lamatsch, S. Adolfsson, G. Christiansen, A. M Senior, M. Pichler, Y. Ozaki, L. Smeds, M. Scharl, S. Nakagawa (submitted)).

EROS in Ostracods (Evolution of Reproduction with Oversized Spermatozoa in Ostracods) (Grant of the German Research Foundation 2011-2013, with Dr. Renate Matzke-Karasz, LMU Munich, Germany)

In 2012 a new project was started on “EROS in Ostracods” (Evolution of Reproduction with Oversized Spermatozoa in Ostracods). Recent cypridoidean ostracods (Podocopa) are living mainly in fresh or brackish water environments. They reproduce with filamentous giant sperm, reaching up to ten times the body length of the animal (Fig. 18). A common origin of their reproduction with giant sperm is well supported by fossil evidence from the lower Cretaceous, speaking for an evolutionary success of this reproductive mode. Considering the energetic costs related to production, transport and storage of giant sperm, the question about the advantages stands to reason.

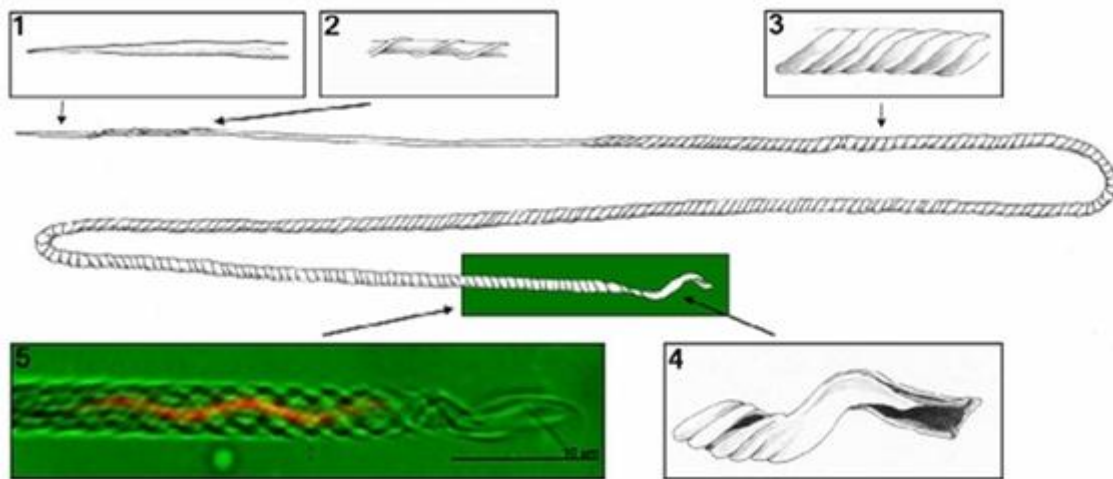


Fig. 18. Graphic overview on the morphology of a giant ostracod sperm.

The present project features two hypotheses: (A) males developed giant sperm in order to fill up the female receptacles and thus to prevent other males from inseminating the female (aim: optimization of fertilization success) and (B) giant sperm help females to reduce the sperm transfer rate per time unit (aim: diversification of paternities).

Paternity analyses of offspring from controlled crosses by amplified fragment length polymorphism (AFLP) will help to reveal which strategy underlies the formation of giant sperm (Grant of the German Research Foundation 2011-2013, with R. Matzke-Karasz, LMU Munich, Germany).

Experimental Evolutionary Ecology

(C.-P. Stelzer, S. Riss, T. Scheuerl, S. Ullrich: *until July 2012*, P. Stadler: *Jan-June 2012*)

Our main activities during 2012 were devoted to the analysis of experimental data and the preparation of manuscripts. Two of these manuscripts were part of the PhD thesis of T. Scheuerl. In the first one we used time series analysis to study 24 experimental populations of obligate (OP) and cyclical parthenogenetic (CP) *Brachionus calyciflorus*. We showed that population dynamics are significantly destabilized in populations consisting of OP clones as opposed to CP populations. For example, OP populations showed overall higher amplitudes in population cycles, which suggests that they might face higher extinction risks in the long term (Fig. 19). The second manuscript dealt with experimental adaptation of *B. calyciflorus* to two varying harsh environments: a high-salt and a food-limited (suppressing sex) environment. After 56 days of selection and adaptation, the populations showed a significant increase of fitness compared to controls, but more pronounced in the high salt population (i.e., the environment with the higher sex levels). This result is consistent with the theoretical expectation that sex is beneficial for adaptation to new environments. Both manuscripts are currently in review.

