

Abstracts of the 25th International Diatom Symposium

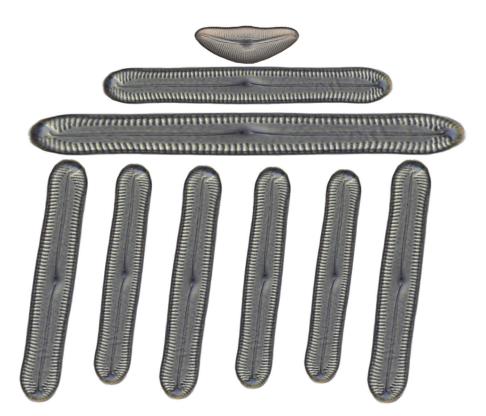
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Abstracts of the 25th International Diatom Symposium Berlin 25–30 June 2018 – Botanic Garden and Botanical Museum Berlin Freie Universität Berlin







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Front cover: IDS 2018 Logo by N. Abarca; back cover: images of living diatoms by O. Skibbe

Preface

The 25th International Diatom Symposium (IDS 2018) was held at the Seminaris Cube and at the Botanic Garden and Botanical Museum, Freie Universität Berlin (BGBM), from 25 – 30 June 2018. The Research Group Diatoms at the BGBM was honored to hold this 25th Symposium in Germany again. After all, these symposia were started in Bremerhaven, Germany in 1970; the 3rd took place in Kiel, Germany, also. The first four were named *Symposium on Recent and Fossil Marine Diatoms* (London, UK, 1972; Oslo, Norway, 1976). The 5th took place in Antwerp, Belgium (1978) and the 6th in Budapest, Hungary (1980) and were called *Symposium on Recent and Fossil Diatoms*. From the 7th Symposium on, the current name *International Diatom Symposium* was used and the meetings became more international. Five Symposia have been held in the USA (Philadelphia, 1982; San Francisco, 1990; St. Paul, 2010) and Canada (Ottawa, 2002; Québec, 2016), three in Asia: Japan (Tokyo, 1996), Russia (Irkutsk, 2006), China (Nanjing, 2014), and one in Australia (Perth, 1998). The symposia in Europe took place in Paris, France (1984), Bristol, UK (1986), Joensuu, Finland (1988), Zeeland, Netherlands (1992), Maratea, Italy (1994), Athens, Greece (2000), Misdroye, Poland (2004), Dubrovnik, Croatia (2008), and in Ghent, Belgium (2012).

At the 25th symposium, 210 participants from 43 countries of all five continents took part in and contributed to 83 Session Talks, 6 Keynote Talks, 10 Workshops and 100 Posters. Important topics of this symposium were: *Taxonomy & Phylogeny, Freshwater Biogeography, Bioindication, Marine & Brackish Biodiversity, Paleoclimatology, Names & Collections*. Current important topics were picked up in the Session *Environmental DNA & High Throughput Sequencing (eDNA & HTS)* by the diatom group in the DNAquanet EU CostAction. The International Code of Nomenclature for algae, fungi and plants (ICNafp) 2018 had just been published before the IDS 2018 and its implications for diatom research were covered in a keynote talk by the chair of the editorial committee.

For the first time, the Young Diatomists who had founded themselves at the last symposium in Québec organized their own day (30 June) with 60 participants in 4 Workshops. As in Québec, they had organized *Speed Talks* within the regular sessions, which were a lot a fun to listen to for the elder diatomists. 20 travel awards were financed by the ISDR (International Society for Diatom Research) and the IUBS (International Union for Biological Sciences), and a number of prizes for the best talks, posters and speed talks were awarded.

In this Abstract Book, 189 abstracts are printed alphabetically, no matter if they were presented as talks, posters, or in workshops. In the index, about 600 (co-)authors are listed; in the text more than 800 diatom taxa are referred to. This is substantial reading material for a symposium of less than a week's length.

We hope that you enjoyed meeting with colleagues and friends in Berlin in summer 2018,

Regine Jahn, Nélida Abarca, Wolf-Henning Kusber, Demetrio Mora & Jonas Zimmermann

25th International Diatom Symposium – Berlin 2018

New data on the postglacial development of the Kandalaksha Bay coast (White Sea) inferred from diatom assemblages

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Recently, interest in the dynamics of the natural conditions of the White Sea coast has significantly increased due to a number of unsolved and topical issues: isostatic and tectonic movements' role in the current relief formation; the relief-value, chronology and spread of ice cover during the last glacial period; the reconstruction of sea level fluctuations during the Holocene and its forecast (Polyakova 1997). We aim to reconstruct the history of relief development, the main features of sedimentation and the dynamics of the natural environment of the Kandalaksha Bay coast of the White Sea during the Holocene using diatom analysis. To achieve this goal, an analysis of data on geomorphological structure of the Karelian and Tersky coasts and diatom analysis of the coast's lacustrine-boggy deposits were made (104 samples). We analyzed six sediment core sections from two study sites of the Kandalaksha Bay coast and obtained results showing that in all studied sediment core sections of the Karelian coast, the identified diatom ecozones characterize the gradual transition from an open sea bay to a modern lake through the stage of a meromictic reservoir. The deposits of the Tersky coast contain diatom assemblages characterized by low diversity and low concentrations. In the sediment core sections of the Tersky coast, we found the stages of isolation from the ancient sea water bodies, which are similar in diatom composition with meromictic lakes of the Karelian coast, but the lithology of the deposits differs greatly. Despite the fact that the Karelian and Tersky coasts are located on different sides of the Kandalaksha graben, the uplift rates of them from the end of the Atlantic were very close. We identified three stages in the history of environmental development of the Kandalaksha Bay coast. In each of them, significant changes in the relief and the natural environment took place. The first stage (from the late Dryas to the beginning of the Boreal period) is the cold marine stage, the second (from the second half of the Boreal to the beginning of the Subboreal) is a transitional one thatis characterized by the isolation of reservoirs and the formation of meromictic lakes, and the third is a modern freshwater stage (started in the middle of the Subboreal time). Owing to the competent choice of the objects of research, we created a strong base for paleogeographic reconstructions. Also, new unique data on the diatoms composition in the coastal peat bogs of the Tersky coast, which has been much less studied than Karelian, have been obtained.

Polyakova Y. 1997: The Eurasian Arctic Seas during the Late Cenozoic. - Moscow: Scientific World. [In Russian].

Revision of the genus *Sieminskia* with description of valve ultrastructure

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In this work we present an ultrastructure-based revision of the diatom genus *Sieminskia* Metzeltin & Lange-Bert. using light and electron microscopy. Only one species belongs to *Sieminskia* but appeared in the literature with different synonyms. The genus was established in 1998 by Metzeltin and Lange-Bertalot to accommodate two *Navicula* Bory species; *Navicula zeta* Cleve and *Navicula wohlenbergii*

C. Brockmann. Another species described by Hagelstein in 1939; *Navicula expansa*, appeared to be synonym to *N. zeta*. A taxonomic comparison with the related genera *Parlibellus* E. J. Cox, *Cosmioneis* D. G. Mann & Stickle, *Scolioneis* D. G. Mann and *Stauroneis* Ehrenb. is provided. *Sieminskia zeta* Metzeltin & Lange-Bertalot (the valid name of the only species of the genus), is widely distributed in brackish-water but its valve structure has not been fully described. The present work is based on material from Southern Iraq where *N. expansa* is found abundantly as epiphyte on some submerged aquatic plants like *Ceratophyllum demersum*.

Life cycle observations of *Eucampia antarctica, Odontella weissflogii* and the discovery of living diatoms on tintinnid loricae from the Southern Ocean.

Armand, Leanne K.

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Over the course of three missions to the East Antarctic and Sub-Antarctic Kerguelen Islands through the 2000's, live diatom communities were collected in phytoplankton nets or concentrated from ship's intake seawater lines. Observation of the living community principally during periods of prebloom, bloom and post-bloom has enabled insights into the life cycles of *Eucampia antarctica* (Castrac.) L. Mangin var. *antarctica* and var. *recta* (L. Mangin) G. A. Fryxell & A. K. S. Prasad and also *Odontella weissflogii* (Grunow) Grunow. The talk will be a short guide to the observations of aberrant forms and life cycle variations of these two species. In addition, through the observation of live material at sea, the first observation of living diatoms on the theca of tintinnids was discovered (Armbrecht & al. 2017).

Armbrecht L. H., Eriksen R., Leventer A. & Armand L. K. 2017: First observations of living sea-ice diatom agglomeration to tintinnid loricae in East Antarctica. – J. Plankt. Res. **39:** 795–802. https://doi.org/10.1093/plankt/fbx036

Molecular phylogeny of "marine gomphonemoid" diatoms, with particular reference to the epizoic genus *Poulinea* Majewska, De Stefano & Van de Vijver

Ashworth, Matt^{1,*}; Frankovich, Thomas²; Sullivan, Michael³; Majewska, Roksana⁴; Arendt, Mike⁵; Schwenter, Jeffrey⁵; Theriot, Edward¹ & Stacy, Nicole⁶

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The "marine gomphonemoids" are a loosely-defined group of raphid pennate diatoms which feature clavate frustules and asymmetric valves. This assemblage has always been assumed to be paraphyletic, with described genera such as Cuneolus Giffen, Gomphonemopsis Medlin, Gomphoseptatum Medlin and Pseudogomphonema Medlin assigned to families across the diatom phylogeny, such as the *Rhoicospheniaceae* and *Naviculaceae*, in the case of *Pseudogomphonema*. Among the marine gomphonemoids are a number of epizoic raphid genera, whose numbers have increased in recent years with the renewed interest in epizoic diatoms, including Tursiocola R. W. Holmes, S. Nagas. & H. Takano, Poulinea Majewska, De Stefano & Van de Vijver, Chelonicola Majewska, De Stefano & Van de Vijver and Medlinella Frankovich, Ashworth & M. J. Sullivan, all documented from sea turtles. We have successfully sequenced three DNA markers (nuclear-encoded SSU rDNA and chloroplast-encoded rbcL and psbC) from several cultured strains of these epizoic diatoms, and SSU DNA data from single-cell DNA extractions and amplifications of several nonphotosynthetic *Tursiocola* species. Though taxonomic diversity in sequenced species is still fairly low, some patterns in the molecular phylogeny are beginning to emerge. For example, no sequenced marine gomphonemoids so far have shown any genetic affinity to the Rhoicospheniaceae, and the epizoic taxa have no genetic affinity to the non-epizoic taxa. Additionally, despite the geographical proximity of the samples taken (south Florida, USA), there appears to be significant genetic variation among Poulinea isolates between host sea turtle species. Though preliminary, we feel these data suggest epizoic diatoms may be a particularly revealing model system to study benthic diatom diversification.

Using fossil and DNA data to investigate the biddulphioid diatom genera *Biddulphia, Stoermeria, Tabulina* and *Biddulphiella* gen. nov.

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Valve ultrastructure, particularly when viewed under scanning electron microscope (SEM), has been particularly useful in resolving taxonomic synapomorphies in the diatom family Biddulphiaceae, allowing for a clear separation of Biddulphia Gray sensu stricto from the Eupodiscoidaceae (like Odontella C. Agardh and Triceratium Ehrenb.) by the structure of the elevated apical pore fields pseudocelli and ocelli, respectively. Defining generic limits within the Biddulphiaceae, however, have been more problematic. DNA sequence data have cast new light on this ambiguity, suggesting the genus is polyphyletic, with Biddulphia biddulphiana (Sm.) C. S. Boyer and B. tridens (Ehrenb.) Ehrenb. as sister to Attheya T. West, Terpsinoë americana (Bailey) Grunow and Neocalyptrella Hern.-Becerril & Meave del Castillo rather than to the Biddulphia alternans (Bailey) Van Heurck / B. sculpta (Shadbolt) Van Heurck clade. With few recognized modern species left to sample for DNA data, a thorough morphological examination of the diverse array of fossil biddulphioid taxa is probably our best hope to resolve the evolutionary relationships within this group. We have started with Biddulphia, defining the genus more strictly based on the frustule ultrastructure of B. biddulphiana specimens collected from the type locality and from collections across the Pacific and Atlantic oceans. For taxa without internal costa or areolae bordered by a hyaline rim, we suggest a transfer to the genus Tabulina Brun (B. shulzei C. S. Boyer, B. costata C. S. Boyer) or the newly-erected Biddulphiella (B. tridens, B. regina W. Sm.). We also suggest the transfer of Terpsinoë americana, which is genetically and morphologically distinct from Terpsinoë Ehrenb. and Hydrosera G. C. Wallich, to the genus Stoermeria Kociolek & al.

More than a name: the importance of voucher micrographs to molecular phylogenetics of diatoms

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Diatoms are one of the few microalgal lineages with complex morphologies which persist even after the death of the cell, making diatoms relatively unique in the way we can utilize both morphological and DNA sequence data in phylogenies. However, often the relationship between these two data types are treated as antagonistic; the ubiquity of molecular phylogenetics software and the relative ease of extracting DNA data from diatoms has led to a flood of papers "testing" taxonomy based primarily on morphological characters with DNA data, without always re-examining those original morphological concepts. One consequence of this is that it creates a pool of publicly-available DNA sequence data which are not directly tied to morphological data. This can create problems when other researchers use those data in their own studies and encounter anomalous results in their phylogenetic trees. These anomalies may not necessarily be due to laboratory (contamination of culture or DNA) or taxonomic (misidentification) errors—our understanding of diatom taxonomic and genetic diversity is changing every year as we gather more data for each. The fraction of diatom diversity represented in public DNA databases is still laughably slim, and it is entirely reasonable to assume that many genetic lines, even within described genera, are completely unknown. This cannot be overstated: taxonomic identification by DNA data alone (such as via a BLAST search) is unlikely to lead to accurate identification, even to the genus level, in all but a few groups of diatoms.

While some public DNA databases, such as GenBank, do not allow for image deposition, there are useful metadata fields to help make voucher image data available. The "strain" field is a far more useful tool to track down voucher image data for a sequence than a species name. Taxonomy from GenBank can be tricky not only because of misidentification, but also due to simple curatorial ignorance—GenBank curators rely on AlgaeBase (www.algaebase.org) for their taxonomy and classification of diatoms. There is also an open "specimen voucher" field on GenBank that can be used to tie a sequence to a voucher image. There are also several web resources available which will host voucher image data for no or minimal cost, such as Dryad (datadryad.org), AlgaTerra or Protist Central (www.protistcentral.org).

Paleoclimate reconstruction for the transition MIS 6 to MIS 5 from Lake Chalco, central Mexico

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The objective of this work is to characterize the diatoms that are present in the sediments between 100 to 122.5 m from lake Chalco, central Mexico, which correspond to a Glacial Termination II (130 ka). We identify two different diatom assemblages indicative of contrasting limnological and climatic conditions. The first is a freshwater assemblage, dominated by Stephanodiscus niagarae Ehrenb., and S. oregonicus (Ralfs) Håk., species that are scarce in modern environments in central Mexico but are common in temperate lakes in USA and Canada; we consider this assemblage indicative of temperate, freshwater conditions. The second is a halophilous assemblage, dominated by Anomoeoneis costata (Kütz.) Hust., nom. illeg., Cyclotella meneghiniana Kütz. and Campylodiscus clypeus (Ehrenb.) Ehrenb. ex Kütz., which are common in modern alkaline, subsaline to hyposaline lakes in central Mexico. Extrapolating the chronological model based on ¹⁴C and U-Th dates on the top 63.5 m of the sequence, we consider that the studied section covers the MIS 6 to MIS 5 transition (ca. 130 ka) (Lisiecki y Raymo, 2005). This transition is recorded by a change from laminated (MIS6) to massive sediments (MIS5) at 106 m. The laminated MIS6 sediments alternate between light diatom ooze lamina, dominated by the freshwater assemblage (S. niagarae and S. oregonicus) and dark laminae dominated by clastic sediments. The massive (MIS5) sediments, on the other hand, are characterized by the halophilous assemblage that indicate the abrupt change in the hydrology basin with a change towards warmer climates and subsaline to hyposaline conditions in the lake.

Lisiecki L. E., & Raymo M. E. 2005: A Pliocene-Pleistocene stack of 57 globally distributed benthic δ^{18} O records. – Paleoceanography **20**: 1–17.

Protected shallow lakes in the Carpathian basin – is nature protection indicated by diatom assemblages?

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Freshwater ecosystems are one of the most vulnerable areas on the Earth. It is essential to protect them not only from ecological but also from economical point of view. Most of the natural lakes and ponds are protected areas (PAs) in the Carpathian basin, and belong to the 'Natura 2000' network. Management activities in these PAs focus primarily on habitat restoration and conservation with special interest to maintain water bird communities. However, some of them provide opportunities for social and economic well-being in many ways (fishing, recreation). Although the non-protected standing waters (NPSWs) also could play essential role in conservation of habitat and species diversity, these waters primarily serve to satisfy social needs.

Here, we compared lowland PAs and NPSWs concerning (i) functional diversity (FD) of benthic diatom assemblages and also of (ii) the diatom based ecological quality (EQ). We hypothesised that (i) FD is strongly influenced by the protection status of waters, that is, lower diversity is expected in NPSWs; (ii) FD also strongly relates to recreational use and other human activities on waters: decreasing FD is hypothesised with the increasing number of services (fishing, or fishing and recreation); and we also hypothesised that (iii) diatom based EQ is highly affected by ecosystem services.

The results only partially confirmed these hypotheses. Both FD and EQ were the lowest in PAs without any social or economic services. While the increasing number of services in PAs increased the FD, diversity did not differ significantly in differently managed NPSWs. There were no significant differences between the EQ of differently managed PAs, but the quality was higher in NPSWs used only for fishing than for fishing and recreation. We have to stress, that protection of ecosystems do not necessarily affect positively the diatom-based FD and EQ of the standing waters.

Our results highlighted the deficiencies of those protection strategies that focus exclusively on macroscopic organisms. The higher abundance of the protected macroscopic organisms might occasionally have a pronounced organic load to the systems resulting in worse ecological state. In a broader perspective our results also indicate that there is a controversy between the aims of nature conservation strategies and that of the Water Framework Directive. Since the conservation concepts focus primarily on macroscopic organisms, increasing ecological quality cannot be expected in these protected ecosystems.

Pipelines for diatom metabarcoding in water quality assessment

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In the scope of developing new techniques for monitoring with diatoms in Sweden (within the WFD), we aimed at comparing the index values and water quality class obtained by traditional microscopy with ones obtained using NGS. A selection of 180 samples were taken in Sweden, Finland, Norway and Iceland, both in streams and lakes, to cover a broad ecological gradient (different, pH, nutrients and altitude, land use). The samples diatoms' communities were analyzed both under light microscope and DNA metabarcoding on a PGM sequencer. We selected two different DNA markers, rbcL and 18S, which are commonly used for diatoms sequencing. The taxonomical assignation of the sequences was done with the python program Diagnosyst (Frigerio & al. 2016) using the curated and open access R::syst database for both markers (Rimet & al. 2016). The molecular data quality was assessed in respect to the morphological data, by comparing the presence/absence of species and their relative abundance in each sample. The IPS index values were calculated for both techniques (and both markers) in order to compare the assigned water quality class. The Dignosyst program was designed to produce species inventories as close as possible to the ones obtained by traditional data (within the limits of the reference database). In order to assess the quality of the taxonomical assignation, a selection of our samples is to be processed using different bioinformatics pipelines (6 currently used within the DNAgua-net diatoms group) with the same reference database. This additional project will compare the outcome of those pipelines with respect to traditional diatoms indices and to ecological status class of the studied aquatic habitats and also detect the need for development in all the current pipelines.

Frigerio J.-M., Rimet F., Bouchez A., Chancerel E., Chaumeil P., Salin F., Thérond S., Kahlert M. & Franc A. 2016: diagno-syst: a tool for accurate inventories in metabarcoding. arXiv:1611.09410 [q-bio.QM]

Rimet F., Chaumeil P., Keck F., Kermarrec L., Vasselon V., Kahlert M., Franc A. & Bouchez A. 2016: R-Syst::diatom: an openaccess and curated barcode database for diatoms and freshwater monitoring. – Database, 2016 pp.baw016. https://doi.org/10.1093/database/baw016

Diatom assemblages in rivers differing in extent of their anthropogenic transformation (Upper Silesia and adjacent areas, southern Poland)

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The study was conducted in summer 2017 and involved sampling five sites located in rivers affected by industrial activities in the Upper Silesian industrial region and adjacent areas. Anthropogenic effects were visible primarily as alteration of the rivers' physical and chemical characteristics as well as the morphology of the river sections visited. Phytobenthos samples were collected from 25 cm² of the bottom in the initial stretch of the Centuria River (unaltered site), the downstream reach of the Mitrega River (the river is channelised, with fascine-reinforced banks and a dam reservoir); the downstream reach of the Mleczna River (the river is channelised, with fascine-reinforced banks and indirect supply of mine waters); and two sections of the Bolina River (the river is channelised, with banks and bottom variously reinforced; very heavy, but varying, mine water supply). The sites differed in the riverbed characteristics, water temperature and salinity, concentration of ammonium and phosphates in the water, and oxygen regime, but were fairly similar in terms of water pH. The Bolina and Mleczna sites, characterised by the highest salinity (7–12 PSU in the up- and 16–34 PSU downstream of the Bolina, and 3–5 PSU of the Mleczna), showed a relatively low taxonomic richness (22 and 32 taxa in the up- and downstream reaches of the Bolina, respectively, and 23 taxa in the Mleczna). The phytobenthos was dominated by species typical of brackish and marine water: Pleurosira laevis (Ehrenb.) Compère var. laevis and var. polymorpha Compère, Ctenophora pulchella (Ralfs ex Kützing) D. M. Williams & Round, Achnanthes brevipes var. intermedia (Kütz.) Cleve, Halamphora coffeiformis (C. Agardh) Levkov, H. luciae (Cholnoky) Levkov, Navicula salinarum Grunow, Gyrosigma attenuatum (Kütz.) Rabenh., and Pleurosigma salinarum Grunow. The initial stretch of the Centuria and the downstream section of the Mitrega supported much higher taxonomic richness (55 and 70 taxa, respectively), the Centuria showing the presence of species typical of oligotrophic and oligosaprobic waters as well as those highly tolerant of trophic conditions, saprobic status, and nutrient contents (the dominants included Planothidium dubium Round & Bukht., Cocconeis pseudothumensis E. Reichardt, C. neothumensis Krammer, Karayevia clevei (Grunow) Bukht., Amphora inariensis Krammer and Achnanthidium minutissimum (Kütz.) Czarn. var. *minutissimum*). The taxa present in the Mitrega River were typical cosmopolitan ones, found in various types of water, but occurring quite frequently in waters of an elevated trophic status (no distinct dominants). The diatom flora at all the five sites sampled was found to closely reflect the extent of anthropogenic alteration of the environment.

Two-way insight into diatom diversity of the Northern Adriatic. High-Throughput Sequencing in marine phytoplankton research

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For the European Marine Strategy Frame Directive (MSFD), marine microphytoplankton is monitored for community structure, overall abundance, toxic and invasive species. Identification of diatom species (the major component in Adriatic phytoplankton communities) based on morphology (light microscopy) requires expert taxonomic knowledge and is limited by the resolution of light microscopy. As demonstrated in freshwater systems, metabarcoding and High-Throughput Sequencing (HTS) are promising tools that might increase taxonomic resolution (Vasselon & al. 2017, Zimmermann & al. 2015).

Here we present diatom diversity data of the Northern Adriatic (Mediterranean Sea) assessed by HTS of ribosomal 18S and plastid *rbcL* gene and compared with light microscopy results. Sampling stations represent a transect from the coastal area to the open waters that are included in monitoring programmes of monthly diatom diversity and abundance assessments (Godrijan & al. 2013). Two DNA barcodes (*rbcL* and 18S V4) were amplified for samples at every station and HTS was performed using the PGM Ion Torrent technology.

Around 14% of the known diatom species in the study area are represented in sequence reference databases (*rbcL* and 18S V4) (Rimet & al. 2016, Quast & al. 2012). In the studied samples, around 35% of the species observed by light microscopy (LM) are represented in sequence reference databases. Around 30% of the species identified by LM were not detected by HTS. This could be the result of incompleteness of the reference database but might also be an effect of DNA extraction and PCR amplification biases. 21% of the species uncovered by HTS (which amounts up to 52% of the species uncovered by LM) are species not identifiable by LM (cryptic species). For unrestrained OTU formation, HTS uncovered up to 3 times more potential species (OTUs) (within diatoms) than with LM.

The known diatom species for the region are not well represented in sequence reference databases (around 14%). Even though the tested samples showed better coverages, our results indicate a negative effect of this low reference database coverage on the alpha diversity (at species level) recovered by HTS. However, unrestrained OTU formation demonstrated that HTS does allow the detection and monitoring of significantly larger diatom diversity if compared to LM. The detection of large numbers of cryptic species additionally demonstrates the potential of HTS for the monitoring of invasive and/or cryptic species. With the correlation between observed cell numbers and read numbers still under discussion, it appears safe to assume that some species might be over- or under-represented in the HTS results. Future research will have to demonstrate, whether HTS will be helpful in the early detection of low abundance (e.g. invasive) species.

Vasselon V., Rimet F., Tapolczai K. & Bouchez A. 2017: Assessing ecological status with diatoms DNA metabarcoding: Scaling-up on a WFD monitoring network (Mayotte island, France). – Ecol. Indicators **82:** 1–12.

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Zimmermann J., Glöckner G., Jahn R., Enke N. & Gemeinholzer B. 2015: Metabarcoding vs. morphological identification to assess diatom diversity in environmental studies. – Mol. Ecol. Resources **15:** 526–542.

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Rimet, F. Chaumeil P., Keck F., Kermarrec L., Vasselon V., Kahlert M., Franc A. & Bouchez A. 2016: R-Syst::diatom: An openaccess and curated barcode database for diatoms and freshwater monitoring. – Database 2016:baw016

A new diatom genus from a thermo-mineral spring of the French Massif Central (France)

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In summer 2016, a survey was performed in the area of the former thermal city of Saint-Nectaire situated in the Massif Central (France). In the thermo-mineral salt spring of Anthonia, due to a drilling linked to the thermal history of the city, a new diatom genus was able to be collected. Light (LM) and scanning electron microscopy (SEM) observations of the new diatom genus are presented. The new genus shows some similarities with other genera previously described. However, based on morphology, the new genus shows particular features that have not been described previously such as, the observed areolae pattern: striae, briefly interrupted at the junction, continuous from valve face to mantle and composed of one slit-like areola on the valve face and another on the mantle. Externally, areolae are covered by hymenes. Thus, compared to other small naviculoid genera such as *Nupela* Vyverman & Compère, *Adlafia* Gerd Moser, Lange-Bert. & Metzeltin, *Chamaepinnularia* Lange-Bert. & Krammer and *Germainiella* Lange-Bert. & Metzeltin, this new taxon does not show evident similarities to any other diatom genus described so far. The ecological preferences of this new monotypic genus are briefly discussed.