In October, S. Riss returned from her maternity leave to resume her postdoc work on a part-time basis (50%). During this time she conducted DNA sequence analyses of *Brachionus plicatilis* populations and analyzed experimental data from a mutation accumulation experiment that took place in 2011. Her contract ended in December 2012 with the official end of the FWF project. In December, the group leader, C.-P. Stelzer, submitted the end report to the FWF. So far, the project has resulted in 9 publications of our group (7 already published, 2 in review). Some remaining datasets are still being analyzed.

In addition, the research within our FWF project “Evolution of asexuality in experimental rotifer populations” has lead to an ongoing collaboration with J. M. Logsdon (University of Iowa, USA). Specifically, the Mendelian inheritance of OP in *B. calyciflorus* (see earlier annual reports from 2009 & 2010) and its possibility to generate full siblings with two contrasting reproductive modes encouraged us to screen for differences in gene expression between CP and OP clones. Currently S. Hanson (PhD student at the Logsdon lab) uses next generation sequencing for analyzing the transcriptomes of OP and CP clones. She also characterized expression of meiosis-specific genes in the two reproductive types (Hanson, Schurko, Hecox-Lea, Mark Welch, Stelzer & Logsdon, in review).

Our research activities during 2012 encompassed an assessment of genome size variation *within* a population of *B. plicatilis* from a small alkaline pond in the vicinity of Neusiedlersee (Burgenland, Austria). Surprisingly, this population exhibited an up to 1.2-fold variation in genome size, a magnitude that is only paralleled by very few examples in the literature. So far, we could establish that this variation is true intrapopulation variation and not confounded by other cryptic species present in this habitat, that the genome size distribution is \pm continuous and close to normal, and that clones with high and low genome size can be

crossed with each other and produce offspring of intermediate genome size. Altogether, this suggests a “quantitative trait”-like variation of genome size in this population. Because of such characteristics *B. plicatilis* should be an exceptionally valuable model system for studying microevolutionary aspects about genome size diversity in eukaryots. We plan to address such questions in the near future.

Other activities. C.-P. Stelzer successfully defended his habilitation thesis at the University of Salzburg in June 2012 (Title: Evolutionary ecology of rotifers). T. Scheuerl submitted his PhD thesis at the University of Salzburg (Title: Evolutionary and ecological consequences of sexual and asexual reproduction in rotifers).

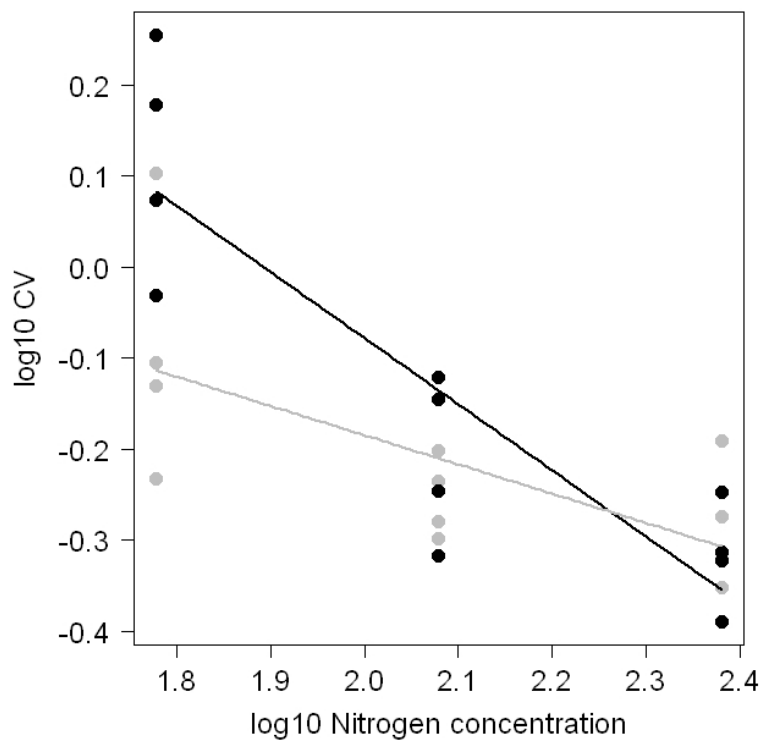


Fig. 19. Relative stability of experimental rotifer populations. Populations experiencing lower nitrogen levels showed greater fluctuations over their mean density. Each dot represents one rotifer population (n=24). Black: OP clones; Gray: CP clones. The coefficient of variation (CV) significantly decreased with the increasing nitrogen level, indicating higher variation in population density at low levels of nitrogen (i.e. predator cycles of larger amplitude). There was a significant difference in the CVs of CP vs. OP clones at 60 μ M nitrogen (F value 9.8816; $P < 0.0056$). At the other nitrogen levels there was no significant difference.

Ecology of Freshwater Fish

(J. Wanzenböck, H. Ficker, S. Mayr: *until June 2012*, T. M. Oberlercher, F. Keil)

The PhD Project of H. Ficker is connected to the project RADICAL (Risk Analysis of Direct and Indirect Climate effects on deep Austrian Lake Ecosystems). He focused on the development of different population models for native and introduced whitefish species (*Coregonus* spp.) in pre-alpine lakes of the Austrian Salzkammergut Lake district. In 2012 he refined his previous models by including demographic and environmental stochasticity. This was accomplished by establishing close cooperation with the International Institute for Applied Systems Analysis (IIASA) where H. Ficker spent three month within the “Young Scientists Summer Program”. Several manuscripts were developed which are currently submitted to international journals. One of those papers clearly shows the detrimental effects of too much stocking of young life stages of whitefish on survival of subsequent year classes and resulting low catches (Fig. 20).

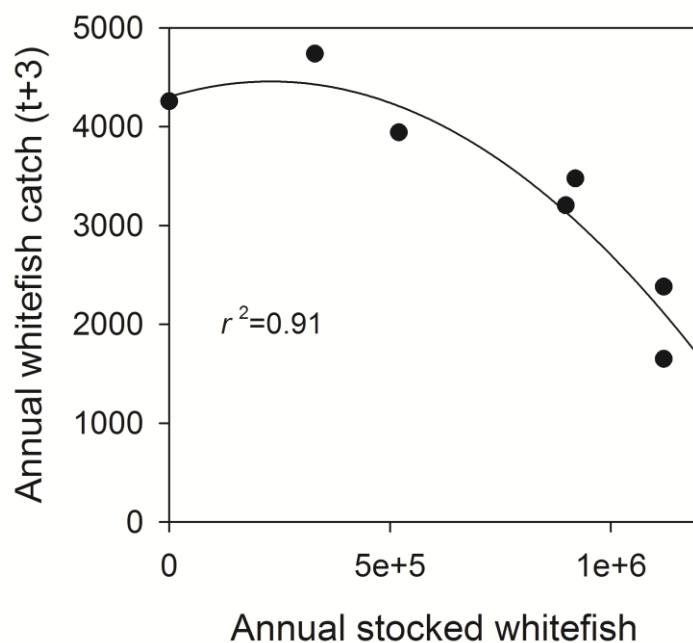


Fig. 20. Non-linear correlation between annual stocking and catch by recreational fishery with a time lag of three years (t+3).

This is equivalent to the stock-recruitment relationship predominantly known from marine fish stocks. Here, a similar relationship was shown for the first time for a freshwater species exclusively exploited by angling where natural reproduction is augmented by stocking and density dependent effects operate on all age classes of the population.