Modern diatoms in Tunisia as indicators of water chemistry and their use for hydrologic and climatic reconstruction

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Modern diatom study reflects the characteristics of waters and their frequency allow for statistical analysis. In Tunisia, salinity is the major discriminant factor, it varies from 0,4 to 74gl-1. Gaussian response curve allow the use of coefficient of regression for a hundred of species. In total, 603 taxa are recorded from fresh to metasaline modern waterbody and autoecolgical data is given for 136 taxa (Ben Khelifa 1989).

Athalassic metasaline species are distinguished as *Rhopalodia musculus* (Kütz.) O. Müll., *Mastogloia aquilegiae* Grunow, *Entomoneis paludosa* var. *subsalina* (Cleve) Krammer, *Amphora coffeaeformis* (C. Agardh) Kütz., *Hantzschia virgata* (Roper) Grunow, etc.

Main thalassic species observed in modern samples are *Biddulphia rhombus* (Ehrenb.) W. Sm., *Cocconeis quarnerensis* (Grunow) Grunow, *Cocconeis scutellum* var. *stauroneiformis* Rabenh., *Diploneis bombus* (Ehrenb.) Ehrenb., *Diploneis constricta* (Grunow) Cleve, *Licmophora gracilis* (Ehrenb.) Grunow, *Dimeregramma fulvum* (W. Greg.) Ralfs, *Nitzschia closterium* (Ehrenb.) W. Sm., *Striatella unipunctata* (Lyngb.) C. Agardh and *Triceratium* Ehrenb. sp.

Water chemistry is mostly sodium-chloride or calcium-magnesium/chloride-sulphate type. *Denticula elegans* var. *africana* Hust., *Fragilaria brevistriata* Grunow and *Nitzschia desertorum* Hust. are more commun in water rich in Ca₂₊ and Mg₂₊, and *Nitzschia linearis* W. Sm., in particular, prefer water rich in Mg₂₊. *Denticula elegans* Kütz. var. *elegans* is dominant in chloride water whereas the variety *africana* is dominant in sulphate waterbody.

Denticula elegans is acidophilous species, *Denticula elegans* var.*africana* is alcaliphilous; the species and its variety are never observed in the same modern biotope.

Samples from hydrothermal springs show a high diversity and assemblages with only one or two dominant species. Temperature of 40°C is a limit for high diversity; few species support T°>60°C as *Pinnularia borealis* var. *brevicostata* Hust., *Pinnularia viridis* (Nitzsch.) Ehrenb., *Rhopalodia gibba* (Ehrenb.) O. Müll., *Navicula veneta* Kütz.

In Quaternary fossil sediments from lens rich with the lamellibranche *Cerastoderma* in the endoreic Chott Fejej and Jerid and from lens and core in the mouth of Wadi El Akarit (PALHYDAF Sector1: southern Tunisia), around 60% of fossil diatom are observed in modern biotope.

Assemblages with *Denticula elegans* var. *africana* and *Fragilaria brevistriata* dominant is associated with *Nitzschia fonticola* Grunow in the mouth of Wadi El Akarit and in the Chott region of Ain Atrous. Thalassic species are observed in the Holocene lens of the mouth of Wadi El Akarit whereas in the Chott lens, only athalassic metasaline species are observed thus no marine incursion in the late quaternary occured in the Chott area.

In South Tunisia, from the last interglacial to 3000yrBP, three major humid phases are observed. Using a transfer function, salinity is recalculated for the Holocene phases and vary from 4 to 8,5 g/l. Diatom abundance (108valves/g), and assemblage type show Holocene sea-level fluctuations in the Wadi El Akarit and humid phases with salinity much lower than present time.

Ben Khelifa L. 1989: Diatomées continentales et paléomilieux du Sud-Tunisien (PALHYDAF site 1) au Quaternaire supérieur : approche statistique basée sur les diatomées et les milieux actuels. – Paris. http://www.theses.fr/1989PA112407

Combining slide scanning microscopy, web-based virtual slide annotation and machine learning for diatom collection mobilization

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In the Hustedt diatom collection, we have over the last years been exploring how current light microscopic imaging (slide scanning along with focus stacking), in combination with image analysis techniques, can facilitate diatom research (Kloster & al. 2014, 2017). These techniques can be useful in different contexts, and so far we mainly used them for intraspecific morphometric studies; in this talk, I will focus on application of these methods in taxonomy and diatom collection mobilization. First, I will introduce a case study in which, along with several members of the Polar Marine Diatom Workshop community, we tried see how multi-expert image annotation, in combination with customized, image analysis based morphometric comparisons can assist clarifying and harmonizing concepts of difficult-to-separate species. Using the thus quantified features, we also tested the performance of automatic classification algorithms. Second, I will introduce a project which we are just starting and which is aiming at using these techniques for what we call "deep" mobilization of the Hustedt diatom collection.

Kloster M., Kauer G. & Beszteri B. 2014: SHERPA: an image segmentation and outline feature extraction tool for diatoms and other objects. – BMC Bioinformatics 15: 218. https://doi.org/10.1186/1471-2105-15-218
 Kloster M., Kauer G. & Beszteri B. 2017: Large-Scale Permanent Slide Imaging and Image Analysis for Diatom

Morphometrics. – Appl. Sci. 7: 330. https://doi.org/10.3390/app7040330

Refined diatom biodiversity assessment of Southern Bug River (Ukraine) via eDNA-Metabarcoding

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Concerning diatoms, the Ukrainian territory is well-studied as algological investigations have been conducted for 140 years. Hitherto, the studies have detected 945 species (1,163 including infraspecific taxa) of *Bacillariophyta* coming from all kinds of waterbodies (Gerasimiuk & al. 2009). The Southern Bug is a large river whose basin is located completely in the territory of Ukraine. The river is subject to several anthropogenic influences, such as canalization, overregulation, hydro-engineering measures and industrial installations, as well as a heavily developed agrarian sector near its banks. Consequences of such activities are nutrient enrichment of the water, especially nitrogen and phosphorus compounds that lead to significant eutrophication effects as well as changes in the flow and temperature regime.

The Southern Bug River was monitored with regard to phytoplankton for eight consecutive years (Belous 2014; Belous & Klochenko 2015; Belous 2016). Along the entire Southern Bug River with its 800 km and 41 sampling stations, the algae in the plankton were collected, analyzed and identified. Identification of species composition involved the steps: microscopical analysis of live samples and processing of permanent preparations of diatoms. The diatom material revealed 100 species (108 including infraspecific taxa), making up 26% of all algae species found. When literature data is added, the diatom diversity of the Southern Bug River amounts to 162 algae species (183 including infraspecific taxa) forming 32% of all investigated algae species from its riverbed. The biodiversity of diatoms is composed of 55 genera. The most common species were *Aulacoseira granulata* (Ehrenb.) Simonsen var. *granulata, Melosira varians* C. Agardh, *Stephanodiscus hantzschii* Grunow and *Navicula gregaria* Donkin. Our investigations revealed that the sampling site with the highest species diversity was near the City Nikolaev. Its increase is attributed to the different ecotone types caused by the border between freshwater and saline; and therefore the transition between the varying communities of hydrobionts.

Furthermore, for a more refined understanding of the diatom diversity within Ukrainian waters the first eDNA metabarcoding (HTS) study was applied on the Southern Bug River.

For that reason, benthic samples were taken, focusing on *Bacillariophyta*, along the lower part of the Southern Bug River from three ecotone stations – one at Nikolayev city, one upstream and one downstream of the city (approximately 5 km away). Epilithic diatoms were harvested with a toothbrush from the biofilm on immersed stones according to the sampling strategy of the EU WFD. The samples then were homogenized and partitioned into two subsamples for each station and fixed with 70% ethanol in the end volume (including the sample water). For every investigated station, one sample was used for morphological identification by light microscope and one for metabarcoding analyses. To evaluate the comparability of both methods, the taxa lists derived from both HTS and morphological approaches were compared in regard to taxa presence or absence and species composition.

Gerasimiuk V. P., Gerasimova O. V., Struk (Konischuk) M. O., Terenko G. V., Tsarenko (Bilous) O. P., Tsarenko P. M., Wasser S. P. 2009: *Bacillariophyta* Vol. 2. – In: Tsarenko P. M., Wasser S. P., Nevo E. (ed.), Algae of Ukraine: Diversity, nomenclature, taxonomy, ecology and geography. – Ruggell: A.R.G. Ganter Verlag.

Belous Ye. P: 2014: Taxonomic structure of phytoplankton in the upper portion of the Southern Bug River (Ukraine). – Int. J. Algae **16(2)**: 107–115.

Belous Ye. P. & Klochenko P. D. 2015: Phytoplankton taxonomical structure in the middle part of Southern Bug River (Ukraine). – Int. J. Algae **17(3)**: 253–262.

Bilous O. P. 2016: Phytoplankton taxonomic structure of the lower part of the Southern Bug River (Ukraine). – Int. J. Algae **18(4)**: 377–386.

The state of the diatom flora of the Vestfold Hills within East Antarctica

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The stepwise re-investigation of the diatom flora from the Antarctic region has challenged long held notions of cosmopolitanism, endemism and species distribution as they pertain to microorganisms (Kociolek & al. 2017). Specifically, the Maritime and sub-Antarctic regions possess both endemic and cosmopolitan taxa across a number of ecologies (Zidarova & al. 2016). These advances led to the combined effort to re-examine the non-marine diatom flora of the Antarctic Continent. By applying the fine-grained taxonomic approach to historic surveys of West and West, new species of *Luticola* D.G. Mann and *Chamaepinnularia* Lange-Bert. & Krammer were described (Van de Vijver & al. 2012) from within the McMurdo Dry Valleys and other localities within East Antarctica. Furthermore, utilizing material from the entirety of the Antarctic region, two new species of *Halamphora* (Cleve) Levkov were described from the east-Antarctic region (Van de Vijver & al. 2014).

Here, we apply a fine-grained taxonomic approach, to re-analyze materials from the Vestfold Hills within East Antarctica. This area features numerous lakes, ranging from freshwater holomictic to marine meromictic habitats. Over the past century, work from this area has resulted in a diatom flora that is in need of revision. Using materials from Roberts & McMinn (1999) we show that the Vestfold Hills possess a diatom flora that is much richer than originally thought, featuring both cosmopolitan taxa and those endemic to the Antarctic region. Finally, by combining surveys with a standardized diatom flora generated from within East Antarctica, such as the Bunger Hills and Rauer Island group, we have increased taxon records from throughout the region.

Kociolek J. P., Kopalova K., Hamsher S. E., Kohler T. J., Van de Vijver B., Convey P. & McKnight D. M. 2017: Freshwater diatom biogeography and the genus Luticola: an extreme case of endemism in Antarctica. – Polar Biol. 40: 1185–1196.
 Roberts D. & McMinn A. 1999: Diatoms of the saline lakes of the Vestfold Hills, Antarctica. – Biblioth. Diatomol. 44: 1–83.

Van de Vijver B., Tavernier, I., Kellogg, T., Gibslin J., Verleyen E., Vyverman W. & Sabbe K. 2012: Revision of type materials of antarctic diatom species (*Bacillariophyta*) described by West & West (1911), with the description of two new species. – Fottea. 12(2): 149–169.

Van de Vijver B., Kopalová K., Zidarova R. & Levkov Z. 2014: Revision of the genus Halamphora (*Bacillariophyta*) in the Antarctic Region. – Plant Ecol. Evol. **147:** 374–391.

ZidarovaR., KopalováK. & Van der Vijver B. 2016: Diatoms from the Antarctic Region. I: Maritime Antarctica. – Iconogr. Diatomol. 24: 1–509.

A data analytics system for Late Quaternary diatom records in the Russian Arctic

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Palaeolimnological records in the Russian Arctic have large spatial research gaps and are not easily comparable to each other in advanced statistical applications. Therefore, we have compiled a standardized data set of available diatom assemblages from radiocarbon dated lake sediment cores in the Eastern Arctic (Biskaborn et al., 2016; Herzschuh et al. 2013) that will facilitate a better understanding of relationships between lake system ontogeny and millennial climate forcing on a continental scale. Our objective is to develop a state-of-the-art data analytics system that allows to detect coupling mechanisms of inherent aquatic ecosystem dynamics and external climate changes and their spatiotemporal pattern in dependence to lake and catchment attributes. Over the last decades, we generated a growing archive of roughly about 100 radiocarbon dated lake-sediment cores with published or unpublished data that is currently curated. The high complexity of taxonomical data and the increasing amount of measurements requires a big-data approach to generate data synthesis products. Our current taxonomic data compilation comprises 413 diatom species, of which 49% are present in multiple locations and the rest in single occurrences. All diatom species occur with at least 1% in two depths of one core. The average temporal resolution of a sediment core is about 300 and its maximum age is ca. 15.000 yrs BP on average. A single lake sediment record comprises about 100.000 sample measurements attributed to >100 different biotic (e.g. organic sediment properties, diatoms, pollen, chironomids) and abiotic (e.g. XRF scanner data, XRD mineral composition, grain-size distribution) proxy data. Detection of ecosystem-climate relationships in a large three-dimensional dataset requires close interdisciplinary collaboration between field-based polar research to provide the original data and their interpretation, as well as data science expertise to guide the management, standardization, quality-control, and multivariate big-data methods.

Biskaborn B. K., Subetto D. A., Savelieva L. A., Vakhrameeva P. S., Hansche A., Herzschuh U., Klemm J., Heinecke L., Pestryakova L. A., Meyer H., Kuhn G., Diekmann B., 2016: Late Quaternary vegetation and lake system dynamics in north-eastern Siberia: Implications for seasonal climate variability. – Quatern. Sci. Rev. 147: 406–421.

Herzschuh U., Pestryakova L. A., Savelieva L. A., Heinecke L., Boehmer T., Biskaborn B. K., Andreev A., Ramisch A., Shinneman A. L. C., Birks H. J. B. 2013: Siberian larch forests and the ion content of thaw lakes form a geochemically functional entity. Nature Commun. 4: 2408.

The role of scale and hydraulics/hydrology in shaping diatom communities in an aridland river

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Biological communities in aridland rivers are often reliant on a "bathtub ring" of autochthonous primary production. For example, the Middle Rio Grande in New Mexico is an aridland river with high turbidity levels and shifting sand and silt substrates, which confine the bathtub ring to a shallow, temporary river edge. We investigated the role of hydrologic and hydraulic variables in the distribution of biological parameters in microhabitats of the Rio Grande. Transverse surveys were conducted at two locations during the summer in 2015 and 2016. We collected samples for biological data (chlorophyll a, diatom species assemblages) and quantified local hydraulics and hydrology (e.g. geomorphology, turbulence strength and intensity, velocity, and turbidity). We used these data, along with US Geological Survey discharge data, in Classification and Regression Tree (CART) analysis. These decision trees are used in data mining to create a model that predicts values of a dependent variable based on the input of several independent variables. Diatom communities were dominated by Cocconeis placentula Ehrenb., C. pediculus Ehrenb., Rhoicosphenia abbreviata (C. Agardh) Lange-Bert., Nitzschia dissipata, and Navicula Bory spp. Local changes in flow (e.g. velocity, turbulence) and large-scale hydraulic events (e.g. discharge) were important variables driving differences in the structure of the diatom community; in part, these hydraulic metrics impacted diatom growth forms differentially. However, we recognize that there are also important variables at the micro-scale that are difficult to quantify. We will discuss the complexities of understanding biological communities in aridland rivers.

Regulation of the xanthophyll cycle in diatoms

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Diatoms are the dominant primary producers in highly mixed waters, characterized by fluctuating light conditions. To avoid oxidative damage during exposure to high light, diatoms possess a very efficient fast response: the dissipation of excess light energy as heat, a mechanism visualized as the Non-Photochemical Quenching of chlorophyll *a* fluorescence (NPQ). In most diatom species, NPQ is proportional to the concentration of the xanthophyll pigment diatoxanthin, which is produced during the xanthophyll cycle. In saturating light conditions, the epoxidized xanthophyll diadinoxanthin is converted into its de-epoxidized form diatoxanthin, whereas the opposite reaction is observed in light-limiting conditions.

Despite the central role of the xanthophyll cycle in light responses, the regulation of the rates of the de-epoxidase and epoxidase enzymes is not yet well understood. For example, most models still attribute a passive role to the epoxidation reaction despite the observations that its rate changes significantly with light conditions. We first measured the light regulation of the epoxidation reaction in the model diatom *Phaeodactylum tricornutum* Bohlin in conditions where the de-epoxidation step was inhibited with dithiothreitol. We could confirm that the epoxidation reaction has an optimum in light-limiting conditions, whereas its activity is strongly inhibited in saturating light conditions. We are now investigating the light regulation of the rates of the two enzymes by modeling the kinetics of NPQ in different light conditions.

SLOSS debate: a new perspective on an old paradigm

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Fragmentation of habitats is one of the most important threats to natural ecosystems, occasionally coinciding with drastic loss of species in the smaller fragmented habitat patches. The question of whether a single large or several small habitats may hold more species (i. e. the SLOSS debate) became a central issue in conservation biology.

This question is not yet decided and also has not been investigated in the case of microscopic organisms. Therefore, we aimed to study the outcome of the SLOSS debate in case of benthic diatoms and phytoplankton. Benthic diatom and phytoplankton diversity in differently-sized water bodies ranging between 10⁻² and 10⁷ m² was studied. Diversity of the neighbouring classes was compared step –by- step. Our results showed, that in most cases, diversity of smaller sized water bodies was higher than that of a single water body in the neighbouring larger size range. Consequently, several small habitats are able to keep more planktonic and benthic diatom species than a single large one. The results imply that protection of small aquatic habitats might be a good strategy in the conservation management of aquatic ecosystems.

New Proschkinia species associated with sea turtles

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The marine diatom genus Proschkinia Karaeva (Karayeva 1978) currently comprises seven valid species occurring worldwide in benthic and planktonic habitats. The taxa are characterized by having delicate frustules, a cingulum composed of numerous copulae and lanceolate valves whose outer surface is often ornamented with longitudinal ridges. A distinctive feature of the genus is the isolated pore called a fistula positioned near the central raphe endings. We have recently observed several distinct populations of *Proschkinia* species growing on skin and carapaces of various sea turtles from different habitats in the Mediterranean Sea, Indian, Pacific and Atlantic Oceans. Based on detailed SEM observations of wild populations as well as the one cultivated strain, we distinguished at least 5 new Proschkinia species whose morphology is presented and compared based on scanning electron microscope observations (SEM). All species presented a different morphology of the fistula along with several other discriminating features. Two species have been observed from loggerhead turtles in the Adriatic Sea (Croatia), of which *Proschkinia* sp. 1., previously found in samples taken from olive ridleys from Ostional (Pacific coast of Costa Rica), has fistulae internally occluded by one domed hymen and Proschkinia sp. 2. has fistulae internally segmented in a series (3-4) of small rounded openings occluded by raised convex hymenes. Proschkinia sp. 3 also has fistulae internally occluded by one domed hymen and was observed growing on Kemp's ridleys, loggerheads, and green turtles from Long Island (New York, USA) and on loggerheads from Florida and South Carolina (USA). Proschkinia sp. 4 was found on Kemp's ridleys and green turtles from Long Island (New York, USA) and on loggerheads from Kosi Bay (South Africa). Proschkinia sp. 5 has been observed from loggerheads and green turtles from Florida, and isolated into culture, and it is the smallest species without external longitudinal ribs and fistula internally occluded by one domed hymen. We will also present DNA sequence data for several strains of Proschkinia sp. 5 isolated from different sea turtle hosts, which suggest an evolutionary relationship to Fistulifera Lange-Bert., Stauroneis Ehrenb.and Craticula Grunow.

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Comparative single-cell diatom population genomics across the world's largest lakes and across the world

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Ecological models accounting for current and predicted warming trends portend dramatic changes to the Lake Baikal ecosystem, which could result in food web collapse and ecosystem restructuring. The planktonic diatom *Aulacoseira baicalensis* (K. I. Mey.) Simonsen is a dominant primary producer in the endemic pelagic food web of Lake Baikal, Siberia. This species is a very large, slow- growing stenotherm that thrives at low irradiances and is thought to be highly adapted to Lake Baikal's cold and hyper-oligotrophic environment. We know that genetic variation can impact an organism's ability to adapt to environmental change, therefore quantitative investigations into the genetics of *A. baicalensis* are needed to evaluate the risk of population declines and potential extirpation of this important endemic phytoplankter. Because there is no population-level genome-wide SNP data currently available for diatoms, it was equally important to develop a benchmark to which our *A. baicalensis* data could be compared.

We therefore took a comparative population genomics approach to investigate the standing genetic diversity, genetic structure, and population genetic statistics of five *Aulacoseira* Thwaites species from Lake Baikal and The Laurentian Great Lakes. Adapting newly-developed molecular tools, we overcame issues with culture establishment and culture bias, procuring high quality DNA from single *Aulacoseira* chains for ddRAD (double digest restriction associated DNA) library preparation, next generation sequencing, and population genomic analyses of the resulting genome-wide SNP datasets.

We found that genetic structure and population genomic parameters varied widely among the *Aulacoseira* species sampled. Given known heterogeneity of warming and nutrient conditions among basins within Lake Baikal, we tested specific temporal and geographic hypothesis for *A. baicalensis*. Fst, STRUCTURE analysis, principal components analysis, and multispecies-coalescent methods all pointed to a single panmictic population of *A. baicalensis* in the world's largest lake. Though *A. baicalensis* was sampled during a bloom, population genetic parameters did not indicate clonality, as observed heterozygosity (0.0422) was statistically significantly lower (P<0.001) than expected heterozygosity (0.0665) and Fis = 0.3573. Mean expected heterozygosity was used as a measure of standing genetic diversity. We found that *A. baicalensis* genetic diversity was three times lower and significantly different (P<0.001) from all four other *Aulacoseira* species measured. This suggests that *A. baicalensis* may be particularly vulnerable to lake-wide changes, as decreased genetic diversity can hinder adaptability.

Use of traits: Reconciling diverse diatom-based lake responses to climate change in the Carpathian lakes – (CRYPTIC: CRYPtogams' Traits In the Carpathians)

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In the last couple of years high resolution diatom-based palaeoenvironmental reconstructions were carried out for several mountain and lowland lakes of the Carpathian region in the late Quaternary; for the last 16,000 cal yr BP (Magyari & al. 2009, Korponai & al. 2010; Buczkó & al. 2017). Remarkable synchronicity in aquatic ecosystem changes has been detected during the late glacial and the Holocene, but the diatom composition was completely different (the number of taxa varied between 80 and 300 in the lakes). We established that despite the different slope aspect, water-depth and basin parameters, diatom assemblage changes show clear synchrony. The most detailed study was conducted in four lakes in the Retezat, South Carpathians, where the most remarkable changes in the aquatic ecosystems were observed around 6500 cal yr BP on the northern slope and around 6100 cal yr BP on the southern slope during the Holocene. Evidences for sharp concomitant shifts were found between 9200-9000 and 3200-3000 cal yr BP in the siliceous algal communities on both slopes. The Late Glacial/Holocene boundary was not pronounced in the shallow lakes, but was significant in a deep lake. The signs of a dry and bipartite Younger Dryas (GS-1) were evident, but floristic changes differed in the lakes. The diversity of diatom assemblages made difficulties in increasing the resolution of the analysis. The local environmental variables (e.g. bedrock, geographic position, vegetation cover) have highly influenced the diatom assemblages of the lakes resulting considerably differing species list. Acidophilous/acidobionta diatoms were dominant in the Lake Saint Anna, boreo-alpin taxa for glacial lakes of the Retezat Mountains, while meso-eutraphenic, alkaliphilous diatoms were found in the Lake Balaton and in the Lake Ighiel. Some attempts were made for diatom-based pH, phosphorous and salinity reconstruction using European database (EDDI), however the lack of a suitable local training set of siliceous algae hampered the fine quantitative reconstructions. The need for using standard methods in paleolimnology is a challenge and an urgent task. One solution can be to find non-species-based traits of siliceous algal assemblages that are objective, well measurable and do not require long practice in taxonomy for completing the analysis. Metrics based on different classifications are tested: (1) life forms, or growth morphology, (2) adaptive strategies (ecological guilds), (3) taxonomical traits (phylogenetic relationship) (4) cell size categories (5) combined eco-morphological functional groups and (6) a morphological/ornamentation patterns of diatom valves.

Cryptic project of NKFIH 119208.

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YOUNG ISDR, a new international platform for early career diatomists

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During the last International Diatom Symposium held in Quebec City (Canada) in 2016, the "Young ISDR" section within the International Society of Diatom Research (ISDR) was launched. The idea behind this formation is (a) to address the interests of early career diatomists directly to the ISDR commitee by an elected early career representative and (b) to assist early career researchers to build collaborations and develop skills needed for career enhancement. A better exchange with experienced diatomists should be facilitated providing workshops dealing with key topics of diatom research within future congresses. The Young ISDR also tries to improve global networking with other international scientific organisations and related diatom research topics.

Here, we would like to present a newly created socializing network of Young ISDR members including an interactive forum and a blog (https://youngisdr.blogspot.de/), which both highlight job offers, possible funding, future workshops and conferences, research reports, the "Diatom of the month"-series and key publications within the field of diatom research.

Size matters: the importance of transapical valve width in diatom biomonitoring

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Water quality biomonitoring using diatoms is still mostly based on light microscopic analysis of the frustules. New developments in (semi-) automatic slide imaging (Kloster & al. 2017) permit a high bulk throughput of samples to obtain comprehensive sets of individual diatom images. This provides a possibility to gather precise morphometric information on large sample sizes, as well as creating a digital record. We have studied benthic diatom samples from the sample library results of the Ebro Basin biomonitoring network (48 slides from 8 sites visited from 2003 to 2013) using a commercial slide-scanning microscope. After modifying the proposed workflow to our needs, 2500-4000 valves per sample were imaged. Individual diatom valves were selected and measured from them using the SHERPA software (Kloster & al. 2014). The measured diatom images were identified manually. Thus, detailed taxonomic and morphometric inventories were obtained for each sample. When comparing time series inventories, the results of multiple linear regression analyses of physicochemical traits showed that transapical valve width was the most important taxonomical diatom trait in the community analysis. Width was dependent on the characteristics of the sampling sites. Comparable and even connected sites showed parallel developments of width means through time. This parameter, in addition to the frustule surface-to-volume ratio, was the only one to display clear Spearman correlations with nutrients and all other physicochemical parameters studied. Among these, nutrients such as silicon dioxide and nitrate were the most affecting parameters. Infraspecific observation of the size parameters has partly confirmed the trends of physicochemically mediated morphometric variations. In this range, the variability is dependent on morphological plasticity of the taxa.

Valve width appears to be a defining trait linked to water characteristics. It affects habitat-dependent cell morphometry such as surface, volume and surface-to-volume ratio. Transapical width is dependent on the initial cell of a clone culture (Cox & al. 2012, Mann 1984, Geitler 1932) and stage of vegetative reproduction. Thus, it could be directly driven by the surrounding traits of the initial cell. We conclude that a better understanding of diatom physiology could improve our way of biomonitoring.

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Diatom taxonomic consistency in the 21st century: Lessons, directions, and updated methodologies

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Diatoms are widely used as freshwater biological indicators in environmental monitoring programs. In some U.S. studies, the problem of diatom counting, and taxonomy is large enough that analyst signal (analyst bias) can be greater than environmental signal. Indeed, the problem threatens the credibility and scientific confidence in using diatoms as indicators in biological assessments. We examine three studies to understand the causes and develop solutions to taxonomic inconsistency within and among microscopy labs. The first study determined that datasets from multiple sources could be harmonized to minimize noise and maximize environmental signal. This study improved taxonomic coherence in a national survey by detecting taxa with "high analyst signal" and combining problematic taxa into "slash" groups based on QA/QC data. The correction process was automated with R scripts for repeatability and transparency. The second study utilized "plate-sorting exercises" to quantify differences in analysts' species concepts. Analysts reviewed a collection of images and grouped specimens into morphological species concepts. Results revealed variability among analysts' species concepts and highlighted the need for a unified, pre-defined taxonomic reference (the "voucher flora") when working with multiple analysts. In the third study, pre-count voucher floras were developed for two survey projects. Analysts used these floras at the bench to direct their identification. Quality assurance protocols were used to assess intra-analyst, inter-analyst, and interlab variability. Efforts were made to reduce other sources of variability by having all samples processed in the same lab, having similar microscope optics, and using Battarbee chambers for sample preparation. When diatom data were examined across all quality assurance levels, no significant differences were found within or between analysts, nor between labs. By combining the lessons learned among studies we identify the primary sources of data inconsistencies as 1) lack of nomenclatural harmonization, and 2) analyst inconsistency in species concepts, especially difficult species complexes. Furthermore, by using a project-specific flora for diatom identification, analystlevel variability can be overcome, which reduces taxonomic bias and increases the power of the information provided by diatom environmental assessments.

Views expressed are the authors' and not views or policies of the U.S. EPA.

Diatom-based transfer functions for Central Mexico and their use in the interpretation of Lake Chaco's 35 ka record

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Canonical correspondence analysis (CCA) is used to explore the relationship between diatom species distribution and environmental variables in a set of 40 lakes in central Mexico. The CCA shows that salinity, expressed as total dissolved solids (TDS), is the most important environmental gradient, followed by average annual temperature (AT) and annual precipitation (AP). Groups of diatoms characteristic of high salinity lakes, of low salinity warm lakes and low salinity cool lakes are identified. Partial CCAs and Monte Carlo permutation tests show that the three variables are also highly significant in explaining diatom distribution in the data set, and therefore transfer functions were developed using a weighted-averaging regression method (WA) with inverse deshrinking (r^2 >0.8). These transfer functions were applied to the Chalco B diatom sequence, to generate a ~35 ka cal BP quantitative paleolimnologic (salinity) and paleoclimate (AT and AP) reconstruction. The conjunction of modern and fossil diatom data offers the opportunity of assessing the intensity and speed of limnologic and climatic change in Lake Chalco, Central Mexico, since the late MIS-3, including the impact of millennial scale climatic events such as Dansgaard-Oeschger interstadials (D-O) and Heinrich stadials (HS).

The Chalco B record shows orbital scale variability, recording the late MIS-3 as a period of variable but generally high salinity in the lake that relates with a peak in summer insolation ~36-29 ka cal BP. MIS-2 is recorded between 27 to 11.5 ka cal BP as a period of low salinity in the lake that relates with a time of low evaporation and summer insolation. The last glacial maximum (LGM) is identified as a two phase event reaching the lowest temperatures (-4.5°C) by 26-25 ka cal BP and 20-19 ka cal BP. The onset of the deglaciation is recorded by 19 ka cal BP and represents the wettest period in the record. The early Holocene shows positive temperature anomalies (+3°C) and high salinities that relate again with the peak in seasonality and summer insolation by 10–9 ka cal BP. Millennial scale events are also evident from the Chalco record, with a general patter of warm-wet D-O interstadials and cool-dry HS; this pattern is common to other tropical sites in the Northern Hemisphere (NH). The Chalco data therefore fits with the model that during HS cold-freshwater inputs to the North-Atlantic slowed deep-water formation, reducing meridional heat transport and favoring a southerly location of the Inter Tropical Convergence Zone and a reduced activity in the Northern Hemisphere monsoon systems.

Effect of thermohaline circulation on diatom distribution in the open South Adriatic Sea

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Dynamics of a diatom community was studied during winter-spring period in span of two years that differed with respect to the oceanographic conditions induced by specific hydroclimatic events in southern Adriatic. Sampling station was situated in the South Adriatic Pit (SAP) with depth of 1200 m. Altogether, 16 research cruises were undertaken and in total 232 bottle samples were observed for physical-chemical and phytoplankton analizes. Two specific phenomena were recorded in SAP during investigated periods: high abundances of diatoms in the aphotic zone associated with strong downward flow, and intense surface diatom bloom in 2017 induced by strong vertical convective mixing which increase nutrient availability in surface layer. Diatoms were the most diverse and abundant group of microphytoplankton (MICRO) during investigated periods, classified into 102 taxa of 48 genera. Contribution of diatoms in MICRO abundance ranged from 8.3 to 97.9% in 2016 and from 0.4 to 99.6% in 2017 with intense development and contribution during bloom in March 2017. At that time (3th and 20th of March) diatom abundances ranged from 6.1x10² to 5x10⁴ cells L⁻¹ and 2x10² to 1.9 x10⁵ cells L⁻¹, respectively. In the begining of bloom (3th of March), intensive development of diatoms was recorded in surface layer (0-50 m). During the peak (20th of March) high abundances spread to 300 m. Four days later (24th of March), diatom abundance decreased in the surface layer and maintained in the reduced values in the deep samples (under 75 m). The diatom community during the winter-spring period was characterized by atypical mix of benthic, epilitic and planktonic species with Asterionellopsis glacialis (Castrac.) Round (2.4x10⁴ cells L⁻¹), Chaetoceros affinis Lauder (2.5 x10⁴ cells L⁻¹), Chaetoceros lorenzianus Grunow (2.3 x10⁴ cells L⁻¹), unidentified *Chaetoceros* Ehrenb. spp. (2.2 x 10^4 cells L⁻¹), and *Pseudo-nitzschia* H. Perag. spp. (4.5 x 10^4 cells L⁻¹) as the most abundant taxa. The great contribution of coastal species at significant distance from the coast suggests the strong influence of different water masses in this area. Such a high abundances of diatoms, accompanied by a high concentration of chlorophyll a (>1 µg L⁻¹), indicated that area of SAP is not exclusively oligotrophic in the winter. Winter-early spring in the open water of South Adriatic could be considered as a productive season with significant phytoplankton activity.

The influence of environmental factors on diatom colonization on glass slides in the marine lake Mrtvo More (island of Lokrum, Adriatic Sea coast)

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In this study we investigated diatom colonization during period of first 6 months of artificial substrate (glass slides) exposure. From April to October 2016 microscopic glasses were submerged in the marine lake Mrtvo more (island of Lokrum, Dubrovnik area, South Adriatic, NE Mediterranean, Croatia). This semi-closed shallow marine ecosystem is connected with the open sea by an underwater passage, and is during summer season under significant anthropogenic influence (swimmers). The parallel oriented glass slides (against the surface) were placed on a seafloor at 1 m beneath the water surface. The samples were collected weekly. For light microscopy (LM) observations diatom frustules were cleaned from the organic material using method with hydrogen peroxide and hydrochloric acid. In order to determine the relationships between diatom community and environmental variables, water samples for analysis of physicochemical variables were taken weekly from the same place where diatom sampling was carried out. Water temperature ranged from 18.3°C (May) to 27.3°C (July). Salinity varied from 26.6 (October) to 37 (August). Oxygen saturation (O2/O2') ranged 0.58 (September) to 1.3 (June). TIN ranged from 0.96 (May) to 10.2 (September) µM. Phosphate (PO4) ranged from 0.112 (May) to 0.578 (July). Silicate (SiO4) ranged from 3.925 (May) to 13.016 (July) μ M. The benthic diatom flora was investigated and diversity was determined in relation to the concentrations of phosphate, silicate, and nitrogen compounds. The composition (% relative abundance) of a total of 133 diatom taxa within 47 genera found in the benthic diatom community of studied artificial substrates were identified in 21 samples. Species Cocconeis scutellum Ehrenb. var. scutellum, Cocconeis dirupta var. flexella Grunow, Pinnularia Ehrenb. sp., Diploneis crabro (Ehrenb.) Ehrenb., Navicula salinicola Hust., and Licmophora paradoxa (Lyngb.) C. Agardh were the most abundant. Genera with the greatest number of taxa were: Nitzschia Hassall (20 taxa), Mastogloia Thwaites ex W. Sm. (11), Amphora Ehrenb. ex Kütz. (9) and *Cocconeis* Ehrenb. (9). Altogether, only three taxa were presented in more than 85% of samples: Cocconeis scutellum var. scutellum, Cocconeis dirupta var. flexella and Cocconeis pseudomarginata W. Greg. In total, 60 taxa were found only once (sporadic) with average relative abundances lower than 1.3%. The number of taxa per sample ranged from 9 (May, June) to 52 (August), with an average of 25.4. The species diversity index varied from 0.74 to 4.51. Pielou's species evenness ranged from 0.23 to 0.86 (the average 0.63). The amount of biofilm increased through study period. Diatom assemblages were significantly different (ANOSIM, P<0.05) between the beginning samples till July and samples afterwards. Throughout the period from end of July till end of September, the community was characterized by a stable composition and high species diversity (Shannon-Weaver, mean H'=4.22). Different environmental conditions such as sea temperature, salinity, oxygen saturation and nutrient concentrations may have influenced unequal colonization between months. This study indicates that the early diatom biofilm formation and composition are affected by different environmental conditions. Additionally, it clarifies what parameters contribute to observed differences between months.

Ecological factors and micromechanics of valve structure in loculate centrics

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The structure of the diatom valve varies among species with respect to wall thickness and the size, density and arrangement of openings. This study applied structural and mechanical engineering theory to measurements of valves to investigate hypotheses about the ecological factors affecting valve structure: 1) porosity is determined by the living cell's need for nutrient uptake from the external environment; 2) pore size is determined by the cell wall's function as a mechanical filter that prevents parasitism; 3) the strength of the valve is determined by its benefit in protecting the cell against predation. For simplicity, this study focussed on diatoms that have circular outline and walls with three-layered sandwich panel structure (i.e. loculate areolae) within the Coscinodiscophyceae (Coscinodiscus, Thalassiosira etc.). The thickness of each layer of the diatom cell wall and the density, diameter, and wall thickness of pores in each layer was measured on electron micrographs of cells of varying diameter. The mechanical properties of the valves were calculated using cellular material theory, modelling the cell wall as a laminate sandwich panel structure with porous solid faces and honeycomb core, composed of the solid material biosilica, whose properties were modelled as a composite material, using published values. The porosity of valves was not significantly higher in cells of larger diameter, a result that does not support the nutrient uptake hypothesis, based on the inference that cells with larger surface area to volume ratios require greater porosity. The cell wall of each species had at least one layer of very small pores (~40-50 nm), a result that supports the parasite filter hypothesis. The mechanical strength and predator defense hypothesis was supported by three observations: larger diameter cells had thicker core layers, lower porosity face layers, and areolae walls of higher thickness to length ratio, compared to smaller diameter cells, which are the three factors most needed to maintain structural strength in a larger diameter valve. Thus, these preliminary results from a very small group of species provide support for the theory that the siliceous cell wall is of primary benefit to the diatom as a defense against predation and parasitism.

Diatom inventory and description of El Mellah lagoon, Algeria

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Diatoms (or unicellular microalgae) are present in all aquatic environmentsThese organisms have adapted to all environments imaginable of the planet, on the condition that there is water. Nevertheless, these algae have adapted to their environment and have evolved with the environment in which they live (there are 200 000 species in the world).

Diatoms are thus indicative of the quality of an environment. This is why the occurrence of diatoms is used to assess the quality of water courses (Maupoix & al. 1991, Rimet & al. 2006a, b). There is a biological index based on the settlement of benthic diatoms: biological diatom index (IBD). The samples are obtained by brushing stones with a toothbrush over an area of 100 cm² spread over at leaest five different stones, or by removing diatoms fixed on plants. The samples are centrifuged, fixed with formaldehyde, alcohol or lugol and stored in a dark place.

The determination and counting of diatoms are carried out under a microscope by observation of the external siliceous skeleton of the diatoms (the only element remaining after the destruction of the organic material carried out above). 400 diatoms were identified per sample. This phase requires a good knowledge of the forms and characteristics of the different species of diatoms.

The Diatomic Biological Index (IBD - standardized AFNOR NF T 90-354, December 2007) thus makes it possible to evaluate the biological quality of a watercourse based on the analysis of diatoms. On the station studied at El Mellah lagoon in the northeast of the Wilaya of El Tarf isa list of some abundant species such as: *Frustulia rhomboides* (Ehrenb.) De Toni, *Neidium iridis* (Ehrenb.) Cleve, *Pinnularia viridis* (Nitzsch) Ehrenb., etc. After the application of the IBD on all the studied stations, the state of El Mellah lagoon was defined.

The purpose of this study, which will be carried out at the level of several water bodies of the Tarf region, is to establish a diatomic atlas of the region and to develop a diatomic index for scientists and technicians capable of assessing the quality of watercourses.

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Diatoms – the indicator of past sea-level changes: A case study from the Neogene sediments of Andaman and Nicobar Basin, India

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The instrumental record of sea-level changes is limited to certain time period, as a matter of fact for quantifying the variations of the sea level in the past, several micropalaeontological and geological proxies are only reliable. Amongst the several micropalaeontological proxies, diatoms can be used for determining the past sea level fluctuations. After their perishment, the distinctive siliceous valves are incorporated in the sediments through time and the diatom assemblages thus formed can be recovered and evaluated for the reconstruction of palaeoenvironment. Analysis of different aspects of diatom assemblages is a unique tool for the interpretation of sea-level change that might have took place in response to global rise of temperature. Studies on the Neogene diatoms from the Andaman and Nicobar Basin (India) indicate that there were sea level fluctuations during Miocene to Pliocene. During the Burdigalian (late early Miocene), the frequency of planktonic and benthic diatoms occurrence is variable and more or less represented by equal percentage. This implies that the deposition took place alternatively in a shallow water and comparatively deeper water environment. During the Tortonian (late Miocene) initially the deposition took place in deep water and gradually at the middle there was presence of comparatively more benthic diatoms in comparison to the planktonic that denotes a relatively shallower sea level. At the end of Tortonian, there was a declining trend of the benthic diatom percentage that is indicative of deeper water. During the Zanclean (early Pliocene) the sea level was shallower as evident by dominance of benthic diatoms; however, in some instances planktonic diatoms were present. Overall the Andaman and Nicobar Basin has experienced fluctuations of sea-level during the Mio-Pliocene Epoch which can be envisaged by the study of recovered diatom valves.

Diatoms from the Neogene sediments of Neill Island, Andaman and Nicobar Islands, India

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Late Miocene - Pliocene marls and limestones on Neill Island within the Ritchie's Archipelago of the Andaman Islands Group, in the northeastern Indian Ocean, are known to be rich in calcareous as well as siliceous microfossils. For the present study, a coastal cliff on the east coast of Neill Island, as well as the Nipple Hill Section of this island, were sampled and analysed for siliceous microfossils. Siliceous sponge spicules and radiolaria were found to be most abundant. Diatoms were studied in greater detail in order to obtain stratigraphic information from this fossil group. In addition, quantitative counts were performed, counting 300 diatom valves per sample. The abundance changes in the more common diatom taxa reflect changing preservation of siliceous microfossils and changing marine productivity in this region.

Moss-inhabiting diatom communities from Ile Amsterdam (TAAF, southern Indian Ocean)

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Ile Amsterdam (77°30'E, 37°50'S) is a very young, small volcanic island situated in the southern Indian Ocean, well north of the polar front. It is quite isolated in geographic position, far from larger landmasses, which is probably one of the main reasons for the presence of a unique diatom flora. The climate on the island shows a clear gradient from temperate at the lower altitudes to almost cold sub-Antarctic at the top of the Caldera (881 m). Running water is almost absent on the island, restricted to some small rivers on the southern side of the island. Most waterbodies are located in the ancient caldera, at an altitude of 700-800 m.

Following two large sampling campaigns in 2007 and 2016, the limnoterrestrial diatom flora of Ile Amsterdam has been thoroughly analysed. A first study focused on the aquatic diatoms of the island (Chattová & al. 2014) clearly separating Ile Amsterdam from all other islands in the southern Indian Ocean. Several new taxa and two new genera were published (Cantonati & al. 2009, Van de Vijver & al. 2017).

The present study shows the results of a taxonomic and ecological survey on the moss-inhabiting diatom flora of Ile Amsterdam. The analysis of 148 samples revealed the presence of 125 diatom taxa belonging to 38 genera. The specificity of the Ile Amsterdam's diatom flora is mainly reflected in the species composition of the dominant genera *Pinnularia* Ehrenb., *Nitzschia* Hassall, *Humidophila* R. L. Lowe & al. and *Luticola* D. G. Mann, with a large number of new species (Chattová & al. 2017, 2018). This highly specific diatom flora, together with differences in sampling habitats and the isolated position of the island, resulted in very low similarity values between Ile Amsterdam and the other islands of the Southern Ocean. From a biogeographical point of view, 42% of the taxa have a typical cosmopolitan distribution, whereas 18% of all observed species can be considered endemic to Ile Amsterdam, with another 16% species showing a restricted sub–Antarctic distribution. The NMDS analysis, based on a cluster dendrogram, divides the samples into six main groups. For each group, indicator species were determined. Both environmental data and diatom distributions indicate that apart from altitude, specific conductance, pH and moisture are the major factors involving the structure of moss-inhabiting diatom communities on Ile Amsterdam.

Cantonati M., Van de Vijver B. & Lange-Bertalot H. 2009: Microfissurata gen. nov. (*Bacillariophyta*), a new diatom genus from dystrophic and intermittently wet terrestrial habitats. – J. Phycol. **45**: 732–741.

Chattová B., Lebouvier M. & Van de Vijver B. 2014: Freshwater diatom communities from Ile Amsterdam (TAAF, southern Indian Ocean) – Fottea **14:** 101–119.

Chattová B., Lebouvier M., De Haan M. & Van de Vijver B. 2017: The genus Luticola (*Bacillariophyta*) on Ile Amsterdam and Ile Saint-Paul (Southern Indian Ocean) with the description of two new species. – Eur. J. Taxon. **387:** 1-17.

Chattová B., Lebouvier M. & Van De Vijver B. 2018: Morphological and taxonomical analysis of the terrestrial diatom genus Humidophila (*Bacillariophyta*) on Ile Amsterdam and Ile Saint-Paul (Southern Indian Ocean. – Phytotaxa **336**: 28–42.

Van de Vijver B., Chattová B., Lebouvier M. & Houk V. 2017: Ferocia gen. nov., a new centric diatom genus (*Bacillariophyceae*) from the sub-Antarctic region. – Phytotaxa **332**: 22–30.

Diatom metabarcoding to evaluate community changes in river biofilms linked to pharmaceutical loads from a wastewater treatment plant

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Hospital wastewaters (HWW) contain more pharmaceuticals than urban wastewaters (UWW), but they are usually discharged in sewers without pre-treatment (Verlicchi et al. 2012). Since traditional wastewater treatment plants (WWTP) are not designed to remove pharmaceuticals, hospital treated effluents (HTE) still contain active molecules that could impair receiving environments. Benthic diatoms are relevant ecological indicators because of their high species diversity and rapid responseto human activities. High-Throughput Sequencing (HTS) allows for accurate characterization of diatom community changes and species identification. This is helpful to describe adaptations of benthic communities to the presence of pharmaceuticals. Environmental biofilms were colonized at the output of a WWTP 1/ in separately treated effluents from UWW and HWW and 2/ in the recipient river up- and downstream from the WWTP output (Chonova et al. 2016). Pharmaceuticals were studied with passive samplers (Wiest et al. 2017) and HTS was used for characterization of diatom communities (Vasselon et al. 2017). Concentrations of nutrients and meteorological conditions were recorded. The ecological status of the recipient river was assessed calculating Specific Pollution Sensitivity Index (SPI) (Vasselon et al., 2017). Pharmaceuticals were more concentrated in HTE than in urban treated effluents (UTE). An increase in pharmaceutical concentration was also observed in the river downstream the WWTP output compared to upstream. HTS showed that diatom communities developed in all locations and differed strongly in their diversity and structure. Multivariate analysis suggested that diatoms were influenced by the present pharmaceuticals. However, other environmental factors also showed an effect that led to a seasonal gradient in the community changes. Calculated SPI score suggested decrease in ecological quality status in the river downstream the WWTP compared to upstream. This trend was expressed more strongly in summer months. Our results showed that in-depth assessment of community composition using HTS, coupled to integrated measurement of pharmaceuticals, highlights efficiently the disturbing effect of pharmaceuticals on natural microbial communities in the environment.

Wiest L., Chonova T., Bergé A., Baudot R., Bessueille-Barbier F., Ayouni-Derouiche L. & Vulliet E. 2017: Two-year survey of specific hospital wastewater treatment and its impact on pharmaceutical discharges. – Environm. Sci. Pollut. Res. Int. 25: 9207–9218.

Chonova T., Keck F., Labanowski J., Montuelle B., Rimet F. & Bouchez A. 2016: Separate treatment of hospital and urban wastewaters: A real scale comparison of effluents and their effect on microbial communities. – Sci. Total Environ. **542**: 965–975.

Vasselon V., Domaizon I., Rimet F., Kahlert M. & Bouche, A. 2017: Application of high-throughput sequencing (HTS) metabarcoding to diatom biomonitoring: do DNA extraction methods matter? – Freshwater Sci. **36:** 162–177.

Verlicchi P., Al Aukidy M., Galletti A., Petrovic M. & Barceló D., 2012: Hospital effluent: investigation of the concentrations and distribution of pharmaceuticals and environmental risk assessment. – Sci. Total Environm. **430**: 109–118.

Volutin distribution pattern as a valuable taxonomic character in the genus *Navicula*

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Diatom taxonomy is mainly based on the characters of siliceous cell covering. Features of protoplast except chloroplast shape, number and position receive little attention. Volutin distribution pattern is rarely considered as a character of taxonomic importance.

Material for the present study were natural population of epipelic diatoms collected in water bodies of Zvenigorod Biological Station (Moscow Region, Russia) during the summer of 2014 and 2017. Diatoms were harvested on cover slips placed on tissue above the sediment. Cover slips with diatom cells were than fixed in Carnoy's solution and volutin was stained with methylene blue and sulphuric acid according to Meyer (1904). Volutin distribution pattern was studied in four species belonging to the genus *Navicula* Bory: *N. capitatoradiata* H. Germ., *N. oblonga* (Kütz.) Kütz., *N. radiosa* Kütz. and *N. viridulacalcis* Lange-Bert.

The results of the study showed three distinct patterns of volutin distribution were revealed. *N. capitatoradiata* and *N. radiosa* possess many tiny volutin grains irregularly distributed through the vacuole volume though quantity of volutin vary between the cells. One or two large, more or less spheric grains are located in each vacuole of *N. oblonga*, small irregularly placed grains are sometimes present along with large grains. In *N. viridulacalcis* grains are numerous, tiny, rod-shaped and located essentially at the cell apices. Noteworthly is the difference in volutin distribution between representatives of the sections *Alinea* (*N. viridulacalcis*) and *Navicula* (other species). Within *Navicula* section different patterns of volutin distribution occur which may indicate that futher splitting of this group is nessesary.

Meyer A. 1904: Orientierende Untersuchungen über Verbreitung, Morphologie, und Chemie des Volutins. – Botanische Zeitung, 2. Abt. **62**: 113–152.

Diatom biodiversity and endemism in tropical Africa

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Ancient lakes are well known to possess a large number of endemic taxa. In Lake Baikal, for instance, 55 % of the 672 reported specific and infraspecific taxa are considered to be restricted to the lake. This high percentage is mainly due to the taxonomic research conducted the last decades. For Lake Tanganyika, 10 % of the about 500 reported taxa are endemic to the lake. Recent taxonomic revision of a couple of genera, e.g., *Iconella* Jurilj, *Surirella* Turpin and *Amphora* Ehrenb., together with the current species concept showed an increase in the number of the endemic taxa in the lake from 30 to 50. Beside the African Great Lakes, diatoms in tropical Africa have attracted little attention during the 20th century, except at the beginning of the 1900s when material collected during the German "Nyassa-See und Kinga-Gebirgs-Expedition" was studied by Otto Müller. From this, he described more than 100 new diatom taxa. This material is the subject of re-investigation. The genera Cymatopleura W. Sm., Iconella and Surirella, and Epithemia subgenus Rhopalodiella.) Cocquyt & al. (formerly Rhopalodia "sippe" Eurhopalodiae) are accomplished; the study of Epithemia subgenus Rhopalodia (O. Müll.) Cocquyt & al., Placoneis Mereschk. and Nitzschia Hassall has been initiated. Afrocymbella Krammer, Actinellopsis J. C. Taylor & al. (recently described from Zambia) and Epithemia subgenus Rhopalodiella have a distribution restricted to tropical Africa or to the African continent. In the frame of ecological and paleoecological projects, some taxonomic diatom investigations were undertaken in tropical East Africa and the Democratic Republic of the Congo. These studies have led among others to the description of three new diatom species (Afrocymbella barkeri Cocquyt & Ryken, Nitzschia fabiennejansseniana Cocquyt & Ryken and N. pseudoaegualis Cocquyt) from a small crater lake near Mount Kilimanjaro, which are up to now only known to be from that lake. In 2010, a diatom monitoring started for streams and rivers in central part the Democratic Republic of the Congo. First results showed that cosmopolitan species were found only in very polluted (eutrophicated) waters, with Nitzschia palea (Kütz.) W. Sm. as the dominant species in the river Makiso, running through Kisangani, the third largest city of this country. On the other hand, less human-impacted sites such as small rivers and streams in the Biosphere Reserve of Yangambi, 100 km north of Kisangani, showed many diatoms unknown to science, or resembling species described from the Amazon basin (e.g., Encyonopsis frequentis Krammer, Eunotia enigmatica L. F. Costa & C. E. Wetzel). However, in-depth study of each taxon is needed to know if a species is new to science, if it distribution is restricted to tropical African or if it has indeed a pantropical distribution. This led already to the description of eight diatom species, up to now only known from the Congo Basin. Because the small rivers and streams are acidic in the Congo region, these taxa have not been found up to now in tropical East Africa where the waters are typically alkaline. However, we must remark that the description of the species was done on morphologic characteristics. It is the aim that genetic analyses should start soon, but the Nagoya protocol may slow down its progress.