In December 2012 the MSc thesis of F. Keil was finished with the defence at the University of Vienna. He compared different methods of analysing echosounder data (single ping based vs. Track based echo integration) and showed that for whitefish dominated pre-alpine lakes the analysis method has a minor effect compared to diurnal or seasonal differences of surveys. The MSc thesis project of T. M. Oberlercher was continued throughout 2012. He could demonstrate significant, though minor reductions of fertilisation rates of eggs from fish

caught by electrofishing. Furthermore, he found a close correlation between Voltage (in experimentally shocked fish) and fertilisation rate.

The lab technician working in this research group, S. Mayr, started a year of external training in June and replacement of his workforce was delayed until January 2013. Nevertheless, with the help of two trainees (T. Theuretzbacher and S. Wanzenböck) the experimental breeding of whitefish was achieved. This was part of a cooperation project with P. Steinbacher (University of Salzburg, FWF project P23739) in which we are analyzing the effects of thermal conditions during egg incubation on subsequent growth and muscle development.

A cooperation project with colleagues from the Hydrobiological Institute of the Czech Academy of Sciences (J. Frouzova & J. Kubecka) was continued, financed by the Austrian Academic Exchange Service. This included the development of hydroacoustic reference regressions for the relationships between echo-strength and fish size, specifically for whitefish and for various echosounder frequencies done in net-cage experiments. In 2012 we extended these efforts to other fish species. The editorial work to produce a special issue of the journal "Fundamental and Applied Limnology" with selected papers from the "11th International Symposium on the Biology and Management of Coregonid Fishes" organized 2011 in Mondsee, continued throughout 2012 and was finished in January 2013. This issue will include the publication Winkler, K.A., Weiss, S., Pamminer-Lahnsteiner, B., Wanzenböck, J. "Multiple stocks of whitefish (*Coregonus lavaretus* (L.) complex in the pre-alpine lake Traunsee: recommendations for habitat-specific conservation units".

A major new research proposal was developed with H. Ficker, entitled "Comparative evaluation of population bottlenecks in whitefish (*Coregonus lavaretus* sp. complex) with regard to global change: Survival during early life vs. habitat availability for older stages". The proposal was submitted in August 2012 to the Austrian Science Fund (FWF), a decision is anticipated in March 2013.

International Post-Graduate Training Programmes in Limnology (IPGL)

(G.Winkler, R. Brandstätter, plus several national and international partners)

21 young professionals in aquatic ecology and water resource management attended academic training courses organized and implemented by IPGL. Six M.Sc. research projects were facilitated by IPGL and successfully finished. In October 2012, IPGL was transferred to the University of Natural Resources and Life Sciences, Vienna (BOKU) and the international joint-degree Master Programme in Limnology and Wetland Management started with 10 participants successfully at BOKU.



Fig. 21 Field work executed within two IPGL-Master theses in Kenya 2012, supervised by Dr. D. Liti (Moi University/Kenya) and Prof. Dr. H. Waidbacher (University of Natural Resources and Life Sciences, Vienna/Austria)

2.6. Publications 2012 (staff members and former staff members in bold)

Peer-reviewed articles

- **Dokulil, M.T. & Teubner, K.** (2012). Deep living *Planktothrix rubescens* modulated by environmental constraints and climate forcing, *Hydrobiologia* doi: 10.1007/s10750-012-1020-5.
- **Hahn, M.W.**, Minasyan, A., Lang, E., **Koll, U.** and Spröer, C. (2012) *Polynucleobacter difficilis* sp. nov., a planktonic freshwater bacterium affiliated with subcluster B1 of the genus *Polynucleobacter*. *Int. J. Syst. Evol. Microbiol.* 62:376 - 383 doi: 10.1099/ij.s.0.031393-0
- **Hahn, M.W., Scheuerl, T., Jezberová, J., Koll, U., Jezbera, J., Šimek, K., Vannini, C., Petroni, G., and Q. L. Wu** (2012) The passive yet successful way of planktonic life: Genomic and experimental analysis of the ecology of a free-living *Polynucleobacter* population. *PLoS ONE* 7(3): e32772.
- **Jezbera, J., Jezberová, J., Koll, U., Hornak, K., Šimek, K., Hahn, M.W.** (2012) Contrasting trends in distribution of four major planktonic betaproteobacterial groups along a pH gradient of epilimnia of 72 freshwater habitats. *FEMS Microbiology Ecology* 81: 467-479.
- **Luoto T.P.** (2012). Intra-lake patterns of aquatic insect and mite remains. *Journal of Paleolimnology* 47(1): 141-157.
- **Luoto T.P.** (2012). Spatial uniformity in depth optima of midges: evidence from sedimentary archives of shallow Alpine and boreal lakes. *Journal of Limnology* 71: 228-232.
- Meincke, L., A. Copeland, A. Lapidus, S. Lucas, K. W. Berry, T. Glavina Del Rio, N. Hammon, E. Dalin, H. Tice, S. Pitluck, P. Richardson, D. Bruce, L. Goodwin, C. Han, R. Tapia, J. C. Detter, J. Schmutz, T. Brettin, F. Larimer, M. Land, L. Hauser,, N. C. Kyrpides, N. Ivanova, M. Göker, T. Woyke, Q. L. Wu, **M. Pöckl, M. W. Hahn,** and H.-P. Klenk (2012). Complete genome sequence of *Polynucleobacter necessarius* subsp. *asymbioticus* type strain (QLW-P1DMWA-1T). *Standards in Genomic Sciences* 6:74-83
- **Nevalainen L.** (2012). Distribution of benthic microcrustaceans along a water depth gradient in an Austrian Alpine lake - Sedimentary evidence for niche separation. *Limnologica* 42: 65-71.
- **Nevalainen L., Luoto, T.P.** (2012). Faunal (Chironomidae, Cladocera) responses to post-Little Ice Age climate warming in the high Austrian Alps. *Journal of Paleolimnology* 48(4): 711-724. doi: 10.1007/s10933-012-9640-3.
- **Ostermaier V., Schanz F., Köster O., and Kurmayer R.** (2012) Stability of toxin gene proportion in red-pigmented populations of the cyanobacterium *Planktothrix* during 29 years of re-oligotrophication of Lake Zürich. *BMC Biology* 10:100, doi:10.1186/1741-7007-10-100.
- **Pamminger-Lahnsteiner, B., Winkler, K., Weiss, S., and Wanzenböck, J.** (2012) Does segregated spawning time prevent the introgression of stocked whitefish species into native species? A morphometric and genetic study in Mondsee (Austria). *Fundamental and Applied Limnology, Advanc. Limnol.* 63: 197-208.

- Sitoki, L., **Kurmayer, R.**, Rott, E. (2012) Spatial variation of phytoplankton composition, biovolume, and resulting microcystin concentrations in the Nyanza Gulf (Lake Victoria, Kenya). *Hydrobiologia* 691:109-122. doi: 10.1007/s10750-012-1062-8
- **Stelzer, C.P.** (2012) Population regulation in sexual and asexual rotifers: an eco-evolutionary feedback to population size? *Functional Ecology* 26:180–188.
- **Wanzenböck, J., Pamminger-Lahnsteiner, B.**, Winkler, K., and Weiss, S. (2012) Experimental evaluation of the spawning periods in a native Alpine whitefish population versus an introduced population of whitefish (*Coregonus lavaretus* complex) in Mondsee, Austria. *Fundamental and Applied Limnology, Advanc. Limnol.* 63: 89-97.
- **Weisse T, Moser M, Scheffel U, Stadler P**, Berendonk T, Weithoff G, Berger H (2012). Systematics and species-specific response to pH of *Oxytricha acidotolerans* sp. nov. and *Urosomoida* sp. (Ciliophora, Hypotricha) from acid mining lakes. *European Journal of Protistology*, pii: S0932-4739(12)00057-0. doi: 10.1016/j.ejop.2012.08.001.
- Zhang J., Khan M.R., Tian Y., Li Z., **Riss S.**, He C. (2012): Divergences of MPF2-like MADS-domain proteins have an association with the evolution of the inflated calyx syndrome within Solanaceae. *Planta*. doi:10.1007/s00425-012-1684-0

Books, Conference Proceedings, Reports, Book Reviews, Abstracts, Others

- **Dokulil, M.T.** (2012). Potamoplankton primary productivity in side-arms, floodplains and major tributaries of the Danube, 39th IAD Conference, August 2012, Szentendre, Hungary, ISBN 978-963-8391-53-7