Cocquyt C. & Ryken E. 2016: *Afrocymbella barkeri* sp. nov. (*Bacillariophyta*), a common phytoplankton component of Lake Challa, a deep crater lake in East Africa. – Eur. J. Phycol. **51**: 217-225.

- Cocquyt C., Kusber W.-H. & Jahn R. 2018: *Epithemia hirudiniformis* and related taxa within the subgenus *Rhopalodiella* subg. nov. in comparison to Epithemia subg. Rhopalodia stat nov. (*Bacillariophyceae*) from East Africa. Cryptog. Algol. **39**: 35–62.
- Jahn R., Kusber W.-H. & Cocquyt C. 2017: Differentiating *Iconella* from *Surirella* (*Bacillariophyceae*): typifying four Ehrenberg names and a preliminary checklist of the African taxa. Phytokeys 82: 73–112.
- Taylor J. C., Karthick B., Kociolek J. P., Wetzel, C. E. & Cocquyt C. 2014: *Actinellopsis murphyi* gen. et spec. nov.: A new small celled freshwater diatom (*Bacillariophyta, Eunotiales*) from Zambia. Phytotaxa **178**: 128–137.

Cocquyt C. & Ryken E. 2017: Two needle-shaped *Nitzschia* taxa from a deep East African crater lake. – Diatom Res. **32:** 465–475.

Proschkinia Karaeva: a marine diatom genus with some unusual wall features

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Karayeva established the genus *Proschkinia* Karaeva for *Navicula bulnheimii* Grunow and it now also includes several species that were previously placed in the *Navicula* section *Microstigmaticae* by Hustedt, based on the possession of numerous girdle bands. Scanning electron microscopy reveals that these girdle bands are folded, with a row of hymenate pores on the pars interior, but a plain pars exterior. In addition to this unusual feature, *Proschkinia* species possess unusual, fistula-like, isolated pores near the central raphe endings. There is interspecific variation in internal arrangement of the isolated pores, the degree of development of a conopeum beside the raphe, and in the extent to which longitudinal ridges develop on the valve surface.

Round & al. (1990) transferred some other former *Navicula* species to *Proschkinia* and created a new monogeneric family (*Proschkiniaceae*) within the Naviculineae, alongside the *Naviculaceae*, *Pleurosigmataceae*, *Plagiotropidaceae* and *Stauroneidaceae*.

This paper will present the distinctive morphological features of *Proschkinia*, some of which are found in apparently more distantly related genera, and consider its taxonomic position.

Round F. E., Crawford R. M. & Mann D. G. 1990: The diatoms. Biology and morphology of the genera. – Cambridge: Cambridge University Press.

Environmental changes of a highly variable saline lake (Laguna Mar Chiquita, Argentina) since Last Glacial Maximum

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Laguna Mar Chiquita (30°54' S – 62°51' W) is an extensive saline lake located in central Argentina. It is a sensitive system to past and present hydroclimatic changes located in the middle latitudes of South America. Prolonged intervals with either negative or positive hydrological balances have severely modified lake water levels, salinity and primary productivity which is reflected on diatoms assemblages, sedimentary features and geochemical proxies. A high resolution multiproxy analysis along 4 m sedimentary record allowed to reconstruct the environmental variability occurred in Laguna Mar Chiquita over the last 23.6 cal ka BP. Here we report the fossil diatom analysis which evidenced throughout the record three main stages. The first stage (12.3 - 23.6 cal ka BP), comprising the LGM, HS1 and ACR, was characterized by an ephemeral hypersaline lake with high abundances of benthic species (i.e., Tryblionella punctata W. Sm., Amphora coffeaeformis (C. Agardh) Kütz.and Amphora Ehrenb. ex Kütz. sp.). The second stage (3.5 – 12.3 cal ka BP) should be considered as a transitional system, since shallower conditions with the predominance of benthic species (i.e, Tryblionella punctata, Diploneis ovalis (Hilse) Cleve, Tabularia fasciculata (C. Agardh) D. M. Williams & Round and Rhopalodia gibberula (Ehrenb.) O. Müll.) moved toward a system with higher water level where the planktonic species Cyclotella striata (Kütz.) Grunow was dominant and then a hypersaline ephemeral system with high percentages of tychoplanktonic species (i.e., Paralia sulcata (Ehrenb.) Cleve) was established. The core chronology allowed us to ascribe this stage to the Mid-Holocene, a period characterized by abrupt hydrological changes alternating between drought and flood episodes in the region. The third stage (2002 AD - 3.5 cal ka BP) is characterized by a perennial productive system with high frequency variability, which was subdivided into three sub-stages. The first sub-stage (1.0 - 3.5 cal ka BP) is characterized by high lake level where the planktonic species Cyclotella striata was predominant. Considering the chronology of this sub-stage, it is contemporaneous of the MCA, a warm and wet period in the Argentinean pampean plain. The second sub-stage (1970 AD – 1.0 cal ka BP) corresponds to a low water level period with the predominance of aerophilic benthic species (i.e., Amphora coffeaeformis, Amphora sp.1, Nitzschia pusilla Grunow), this sub-stage being ascribed to the LIA, a cold and arid period. The third sub-stage (2002 – 1970 AD) marked the return to high lake levels associated with high percentages of Cyclotella striata. These diatom-based results, allowed us to reconstruct the magnitude and the expression of the hydroclimatic variability at a regional scale as well as the response of the lake system to different environmental and climatic conditions.

Changing contribution of global climate and local environmental influence on diatom community structure over time in ancient Lake Ohrid

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Very few ecosystems, such as ancient lakes, offer the potential to understand the environmental drivers of community structure on long temporal scale. The 584 m long sediment record from the site DEEP, recovered within the project Scientific Collaboration on Past Speciation Conditions in Lake Ohrid is unique in diatom preservation. Due to the depth of the coring location (i.e., 243 m) in the centre of the lake, planktonic diatoms dominate the microfossil record. We here present the stratigraphic succession of planktonic diatom diversity and test how global climate and local environmental drivers shaped the community structure over time.

Our biostratigraphic record shows that three types of major planktonic communities have existed in the lake since the onset of full lacustrine conditions, ca. 1.4 Ma ago, each community being characterized by distinct endemic taxa. Community turnovers occurred at glacial-interglacial transitions, caused by the extinction of dominant endemic species and emergence and/or increase in the relative abundance of newly immigrating or evolved taxa. By using constrained ordination and variation partitioning analyses, we tested the influence of climatic and environmental drivers for each major type of community individually. This shows that different global and local drivers affected the community structure over time. The diatom community present in the lowermost stratigraphic interval (~440–330 m core depth) is primarily structured by local habitat structure and nutrient availability, whereas global-scale climate variability had relatively low effects. The 100 ka orbital cycle, global and Mediterranean climate variability became more important from, ~330-80 m. During this second phase, local variation in precipitation, depositional environment, catchment dynamics, nutrient availability and lake mixis drove community dynamics. The last community turnover at ~80 m, marked a complete change of the prevailing drivers of community structure, with global-scale changes in temperature, and regional changes in precipitation having a large effect on the local environment. Diatom community structure from ~80 m on appears therefore driven by global and Mediterranean climate.

The change in the relative importance of the local environmental and global-scale factors in shaping diatom community structure in Lake Ohrid reflects the lake development from a shallow, productive lake 1.4 Ma ago to the deep, oligotrophic ecosystem seen today. This study thus provides a better understanding of the complex role of the environment in structuring community and diversity patterns over long temporal scales.

Biodiversity and taxonomy of South African marine coasts' diatom floras – what do we know 30 years after M.H. Giffen?

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Malcolm H. Giffen, Botany Professor at University College of Fort Hare, Cape Province, South Africa is an example of a most astonishing career in the history of diatomology. He was able to start his research on diatoms only after retirement. Because of this, his significant work on South African marine littoral benthic diatoms appears almost explosive. In the period of ca. 20 years, he published just 10 papers describing one genus – Cuneolus Giffen - and 134 taxa, including 121 new species, 5 new varieties and 8 new forms. Taxa described by Giffen were exclusively observed with light microscopy and documented with excellent line drawings. Access to original slides and to unmounted material housed in European collections (London, Bremerhaven, Berlin and Frankfurt am Main) and in Potchefstroom in South Africa made further EM observations possible. Within the time period following his last publication in 1984, almost all taxa described by Giffen have been imaged under LM and many also under EM (SEM or TEM). Many of his taxa have been used as basionyms for new genera or transferred to more appropriate genera; very few turned out to be synonyms of established taxa. The backbone of his research was collections from the South Africa coasts analyzed in the 19th and early 20th centuries. In his papers, Giffen also identified several hundreds of established species, suggesting the marine benthic diatom assemblages of South Africa are moderately to highly diverse. Beginning in the early 21st century, an extensive bilateral research program on the South African marine littoral was carried out between Poland and South Africa. Within the framework of this cooperation, Giffen's sampling sites were revisited, new samples collected, environmental variables measured and ca. 350 cultures at the Szczecin Diatom Culture Collection (University of Szczecin) were established. Our recent results support the idea that benthic diatom diversity of the South African coasts is high and strongly underscored. New genera and new species, characterized by both morphology and DNA sequence data, have been established based on this joint research, including new genera belonging to the Cymatosiraceae, Fragilariaceae, Plagiogrammaceae and Bacillariaceae. Molecular markers as also suggest some taxa described by Giffen are globally distributed.

The bilateral cooperation between University of Szczecin and the South African Environmental Observation Network and Nelson Mandela University continues, funded by the Polish National Research and Development Centre (NCBiR – grant no. PL-RPA/TemBioDiaSA/02/2016) and the South African National Research Foundation (NRF).

Reproductive compatibility of Eurasian populations of Ulnaria ulna

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Biogeographic delineation of species based on morphology or gene sequences analyses may not correspond to real biological relations between field populations supposing actual or potential gene exchange. While similar morphological features of cells taken from different populations support an idea of the species uniformity, possible existence of cryptic species or species complexes cannot be rejected. Fortunately, species boundaries in diatoms can be verified experimentally (Chepurnov & 2004). It is the concept of reproductive isolation that provides the yardstick for both delimitation of cryptic species taxa and recognition of conspecific populations. This approach could not be recommended for routine purpose, but it allowed us, in the case of Ulnaria ulna (Nitzsch) Compère, to discover mechanism providing species boundaries and operating on the second level of incompatibility, i.e. incompatibility of gene pools. The morphotype of the freshwater diatom U. ulna is known from around the world. Following the biological species concept (BCC) claiming that "species are groups of actually or potentially interbreeding natural populations, which are reproductively isolated from other such groups" (Mayr 1942, p. 120) we checked sexual compatibility of clones derived from ten distantly located populations on Eurasian continent with the aim of testing a hypothesis about Pan-Eurasian distribution of the species. All isolated clones turned to be sexually compatible, and mated readily in the combinations corresponding to their mating types. The descendants (F1 generation) were fertile in back-crosses with parental clones, excepting those hybrids which were obtained with the participation of clones originated from East Eurasia. East Eurasian and West Eurasian populations revealed post-zygotic isolation thereby demonstrating an evolutionary divergence and they could be regarded as separate species according to the BCC. However, this isolation was not complete enough to prevent hybridisation in the first generation. The data obtained stimulate further discussion on dissemination and speciation of diatoms.

Chepurnov V.A., Mann D.G., Sabbe K. & Vyverman W. 2004: Experimental studies on sexual reproduction in diatoms. –Int. Rev.Cytol. 237: 91–154.

Mayr E. 1942: Systematics and the Origin of Species from the Viewpoint of a Zoologist. – New York: Columbia University Press.

Sexual reproduction of diatom species *Climaconeis scalaris* (Bréb.) E. J. Cox from the Black Sea

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Grunow described the genus Climaconeis by incorporating into it two species, C. lorenzii Grunow and C. frauenfeldii Grunow. Later on Mereschkowsky based on plastid morphology amended the generic diagnosis of the genus Okedenia Eulenst. ex De Toni. Taxa included in Climaconeis have H-shaped chloroplasts with centrally positioned pyrenoid. Cox reviewed the nomenclatural and taxonomic history of the two genera and found many structural similarities between Okedenia and Climaconeis. She proposed to merge them in *Climaconeis*, which has nomenclatural priority over *Okedenia*. Clones of C. scalaris were isolated into culture from natural population that inhabit the sublittoral pebbles near the Karadag biological station (44° 54' 41" N, 35° 12' 04" E) in the Crimea, the Black Sea. Crossing experiments were performed by mixing pairs of clones that had been maintained in the exponential phase of growth by sub-culturing into fresh medium every 5-6 days. Each crossing combination was performed at least in duplicate. Heterothallic mode of sexual reproduction was observed. Here, we provide for the first time a description of the sexual reproduction process in this species. Cells from clones which were sexually compatible, arranged gametangial pairs. Diploid maternal cells touching each other began to move. During an active gliding, cells extruded mucilage forming mucous track. Each gametangium in the pair produced two ellipsoidal haploid gametes, which to a large extent were morphologically and behaviorally isogamous. The division of the contents of gametangia occurred in the transapical plane, without gamete rearrangement. Pairwise fusion of gametes resulted in appearance of two zygotes which shortly after started to grow. The young auxospores were ellipsoidal and positioned between the empty gametangial frustules. Parental valves were parallel to the growing auxospores. Intraclonal sexual reproduction was not observed.

The Byelovezhian Interglacial diatom flora of Belarus: new data

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Diatoms of the Byelovezhian Interglacial (=Ferdynandovian, Muchkapian), of the most ancient Interglacial of the Pleistocene in Belarus, so far, have been studied in nine sections located in the western and southeastern parts of the country. New data on the study of the Byelovezhian Interglacial deposits by diatom methods has been recently received. It is the first diatom study of these sediments in the territory of the Belarusian Poozerie in the northern part of the country. 17 samples of lake sapropelite with fossils (fruits and seeds, shells of mollusks) revealed at a depth of 71.5-79.6 m near the city of Novopolotsk, Vitebsk region, were investigated. 115 species belonging to 46 diatom genera were identified. The bulk of the flora consists of representatives of the planktonic genera Aulacoseira Thwaites, Stephanodiscus Ehrenb., Handmannia Perag. and Cyclotella (Kütz.) Bréb. In addition, species characteristic of the Middle Pleistocene and Byelovezhian times were abundant. Cyclotella reczickiae Loginova var. reczickiae and C. reczickiae var. diversa Loginova were described as taxa new to science from Byelovezhian deposits of Belarus; also recorded were Handmannia (Cyclotella) comta var. pliocaenica and H. (Cyclotella) comta var. lichvinensis; Stephanodiscus niagarae var. insuetus Khurs. & Loginova with transitional forms to S. rotula (Kütz.) Hendey; spores of Aulacoseira granulata (Ehrenb.) Simonsen. The species Aulacoseira ambigua (Grunow) Simonsen dominates in the section, amounting to more than a half of all valves in the samples. Planktonic species Stephanodiscus rotula (Kütz.) Hendey, Handmannia comta (Ehrenb.) Kociolek & Khurs., nom. inval., Aulacoseira subarctica (O. Müll.) E. Y. Haw., Cyclostephanos dubius (Hust.) Round stand out as abundant taxa. Among benthic diatoms, Tabellaria fenestrata (Lyngb.) Kütz., Staurosira construens Ehrenb. with varieties, Pseudostaurosira brevistriata (Grunow) D. M. Williams & Round, Staurosirella martyi (Hérib.) E. Morales & Manoylov, Amphora ovalis (Kütz.) Kütz. quantitatively dominated. As seen in the unchanging dominance of one planktonic group (up to 80%) in the diatom assemblages, the paleoecological conditions in the lake during the characterized period of time did not change significantly: the paleobasin most likely remained deep, stagnant and oligomesotrophic.

Overview of study background of the fossil diatom flora of Belarus

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In 1967, for the first time in Belarus, L. Loginova and G. Khursevich began to study fossil diatom flora for geological purposes (defining the age of sediments and paleogeographic conditions of their formation) at the Institute of Geochemistry and Geophysics of the Academy of Sciences of the BSSR (now "The Institute of Geology" branch of the Republican Unitary Enterprise "Research and Production Center for Geology") on the initiative of the academician G. Goretsky. S. Fedenya and S. Demidova later started diatom analysis. Work is being continued at the present time at the same Institute, where the original materials from diatom research and the diatom fossils have been kept for 50 years and are still being kept. The diatom collection includes also some materials from other countries. It represents permanent samples for light microscopy (slides) and powders consisting of refined diatom valves to make preparations for light and scanning electron microscopy. Holotypes of the newly described taxa are particularly valuable.

Comprehensive data on the freshwater diatom flora of the Late Cenozoic in Belarus has been accumulated. Diatom flora was obtained from different-age ancient lake sediments from sections of boreholes and natural and artificial outcrops. Changes in diatom assemblages from bottom to top in the sections reflect the dynamics of paleoecological conditions in paleobasin (depth, salinity, pH, trophicity, etc.).

The studied flora refer to several age levels of the Neogene and Quaternary. In the Neogene, these are the Middle and Upper Miocene (5 sites); in the Quaternary are the three Interglacial intervals of the Pleistocene: Byelovezhian (=Ferdynandovian, Muchkapian; 8 sites), Alexandrian (=Holsteinian, Mazovian, Likhvian; 11 sites), Muravian (=Eemian, Mikhulian; 18 sites), and the Late Glacial and Holocene (5 sections of lake sediments). For each age interval, a complex of characteristic species, including indicative taxa, was determined. In the process of studying the fossil diatom flora of Belarus, 20 new species and intraspecific taxa have been identified. From the Upper Miocene deposits, the following species are described: *Mesodictyon (Stephanodiscus) nemanensis* (Khurs.) Khurs., Eunotia goretskyii Khurs., E. goretskyi var. flexuosa Khurs., Tabellaria celatom Khurs. var. celatom, T. celatom var. elongata Khurs., T. poretzkiae Loginova & Khurs., Achnanthes pliocenica Khurs. & Loginova, Pseudoaulacosira moisseeviae (Lupikina) Lupikina & Khurs. From the Byelovezhian Interglacial deposits, Cyclotella reczickiae Khurs. & Loginova var. reczickiae, C. reczickiae var. diversa Loginova, Stephanodiscus determinatus Khurs., S. niagarae var. insuetus Khurs. & Loginova, S. peculiaris Khurs., S. raripunctatus Khurs. & Loginova, S. styliferum Khurs. were discovered as new taxa to science. Cyclotella temperiana Loginova, C. michiganiana var. parvula Loginova, Stephanodiscus alexandriensis Khurs., S. immemoratus var. minor Khurs., S. fascicularis Khurs. as novel taxa were studied from the Alexandrian Interglacial deposits. Most of these taxa belong to the stenochronous representatives of the flora, which are important biostratigraphic markers that are also found in coeval-age deposits of other regions of Western and Eastern Europe. Fossil diatoms of Belarus are very diverse taxonomically. A consolidated systematic list of fossil diatoms includes more than 600 species, varieties and forms, among which 32 species and 15 intraspecific taxa are considered extinct. Work on the compilation of an atlas of the fossil diatom flora of Belarus has begun.

Sex and size in diatoms

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The diatom life cycle is dominated by long periods of vegetative or mitotic division, punctuated by short periods of sexuality (haplobiontic-diploid). Critical in this life history strategy is the recovery of cell size and form following sexual reproduction and auxosporulation. The end product of sexuality is the initial cell(s), which represents the largest size that a diatom species can attain. Earlier work has shown that initial cell size is most strongly predicted by gametangial cell size; large gametangia produce large initial cells. Less work has been directed at other factors potentially involved in controlling initial cell size such as environment, mating strategy, or genetics. We analyzed natural populations undergoing sexuality and used the literature to explore the relationships between mating partners, between initial cells, and between gametangial and initial cell size undergoing various sexual strategies including Type I and II allogamy and automixis. We consider the effect of initial cell size in structuring diatom communities and ramifications for bioproduction, food web dynamics, nutrient uptake, and the impact of temporal and spatial variation in diatom cell size on ecology and taxonomy.

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Latest Miocene diatoms from lacustrine sediments in Cappadocia, Turkey

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In the context of a study of Neogene paleosols in Cappadocia, Central Anatolia, Turkey, near the city of Sahinefendi, Late Miocene lacustrine sediments were sampled. These freshwater sediments were deposited in a region with active volcanism and are preserved between two thick ignimbrites, the Kizilkaya – and the Gördeles ignimbrite. New ages obtained for these ignimbrites by analyzing glassparticles for their 40 Ar/ 39 Ar ratio: 5,6 ± 0,06 Ma and 6,22 ± 0,04 Ma respectively, provided the time frame. During the upper part of this interval, just above a thick massflow deposit below the Kizilkaya Ignimbtrite, the presently studied lacustrine sediments rich in diatoms formed. Quantitative analysis of these sediments showed that there are samples which are very rich in diatoms, with 10⁷ valves per gram of sediment. Other samples rich in fine clastic components have diatom abundances of 10⁶ to 10⁵ per gram sediment. The diatom assemblages in most samples are dominated by Cyclotella (Kütz.) Bréb. species. Besides these, epiphytic or epilithic living pennate species of the Cocconeis placentula Ehrenb. group, Epithemia aff. smithii Carruth., Mastogloia aff. elliptica (C. Agardh) Grunow are likely to be common. Present but less abundant are species of the genera Surirella Turpin, Staurosira Ehrenb., Denticula Kütz., Amphora Ehrenb. ex Kütz., Rhopalodia O. Müll., Cymbella C. Agardh, Hantzschia Grunow, Nitzschia Hassall, Navicula Bory, Achnanthes Bory, Pinnularia Ehrenb., Fragilaria Lyngb., Diploneis Ehrenb. ex Cleve. In some samples, chrysophycean cysts far outnumber the diatoms. These might represent springbloom deposits. The different types of sediment and diatom assemblages encountered suggest fluctuating water levels between a shallow lake and swamp at the sampling site.

"Pinnularia baetica": a new diatom species found in an alkaline mountain lagoon in the south of Europe (Granada, Spain)

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A new benthic freshwater diatom species, belonging to the genus *Pinnularia* Ehrenb., was found in Laguna Seca of Sierra Seca in the north of the province of Granada, Spain. *"Pinnularia baetica"* Fern. Moreno & Sánchez Castillo (paper submitted) is proposed as a new species based on observations under light (LM) and scanning electron microscopy (SEM) and its special ecology typical of a calcareous lagoon. The most similar taxa to *"P. baetica"* are *P. atlasi* J. Darley and *P. infirma* Krammer , which were studied through material obtained in lagoons of northern Morocco. Although there are similarities in the morphological characters of the frustule, it was possible to verify through LM and SEM micrographs clear differences between *"P. baetica"* and the other two taxa; on the one hand, *"P. baetica"* has a panduriform shape more pronounced than *P. infirma*. On the other hand, the absence of spines in *"P. baetica"* and the smaller average length of the frustule are the main differences with *P. atlasi*.

Eunotiaceae biodiversity from Serra of Itabaiana, Sergipe, northeastern Brazil

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Species of Eunotiaceae Kütz. are commonly found in benthic freshwater habitats, particularly in acidic environments, and are widely distributed in the tropical and subtropical regions of the planet. Eunotia Ehrenb. is one of the most representative genera in Brazil, in which around 100 species have already been reported. In the northeastern Brazil, about 30 infraspecific taxa of Eunotia and two of Actinella F. W. Lewis are known. The Serra of Itabaiana, located in the municipality of Itabaiana, Sergipe, is formed by residual mountain ranges, ranging from 400 to 659 m elevation, in a transition area between the Atlantic forest and the Caatinga. The objective of this study is to discuss the taxonomy of Eunotiaceae species of Serra of Itabaiana, using electron and optical microscopy. The study was based on periphytic and planktonic samples collected at four points. A total of 31 infrageneric taxa were identified, one Actinella and 30 Eunotia. Eunotia incisa W. Greg., E. intermedia (Krasske ex Hust.) Nörpel & Lange-Bert., E. pseudogroenlandica Lange-Bert. & Tagliaventi and E. rhomboidea Hust. were the most common taxa. We highlight five pioneer citations for Brazilian waters: E. frickei var. elongata Hust. ex Simonsen, E. julma Lange-Bert., E. pseudogroenlandica Lange-Bert. & Tagliaventi, E. quaternaria Ehrenb., E. valdespectabilis Metzeltin & Lange-Bert. The Eunotiaceae inventory from Itabaiana is richer than about 80% of the similar diatom floras studied in Brazil. No freshwater diatom taxonomic studies on the Sergipe state were hitherto developed, thus this represents an unprecedented contribution to the *Eunotiaceae* biodiversity and biogeography knowledge from Brazil.

Environmental factors influencing the composition of soil diatom communities: preliminary results

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In 1843 C.G. Ehrenberg described the first diatoms from soils currently known as Hantzschia amphioxys (Ehrenb.) Grunow (= Eunotia amphioxys Ehrenb.) and Pinnularia borealis Ehrenb. Since then, around 300 papers concerning terrestrial diatoms were published, most of them with a floristic approach (i.e. limited ecological knowledge on the species). Within the last couple of years, the interest in soil diatoms increased, particularly regarding their potential use as hydrological tracers (Pfister & al. 2017) and as soil bio-indicators (Antonelli & al. 2017). In this line, we want to obtain more general and specific ecological information (spatial and temporal resolution) about soil diatoms by investigating the monthly variation over the course of one year. Diatom and soil samples were taken at 16 sites with different combinations of geological, soil (schist, marl and sandstone) and land use (forest, grassland and agriculture) features. Sampling in such complex environment will give us a wider picture of the diatom diversity. For instance, we have identified around 200 taxa containing some poorly recorded species such as Sellaphora lundii C. E. Wetzel & al., Sellaphora harderi (Hust.) Foets & C. E. Wetzel, Humidophila irata (Krasske) R. L. Lowe & al. The most common diatoms were, among others, H. amphioxys, Nitzschia pusilla Grunow, Mayamaea permitis (Hust.) Bruder & Medlin, Mayamaea atomus (Kütz.) Lange-Bert. and Stauroneis thermicola (J. B. Petersen) J. W. G. Lund. Concerning the seasonal variation, we observed that towards the winter season (i.e. harsher weather conditions), the abundances of certain species decrease and eventually even disappear (e.g. Fragilaria rumpens (Kütz.) G. W. F. Carlson, Fragilaria pectinalis (O. F. Müll.) Lyngb. and Psammothidium subatomoides (Hust.) Bukht. & Round, while other taxa benefit from those changes (e.g. Craticula minusculoides (Hust.) Lange-Bert. and Pinnularia cf. bullacostae Krammer & Lange-Bert.). Except for those changes, the overall composition of the communities remained the same from October to March. However, most of the sites could be distinguished from each other based on the composition of the communities and the presence of certain (indicator) species such as Mayamaea fossalis (Krasske) Lange-Bert., Planothidium lanceolatum (Bréb.) Lange-Bert. and S. lundii. Particularly the sites located in or near forest area consisted of unique diatom composition and in most cases very species rich communities (up to 35 species). Furthermore, soil pH, soil moisture, habitat type, amount of shading, nitrogen content and iron (Fe) content were identified as the variables having the largest impact in structuring the communities, and are among the features with the highest importance in defining the ecological status of the sites. Optima and tolerances were determined for pH, soil moisture and nitrogen for the most common soil diatoms.