Diploma & Masters Theses

- Benard M. Simiyu (2012) The concentration of microcystins in *Rastineobola argentea* in Nyanza Gulf, Lake Victoria, Kenya. UNESCO-IHE Institute for Water Education, Delft, the Netherlands, 55pp. Supervision: Rainer Kurmayer
- Keil, Florian (2012) Comparing two hydroacoustic analysis methods for fish abundance and biomass: Sv/TS scaling vs. fish tracking. Universität Wien, 29pp. Supervision: Josef Wanzenböck

Dissertation

- Schober, E. (2012). Diversity in abundance of toxic genotypes in natural populations of cyanobacteria (*Planktothrix* spp.), University of Vienna, 129 pp., Supervision: Rainer Kurmayer

Habilitation

- **Stelzer, C.P.** (2012) Evolutionary Ecology of Rotifers. Habilitation Thesis

2.7. Presentations 2012 (talks, posters) (staff members and former staff members in bold)

Talks

Blank, S, Kurmayer, R. : Charakterisierung der mikrobiellen Biodiversität im Pelagial von alpinen Seen mittels Hochdurchsatz-Sequenzierung. SIL-Austria Meeting, Pörschach, Austria, September 28-29, 2012.

Christiansen, G.: Characterization of a bi-specific NRPS adenylation domain activating both Arg and Tyr during biosynthesis of the cyanobacterial secondary metabolite Anabaenopeptin. 2nd Austrian Peptide Symposium, Vienna, Austria, November 29, 2012.

Hahn, M.: Polynucleobacter: Lazy planktonic bacteria of global significance in the species-like freshwater taxon *Polynucleobacter necessarius* (Betaproteobacteria). Biologické centrum Akademie věd České republiky / Biology Centre of the Academy of Sciences of the Czech Republic, České Budějovice, Czech Republic, October 1, 2012 (seminar talk).

Kammerlander, B., Trattner, F., Tartarotti, B., Sommaruga, R., **Sonntag, B.**: Ciliate community composition in two lakes of different turbidity resulting from glacier retreat. - 31st annual meeting of the German society of protozoology, Wuppertal, Germany (presented by BK) February 29 – March 3, 2012.

Kurmayer, R.: Microevolution of Toxin Production in Cyanobacteria. INRA Unité mixte de Recherche (UMR) Centre Alpin de Recherche sur les Réseaux Trophiques des Ecosystèmes Limniques (CARTEL), Thonon Cedex, France. October 25, 2012 (invited lecture).

Kurmayer, R.: Microevolution of Toxin Production in Cyanobacteria. Zoological Institute, Cologne Biocenter, University of Cologne, Köln, Germany, January 25, 2012.

Kurmayer, R.: Molecular Ecology and Physiology of Cyanobacteria. CYANOCOST Meeting, November 2-4, 2012, Miraflores, Madrid, Spain, (lecture at project meeting).

Kurmayer, R.: Wasserqualität im Mondsee: Modellierung des Algenwachstums in Abhängigkeit von sich verändernden klimatischen Bedingungen. Fachtagung Archäologische Arbeitsgemeinschaft Ostbayern / West- und Südböhmen / Oberösterreich, Mondsee, June 20-23, 2012.

Lamatsch, D.: Sex-specific marker development from transcriptome in the invasive Western mosquitofish *Gambusia affinis*. Project Meeting Marsden Fund, Otago, New Zealand, November 10, 2012 (lecture at project meeting).

Kurmayer, R.: CYANOCOST-Cyanobacterial blooms and toxins in water resources: Occurrence, impacts and management. SIL-Austria Meeting, Pörschach, Austria, September 28-29, 2012.

Schories, S., Matos, I., Trifonov, V., Kneitz, S., Reichwald, K., Nanda, I., **Lamatsch, D.**, Platzer, M., Schmid, M., Coelho, M., Warren, W.C., Walter, R.B., Scharl, M.: The *Xiphophorus maculatus* Jp 163 A genome, 5th International Conference of Poeciliid biologists, Trinidad, June 24–27, 2012 (held by MS)

Sonntag, B., Pöll, D.: Do ciliates suffer from sunburn? – 31st annual meeting of the German society of protozoology, Wuppertal, Germany, February 29 – March 3, 2012.

- Sonntag, B.:** Taxonomy and ecology of planktonic ciliates. – University Duisburg-Essen, Botanic Institute, Germany.
- Sonntag, B.:** Die Reaktion von Planktonorganismen auf UV-Strahlung in Hochgebirgsseen. Universitäts-Vortragsreihe im Großvenedigerhaus-Mitterkratzerhof (Osttirol) des Österr. Alpenvereins, Austria.
- Trummer, P., Kurmayer, R.:** Modellierung der Auswirkung veränderlicher Umweltbedingungen auf das Wachstum von Cyanobakterien in einem tiefen See der Voralpen. SIL-Austria Meeting, Pörschach, Austria, September 28-29, 2012.
- Stelzer, C.-P.:** Experimental evolutionary ecology of rotifers. Leopold-Franzens-Universität Innsbruck - Institut für Ökologie, Innsbruck, Austria, November 5, 2012 (ecological colloquium).
- Wanzenböck, J.:** Risk Analysis of Direct and Indirect Climate effects on deep Austrian Lake ecosystems (RADICAL) – Eine Zwischenbilanz. 13. Österreichischer Klimatag - Forschung zu „Klima, Klimawandel, Auswirkungen und Anpassung sowie Klimaschutz“ in Österreich. University of Natural Resources and Life Sciences Vienna, Austria, June 14–15, 2012.
- Wanzenböck, S.:** Präsentation zum Girls' Study Day 2013 am Forschungsinstitut für Limnologie, Mondsee der Universität Innsbruck. Landhaus Linz, Austria, November 6, 2012 (public lecture).
- Weisse, T.:** Population dynamics of microorganisms - Adaptation and tolerance to physical conditions in the (freshwater) environment. New Directions for Investigating Biodiversity of Ciliates. Workshop Presented By the International Research Coordination Network for Biodiversity of Ciliates, National Evolutionary Synthesis Center and North Carolina Central University, Durham, NC, USA, September 19-22, 2012 (invited keynote lecture).
- Weisse, T.:** Sex, cysts, and local adaptation in freshwater protists. VIII. International Chrysophyte Symposium (ICS) in Prague, Czech Republic, August 12–17, 2012 (invited keynote lecture).

Posters

- Blank, S., Kurmayer, R.;** Deng, L.; Niklas, G.; Pröll, J.; Gabriel, C.: Structure of pelagic bacterial diversity in alpine lakes using high throughput sequencing. Workshop "Next Generation Sequencing at the Poles", Liège, Belgium, November 21- 23, 2012.
- Breiner, H.-W., **Sonntag, B.**, Kammerlander, B., Stoeck, T. 2012 The ecological function of the rare biosphere. - 31st annual meeting of the German society of protozoology, Wuppertal, Germany, February 29 - March 3, 2012.
- Christiansen, G., Kurmayer, R.** Transformation of the cyanobacterium *Planktothrix* with a synthetic *mcyT* gene encoding a type II thioesterase and its effect on microcystin production. ISPP, Porto, Portugal, August 5-8, 2012.
- Ficker, H.:** Alpine fish populations under temperature stress. IIASA 40th Anniversary Conference – Worlds within reach from science to policy, Hofburg Congress Center Vienna and IIASA, Laxenburg, Austria, October 24-26, 2012.

- Kurmayer, R., Christiansen, G.:** Genotype determined microcystin content in *Planktothrix* spp. ISPP, Porto, Portugal, August 5-8, 2012
- Weisse, T., Moser, M., Scheffel, U., Stadler, P.,** Berendonk, T., Weithoff, G. & Berger, H.: Morphology, phylogenetic relationships, and pH response of two as yet undescribed *Oxytricha* species (Ciliophora, Hypotricha). 31. Wissenschaftl. Tagung der Deutschen Ges. für Protozoologie, Wuppertal, Germany, February 29 - March 3, 2012.