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Epiphytic diatom communities in a eutrophic reservoir in the second year of the management cycle

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Epiphytic diatom communities from the Dehtář fishpond (Southern Bohemia, Czech Republic) were studied in terms of species composition, substrate affinity and functional traits. The Dehtář fishpond is a large hypertrophic reservoir near České Budějovice with fluctuations of oxygen and fast changes in stratification of main physical and chemical water parameters. These changes were recorded by several sensors placed on three stations at different parts of the pond providing high-frequency monitoring. This monitoring system took part in a complex study conducted within the NETLAKE – COST action including also observation of phytoplankton, zooplankton, vegetation and seed bank (Potužák & al. 2017).

22 samples of 17 species of vascular plants were collected at two sites (the Babický Stream Bay - BSB and the Fishpond Dam - FD) within the fishpond near the high frequency monitoring stations (with temperature and oxygen sensors) during one sampling event in June 2016, which was the second year of the fishpond management cycle with higher water level and increased nutrient content in fishpond water. 400 individual diatoms were counted in each permanent slide. Altogether, 119 diatom taxa were identified, which is 23 more than was found in 2015 (the first year of the fishpond management cycle). The species richness ranged from 17 to 46 taxa per sample, with the highest richness for Ranunculus sceleratus and the lowest for Lemna gibba. In terms of set functional types characterizing relation of diatoms to the host plant surface, the plant substrate of the FD was dominated by typically periphytic taxa (mainly Achnanthidium saprophilum (H. Kobayasi & Mayama) Round & Bukht., Cocconeis placentula Ehrenb. and Gomphonema saprophilum (Lange-Bert. & E. Reichardt) N. Abarca & al.), while the plant substrate of the BSB was dominated by facultatively periphytic taxa of the Bacillariales (mainly Nitzschia archibaldii Lange-Bert. and Nitzschia palea (Kütz.) W. Sm.). This result differs from the first year of the fishpond management cycle when actively moving epipelic taxa of the Naviculales dominated at the FD and facultatively periphytic taxa of the Fragilariales dominated at the BSB (Fránková & al. 2017). These interannual differences can be explained by anoxic conditions and increased nutrient content together with changed light conditions in 2016, while the differences between the FD and the BSB in 2016 can be explained by the differences in environmental conditions among the sites, especially very intensive and frequent wave action typical for most parts of the Dehtář fishpond.

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Late Quaternary palaeoenvironmental reconstruction by downcore diatom variability in Lake Bolshoe Toko sediments, Yakutia (Russia)

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The northern Eurasian region is regarded as being notably sensitive to a changing climate. Recent changes are currently threatening the stability of permafrost environments and the natural local ecosystems (Biskaborn et al. 2016). Using palaeoecological proxy data in lake sediments like diatoms as sentinels of environmental changes foster the understanding of transitions from past pristine to Anthropocene conditions. The large and deep Lake Bolshoe Toko is located at the marginal permafrost zone in south-eastern Yakutia, Siberia, at the foot of the northern slope of the eastern Stanovoi mountain range. We performed multiproxy analyses focusing on diatoms in a sediment core dated to 18.000 years BP, located in the deepest waters of the lake (approx. 70m). In this study, the diatom species assemblage with a temporal downcore resolution of at least 1000 years was analysed. The counts show a total amount of 160 different species. Diatoms began to appear from 14,600 years BP. In the Late Pleistocene, only a few Cyclotella (Kütz.) Bréb. species were preserved in the record, whereas since the beginning of the Holocene we find a complex biodiversity in the diatom assemblage. The entire core is dominated by either small achnanthoid taxa or a variety of Cyclotella taxa. In addition, the ultra-oligotrophic, mostly endemic taxa Lindavia costata (Loginova & al.) T. Nakov & al. (Pliocaenicus costatus (Loginova & al.) Round & Håk.) appears in different varieties over the whole core. Three methods were used: A) Data visualisation using Tilia. B) Combining characteristics of each taxa based on gualitative limnochemical information from the literature with their relative abundance found in the core to estimate environmental conditions. The information is mostly taken from the collection of ecological species attributes created by S. Barinova (Barinova & al. 2011). C) Application of training dataset from NE Siberia (Herzschuh & al. 2013) to reconstruct limnohydrological parameters quantitatively using a transfer function. Additionally, multivariate statistics are used to detect the main influences in data variabilities or changes in diatom assemblages using a principle component analysis (PCA) in the R environment.

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Diversity of introns in the marine planktonic diatom family Chaetocerotaceae

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Introns (intragenic regions) are non-coding DNA fragments in rRNA- and protein-coding genes and are spliced out prior to rRNA maturation or mRNA translation. They have been found in all lineages of the tree of life. During our molecular and morphological explorations of the diversity of the family Chaetocerotaceae we encountered several short (ca. 100 bp) and long (ca. 400 bp) introns in the 18S and 28S rDNA sequences. Introns were detected at 14 locations in the alignment of the 18S, and at one location in the 28S rDNA alignment. The introns were not distributed all over the Chaetocerotacean diversity, but instead concentrated in three clades. To characterise the introns and assess their relationships, we performed BLAST searches using them as queries against the nucleotide database of NCBI and Comparative RNA Web Site and Project (CRW) and gathered all results down to 90% identity. Introns were aligned manually into two sets (one with the short introns and one with the long ones). Long Chaetoceros introns grouped into two clades, defined by insertion sites within the SSU rDNA. Both clades were recovered within the lineage of the family IC1 of the Group-I introns. Characteristics of the secondary structure of their rRNA sequences confirmed this characterisation. Phylogenetic relationships among the long introns did not corroborate the Chaetocerotacean phylogeny inferred from the 18S or 28S rDNA sequences, suggesting that these introns are transferred horizontally across lineages in the tree of life. The short introns were characterized as "spliceosomal introns" based on their conserved, functional sites. Alignment of these signature sites was straightforward, whereas in between these sites, alignment was fraught with ambiguity. Only strains of identical species shared similar or identical introns at the same locations, whereas differences were apparent between strains from different seasons, and became substantial between closely related species. Thus, the introns accumulate base substitutions more rapidly that the rRNA coding regions, and therefore, may provide tools for population studies. The introns are relevant also in high throughput sequencing (HTS) meta-barcoding approaches. Short introns are located in the 18S V4 region of six species and in the V9 region of seven species, thereby affecting the detectability of these species in HTS metabarcoding approaches. So, depending on the bioinformatics procedures, one might eliminate such sequences from the database because of them "being too long", thereby underestimating the actual diversity.

Re-examination of type material of *Melosira perpusilla* Freng. and description of two new *Aulacoseira* species from Santa Cruz Province (Argentina)

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During analyses of lacustrine sediments for palaeoenvironmental reconstructions, the occurrence of new species with unknown ecological requirements become a challenge for an accurate interpretation of the diatom record. Working on diatom taxonomy in an isolated region such as southern Patagonia is a complicated task due to lack of supporting bibliography. The use of references for the Northern Hemisphere has caused identification errors since southern taxa have been force-fitted into European and North American concepts. In the case of the genus *Aulacoseira* Thwaites, there is a long history of misidentifications due to use of literature for other continents and a renewed interest in this group has produced a number of new taxa and the documentation of known taxa (Tremarin & al. 2014, Morales & al. 2015, Casa & al. 2017). In the present work, we examine the type material of *Melosira perpusilla* Freng., analyse its transfer to *Aulacoseira* and provide the basis for the description of two new small species of *Aulacosiera* found in sediment samples from Laguna Verde (49.20°S; 72.98°W) located in southern Santa Cruz province (Patagonia, Argentina). We present light and scanning electron microscopy data for the three taxa and a comparison with similar species.

- Casa V., López Bedogni G. & Van de Vijver B. 2017: A new *Aulacoseira* species (*Bacillariophyta*) from Tierra del Fuego (Argentina) and comparison with the type material of *Melosira laevis* var. *fuegiana* Frenguelli. Diatom Res. **32**: 409–416. https://doi.org/10.1080/0269249X.2017.1401010
- Morales E. A., Rivera S. F., Rubin S. D. C., Vis M. & Houk V. 2015: *Aulacoseira kruegeriana* (Diatomeae, *Coscinodiscophyceae*): a new centric diatom from high elevation Andean rivers and streams of Bolivia. Diatom Res. **30**: 269–277.
- Tremarin P. I., Ludwig T. A. V. & Torgan L. C. 2014: Four new *Aulacoseira* species (*Coscinodiscophyceae*) from Matogrossense Pantanal, Brazil. Diatom Res. **29:** 183–199.

Phylogenetic analysis reveals that the 'radial centric' genus Orthoseira Thwaites is a member of a 'multipolar' diatom lineage

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The diatom genus *Orthoseira* Thwaites (*Bacillariophyta*) is a ubiquitous taxon in aerial diatom assemblages, with species found globally. Cylindrical cell shape and radial symmetry of this genus has led to its historical placement in the *Coscinodiscophyceae* ('radial centric' diatoms), but its systematic relationships have remained uncertain. I present a five-gene phylogeny, based on nuclear (nSSU rDNA) and chloroplast (*rbcL*, *psbC*, *psbA*, and *psa*B) genes to determine the phylogenetic placement of *Orthoseira* among the diatoms. The concatenated multi-gene phylogenies and nSSU-only gene tree demonstrate that *Orthoseira* is deeply embedded within a clade of the *Mediophyceae* ('multipolar centric' diatoms). Throughout all phylogenetic analyses, *Orthoseira* was shown to be sister to the genera *Terpsinoë* Ehrenb. and *Hydrosera* G. C. Wall. Through constrained phylogenetic tests, it was determined that the hypothesis that *Orthoseira* is a member of the *Melosirales* could be rejected. Therefore, lack of morphological similarity between *Orthoseira*, *Terpsinoë*, and *Hydrosera* is hypothesized to be the result of an ancient divergence event between the *Orthoseirales* and the *Hydrosera*, *Terpsinoë* clade.

Variations of Indian Summer Monsoons during the Miocene: evidences from diatom assemblages of the northern Indian Ocean

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The Miocene epoch is characterised by some significant events viz., upliftment of Himalayas and Tibetan plateau, intensification of Asian Monsoonal system etc. A monsoon can be considered as a manifestation of the seasonal migration of the Inter Tropical Convergence Zone (ITCZ) or equatorial trough in response to the seasonal variation. Phytoplankton, specifically the siliceous microfossils preserved in the Miocene sedimentary sequence of northern Indian Ocean, can play a significant role in the estimation of monsoonal variability. The siliceous microfossils of Andaman and Nicobar Basin, also designated as the northern Indian Ocean, are represented by diatoms, radiolarians, silicoflagellates, sponge spicules etc. As observed, in most of the samples, the silicified microfossils are present in association with the calcareous nanofossils. The relative ages of the outcrops have been precisely dated with calcareous nanofossils and silicified radiolarians. The siliceous microfossils from the early to middle Miocene outcrops on the Havelock Island of Andaman and Nicobar Basin are poorly preserved and most of them are broken. In all cases, dissolution was likely a major factor for poor preservation with low nutrient availability. The diversity of diatoms is also very low and the assemblage is represented by 17 taxa belonging to 14 genera. The commonly-occurring species of diatoms are Coscinodiscus rhombicus Castrac., Rossiella paleacea (Grunow) Desikachary & C. L. Maheshw., Thalassiothrix longissima Cleve & Grunow, Cestodiscus cf. kugleri Lohmann, Nitzschia Hassall sp. and Syndera Ehrenb. sp. Abundance and diversity of well preserved siliceous microfossils remarkably increased in the late Miocene outcrops on Neil Island of the basin. This may be correlated with ocean upwelling and a nutrient rich condition. The assemblages are represented by 82 taxa belonging to 35 genera. The significant diatom taxa present in the late Miocene assemblages are represented by Actinocyclus ellipticus Grunow, A. ellipticus var. javanica Reinhold, Actinoptychus senarius (Ehrenb.) Ehrenb., Paralia sulcata (Ehrenb.) Cleve and Thalassionema nitzschioides (Grunow) Merschk. The abundance and diversity of diatoms as well as the planktonic/benthic ratio of the diatoms have been taken into consideration for the evaluation of monsoonal variability during the Miocene in the northern Indian Ocean.

Fossil diatom flora from the marine Cenozoic stratigraphic section of West Kamchatka at the Kvachina Bay, Russian Far East

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The stratigraphic section at the Kvachina Bay is a key section for the marine Cenozoic in West Kamchatka with an essentially continuous sequence composed of about 500 m of Paleogene through Neogene sediments. Sampling for diatom analysis was done here during recent field work. Samples collected throughout the upper part of this section (the upper part of the "Whitish" Series, about 300 m thick) yield diverse preserved fossil diatoms. The flora is dominated and subdominated by marine neritic-planktic and sublittoral taxa, but open-sea planktic elements are also documented. Analysis of stratigraphic occurrence of diatoms throughout the section allowed determination of seven local zones for diatom-bearing deposits. Stratigraphically from bottom to top these are: *Odontella sawamurae* Akiba Local Zone, *Rhizosolenia oligocaenica* H.-J. Schrad. Local Zone, *Thalassiosira nansenii* R. P. Scherer & N. Koç Local Zone, *Cestodiscus kugleri* Lohman Local Zone, *Lisitzinia ornata* Jousé Local Zone, *Rocella gelida* (A. Mann) Bukry Local Zone, and *Thalassiosira* cf. *praefraga* Gladenkov & J. A. Barron Local Zone. Their boundaries are characterized by the successive first occurrences of marker species in the section.

The presence of biochronologically significant marine taxa such as Odontella sawamurae, Ikebea tenuis (J. Brun) Akiba, Kisseleviella carina Shesh.-Por., K. ezoensis Akiba, Cavitatus jouseanus (Shesh.-Por.) D. M. Williams, C. miocenicus (H.-J. Schrad.) Akiba & Yanagisawa, Rhizosolenia oligocaenica H.-J. Schrad., R. miocenica H.-J. Schrad., Eurossia irregularis (Grev.) P. A. Sims, Thalassiosira nansenii, Asteromphalus symmetricus H.-J. Schrad. & J. Fenner, Cestodiscus kugleri, C. trochus Castrac., Pseudodimerogramma elegans H.-J. Schrad., P. filiforme 'filiformis' H.-J. Schrad. & J. Fenner, Sceptroneis tenuis 'tenue' H.-J. Schrad. & J. Fenner, S. humuncia H.-J. Schrad. & J. Fenner, S. humuncia var. rondipoda R. P. Scherer & N. Koç, Rhaphoneis angulata J. Fenner, R. elongata G. W. Andrews, Lisitzinia ornata, Rocella gelida (A. Mann) Bukry allowed correlation of the proposed local zones with the North Pacific Cenozoic diatom zonation and age determination of the host sediments. A correlation with the lower Oligocene to lower Miocene zones (the North Pacific Rhizosolenia oligocaenica Zone through Thalassiosira praefraga Zone) is supposed. As a result, it is inferred that the Odontella sawamurae Local Zone through Lisitzinia ornata Local Zone may be dated as early Oligocene (from the middle part to terminal part of the Rupelian Stage), the Rocella gelida Local Zone - as late Oligocene (the Chattian Stage excepting its terminal part), and the *Thalassiosira* cf. praefraga Local Zone – as latest Oligocene to early Miocene.

It should be noted, that some taxa including *Lisitzinia ornata*, *Thalassiosira nansenii*, *T. irregulata* H.-J. Schrad., *Asteromphalus symmetricus*, *Pseudodimerogramma elegans*, *P. ellipticum 'elliptica'* H.-J. Schrad., *Eurossia irregularis*, *Rhizosolenia oligocaenica*. *R. miocenica*, *Rocella praenitida* (J. Fenner) J. Fenner, *Sceptroneis humuncia*, *S. propinqua*, *S. ligulata 'ligulatus'* J. Fenner are documented in West Kamchatka for the first time. Moreover, in their entirety and paleontological characteristics Oligocene assemblages from the studied section are the most representative among all assemblages of this age known in the whole Kamchatka region.

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Influence of the cell size and life cycle on the lipid content of the selected set of diatom strains

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The main goal of this study is to investigate a selected set of clonal diatom cultures representing two entities of the genus *Schizostauron* Grunow and compare their lipid content during various stages of their life cycle. The maximum amount of lipid production by diatoms is considered to be species-specific and a heritable trait, which means that some lineages are able to produce more lipids than others. Moreover, diatom cell size is somewhat limited due to solid siliceous cell wall, but it can vary during the life cycle. Considering that larger cells have greater potential to store lipids due to increased cell volume, we tested the influence of cell size within closely-related strains on the lipid content per cell.

The choice of strains was based on their well-known life cycle – type of sexual reproduction, cardinal points and size range. Nine strains ranging in size from 20 μ m to 24 μ m (set 1 - 6 strains) and 30 μ m to 34 μ m (set 2 - 3 strains) were isolated from a marine environment off the coast of Saudi Arabia. In order to obtain the cells of larger size, mating experiments were conducted. Successful auxosporulation, resulting in the production of initial cells, was observed in 5 different pairs from set 1. Six initial cells of size 30-32 μ m were isolated and included in further analyses. The initiation of sexual reproduction in some of the strains enabled us to investigate lipid content in cells of different stages along the size range of this species – from initial cells throughout the vegetative stage to the smallest, parental cell – to determine whether the lipid concentration in cells really is size-dependent. Lipid content in cells was extracted from strains and quantified as % of dry biomass. Lipid droplets were visualized with Nile Red stain using confocal microscopy.

Climate- and human-induced changes in lake ecosystems in the mid-Holocene inferred by diatom analysis

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Prehistoric humans began to significantly reshape their surroundings during the early Neolithic, a transition period from hunter-gatherer to agrarian societies. In Switzerland, numerous archaeological remains from pile-dwellings and lake-side settlements have been found for the Neolithic period. These settlements form a unique group of well-preserved archaeological sites that constitute one of the most important sources for the study of early agrarian societies in the region.

Pollen studies in the sediments of Burgäschisee and Moossee, two lakes on the Swiss Plateau for which the remains of pile dwellings were found, reveal numerous phases of human activity (Rey 2017). It appears that some of these were accompanied by higher lake-water nutrient concentrations and climate-induced lake level changes.

The aim of the presented study is to apply diatom analysis to the sediments at exceptionally high temporal resolution to provide independent evidence of whether human settlements coincided with changes in lake hydrology and to find out if past ecosystem changes were mainly driven by climate or human activities around the lakes.

Preliminary results show remarkable changes in diatom assemblages along with the first appearance of anthropogenic indicators, such as *Cerealia-*, *Hordeum-* and *Triticum-*type pollen, as well as increased concentrations of microscopic charcoal, in the sediments of Lake Burgäschisee (5740 – 5560 cal BP). Rapid increases of *Staurosira construens* Ehrenb. and *Staurosira venter* (Ehrenb.) H. Kobayasi indicate a turbid environment as a result of landscape opening and soil erosion due to agriculture. Planktonic *Pantocsekiella pseudocomensis* (Scheffler) K. T. Kiss & Ács, *P. costei* (Druart & F. Straub) K. T. Kiss & Ács and *Cyclotella radiosa* (Grunow) Lemmerm. are replaced by periphytic diatoms, such as *Gomphonema parvulum* (Kütz.) Van Heurckand *Navicula vulpina* Kütz., which might indicate nutrient enrichment due to anthropogenic impact, as well as climate-driven lake level lowering. The subsequent increase of planktonic diatoms, such as *P. pseudocomensis* and *C. radiosa* could be indicative of ecosystem recovery from human induced disturbances, as well as lake level rise.

The obtained information is relevant for understanding lake ecosystem response to climatic and anthropogenic change. Besides improved understanding of past human-climate-environment interactions, this research will provide information on the resilience of lake ecosystems to repeated human induced disturbance, information also relevant for understanding future ecosystem response to ongoing global change.

Rey F. 2017: Exploring eight millennia of climatic, vegetational and agricultural dynamics on the Swiss Plateau by using annually layered sedimentary time series. Dissertation. – Bern: University of Bern.

SYNAQUA: a French-Swiss program for biomonitoring and preservation of Lake Geneva ecosystems

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Lake ecosystems are exposed to strong anthropogenic pressures coming from their watersheds. These pressures are affecting firstly coastal areas, before affecting the pelagic ecosystem. A better understanding on those pressures and their impacts is necessary to bring environmental and social sustainable solutions.

Biomonitoring of lakes is usually based on pelagic phytoplankton. However, this biotic indicator is not appropriate to identify coastal pressures, for which benthic indicators as diatoms would be more appropriate. Contrary to pelagic phytoplankton needing only a few samples from the water column, coastal biomonitoring requires several samplings along the shore to obtain a good characterization of the hot-spot pressures. This leads to the need of a quick methodology to handle those analyses. In order to increase the biomonitoring throughput and to adapt it to lake coastal areas, the SYNAQUA project proposes to use genetic tools based on the recognition of bioindicator organisms (diatoms and oligochaetes) present in the aquatic environment directly from their DNA. Indeed, the DNAmetabarcoding approach can be faster and less expensive than the usual microscopy approach. The program focuses on the French-Swiss lake, Lake Geneva, which is an alpine lake with a large watershed area (580km²) mainly urbanized (1,083,431 residents; 556,227 tourists per year) and agricultural (35%). Periphyton was sampled in 153 coastal sites in June 2017, together with a characterization of each site (water physico-chemistry, land use, anthropisation). Diatom communities were studied using DNA-metabarcoding with rbcL gene, Illumina Miseq sequencing, Mothur and RSyst::diatom database.

In this presentation, we will highlight links between diatom communities and anthropogenic pressures. We will especially see how diatom communities react to pressures such as urbanized areas or river mouths. Statistical analysis will allow to spot pressures and to create a quality index adapted to the evaluation of the ecological quality of lake-shore zones. Such evaluation tool will help environmental managers to identify specific zones to be preserved or restored, and undertake appropriate management decisions.

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Diatom responses to abrupt Late Quaternary climate change in southern Siberia

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The Quaternary period is well known for its orbitally-driven and abrupt climatic changes. The Late Quaternary is the most recent period to include orbitally-induced climatic changes, seen across the Late Pleistocene to Holocene transition, overlain by abrupt sub-Milankovitch events, occurring over millennia to centuries. The latter are driven by internal feedbacks, and additionally volcanic and solar activity (Clement & Peterson 2008). These have triggered significant environmental shifts, which have been investigated through high resolution, well dated, multiproxy studies in several regions, including Northern Europe. Responses to these events are still uncertain in many remote regions, including the continental region of southern Siberia in central Asia. Southern Siberian is highly sensitive to current climatic changes, with warming occurring at higher rates than the global average (Tingley & Huybers 2013). Several warming impacts are already documented, including alterations in permafrost distribution, increased forest fires, shifts in the sensitive forest-steppe-tundra biomes, warming of seasonally ice-covered lakes and the appearance of thermokarst lakes. In addition to its sensitivity, Siberia's continentality also offers a rare opportunity to consider the impacts of abrupt climatic changes remote from oceanic sources. Despite this, central Asian studies are limited and have been hindered by issues including proxy preservation, sampling resolution and chronological controls, which have caused uncertainty over regional responses to specific climatic events. This presentation outlines work from Lake Baunt (55°11'15" N, 113°01'45" E), a site located at the southern limits of Siberian permafrost. Our palaeoenvironmental record extends back to ~30ka cal BP (based on multiple ¹⁴C dates, ²¹⁰Pb dating, all integrated by Bayesian age modelling), with multiple environmental and climate proxies (biogenic silica, diatom analyses, $z^{18}O_{diatom}$ and $z^{13}C_{diatom}$ analyses), highlighting significant changes in freshwater ecosystems. These include major shifts between two diatom species Pantocsekiella ocellata (Pant.) K. T. Kiss & Ács and Aulacoseira granulata (Ehrenb.) Simonsen, which broadly correlate with climatic events found in the Greenland Ice Core stratigraphy, including GS2.1a, GI-1 and GS-1. Our g¹⁸O_{diatom} Holocene record documents a general cool trend alongside several abrupt shifts, particularly during the early Holocene, including at 9.3ka and 8.3ka cal BP, which may correlate to abrupt events including the 9.3ka cal BP and 8.2ka events documented in Greenland. We compare these records to regional sites (Lake Baikal, Lake Kotokel and Hulu Cave) and consider the influence and interactions between different atmospheric systems, including the Siberian High, Westerlies and Asian Monsoon (Tubi & Dayan 2013) for propagating abrupt climatic change, driving ecosystem shifts.

Clement A. C. & Peterson L. C. 2008: Mechanisms of abrupt climate change of the last glacial period. – Rev. Geophys. **46:** 1-39.

Tingley M. P. & Huybers P. 2013: Recent temperature extremes at high northern latitudes unprecedented in the past 600 years. – Nature **496:** 201–205.

Tubi A. & Dayan U. 2013: The Siberian high: teleconnections, extremes and association with the Icelandic low. – Int. J. Climatol. **33:** 1357–1366.

A diatom-based Biological Condition Gradient (BCG) approach for assessing impairment and developing nutrient criteria for streams

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Over-enrichment leading to excess algal growth is a major problem in rivers and streams. Regulations to protect streams typically incorporate nutrient criteria, concentrations of phosphorus and nitrogen that should not be exceeded in order to protect biological communities. A major challenge has been to develop an approach for both categorizing streams based on their biological conditions and determining scientifically defensible nutrient criteria to protect the biotic integrity of streams in those categories. To address this challenge, we applied the Biological Condition Gradient (BCG) approach to stream diatom assemblages to develop a system for categorizing sites by level of impairment, and then examined the related nutrient concentrations to identify potential nutrient criteria.

The six levels of the BCG represent a range of ecological conditions from natural (1) to highly disturbed (6). A group of diatom experts developed a set of rules and a model to assign sites to these levels based on their diatom assemblages. To identify potential numeric nutrient criteria, we explored the relation of assigned BCG levels to nutrient concentrations, other anthropogenic stressors, and possible confounding variables using data for stream sites in New Jersey (n = 42) and in surrounding Mid-Atlantic states, USA (n = 1443). In both data sets, BCG levels correlated most strongly with total phosphorus and the percentage of forest in the watershed, but were independent of pH. We applied Threshold Indicator Taxa Analysis (TITAN) to determine change-points in the diatom assemblages along the BCG gradient. In both data sets, statistically significant diatom changes occurred between BCG levels 3 and 4. Sites with BCG levels 1 to 3 were dominated by species that grow attached to surfaces, while sites with BCG scores of 4 and above were characterized by motile diatoms. The diatom change-point corresponded with a total phosphorus concentration of about 50 μ g/L.

Hausmann S., Charles D., Gerritsen J. & Belton T. 2016: A diatom-based Biological Condition Gradient (BCG) approach for assessing impairment and developing nutrient criteria for streams. – Sci. Total Environm. **562:** 914-927.

Morphological and molecular characterization of *Pleurosigma* sp., isolated from Puerto Ángel, Oaxaca, tropical Mexican Pacific

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Pleurosigma W. Sm. is a diverse diatom genus with approximately 306 species, which has continental, estuarine and marine representatives. Their species may be found in large populations within soft and fine sediments, and may extend from the supralittoral to sublittoral zone. Pleurosigma species are important members of the marine community as a diverse genus and some species are also part of phytoplankton. In the present work, a putative new species, *Pleurosigma* sp. is described, and its belonging in the Pleurosigmataceae family is also confirmed through the reconstruction of molecular phylogenies using LSU sequences. The isolates were obtained from the bay of Puerto Ángel, Oaxaca in the tropical Mexican Pacific, and the cultures were maintained in f/2 medium, with a photoperiod of 12:12 h light: darkness and at a temperature of 24 ± 1° C. Morphological and reproductive characteristics were observed using light (LM) and confocal microscopy (CM), as well as scanning (SEM) and transmission electron microscopy (TEM). DNA extraction was performed with CTAB and the corresponding fragments were amplified to the ribosomal partial regions of the LSU, using D1R-1 (forward: 5'-ACC CGC TGA ATTTAA GCA TA-3') and D3B-R (reverse: 5' -TCG GAG GGA ACC AGC TAC TA-3). The reconstruction of the phylogeny was performed with maximum likelihood (raxmIGUI 1.5 beta) and Bayesian Inference (MrBayes v 3.2.6) programs. Cultures of *Pleurosigma* sp. showed benthic growth with few cells floating; also, possible zygotes or pre-auxospores could be observed, with no spermatogenesis. Morphology includes solitary cells characterized by slightly lanceolate valves, 90-102 μ m long and 16-19 μ m wide, with poles barely deviated in the opposite direction and rounded apices. Parallel striations (with densities 22-25/10 μ m), oblique striate in center (11-13/10 μ m), and slightly curved at the poles (10-15/10 μm). Molecular phylogenies showed that *Pleurosigma* sp. clades within the family Pleurosigmataceae, and it was placed in the same clade of the order Naviculales, which was represented by the genera Navicula Bory and Gyrosigma Hassall. In conclusion, it is suggested that Pleurosigma sp. is a new species due to the distinctive morphological features: shape, size and number and pattern of striae. New descriptions, illustrations (microphotographs) and videos are provided. In culture the species should be given a habitat which can be mostly benthic and tychoplanktonic. A new sequence, using the LSU gene, is also provided for a *Pleurosigma* species.

Assessing environmental controls on diatom variability in paleomarsh reconstructions, Washington State, USA

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Coastal land-level change during past earthquakes along the Cascadia subduction zone has been estimated from diatom assemblages across mud-over-peat contacts in tidal-marsh stratigraphic sequences. However, the application of diatoms to coastal land-level change reconstructions from the tidal marshes of Washington state is restricted by the absence of a local modern diatom dataset to serve as a fully quantitative modern analogue.

In the process of building a modern diatom dataset from the tidal marshes of Washington State, USA, we consider the influence of environmental controls and spatial variability on diatom assemblages. We test the spatial variability of modern diatom assemblages by comparing the results of over 200 species across 60 genera found at three tidal marshes located within Willapa bay: (1) the Niawiakum River, (2) the Bone River, and (3) the Naselle River. At each site, we collected modern surface samples of diatoms at stations along a shore-perpendicular transect that transitions from an intertidal mudflat to a freshwater wetland. The transects capture the variations in elevations, substrates, bulk geochemistry, and vegetation recorded in sedimentary sequences from repeated subduction zone earthquakes. Measured elevations cover tidal datum from 0.5 m mean tide level to greater than highest astronomical tide. We identified diatoms to species level and classified the species by salinity and substrate. Our results will guide the development of a regional modern diatom dataset that can be applied to diatom-based reconstructions of coastal land-level change along the Cascadia subduction zone.

Paleoenvironmental reconstruction of the Japan Sea during the Mid-Brunhes Event using microfossils

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The Mid-Brunhes Event occurred approximately 450 kyrs ago, when there were increases in CO₂ concentrations during interglacials, with Marine Isotope Stage (MIS) 11 being the warmest interglacial. Thus, this event can be used as an analogy for predicting what the Japan Sea will be like in the future if global warming continues. The purpose of this study is to reconstruct the paleoenvironmental conditions in the Japan Sea during the Mid-Brunhes Event using changes in the microfossil assemblage composition and the relative abundances of warm and cold water diatom species (using the so-called Td index) to differentiate between glacial and interglacial periods. Samples from an interval equivalent to 344-464 ka of IODP Expedition 346 Site U1425 (Tada & al. 2015) were analyzed for microfossils every 1000-2000 years.

In this study, there were three main results. (1) The core could be divided into five sections based on the intensity of the light and dark layers; coccoliths (mostly dominated by *Reticulofenestra* W. W. Hay & al. spp.) and Stephanopyxis spp. occurred in the lowest section, Section E, which indicates the presence of warm and nutrient-rich water. Section D is characterized by *Thalassionema* (H. Perag. & Perag.) Perag., Proboscia Sundström and Rhizosolenia Brightw., which indicates strong upwelling. Section C can be further divided into three sub-sections based on the abundance of cold and warm water diatom taxa. At first, only cold water flowed into the Japan Sea from the north, then the Tsushima Strait opened and warm water from the Kuroshio mixed with the cold water. Finally, the Tsushima Warm Current became stronger. In Section B, the color of the light and dark layers is strong, and the relative abundance of Paralia sulcata (Ehrenb.) Cleve (indicator of East China Sea coastal water) increased. Section A has few diatoms. (2) In a comparison between MIS11 and living assemblages, there were more warm water species in the former. Furthermore, the sea surface temperature reconstructed from the Td index shows an increase of about 2 degrees during an interval of 2000 years in MIS11. (3) The reconstructed paleoenvironment of MIS11 (notably at about 398 ka) can be used to predict the future Japan Sea. Assuming that warming continues for another 10 kyrs, the sea level will rise, and a gradual cooling (due to the weakening of the Tsushima Warm Current) will follow about 5000 years later - a scenario similar to the three sub-sections of Section C, but in reverse.

^{Tada R., Murray R.W., Alvarez Zarikian C.A., Anderson Jr. W.T., Bassetti M.-A., Brace B.J., Clemens S.C., da Costa Gurgel M.H., Dickens G.R., Dunlea A.G., Gallagher S.J., Giosan L., Henderson A.C.G., Holbourn A.E., Ikehara K., Irino T., Itaki T., Karasuda A., Kinsley C.W., Kubota Y., Lee G.S., Lee K.E., Lofi J., Lopes C.I.C.D., Peterson L.C., Saavedra-Pellitero M., Sagawa T., Singh R.K., Sugisaki S., Toucanne S., Wan S., Xuan C., Zheng H. & Ziegle M. 2015: Site U1425. – Proceedings of the Integrated Ocean Drilling Program, 346, 136p.}

Diatom-based evidence of limnological changes in two subarctic lakes (Quebec, Canada) following the onset of the Industrial Era

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Paleolimnological investigations were undertaken on lakes Sans Nom and Carheil located in the Fermont region of eastern subarctic Quebec (Canada). Recurrent cyanobacterial blooms have affected both lakes in recent years, and our study aimed to characterize the lakes' baseline conditions and their natural variability in order to help develop plans for their restauration and management. Analysis of fossil diatom assemblages preserved in sediment cores collected from lakes Sans Nom and Carheil, coupled with ²¹⁰Pb and ¹⁴C dating, revealed that both experienced notable limnological changes following the onset of the global industrial era (~ 1850 AD), more than a hundred years before human settlement in their catchment in the early 1970s. Paleolimnological data demonstrate that diatom community composition remained relatively stable for more than two thousand years before undergoing significant change associated with this time period. Most notably, a decrease in the relative abundance of Discostella stelligera (Cleve & Grunow) Houk & Klee was observed and thought to be associated with changing lake thermal structure induced by higher water mixing due to stronger winds. This hypothesis was further supported by the coincident increase in the relative abundance of other diatom taxa, such as Aulacoseira subarctica (O. Müll.) E. Y. Haw. which is known to benefit from turbulent waters. These changes were then accentuated by the establishment of the town of Fermont in 1974 and the onset of waste water inputs from the catchment. The results we obtained regarding the succession of diatom community composition in the lakes from the Fermont region are contrary to the trends generally observed in North American arctic, subarctic and temperate lakes experiencing limnological transformations related to the industrial era (Rühland & al. 2003, 2008). This suggests that the effects of modern climate change manifest themselves differently in lakes of this region in subarctic Quebec.

Rühland K., Priesnitz A. & Smol J. P.: 2003: Paleolimnological evidence from diatoms for recent environmental changes in 50 lakes across Canadian Arctic treeline. – Arctic Antarc. Alpine Res. **35**: 110–123.

Rühland K., Paterson A. M. & Smol J. P.: 2008: Hemispheric-scale patterns of climate-related shifts in planktonic diatoms from North American and European lakes. – Global Change Biol. 14: 2740–2754.

How Proboscia valve features evolved through time

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Fossil species of Proboscia Sundström are usually present in temperate and polar marine sediments of Late Cretaceous to the recent age, with some of them used as stratigraphic marker species in diatom zonation schemes. Since the junction between the valve face and the distal process (proboscis) is the narrowest and thus weakest point of the valve, the probosces are often the only recognisable fragments in the sediments. This means that the pocket (claspers) into which the proboscis tip of an opposing cell fits is rarely observed on fossil fragments – making it difficult to determine whether these fossil species were solitary or colonial. Fortunately, one of the most distinguishing features used to separate the species in the genus is the proboscis tip, which together with the morphology of the rest of the proboscis, provides enough information to show evolutionary trends. The oldest species are from the Late Cretaceous, characterised by ridges on an extremely long proboscis and one or two large polar spinulae (Jordan & Ito 2002). Similar forms continued into the late Oligocene, although ridgeless forms started appearing in the early Oligocene. These early ridged forms (Cretaceous-Oligocene) can be assigned to a single lineage, hereafter called the 'cretacea' lineage. Later, two ridge-less lineages emerged, one bearing large polar spinulae at the tip and with pores mainly down the lateral sides of the long (usually curved) proboscis (hereafter called the 'barboi' lineage), and another bearing only small spinulae at the tip and with pores covering the entire surface of the short (usually straight) proboscis (hereafter called the 'alata' lineage). These two lineages can be clearly separated throughout the Neogene and Quaternary. Although rarely preserved, claspers have been observed on valves of 'alata' lineage species in samples as old as the Miocene. Surprisingly, morphological diversity is high in marine sediments (e.g., Jordan & Saito 1999), with some forms exhibiting swollen or strongly curved probosces, extremely long longitudinal slits and elbow spines. Interestingly, ridged forms reappear in the northern hemisphere during the Quaternary, but only in the 'barboi' lineage, and today, one survivor remains; P. subarctica K. Takah. & al. found in subarctic waters (Takahashi & al. 1994). This living species lacks claspers, suggesting a solitary life style, which could shed light on the ecology of similar ridged forms in the much older 'cretacea' lineage.

Jordan R. W. & Ito R. 2002: Observations on *Proboscia* species from Late Cretaceous sediments, and their possible evolution from *Kreagra*. – Pp. 313–329 in: John J. (ed.), 15th International Diatom Symposium. – Ruggell: A.R.G. Gantner Verlag.
 Jordan R.W. & Saito M. 1999: The genus *Proboscia* from the *Thalassiosira yabei* Zone (Middle-Late Miocene) sediments of Hokkaido, Japan. – Pp. 565–580 in: Mayama S., Idei M. & Koizumi I. (ed.), 14th International Diatom Symposium. –

Hokkaido, Japan. – Pp. 565–580 in: Mayama S., Idei M. & Koizumi I. (ed.), 14^{ee} International Diatom Symposium. – Koenigstein: Koeltz Scientific Books.

Takahashi K., Jordan R. W. & Priddle J. 1994: The diatom genus *Proboscia* in subarctic waters. – Diatom Res. 9: 411–428.

Acidification of streams and recovery after liming in Wales, United Kingdom

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The diversity and composition of diatom assemblages in the upland streams of Wales are determined by the type of semi-natural terrestrial vegetation, geology, agricultural land use, forestry and airborne pollution. Long-term monitoring of the River Wye and River Irfon and their tributaries between 2003 and 2013 was used to document the effect of land use, in particular the presence of conifer plantations, on water chemistry, diatom assemblages and fish. Two methods of liming, hydrological source and sand liming, were applied to increase stream water pH and reduce acid episodes during high flow, and thereby facilitate the return of salmonid fish. The liming methods differ in the efficiency with which they alter stream chemistry, and allow the establishment of diatom assemblages which indicate conditions suitable for diverse macroinvertebrate communities and for fish. The recently developed UK diatom acidification metric DAM is applied for the first time to a large-scale and long-term data set to test its suitability to reflect differences in stream acidity resulting from different types of land use, acid deposition and remediation through liming. Diatom assemblages are compared between areas of conifer plantations, natural broad-leaved woodlands, upland grassland areas, and naturally acidic moorland streams, and the applicability of the index for these stream types is assessed.

The genus *Odontidium* in the Himalaya, morphology of four new species and their distribution in alpine freshwater habitats

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Species in the genus *Odontidium* Kütz. are typically found in high altitude freshwater habitats. Four new species, recently described from the Nepalese and Indian Himalaya, are shown in light and electron microscopy and compared with similar species from Europe. A comparison of cell size showed a decline in size from the European Alps and southern Europe to the Himalaya. The Himalayan species were restricted to altitudes from 2500–4400 m. Their geographical distribution shows a divide between the eastern and western areas of the Himalaya. *Odontidium nepalense* Jüttner & al. and *Odontidium longiovalum* Jüttner & al. were only found in the central and eastern Himalaya. *Odontidium himalongissimum* Jüttner & al. was only present in western areas of the Nepalese Himalaya and in the Kumaon Himalaya in India, and *Odontidium parvoapiculatum* Jüttner & al. only occurred at one site in the Garhwal Himalaya of India. The species were rare and altitudinal distribution. They are an important taxonomic group which should be included in assessments of the effects of climate change on freshwater assemblages in high altitude ecosystems.

Evolutionary diversification in diatoms: an auxospore perspective

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Diatoms are the most species-rich heterokont algae and are of tremendous ecological and economic importance. Therefore, it is not surprising that the emergence and subsequent diversification of diatoms has been of interest to generations of scholars. Every major advancement in technology has allowed new insights into the diatom frustule, valve or cell structure, and generated new ideas about diatom evolution (Simonsen 1979, Round & Crawford 1981, Mann & Marchant 1989, Round & al. 1990, Mann 1993). Improvements in culturing methods, the discovery of oogamy in centric diatoms (von Stosch 1950), followed by documentation of the unique ultrastructure of the diatom sperm flagellum (Manton & von Stosch 1966), and modern research into the sexuality and life cycles of centric diatoms generated even more intriguing ideas about deep evolutionary relationships among diatoms (von Stosch 1982).

Sexual reproduction is of great importance to all eukaryotes in generating and sustaining specific genetic heterogeneity. In diatoms, the sexual process is of even greater importance for species survival because it re-introduces large post-sexual cells to their populations, thus counteracting mean population cell size decline due to so-called mitotic "cell diminution". This process would otherwise eventually lead to population, and species, extinction. In general, cells, structures and behaviour associated with sexual reproduction are strongly conserved across a wide range of biota. For this reason, characters associated with sexual propagation are used in evolutionary inferences, including those for deep divergences and high-level systematics (Renzaglia & al. 2000, Williams & al. 2008, Webster & Weber 2010). There is no compelling evidence documented thus far that suggests that this does not apply to diatoms.

The auxospore is a sex-related cell known only in diatoms and is present in all species examined to date. It contains the product of syngamy, including chloroplasts, and is capable of growing much larger than the combined size of the parents. It is within the auxospore that sexual progeny with valves restored to a large size develop. Diatom auxospores are complex cells with identifiable developmental stages and a set of structural characters that can be analysed and compared across all diatoms. The idea that auxospores contain evolutionary informative characters was first postulated by von Stosch (1982), and subsequent research has confirmed his insight.

In this presentation we will review and summarise the advances made in the field of diatom sexual reproduction, and centric diatoms in particular (Kaczmarska & al. 2001, Sato & al. 2008, Kaczmarska & Ehrman 2015, Samanta & al. 2017, Davidovich & al. 2017; among others). We will combine this new data with evidence derived from nearly 100 centric species illustrated in published, earlier sources in sufficient detail to determine the nature of their auxospores. We will also illustrate how a number of early "generally" accepted assumptions have been proven to be less than generally applicable to diatoms. We will demonstrate how systematic examination of diatom sexuality, mating behaviour, auxospore development and structure offers valuable insights into the relationships between the major lineages of diatoms.

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Unravelling the relation of the morphological species concept to the molecular one in the genus *Fragilaria*

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This project aims to evaluate taxonomic relationships in *Fragilaria* Lyngb. sensu stricto, an abundant and ecologically important genus, taking advantage of cultured and barcoded material from two different collections (Royal Botanic Garden Edinburgh, UK; Thonon Culture Collection, France). The long-term goal of this project is a harmonization of taxon identification of this complex within Europe, providing a unified view on morphological, molecular and ecological relationships. A harmonized taxonomy will simplify both research and environmental assessment based on either microscopical counts or molecular approaches. There is broad agreement that the separation of species within the group of *Fragilaria* is difficult. Krammer & Lange-Bertalot (1991), for example, stated that this taxon complex needs more taxonomical studies, encompassing both higher systematic levels as well as separation and detailed study of most of species then considered to be *Fragilaria*.

Our study demonstrated that some species defined on morphological criteria could be confirmed by using a long part of the *rbcL* barcode, i.e. *F. gracilis* Østrup, *F. tenera* (W. Sm.) Lange-Bert., and *F. subconstricta* Østrup. However, even for those species, a preliminary identification based on morphology was often different to the identification established by phylogenetic clustering and a deeper study of morphological characters both from light microscopy and SEM, confirming that identification of *Fragilaria* by light microscopy is indeed very difficult, and that NGS here may provide us with an effective tool to overcome these problems. We conclude further, however, that more strains are needed to confirm clusters. Finally, we found well-defined subgroups within one morphological species (*F. gracilis*), whose biogeography and ecology requires further study.

This research received support from the SYNTHESYS Project http://www.synthesys.info/ which is financed by European Community Research Infrastructure Action under the FP7 "Capacities" Program and from The Swedish Agency for Marine and Water Management.

Krammer K. & Lange-Bertalot H. 1991: Bacillariophyceae. 3. Teil: Centrales, Fragilariacease, Eunotiaceae. – In: Ettl H., Gerloff J., Heynig H. & Mollenhauer D. (ed.), Süßwasserflora von Mitteleuropa. Band 2/3. – Stuttgart: Gustav Fischer Verlag.

DNAqua-Net Group Meeting

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DNAqua-Net is an official partner of the IDS session "Environmental DNA & High Throughput Sequencing (eDNA & HTS)" and of the Workshop "Curation of Molecular Reference Libraries". DNAqua-Net is also organizing a satellite meeting with an open and a closed part. The protection, preservation and restoration of aquatic ecosystems and their functions is of global importance. For European states this is a legally binding duty mainly through the EU-Water Framework Directive (WFD, Directive 2000/60/EC)), the Marine Strategy Framework Directives (MSFD, Directive 2008/56/EC) and Habitats Directive (Directive 92/43/EEC). In the last few years, several research groups have been exploring how to apply genomic tools to ecological assessment. The goal of DNAqua-Net (EU COST Action CA15219) is to nucleate a group of researchers to identify goldstandard genomic tools and novel eco-genomic indices and metrics for routine application for biodiversity and ecological assessments of European water bodies. The central aim of the open part of the DNAqua-Net Group Meeting at IDS is to present the progress that has been made in complementing routine morphology-based procedures with novel genomic DNA-based approaches for ecological assessment. This includes standardisation of the various protocols, methods and biotic indices and integration of DNA-based datasets (e.g. resulting from DNA metabarcoding, mito- and metagenomics) with existing data standards. During the closed part of the meeting, we will address ongoing concerns of the diatom group of DNAqua-Net (http://dnaqua.net/).

Leese F. & al. 2016: DNAqua-Net: Developing new genetic tools for bioassessment and monitoring of aquatic ecosystems in Europe. – Research Ideas and Outcomes 2: e11321. https://doi.org/10.3897/rio.2.e11321.

Morphology and distribution of a new diatom genera from Indonesia

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Southeast Asia has a rather diverse diatom flora. In recent years, several new endemic diatom genera have been described from Indonesia (Hamsher & al. 2014; Kapustin & al. 2017), Vietnam (Liu & al. 2018) and Laos (Kulikovskiy & al. 2018). In this presentation we briefly characterize endemic diatom genera, both newly described and potentially new ones, from Indonesian lakes. The genus Tetralunata Hamsher & al. (2014) was described to accommodate Denticula vanheurckii Brun and its allies. The genus is characterized by slightly asymmetrical valves with a medial raphe, composed of two branches; distinct fibulae, extending entirely transapically across the valve; and finally, clover-shaped areolae with 4-5 c-shaped occlusions. We studied by means of SEM the valve morphology of three species from this genus (*T. vanheurckii* (Brun) Hamsher & al., *T. elonaata* (Hust.) Hamsher & al. and T. dubia (Hust.) Hamsher & al.). The genus is restricted to Sumatra, Java and Bali. The monotypic genus Celebesia Kapustin & al. (2017) was established to accommodate Cymbella distinguenda Hust. The valves of this species are only slightly asymmetrical to the apical axis; the raphe is distinctly undulate with external distal raphe ends deflected dorsally and external proximal ends deflected ventrally. A small round or elongate stigma is evident on the ventral side of the axial area and striae are composed of double rows of small round and unoccluded areolae; at the poles there are apical pore fields that are not clearly differentiated from the areolae. The valve face is separated from the mantle by a marginal ridge and the whole valve (except the striae) can be covered with an extra silica layer and numerous silica granules between areolae and along the marginal ridge. The genus is restricted to Lake Matano, Sulawesi Island.

Recently we have rediscovered *Cymbella mirabilis* Hust., "a single specimen taxon" and studied it by means of LM and SEM. The striae of this species are alveolate and composed of double rows of round or slightly elongated areolae. Externally distal and proximal raphe ends deflected toward the secondary side of the valve. At the both apices a pseudosepta is present. Neither apical pore fields nor stigmata are present. *C. mirabilis* is an endemic to Lakes Matano and Towuti, Sulawesi Island. We believe that *C. mirabilis* represent a new genus to science.

SEM investigations of valve morphology of *Denticula parva* Hust. showed that it is much closer to *Tetralunata* rather than *Denticula* Kütz. Like *Tetralunata*, *D. parva* Kütz. has lunate areolae but it has 2-3 semicircular slit-like openings per areola. Additionaly, *D. parva* has distinctly undulate (externally) canal raphe. It is very likely that separate genus could be established for *D. parva* but further studies on valve ultrastructure are necessary. *Denticula parva* is an endemic species for Malili Lakes, Sulawesi Island.

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Patterns and drivers of phylogenetic diversity in freshwater diatom communities

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Understanding the mechanisms determining the distribution of biodiversity and the structure of biological communities is a major concern of ecology. Despite important progress, uncertainty persists regarding ecological forces driving diatom community assembly. In diatoms, these issues have been traditionally addressed using a taxonomic perspective of diversity. In recent years, trait-based ecology was promoted as it offer more insights into the processes at the origin of the observed biodiversity and a better link between biodiversity and ecosystem functioning. However, given their large diversity and their microscopic size it is challenging to collect trait data for diatoms and a comprehensive trait database for ecological studies is still missing.

Ecophylogenetics, the merging of community ecology and phylogenetics (Webb & al. 2002), offer a promising alternative for studying diatom ecology by using phylogeny as a proxy for species ecological similarity. Phylogenetic diversity captures the evolutionary history of species both in terms of richness (how much evolutionary history is associated with a set of species) and divergence (how closely related are species within a set).

Our study aims at assessing the differences between taxonomic diversity (species richness) and phylogenetic diversity in Sweden and to use phylogenetic information to interpret the structure of ecological communities.

We used a dataset of 595 diatom communities sampled across Sweden. A phylogenetic tree of the species was reconstructed by combining genetic data and taxonomic information. For each community we compared Faith's phylogenetic diversity (PD, i.e. the sum of the branch length) to species richness. We also investigated the phylogenetic structure within communities using the mean nearest taxon distances (MNTD) diversity metric. Finally, we investigated how phylogenetic diversity is influenced by gradients in nutrients, pH, organic matter, surface of the catchment and altitude. We found that phylogenetic diversity is highly correlated to taxonomic diversity. When controlling for taxonomic richness, some sites were found to host a larger amount of evolutionary history than other. Overall, diatom assemblages tended to be phylogenetically clustered, which suggests environmental filtering. However the degree of clustering showed no patterns along the environmental gradients, indicating that the importance of niche-related processes is independent of environmental conditions in Sweden.

Webb C. O., Ackerly D. D., McPeek M. A. & Donoghue M. J. 2002: Phylogenies and community ecology. – Annual Rev. Ecol. Syst. **33:** 475–505.

Development and adoption of a high-throughput-sequencing approach to diatom-based ecological assessments in the UK

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Diatoms have been used for assessing the ecological condition of UK freshwaters since 1995 and, following the introduction of the Water Framework Directive, diatoms have been used to fulfil obligations to assess "phytobenthos" in rivers and lakes in the EU. Assessments have hitherto been based on microscope counts of a few hundred individuals per sample, followed by calculation of the Trophic Diatom Index (TDI) as a basis for assessment of ecological status relative to reference pristine conditions. Following preliminary tests and a literature review, in 2012 the UK Environment Agency funded an R&D project to replace microscope-based counts by a DNA metabarcoding approach. This has involved (1) developing an *rbcL* reference library, evaluating candidate barcode regions within the rbcL gene, and establishing a bioinformatics pipeline to check, classify and identify highthroughput-sequencing (HTS) barcode reads; (2) comparisons of molecular and microscope-based assessments of community composition in 1337 paired HTS and LM samples; and (3) formulation of new HTS-based trophic diatom indices (TDI4-HTS and TDI5-HTS) and their calibration with respect to microscope-based TDIs. A report describing the initial project development and results has recently been published by the Environment Agency (Kelly et al. 2018). Despite the absence of many species from the barcode reference library and absence of a clear understanding of how numbers of rbcL reads relate to cell counts (for example, limited information is available about how copy number per cell varies within and among diatom species), HTS-based TDI indices provide assessments of ecological status for UK rivers that are comparable to microscope-based TDI assessments and that are usable for monitoring under the Water Framework Directive. Therefore, given the cost savings of the HTS approach, from 2017 onwards diatom identification and enumeration in England has moved from light microscopy to a DNA metabarcoding approach using Illumina MiSeq high-throughput sequencing (HTS).