2.8. Personnel

AS = administrative staff; SCS= scientific staff

| Name | Position | Funding |
|------------------------|--|--------------------------|
| Blank, Stephan | SCS/PhD student | <i>third-party funds</i> |
| Brandstätter, Regina | AS/IPGL-Programmes | <i>third-party funds</i> |
| Chen, Qin | SCS/PhD student | <i>third-party funds</i> |
| Christiansen, Guntram | SCS/Functional Genomics | general budget |
| Eisl, Liselotte | AS/Lab (partial retirement) | general budget |
| Ficker, Harald | SCS/PhD student | <i>third-party funds</i> |
| Frei, Mark | SCS/MSc student | <i>third-party funds</i> |
| Gadermaier, Maria | AS/Lab | <i>third-party funds</i> |
| Gröschl, Birgit | SCS/MSc student | <i>third-party funds</i> |
| Hahn, Martin | SCS/Environmental Microbiology | general budget |
| Höllerer, Hannes | AS/workshop manager | general budget |
| Huber, Franziska | SCS/MSc student | -- |
| Kammerlander, Barbara | SCS/ PhD student | <i>third-party funds</i> |
| Käferböck, Anna | SCS/trainee | <i>third-party funds</i> |
| Keil, Florian | SCS/MSc student | -- |
| Koll, Ulrike | AS/Lab (on maternity leave) | -- |
| Knoll, Johann | AS/Lab (sickness absence) | -- |
| Kurmayer, Rainer | SCS/Molecular ecology and physiology of cyanobacteria | general budget |
| Lamatsch, Dunja | SCS/Molecular & Cytogenetic Evolution of Asexual Aquatic Organisms | general budget |
| Landertshammer, Jasmin | SCS/trainee (BSc) | <i>third-party funds</i> |
| Mayr, Stefan | AS/Labor (leave of absence) | -- |

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|-------------------------|--|---|
| Mayrhofer, Kurt | AS/electrician and janitor | general budget |
| Moosbrugger, Katharina | AS/Lab | <i>third-party funds</i> |
| Oberlercher, Thomas | SCS/MSc student | -- |
| Ostermaier, Veronika | SCS/PhD student | <i>third-party funds</i> |
| Pichler, Maria | AS/Lab | general budget |
| Ployer, Harald | AS/IT-Administration | general budget |
| Riedl, Irene | SCS/trainee (BSc) | <i>third-party funds</i> |
| Riss, Simone | SCS/PostDoc | <i>third-party funds</i> |
| Scheffel, Ulrike | AS/Lab | general budget / <i>third-party funds</i> |
| Scheuerl, Thomas | SCS/PhD student | <i>third-party funds</i> |
| Schmidt, Johanna | AS/Lab (on maternity leave/part time) | --/general budget |
| Schweighofer, Christina | SCS/voluntary service | -- |
| Sonntag, Bettina | SCS/Ciliate ecology and taxonomy | general budget |
| Stadler, Peter | AP/Lab | general budget |
| Strasser, Lisa | SCS/trainee | <i>third-party funds</i> |
| Steinkogler, Hildegard | AS/cleaning | general budget |
| Stelzer, Claus-Peter | SCS/Experimental Evolutionary Ecology | general budget |
| Theuretzbacher, Theresa | SCS/trainee | <i>third-party funds</i> |
| Tibitanzl, Karin | AS/secretary (part time) | general budget |
| Trummer, Philipp | SCS/PhD student | <i>third-party funds</i> |
| Ullrich, Sabine | AS/Lab (deputyship for maternal leave) | general budget |
| Wanzenböck, Josef | SCS/Ecology of Freshwater Fish | general budget |
| Wanzenböck, Sabine | AS/Public relations, library | general budget |
| Weisse, Thomas | SCS/Microbial Ecology (head) | general budget |

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|-------------------------|---------------------|---|
| Wiedlroither, Anneliese | AS/Lab | general budget / <i>third-party funds</i> |
| Winkler, Gerold | SCS/IPGL-Programmes | <i>third-party funds</i> |
| Zopf, Michaela | SCS/trainee (BSc) | <i>third-party funds</i> |

3. Gallery