Kelly M., Boonham N., Juggins S., Kille P., Mann D., Pass D., Sapp M., Sato S. & Glover R. 2018: A DNA based diatom metabarcoding approach for Water Framework Directive classification of rivers. SC140024/R, Environment Agency, Bristol. Available at http://www.gov.uk/government/publications.

Reports of new diatom species from the hottest point of the world (Lut Desert), Iran

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Extreme (hypersaline) habitats have been the point of attention for taxonomists recently. Central Lut, near Kaluts of Kerman is recorded as the hottest point of world (see Mildrexler & al. 2006). In this study, an epipelic sample was collected from a waterbody located in the Central Lut in 2014. Considered as a hypersaline environment, the crystals of gypsum and halite were observed within the waterbody as well. The physicochemical parameters measured proves the extreme amounts of calcium (7272.7 mg/l), sulphate (1968 mg/l), chloride (75685 mg/l) and sodium (1417.8 mg/l) in the mentioned waterbody. This research presents a number of new diatom taxa from this interesting and unique environment. The variety of new species belong to different genera including *Navicula* Bory, *Seminavis* D. G. Mann, *Amphora* Ehrenb. ex Kütz., *Proschkinia* Karaeva and *Haslea* Simonsen.

Mildrexler D. J., Zhao M. & Running S. W. 2006: Where are the hottest spots on Earth? – EOS Trans. AGU 87(43): 461, 467. https://doi.org/10.1029/2006EO430002

Cryptic species in *Fragilariopsis kerguelensis* unveiled by morphometry and genetics

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Fragilariopsis kerguelensis (O'Meara) Hust. is one of the most important diatoms of the Southern Ocean. It is used as proxy for paleo-environmental studies, based on species-composition transfer functions as well as by its intra-specific morphometric features. While investigating a sediment core from the Polar Frontal Zone of the Southern Ocean, we found two hitherto unrecognized morphotypes with slightly different valve outline shapes. One of these morphotypes occurred throughout the core, where the other was mostly confined to glacial regimes. Using fossil material only, it was difficult to decide whether these morphotypes represent distinct species, or whether they rather represent phenotypic variants of a single taxon. To better understand the biogeography and taxonomy of these morphotypes, we looked at their distribution along several latitudinal transects and compared strains isolated from different locations of the Southern Ocean using different molecular techniques. Our results provide evidence of the presence of three (semi-)cryptic species in *F. kerquelensis* s.l., one of them corresponding to the morphotype previously found mainly in glacial segments of the sediment core. This morphotype seems currently restricted to cold waters south of the Antarctic Circumpolar Current. We conclude that its appearance in the sediment core further north represents biogeographic shifts which accompanied cooling of the Southern Ocean, or a re-organization of circulation patterns leading to a northward shift of the southern boundary of the ACC.

MobiDiC – MOBIlization of a Dlatom Collection

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Taxonomic collections of diatoms are not digitized at a substantial depth because thousands of specimens representing dozens of taxa usually present on a single microscopic slide. Usually only one to a handful of selected specimens is documented by manual microscopic photography and/or taxonomic labelling. We want to use microscopic slide scanning, followed by computer assisted taxonomic indexing, to substantially increase the amount of information that can be made available for collection mining and collection-based research.

Anthropogenic impact on springs with various levels of isolation from direct and indirect human influence based on diatom analysis

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Crenic habitats are one of the most precious elements of the Polish landscape. Due to the limited surface of springs and low influence on economy, springs habitat related aspects seems to be insufficiently researched. However, in times of rapid growth of urbanization and industrialization part of them have remained features characteristic for natural ecosystems, which may lead to maintain high biodiversity e.g. for microorganisms such as diatoms. It is important to highlight that crenic ecosystems might be described as a relatively stable in terms of physical and chemical parameters, as a result of influence of the underground waters inflow. In this study, diatoms, highly effective bioindicators are used in analyses of selected springs which are under stress originated from human activity, both direct and indirect. For the purpose of this research, the classification of the degree of anthropogenic disturbance of ambient springs (oligotrophic character) [°AD] proposed by Nowicka-Krawczyk & Żelazna-Wieczorek (2017) has been taken into consideration. In addition, an investigation of the structure and dynamics of diatoms assemblages in relation to hydrochemical parameters and selected ions (ammonium, nitrate, phosphate) have been carried out. On the basis of the diversity of diatom communities in particular springs (including spatial and temporal changes), described by species diversity and their requirements regarding environmental conditions, sensitivity to potential and diverse human impact for crenic habitats will be determined. In this work we present results of studies carried in four out of twelve selected crenic habitats (sampling site 1: Podwierzchowiec; sampling site 2: Podwódka; sampling site 3: Bukowa Góra; sampling site 4: Łagiewniki) located in the Łódź Province (Central Poland, Central Europe) which morphology is related to early-post glacial landscape. Sampling site 1 and 3 are well isolated, these are midforest localizations with low risk of direct human impact, and in both cases there are no significant seasonal changes. However, diatom assemblages differ in time. Furthermore, site 3 is located on Tetrary sediments while the rest are on Quaternary geological formations. Sampling site 2 is under constant anthropogenic pressure which is reflected in analysis showing no visible similarity between studied time intervals and in low biodiversity of diatom assemblages. Sampling site 4 is the only site within city boundaries which additionally put higher risk to be disturbed by direct and indirect human activities. Samples used in taxonomical analysis of diatoms are based on archival samples from the Phycological Collection of Laboratory of Algology & Mycology (University of Łódź) from years 1998-2014, and on recent samples, from years 2016–2018. Final analysis composed of twelve crenic habitats will attempt to characterize environmental capacity of crenic habitats, the degree of resilience to human disturbances and to test the hypothesis that springs being under human impact are resistant to anthropogenic disturbance and potentially maintain a high environmental stability determining a unique taxonomical diversity of diatoms.

Nowicka-Krawczyk P. & Żelazna-Wieczorek J. 2017: Dynamics in cyanobacterial communities from a relatively stable environment in an urbanised area (ambient springs in Central Poland). – Sci. Total Environm. **579:** 420–429.

Diatom diversity and water quality in the Makuleke Wetlands, Kruger National Park, South Africa

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Monitoring of wetland ecosystems can be problematic at times as the variability in depth and inundation time makes it difficult to support fish and macroinvertebrates. Therefore, the aim of the study was to determine the diatom diversity of the Makuleke Wetlands, a Ramsar site, as well as the influence of water quality on their distribution. Monitoring of these wetland ecosystems is crucial as they provide numerous ecological services and resources to humans. Diatoms, then, are perfect to use as a biological indicators to monitor wetlands as they rapidly respond to changes in the environment, have a worldwide distribution and are the most diverse algae group. Literature indicated that there is a paucity of diatom information of South Africa's Ramsar wetlands. One such wetland is the Makuleke Wetlands which faces increased anthropogenic impacts from rural and industrial development outside of the immediate catchment area. Diatom and water samples were collected using standard methodology, from ten depressions or pans during a wet and a dry season in April and September 2015 respectively. Preserved samples were brought back to the laboratory and microscope slides were prepared using the hot hydrochloric acid and potassium permanganate method. Diatoms were identified using relevant guides. Relevant statistical analyses were conducted to determine the BDI, GDI, SPI and %PTV. Results indicated that there was a diverse community of diatoms, with Nitzschia Hassall species, Craticula accomodiformis Lange-Bert., Gomphonema parvulum Kütz. and Cyclotella meneghiniana Kütz. being the dominant species within the Makuleke Wetlands. As expected, the data indicated water quality influenced the distribution of the diatom community, and indicated the selected pans had a diverse community. Both the diatom community structure and measured water quality values indicated the wetland as nutrient enriched. However, as nutrients accumulate in wetlands it is unclear whether the increased nutrients were from anthropogenic or natural sources.

A polyphasic approach to the delimitation of diatom species: a case study for the genus *Pinnularia*

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Diatoms are one of the most abundant and arguably the most species-rich group of protists, with estimates of the total number of extant species ranging between 30,000 and 200,000 (Mann & Vanormelingen 2013). Diatom species taxonomy has been often based exclusively on the recognition of morphological discontinuities without investigation of other lines of evidence. Even though DNA sequences and reproductive experiments have revealed several examples of (pseudo)cryptic diversity (e.g. Vanormelingen & al. 2008, Poulíčková & al. 2010, Pinseel & al. 2017), our understanding of diatom species boundaries and diversity remains limited. The cosmopolitan pennate raphid diatom genus Pinnularia Ehrenb. represents one of the most taxon-rich diatom genera with 704 currently accepted taxa (Guiry & Guiry 2018). In this study, we focused on the delimitation of species in one of the major clades of the genus, the Pinnularia subgibba Krammer group, based on 58 strains from a worldwide origin. We compared genetic distances between the sequences of seven molecular markers and selected the most variable pair, the mitochondrial cox1 and nuclear encoded LSU rDNA, to formulate a primary hypothesis on the limits of species using three single-locus automated species delimitation methods. We compared the DNA-based primary hypotheses with morphology and with other available lines of evidence. The results indicate that our dataset comprised 15 species of the P. subgibba group. The vast majority of these taxa have an uncertain taxonomic identity, suggesting that several may be unknown to science and/or members of (pseudo)cryptic species complexes within the *P. subgibba* group.

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The Holocene evolution of freshwater diatoms within two lakes from Vega Island, Antarctica

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Rapid climatic changes have been reported in polar regions over the last decades (e.g. Verleyen & al. 2012), which may have profound impacts on resident microbial communities. In existing habitats such as lakes and soils, warming increases hydrologic connectivity and altering sediment and nutrient inputs. Additionally, changes in climate patterns may lead to altered dispersal and migration patterns (Chown & al. 2012). Unfortunately, our understanding of how these changes influence microorganism diversity over the time is limited despite the importance of microbes to Polar Regions. Diatoms are dominant components of polar ecosystems, and among the most species-rich algal group there. Thanks to their taxon-specific morphology and response to the chemical-physical conditions and clear bioregionalism, make diatoms valuable tool for interpreting the past effects of climate changes and predicting the future ones. Our research focused on paleolimnological multi-proxy study of two freshwater lakes from different sides of Vega Island (Antarctica) where sedimentary cores were withdrawn during the austral summers 2013 and 2014.

According to the age-depth, lake Anonima sedimentary record spans the last 2450 years (sediment base 2440 cal. yrs b2k) attaining thus environmental and climatic history over the major part of the Late Holocene. The 69-cm long sediment core was extracted, and the complete diatom flora resulted in 80 species, belonging to 26 genera. Based on the CONISS cluster analysis, the core was divided into six diatom zones of four of which were statistically significant based on the broken stick model. The core was dominated by the genus *Nitzschia* Hassall followed by *Planothidium rostrolanceolatum* van de Vijver & al. All other taxa contribute by smaller proportions and were more variable within the core with specific community patterns in individual biozone.

Lake Esmeralda surprisingly showed that the sediments ages are much younger than expected. Age of 177 cm long core was about 400 years instead of cca 6 ka that would one assume based on previous studies (Irurzun & al., 2013; 2017). A diverse flora of 86 taxa was observed, however no distinct arrivals or disappearances in the analyzed section were observed, although changes in the relative abundances occurred. The most abundant species was *Microcostatus australoshetlandicus* van de Vijver & al.followed by *Nitzschia kleinteichiana* Hamsher & al., *Psammothidium papilio* (D.E. Kellogg & al.) Kopalová & Van de Vijver and *Pinnularia magnifica* Zidarova & al. The genus *Microcostatus* J. R. Johans. & Sray, mainly *M. australoshetlandicus*, dominated most of the core, although it is rarely observed in recent material from the Maritime Antarctic Region (Bulínová & al., in prep.). Aerophilic genera, such as *Luticola* D. G. Mann, *Muelleria* (Freng.) Freng., *Humidophila* R. L. Lowe & al., usually very common in Maritime Antarctic Region (Zidarova & al. 2016), represented only a small proportion of the total diatom flora suggesting permanent aquatic conditions. Our results of individual proxies including diatoms showed significant changes in environmental, climatic and lake conditions of the northeastern AP region, especially in the lake Anonima.

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Aquatic ecosystem response to late Holocene environmental variability recorded in Lake Apastepeque (Central El Salvador)

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The Late Holocene is marked by centennial- to millennial-scale climate variations. However, the response of aquatic ecosystems to these variations in tropical regions is still poorly investigated. Here, we present a diatom record of Lake Apastepeque (13°41'32.84"N 88°44'42.41"W, 509 m a.s.l.) spanning the last ~ 600 years. Apastepeque is a closed, nearly round crater lake with a depth of 54 meters and an area of ~0.6 km², so therefore expected to react sensitively to climatic oscillations. Results are compared with other biological and geochemical proxies to identify environmental drivers of lake development.

Three main zones and one event were identified in the diatom record. From ~1390–1500 AD, the record is dominated by high abundances of planktonic taxa (needle-shaped Fragilaria Lyngb. spp., Aulacoseira granulata (Ehrenb.) Simonsen var. granulata and Aulacoseira granulata var. angustissima (O. Müll.) Simonsen) indicative of open waters and presumably higher trophic state as well as turbulence. These conditions are supported by high percentages of Bosmina longirostris (Cladocera). The second zone (~1500-2000 AD) is characterized by the overall dominance (>80%) of the benthic Achnanthidium aff. pseudolineare Van de Vijver & al. Such a drastic shift from planktonic to benthic species could either indicate a considerable lake level drop or, alternatively, its increase by significantly broadening the littoral zone leading to an expansion of benthic habitats. Low K/Ti ratio hint at wetter conditions during zone 1 compared to zone 2 while Chironomidae point to a shallower lake covered with aquatic plants in the beginning (zone 1) followed by higher lake levels with possibly temporarily anoxic lake bottom conditions. Around 1670 AD, a short return to higher abundances of planktonic diatom taxa possibly indicates a short climate oscillation back towards conditions comparable to those in Zone 1. This event is neither reflected in the cladoceran nor the chironomid record. Overall, cladoceran and chironomid abundances were low until ~1950 AD and increased afterwards. Together with increased spheroidal carbonaceous particles (SCP's), this presumably hints at enhanced human influence on the lake. Interestingly, no major changes in the diatom assemblages are apparent between ~1950 and 2000 AD. In the most recent zone (~2000–2013 AD), a significant change in all proxies is apparent. The assemblage is dominated by Aulacoseira granulata var. granulata. Diatom concentration increased considerably, while Cladocera and Chironomidae concentrations dropped. We propose that these changes were caused by a great earthquake occurring in 2001. Earthquakes are important drivers of erosion and landslides that affect the aquatic ecosystem and possibly lead to drastic reduced light availability, turbulence and higher trophy. Moreover, a change in the water coloration has been observed after the earthquake, indicative of higher sulfur concentrations.

From analysis of silica biogenesis in diatoms to the synthesis of functional materials

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The intricately structured cell walls of diatoms are composed of amorphous silica (~90 %) and tightly associated organic macromolecules (~10%). Silica biogenesis in diatoms shares many features with the biomineralization mechanisms in other organisms (sponges, mollusk shells, bone) irrespective of differences in the mineral chemistries. Diatoms are unicellular, can be easily cultivated, are readily accessible to genetic manipulation, and are thus excellent model systems for studying fundamental mechanisms of biomineralization. I will present recent discoveries about the molecular machinery for silica biomineralization in diatoms particularly regarding the identification of biosilica-associated proteins ("biosilicome") and the role of insoluble organic matrices in silica morphogenesis. I will also provide examples how such insight can be translated into the synthesis of diatom biosilica with tailored properties for applications in catalysis and targeted drug delivery.

Interactions between diatoms and bacteria in photautotrophic biofilms

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Phototrophic, epilithic biofilms are a typical feature of aquatic ecosystems. In order to study interactions between diatoms and bacteria in biofilms, we have isolated and identified different diatoms and associated satellite bacteria from Lake Constance. Interestingly, purified diatom cultures showed significant differences with respect to growth and biofilm formation when compared to the corresponding xenic cultures. The diatom Achnanthidium minutissimum (Kütz.) Czarn. forms capsulelike structures in the presence of an isolated bacterial strain, but not in axenic state (Windler & al. 2015). Interestingly, formation of capsules can be induced by adding substances secreted by the satellite bacteria. SEM analyses show that the diatom capsule material, that was mechanically stressed by being stretched between or around cells, displayed fibrillar substructures (Leinweber & Kroth 2015). Fibrils were also found on the frustules of non-encapsulated cells, implicating that A. minutissimum capsules may develop from fibrillar precursors. We furthermore have screened the genome of the marine diatom *Phaeodactylum tricornutum* Bohlin for gene models encoding proteins exhibiting leucine-rich repeat (LRR) structures (Schulze & al. 2015). We were able to identify several transmembrane LRR-proteins, which are likely to function as receptor-like molecules. Moreover, P. tricornutum encodes a family of secreted LRR proteins likely to function as adhesion or binding proteins as part of the extracellular matrix. We furthermore have analyzed the extracellular proteome of P. tricornutum in the presence and absence of Roseovarius bacteria (Buhmann & al. 2016).

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Biodiversity and preliminary results on molecular phylogeny of diatom assemblages of the tropical Indian Ocean Island – Nosy Be, NW Madagascar

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Madagascar is an isolated oceanic island characterized by high degrees of endemism at all taxonomic levels. Marine waters surrounding Madagascar are still poorly studied for benthic marine diatom assemblages. The aim of our study was to analyze the taxonomic biodiversity and molecular phylogeny of the diatom assemblages of the Nosy Be archipelago. Samples were collected from the Nosy Be and Nosy Tanikely islands in June/July 2014, for a total of 65 samples collected from 14 sampling sites. Measurements of environmental variables were also taken at diatom collection sites. Diatom identification, based on light and electron microscopic examination, revealed 332 diatom taxa. From those, ca. 90 strains have been isolated and successfully cultured. So far, DNA was extracted and one chloroplast gene (rbcL) sequenced from 21 strains and their molecular phylogeny was reconstructed. Taxa selected for sequencing and the preliminary phylogeny are from genera considered common in the marine littoral: Bellerochea Van Heurck, Melosira C. Agardh, Paralia Heib., Triceratium Ehrenb., Navicula Bory, Hippodonta Lange-Bert. & al., Cocconeis Ehrenb. and some araphids. For each site, the Shannon biodiversity index was calculated. Diatom assemblages of Nosy Be Archipelago were characterised with high biodiversity – Shannon index 0.6–4.5 (average 3.3)). Species richness ranged from 12 to 87 (average 57). The most abundant species was Cocconeis scutellum. Many of the taxa identified to the generic level may turn out to represent taxa new to science after EM examination and DNA sequencing, particularly among the small staurosiroids and monoraphids. However, most of the cultured taxa seem to represent cosmopolitan forms: Bellerochea malleus (Brightw.) Van Heurck, Triceratium dictyotum P. A. Sims & R. Ross, Melosira cf. lineata (Dillwyn) C. Agardh or Navicula ramossisima (C. Agardh) Cleve. Some of these common taxa, such as Paralia longispina S. Konno & R. W. Jord., show quite distinct genetic variation. In conclusion, diatoms of the marine littoral of an Island neighbouring NW Madagascar are very rich in species number and occur in very diverse assemblages. The provenience of the diatom species seems to be mixed and beside unique taxa, possibly endemic, the dominant seem to be of broad distribution with Indo-Pacific and global affinities.

Diatoms of the high-mountain lakes of the Ukrainian Carpathians

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Diatoms are an important part of the water ecosystems diversity of the Ukrainian Carpathians. Nonetheless, they have yet to be studied in detail. For the water bodies of the Carpathian region of Ukraine, only 312 species (347 intraspecific taxa) of diatoms are known, according to the monograph "Algae of Ukraine" (Tsarenko & al. 2009). However, the majority of these data refer to the water bodies in the Prykarpatya and Zakarpatya regions. Information about the diatoms diversity in the water bodies directly in mountainous areas is insufficient. So, only 32 species (33 i.t.) of diatoms are known for the high-mountain lakes of the Chornohora massif of the Carpathians: Brebeneskul Lake (N48°06'06.0'', E24°33'44.2'', 1793 m a.s.l.; oligotrophic; oligosaprobic; rocky bottom; pH 7,0) and Nesamovyte Lake (N48°07'21.7'', E24°32'22.1'', 1748 m a.s.l.; oligotrophic; β-mesosaprobic; the bottom is from rocky to sandy and muddy; pH 6,2) (Mykitchak 2014).

As the results of the research, 100 species (101 i.t.) of diatoms were found in periphyton samples from lakes Nesamovyte and Brebeneskul. It has been shown that the species composition of *Bacillariophyta* is represented by the three classes, 5 subclasses, 12 orders, 24 families and 43 genera. The given species diversity is divided unevenly between two lakes: 86 species were found in the Nesamovyte Lake and 38 species (39 i.t.) – in the Brebeneskul Lake; 32 species are common for both lakes (32 % from total species composition of *Bacillariophyta*). Dominant species in the lakes are also different: for the Brebeneskul Lake *Cymbella cymbiformis* C. Agardh, *Denticula tenuis* Kütz., *Encyonema silesiacum* (Bleisch) D. G. Mann are characteristic, and for the Nesamowyte Lake – *Tabellaria flocculosa* (Roth) Kütz., *Eunotia minor* (Kütz.) Grunow and *Frustulia crassinervia* (Bréb. ex W. Sm.) Lange-Bert. & Krammer. Such differences are caused primarily by the ecological and morphometric features of these lakes. Despite this, in both lakes the proportions of oligosaprobic and β -mesosaprobic species are approximately the same and they are dominant. The situation is the same with ratio between oligotrophic and oligomesotrophic species. This may indicate pollution as a result of anthropogenic impact.

It was found that 3 species from lake Nesamovyte are new for the flora of Ukraine (*Brachysira brebissonii* R. Ross, *Navicula recens* (Lange-Bert.) Lange-Bert., *Pinnularia falaiseana* Krammer) and 11 species were firstly recorded for the water bodies of the Ukrainian Carpathians (lake Nesamovyte: *Encyonema neogracile* Krammer, *Eunotia glacialis* F. Meister, *Gomphonema italicum* Kütz., *Karayevia clevei* (Grunow) Round, *Navicula vulpina* Kütz., *Pinnularia subrupestris* Krammer, *Skabitschewskia pergalloi* (Brun & Hérib.) Kulikovskiy & Lange-Bert., *Stauroneis kriegeri* R. M. Patrick; lake Brebeneskul: *Pinnularia divergens* W. Sm., *Psammothidium helveticum* (Hust.) Bukht. & Round, *Staurosira construens* var. *binodis* (Ehrenb.) P. B. Ham.).

Tasarenko S. P., Wasser S. P. & Nevo E. (ed) 2009: Algae of Ukraine: Diversity, Nomenclature, Taxonomy, Ecology and Geography, Vol. 2. *Bacillariophyta*. – Ruggel: A.R.G. Gartner Verlag.

Mykitchak T. (ed.) 2014: Ekosystemy lentychnykh vodoym Chornohory (Ukrainski Karpaty) [Ecosystems of lenthic water bodies of Chornohora massif (Ukrainian Carpathians)]. – Lviv: ZUCK.

The influence of sea turtles on the biogeography of marine diatoms based on a case study from the Mediterranean coasts

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Marine turtles are known to be hosts of diverse groups of organisms (epibionts), both plants and animals, particularly on their carapaces. Many of these epibionts attach to a variety of substrates in habitats where sea turtles spend time between nesting events or while foraging; however, a small group of taxa are limited in their distribution solely to the marine animals. The association between diatoms and turtles potentially exemplifies how epibiont data can be used to identify and corroborate patterns of turtle habitat use and movement. It is expected that vertebrates in general and marine turtles in particular play an important role in the dispersal of benthic diatoms, and could be significant contributors to the spread of invasive species. By studying diatom assemblages living on turtles, we expect to gain information about the role that turtles play in the dispersal of diatoms. We expect that benthic diatoms hosted by marine vertebrates will be characterized by a high degree of specialization, similar to other epibiont communities.

In this study we have combined the analysis of species composition of diatoms incorporated into the biofilm formed on the carapaces of sea turtles with isolation and culture experiments. The diatom assemblages targeted inhabit the carapaces of loggerheads (Caretta caretta) and green turtles (Chelonia mydas) from the Mediterranean coasts in Turkey and Croatia. Altogether, several sampling seasons in the Aegean Sea in Turkey and one season in Croatia allowed us to isolate and successfully grow in culture ca. 120 strains. These include small Navicula Bory, Nitzschia Hassall, Diploneis (Ehrenb.) Cleve and Halamphora (Cleve) Levkov species, apparently incorporated into the carapace biofilm. Interestingly, stalk-forming species of Achnanthes Bory s. str. and tube-dwelling Parlibellus E. J. Cox were included among these epibionts, and grew well in culture. These species in particular may provide an insight into the role of sea turtles in diatom distribution. This will be tested determining the species composition from cleaned and processed samples as well as with molecular analysis of the isolated strains. Extraction of DNA from cultured strains and use of molecular markers (rbcL, psbC and SSU) was applied in testing the hypothesis that the diatoms present on turtle carapaces will exhibit biogeography and possess geographic ranges that match those of their hosts. Additionally, recent results based on species composition analysis solely suggest that the same epibiontic diatom species can be found on the loggerhead turtles and, for example, green turtles from the distant geographic regions e.g. Mediterranean and the Caribbean Sea.

Mountain lake diversity reflects multiplicity of climate change effects – paleolimnological studies in various Alpine lakes

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Mountain lakes constitute highly sensitive ecosystems, which are adapted to extreme conditions. Their characteristics vary widely and thus, the influence of climate warming may differ between different lakes. The basic hypothesis states that the bigger the water body, the better the ability to buffer the impact. The lake set of the study consists of 15 mountain lakes in the Bavarian Alps with a wide range of altitudes, surfaces, depths, and even geological origins. To investigate the individual history and climate warming-related change in a lake, we used sediment cores and its subfossil diatom assemblages. Each centimeter layer was 'scanned': diatoms were counted, the dry weight was measured and the diatom density/biomass out of the two former proxies was estimated. Additionally, the sediment layers' age was determined. The climate in the Alps indicates the onset of a significant warming approximately 30 years ago. In our sediment cores, this is characterized by a shift in the diatom assemblages and an increasing dissimilarity among adjacent layers. This fact occurred in each studied sediment core. Nevertheless, the extent of this change varied considerably across the mountain lakes. Apart from the sedimentation rate, the onset of the impact of global change was detected in different sediment depths and the diatom transition in bigger lakes was much smoother than in those of small shallow water bodies, confirming our hypothesis. Furthermore, the geological origin is very decisive. The diatom assemblages of a montane doline lake, which is exclusively fed by ground water, most likely acts like an alpine lake in the context of climate warming. The mere altitude's effect is less important than changes in the catchment, e.g. vegetation, like the climate change-related uphill-movement of the tree line.

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What can cryptic asymmetry say about diatoms?

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Diatom cells show extraordinary variety of forms that resemble geometric objects. Their shapes are circular, elliptical, elongated, triradiate or multi-angled. They can be heteropolar (longitudinal symmetry), dorsiventral (transapical symmetry), sigmoid or isobilateral (two planes of symmetry). Despite the symmetric appearance of bilaterally symmetric diatoms, they exhibit a cryptic lateral polarity which is associated with their asymmetric ontogeny. During the formation of the cell wall of pennate diatoms, the synthesis of the one side along the apical axis starts later than the other side. The secondary side and primary side of valve can be recognized by Voigt discontinuities and by the curvature of the raphe ends. Furthermore, other morphological characters and developmental processes are also asymmetrical. These asymmetric features are important in separation of diatom genera (e.g., separation of Encyonema Kütz. from Cymbella C. Agardh). In the present study, asymmetric patterns of 23 Luticola species from worldwide localities were examined to answer the following questions: i) Do smaller frustules within species exhibit higher fluctuating asymmetry (i.e., random deviations from perfect symmetry) than large frustules? ii) Is there a significant effect of directional asymmetry (i.e., systematic differences between primary and secondary side)? The results showed that fluctuating asymmetry within species is not significantly related to the size diminution during the asexual cell cycle except in three cases (two positive and one negative correlation). Higher fluctuating asymmetry of small frustules would indicate accumulation of errors in synthesis of hypovalves. However, this relationship has not been supported by our data (except one case) nor by the data from two monoclonal Luticola D. G. Mann strains cultivated under stable conditions (Woodard & Neustupa 2016). Directional asymmetry was present in 21 species and mostly modify the shape similarly across species. The primary side, where the proximal raphe ends are deflected, was externally swollen near the central area, which obscured the wavy margin in undulated species. The secondary side, where a distinct stigma is situated, was deepened internally and wavy margins were more pronounced in undulated species in comparison with the mean shape of species. Consistency in the shape of directional asymmetry across species indicates their evolutionary relatedness and dissimilarity indicates evolutionary diversification within the genus Luticola.

Woodard K. & Neustupa J. 2016: Morphometric asymmetry of frustule outlines in the pennate distom Luticola poulickovae (*Bacillariophyceae*). – Symmetry 8: 1–22. https://doi.org/10.3390/sym8120150

Meta-barcoding insights into the spatial patterns in community structure of freshwater diatoms in oligotrophic habitats

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Autecological characteristics of diatom morphospecies has been used in the development of biotic indices for assessment of the ecological status of the ecosystem, e.g., with respect to trophic status, saprobity, acidity, and salinity. However, with the increasingly common discovery of hidden diversity within morphospecies, new approaches, which do not rely on microscopic identification of species, have been tested to examine the relevance of genetic variability for ecological questions. In the present study, genetic variability of freshwater diatom communities was examined at different spatial scales. We focused on two major questions: i) Is genetic diversity and phylogenetic relatedness significantly affected by local and regional environment? These results would show the relative importance of environmental and spatial factors on diatom communities. ii) Is variability within a diatom genus comparable with the variability of the diatom community? Investigation of this question would show whether phylogenetic signal is similar at different levels of taxonomic resolution.

Molecular phylogeny, morphology and biogeography of genera from the family *Mastogloiaceae* Mereschkowsky

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It was considered that the genus *Aneumastus* D. G. Mann & Stickle is closely related to *Mastogloia* Thwaites ex W. Sm. species due to them sharing a chloroplast type and some aspects of valve morphology, with the exception of partectal chambers on the valvocopulae as in the genus *Mastogloia* (Hajos 1973). This assumption was represented in the useful system of diatoms, where genus *Aneumastus* together with *Mastogloia* was included within the family *Mastogloiaceae*, order *Mastogloiales* (Round & al. 1990). Determination of the phylogenetic position of *Aneumastus* using molecular approaches has not yet been performed. The genus *Mastogloia* Thwaites ex W. Sm. includes epipelic and epiphytic species that inhabit marine, brackish and fresh waters (Round & al. 1990). Our strain of *M. recta* Hust. Ind 427 was isolated from freshwater habitat Mahalona river (Indonesia). According to two-gene maximum likelihood (ML) and Bayesian inference (BI) phylogenetic analyses, strain *M. recta* appeared most closely related to the freshwater strain *Aneumastus* mongolotusculus Maltsev, Andreeva & Kulikovskiy. The phylogenetic positions of species from *Aneumastus* and *Mastogloia*, as well as from other *Mastogloiales*, is discussed, along with analysis of their morphology and biogeography.

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Round F. E., Crawford R. M. & Mann D. G. 1990: Diatoms: Biology and Morphology of the Genera. – Cambridge: Cambridge Univ. Press.

Registration of diatom novelties in Phycobank.org

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The International Code of Nomenclature for algae, fungi, and plants provides for nomenclatural indexing through nomenclatural repositories (Turland & al. 2018, Art. 42). Registering nomenclatural novelties and nomenclatural acts means that repositories will keep track of new names (species and names at all ranks, replacement names, names proposed for conservation or rejection, validated names) and of nomenclatural types, including lectotypes and epitypes.

PhycoBank has been advocated by the International Society for Diatom Research (ISDR), the Global Biodiversity Information Facility (GBIF), and the Special Committee on Registration of Algal and Plant Names (including fossils). Aided by a grant from the German Research Foundation (DFG, JA 874/8-1), PhycoBank has been established at the BGBM Berlin as the repository for nomenclatural acts of algae. By June 2018, PhycoBank staff will be operating a fully functional data entry portal. A user access portal is available under https://www.phycobank.org. A web user interface for voluntary data entry has functioned as a prototype since the summer of 2017. PhycoBank assigns globally unique http-based identifiers for nomenclatural acts, e.g. https://www.phycobank.org/100005. Via these PhycoBank identifiers, the corresponding data and metadata can be retrieved in human- and machine-readable formats.

Journals pioneering the publicaton of PhycoBank identifiers are *Cryptogamie Algologie*, *Diatom Research*, *Fottea*, *Journal of Phycology*, *Notulae Algorum*, *PhytoKeys*, *Phytotaxa*, *Protist*, *Systematics and Biodiversity*, *Taxon* and *Willdenowia*.

Classifications are frequently subject to changes. Currently, the diatom classification is under discussion (Cox 2015, Guiry & Guiry 2018, Kociolek & al. 2018). Therefore, PhycoBank aims to be neutral with respect to higher classification, but will project classification information of each name that is registered into a directed graph of available higher rank names to record higher classification information and to facilitate search functionalities.

All scientists, editors, and publishers involved in the publication of nomenclatural novelties are invited to contact PhycoBank to influence the prototypical registration process and to improve PhycoBank functionality.

Cox, E.J. 2015: Diatoms, Diatomeae (*Bacillariophyceae* s.l., *Bacillariophyta*). – In: Frey W. (ed.): Syllabus of plant families. – Stuttgart: Borntraeger.

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Patterns of diatom flora in Northern European bogs: a case study in Estonia

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Peat bogs provide unique habitats for biodiversity at the species and ecosystem levels because of their extreme environment (e.g. low pH, naturally nutrient-poor, waterlogged soils). Although they are one of the most threatened ecosystems elsewhere in the world, bogs are still common in Northern Europe. However, continuous natural and anthropogenic environmental stressors, including climate change, artificial drainage, pollutants through the air and ground water, and intensified recreational activities continue to affect the habitats there as well. Peat bog studies are generally well advanced in Northern Europe, but diatoms in bogs are poorly studied. The abundance and diversity of bogs in Estonia offers a good opportunity to describe the diatom communities on various types of bogs. This study aims to (1) describe diatom species composition of several Estonian bogs, (2) identify diatom species that are typical bog-dwellers, and (3) evaluate the effect of substrata on diatom assemblages. We collected Sphagnum moss samples from several microhabitats of three bogs in May 2014. Total of 181 diatom species were identified from three bogs. The most common species in this study were Eunotia paludosa Grunow and Kobayasiella parasubtilissima (H. Kobayasi & Nagumo) Lange-Bert., associated with Achnanthidium minutissimum (Kütz.) Czarn. s.l, Eunotia superpaludosa Lange-Bert. and Eunotia fennica (Hust.) Lange-Bert. Most species found were site-specific and recorded exclusively in one of the studied bogs. Only 28 species were present in all three study sites. One of the studied bogs differed significantly from the other sites, both in species composition and environmental factors. While pH and moisture content of the substrata influenced the diatom assemblages in two bogs, electrical conductivity primarily affected those in the remaining bog. Even though many acidophilic and aerophilic taxa occurred, large part of the diatom taxa identified has not been exclusively classified as those associated with bogs and acidic environments in previous studies. Additionally, many species identified in this study have not been previously classified as bog-dwellers. Those results from Estonia show a need of further studies for a better understanding of the autecology of mire diatoms.

Morpho-physiological reactions to phosphate limitation and resulting implications for diatom life strategies

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The northern Adriatic is characterized by a multitude of steep and quickly-changing gradients (e.g. nutrients), both temporal and spatial. The current systems and the major freshwater input (River Po), in particular, generate strong gradients in nutrient concentrations with an expressed N/P imbalance and sustained phosphate limitation. This results in a highly structured planktonic ecosystem that allows us to investigate the performance of planktonic species along those gradients and in contrasting conditions. We analyzed several diatom species with respect to their metabolic reaction towards phosphate limitation. Here we report data on species specific growth rates under different nutrient regimes, phosphate uptake rates, alkaline phosphatase activity, localization and activation patterns and characteristics of alkaline phosphatase activity as well as on morphological reactions to phosphate stress. The Leptocylindrus danicus Cleve species complex and Chaetoceros peruvianus Brightw. are two common taxa/species in the northern Adriatic. We compared their performance in situ as well as performed phosphate limitation experiments ex situ. Physiological changes observed include changes in generation time, expression of alkaline phosphatase as well as morphological reactions to phosphate limitation. L. danicus species complex showed cell and chain elongation in phosphate limitation, while C. peruvianus showed elongation of setae and apical axis. We could demonstrate that both morphological changes are increasing volumes and surface areas, where alkaline phosphatase activity is localized and thus increase the species' capability to make use of organic phosphate resources. In the case of *C. peruvianus*, the morphological changes resemble the transition between two described variabilities, (C. peruvianus var. peruvianus and C. peruvianus var. gracilis Schröd.). Our results show that careful morphological analysis of in situ samples can be a good indicator for the detection of specific and complex ecological circumstances like e.g. phosphate limitation. We furthermore combine the results of our physiological experiments and in situ performance analyses into a model for the life strategies of L. danicus species complex and C. peruvianus.

Small is beautiful but overlooked: role for nanoplanktonic diatoms in spring blooms and carbon export

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Diatoms are one of the major primary producers in the ocean, responsible annually for ~20% of photosynthetically fixed CO_2 on Earth.

In oceanic models, they are typically represented as large (>20 μ m) microphytoplankton. However, many diatoms belong to the nanophytoplankton (2–20 μ m) and a few species even overlap with the picoplanktonic size-class (<2 μ m). Due to their minute size and difficulty of detection they are poorly characterized. Here we describe a massive spring bloom of the smallest known diatom (*Minidiscus* Hasle) in the northwestern Mediterranean Sea. Analysis of Tara Oceans data, together with literature review, reveal a general oversight of the significance of these small diatoms at the global scale. We further evidence that they can reach the seafloor at high sinking rates, implying the need to revise our classical binary vision of pico- and nanoplanktonic cells fueling the microbial loop, while only microphytoplankton sustain secondary trophic levels and carbon export.

Two endpoint metrics of diatoms for ecotoxicological studies

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Diatoms are used to assess the ecological status of aquatic systems because of their cosmopolitan nature, diversity with about 100,000 genera reported, short life span and quick response to environmental and anthropogenic disturbances. The key advantage of diatoms for use in ecotoxicology is that it is possible to examine the effects of toxicants at different levels of biological organization, i.e., from individual cell to community levels in addition to the ease of sampling, storing, observation of live features and identification. However, diatoms are relatively underutilized as a tool for risk assessment and for evaluation management options for fluvial ecosystems. The main reason is the limited types of traditional taxonomic-based metrics including cell counts, biovolume estimates, species richness, diversity indices and metrics using sensitive and tolerant diatom species. No direct cause-effect relationship between chemical pollution and some of these traditional endpoints has been observed with consistency. The traditional methods also appear to require professional expertise and time-consuming. The aim of this study was to introduce new endpoints, the quantity and biovolume of lipid bodies and deformations of diatoms as early warning measures of anthropogenic impact on aquatic ecosystem. Bio-volume of individual LBs was calculated by considering that the LBs are more or less spherical and thus the mathematical formula for a sphere could be applied. Deformities in diatom frustules were categorized into four types: (1) deformities in the valve outline, (2) deformities in the striae, (3) deformities in the raphe and (4) mixed deformities. When diatom samples were collected from 31 sites (14 fresh, 10 brackish and 7 marine waters), which included less impacted (upstream) and impacted (downstream) sites in each water type, diatoms of the impacted sites showed more lipid bodies (also higher biovolume) and a higher percentage of frustules. Principal component analysis (PCA) also showed clear segregation of impacted from less impacted sites by the extent of the presence of lipid bodies (higher both in number and biovolume) and deformities in diatom frustules. Pearson correlation analysis revealed that lipid body induction and deformities were positively correlated with metals (Cd, Co, Cr, Cu, Fe, Pb and Zn) and nutrients (total phosphorus and total nitrogen), whereas they showed negative correlation with salinity, dissolved oxygen, suspended solutes and pH. LBs and DFs are quick, easy to measure, require less human expertise, and have good reproducibility, and more importantly, can be adopted worldwide. They also may allow early detection of stress after exposure to doses below those needed to cause cell death which is the endpoint detected by traditional methods.

Pandey L. K., Sharma Y. C., Park J., Choi S., Lee H., Lyu J. & Han T. 2018: Evaluating features of periphytic diatom communities as biomonitoring tools in fresh, brackish and marine waters. – Aquatic Toxicol. **194:** 67–77.

The complex *Nitzschia amphibia-semirobusta-amphibioides*: a bibliographic revision

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Taxonomic confusion was detected involving Nitzschia amphibia Grunow, N. amphibioides Hust. and N. semirobusta Lange-Bert., a group of cryptic species that urge to be studied. Misidentifications and problems of species delimitation are somewhat common in the literature. This confusion is due to the lack of some details in *N. amphibia*'s original description in 1862, as for instance a partial coincidence in valve shape and length, fibulae and striae density between the three species. Fibulae shape may be considered the same as in *N. amphibia* and *N. amphibioides*. A question may be noticed in Krammer & Lange-Bertalot (1988) identification of some material as "(?) N. amphibioides", that should really be a Nitzschia sp. representative. Observing the original illustration of the later species is possible to verify characteristics of *N. semirobusta* which were described five years later. This reference is used to provide basic information for the species identification during biodiversity and ecological studies round the world. Based on a bibliographic review, we aimed at clarifying the morphological differences to know which ones should be used in new studies. Nitzschia amphibia and N. semirobusta can be separated by their fibulae length and shape, shorter tooth-root-like in N. amphibia. Fibulae in N. semirobusta are longer than in N. amphibia, reaching ¹/₃ of valve width and are thicker near the margin, however, getting thinner along the valve face. Nitzschia amphibioides is the most coarse species of all three, despite its similarities with N. amphibia that include valve ends and fibulae shape, the differences being evident if valve length (32-115 μ m) and width (9-10 μ m), and smaller fibulae (5-7) and striae (11.5-14) density in 10 μm in *N. amphibioides*, against 14-37 μm valve length and 4-4.5 μm width, 7-9 fibulae and 14-18 striae density in 10 μm in *N. amphibia*. Measurements of *N. semirobusta* are also different from those of *N. amphibioides*, but there is some partial overlapping in the valve length (12-50 μ m) and fibulae density (5-9 in 10 μ m). The two last species differ, however, in the valve width (4-6 μ m) and striae density (14-18 in 10 μ m). Present information can be somewhat easily used working with a light microscope in addition to enabling the knowledge of geographic distribution and ecological preferences.

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The ecological response of diatom assemblages in sediment traps to mariculture activity (*Gracilaria lemaneiformis* cultivation) in Shen'ao Bay, Nan'ao Island, China

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Revealing the ecological response of biological components in a mariculture ecosystem to the aquaculture stresses and clarifying the underlying operation mechanisms are crucial for the sustainable development in mariculture industry. The study was undertaken to investigate the temporal and spatial variations of physicochemical properties of seawater (TN, TP, SiO₂, COD_{Mn}, DO, pH, temperature, salinity, and transparency) and diatom assemblage dynamics in the time-series sediment traps set in Shen'ao Bay, Nan'ao Island, a typical base for cultivating the seaweed Gracilaria *lemaneiformis* (Bory) Grev. in southern China. The results from both the monthly histograms and the PCA of physicochemical properties implied that the water quality in the Shen'ao Bay was distinctly better during seaweed cultivating seasons (last Dec.- May) than that in the non-cultivating seasons (Jun.-Nov.). The diatom communities from two designed sediment traps (the Trap A was positioned near the fish cage, while the Trap B was located within the *Gracilaria* cultivation area) exhibited two different dynamic patterns in the 3-year field survey. In the variance analysis T-tests, the diatom diversity data (Richness, Shanon-wiener Index, and Pielou's evenness) of Trap B showed significant differences between the two periods of seaweed cultivation and non-cultivation, while the data from Trap A did not have significant differences between these two periods, indicating that the seasonal changes of diatom assemblages in seaweed cultivating area were strongly impacted by the Gracilaria-cultivated activities, and which was reconfirmed by the NMDS ordinations performed with diatom communities of Trap A and B, respectively. The diatom assemblages of Trap B were dominated by the species Thalassionema nitzschioides (Grunow) Grunow ex Hust., Thalassiosira binata Fryxell, Cocconeis scutellum var. parva (Grunow) Cleve and Paralia sulcata (Ehrenb.) Cleve, and they presented a pattern of periodical fluctuation almost concurrently with the annual schedule of Gracilaria cultivation. Generally, during the period of seaweed production, the relative abundance of planktonic species (e.g. Thalassionema nitzschioides) decreased while the benthic taxa (e.g. *Cocconeis scutellum* var. *parva*) increased, resulting in the relatively low P/B ratios. Additionally, the diatom diversity remained higher and the diatom density stayed lower in the seaweed-cultivated time relative to the rest of the year. All above results suggested that the cultivation of Gracilaria lemaneiformis can effectively remove the nutrients in the mariculture ecosystem and help to form a typical diatom community featured with low density but high biodiversity.

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High species diversity of *Neidium* Pfitzer in an alpine intermittent pond on Mt. Shar Planina, Republic of Macedonia

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The genus *Neidium* Pfitzer is considered a large genus with more than 300 species distributed in freshwater habitats worldwide. Neidium is typically represented in natural environments with a small number of species in low abundance, although with the correct environmental conditions, *Neidium* populations can become co-dominant in occurrence. Some of species have restricted distribution, for instance, Antarctic, South America, North America, or in particular ecosystems like ancient lakes Ohrid, Baikal, and Tanganyika. Observations of more than 2000 samples from Macedonia reveal the existence of ca. 40 different species. However, one sample showed extraordinary diversity with the occurrence of 17 different *Neidium* taxa. Some of them are already known and considered as rare species such as *N. bergii* (Cleve-Euler) Krammer, *N. bobmarshallensis* Bahls, *N. decoratum* Brun, *N. distincte-punctatum* Hust., *N. fogedii* Bahls, and *N. kozlowii* var. *parva* Mereschk. At least eight taxa possess unique morphological features that distinguish them from the existing species. Their morphological features are examined with LM and SEM and compared with the most similar taxa. Also, discussion about morphological groups within *Neidium* and important separating characters such as morphology of the raphe, striae and longitudinal canal is provided.

A new genus of cymbelloid diatoms from Yunnan Province, China

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Freshwater cymbelloid diatoms are characterized by their valves being asymmetrical about the apical axis, with or without apical pore fields (APF's), deflection of the raphe ends towards the dorsal or ventral margin, location and structure of the stigma(ta), and position and type of pore occlusions. Based on details of valve ultrastructure, we have gone from a single genus *Cymbella* C. Agardh, to the group being comprised of 16 genera as of 2017.

As one of the most illustrated diatom groups in China, Cymbelloid diatoms have a long historical record in the country and the group is well-represented in recent publications. In total, 12 genera and 401 taxa of cymbelloid diatoms have been reported from across China (unpublished observations).

The Yunnan – Guizhou plateau is one of the most important areas of the freshwater lakes in China. Study on the diatom flora of Yunnan province has yielded two species that resemble *Cymbella* in symmetry and the presence of apical pore fields, but exhibited unique features seen with both light and scanning electron microscopy. These features suggest that based on the current circumscription of the genus, they could not be placed in *Cymbella*. A new diatom genus, is established and described in this paper, based on light and scanning electron microscopic observations of the valve. Distinctive characters for the new genus include asymmetry about the apical axis, distal raphe ends deflected dorsally, apical pore fields present at each pole bisected by the external distal raphe ends, areolae with slit-like external openings and occluded by elliptic projections internally. Two new species are described as belonging to this new genus. These two new taxa have been found only from northern Yunnan Province in China, at relatively high altitude. The relationship between this new genus to *Cymbella* C. Agardh and other members of the *Cymbellaceae* are discussed.

Extreme acid environments: biogeochemical effects on algal biofilms

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The objective of this study was to evaluate the effect of water acidity on biofilms from two sites of very low pH (2.6-2.8): a pond and a stream, and a control site, with pH around 7. Considering the hydrological regime, the acidic sites are different because one is a lenthic permanent water body, while the other is a temporary stream. In terms of physico-chemical characteristics, the Acid Pond (AP) and the Acid Stream (Ribeira Achada do Gamo, (AS)) showed very high conductivities and high concentration of dissolved metals in the water and sediments with Al, Cu, Fe, Mn, Zn and SO_4^{2-} showing the highest concentrations. On the other hand, the control site (C), located in S. Domingos Mine Fluvial Beach, showed much lower conductivity than the two acidic sites and metals concentration was similar to background levels. It was found that the low pH of the medium caused stress in the biofilms that in turn induced the increase of CAT, SOD, GSTs activities and an increase in the amount of peroxidized lipids, confirming cell membrane damage within biofilm communities. The low values of photosynthetic pigments in the AL and AS sites in comparison with C (control) may indicate the reduction of the biomass due to the lower number of diatom species and other autotrophic organisms as well as the reduced amount of proteins. The effect of acidic environment on the community provoked a stress response, reflected by the reduction of diatom diversity and proliferation of acid tolerant species, such as Pinnularia aljustrelica Luis & al.

Lake monitoring and sediment trapping in a varved lake reveals inter-annual variations in seasonal responses recorded in diatom sediment records

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A major effect of global warming on lake ecosystems is manifested in changes to temperature-driven seasonal processes. We investigated the influence of seasonality on the formation of diatom sediment signals by comparing continuous diatom records collected by a sequential sediment trap with the diatom record in the annually laminated (varved) sediment of a boreal lake (Nylandssjön). Through high-resolution water column monitoring over three consecutive years and the analysis of a decadal sequential sediment trap record, we identified large year-to-year variations in the seasonal formation of the annual diatom sediment signal. The annual diatom record in the sediment trap corresponded well with the annual record in the varved sediment. Throughout the decadal record, relative diatom abundance was mainly dominated by either Cyclotella glomerata H. Bachm. or Asterionella formosa Hassall. Year-to-year differences in relative abundances of these two taxa could be explained by (i) seasonal weather anomalies, (ii) catchment processes, and (iii) specific timing of seasonal thermal structure of the lake. The detailed physicochemical lake monitoring suggests that the timing of physical in-lake process has a large influence on the buildup of Cyclotella glomerata blooms before spring over-turn, particularly in warm winters. In addition, the decadal monitoring identified anomalies in autumnal discharge and the combined effect of forestry and air temperature to be related to the relative abundances of Cyclotella glomerata vs. Asterionella formosa. For these two dominant taxa, the timing of nutrient delivery from the catchment during stratified conditions under ice (late winter) or before autumn over-turn was most important. Inter-annual variation of seasonal weather, catchment and in-lake processes highlight the importance of specific seasonal mechanisms in contrast to, for example, mean annual temperatures for the understanding of biological sediment formation.

Plankton diatom response to environmental change in a mid-sized hardwater stream (Midwestern USA)

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The watershed of the Upper Cedar River in NE Iowa has received heavy N fertilization since the mid-1980's due to 75% row crop agriculture. Flood-related disaster payments to communities along the Cedar River during the last 20 years increased to the top 10% of the United States (the only noncoastal area so ranked).

Diatom samples for this study came mostly from the Cedar River in Waverly, Iowa, a fifth-order stream, at a riffle site 1 km downstream from a low-head inflatable dam having a 5 km long shallow reservoir. Plankton (and epibenthon) samples have been collected at this site since 1974 with intensive sampling since 2013. Diatoms dominate these samples. Several government agencies sample water quality and quantity at near-by stations; these data are accessible in on-line sources. Plankton diatom 10-fold concentrations are based on 3L grab samples fixed in Lugol's. Counts use 0.5 ml (= 5 ml of the original) of concentrated suspension dried on cover-slips, incinerated, and mounted in high index of refraction media for counting at 1000X oil LM or placed on Al stubs for SEM taxonomic evaluation.

Since the mid-1970's, the N:P Redfield ratio has reversed; P has been the limiting nutrient since the 1980's. The proportion of centric diatoms in the plankton showed initial inhibition and more recent adaptation to the N:P change. Taxonomic changes are not apparent, perhaps related to historically high nutrient levels in the original prairie soils.

The spring and fall diatom bloom pattern has changed in several ways in response to increased flood discharges. Summer floods lower the water temperature, and since nutrients are seldom limiting, summer diatom blooms are more frequent. Extreme flood events in spring or fall also inhibit typical seasonal blooms and introduce more edaphic diatoms into the river. The few diatom taxonomic changes observed will be described.

These observations further verify and enhance the precision of diatoms as environmental monitors.

Morphological variations in sea turtle-associated "gomphonemoid" diatoms

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Very recently, several new diatom taxa have been described living epizoically on sea turtles. Among them, two new genera, Poulinea Majewska & al. and Chelonicola Majewska & al. (Majewska & al. 2015), described from nesting olive ridleys in Costa Rica, were later observed in multiple samples collected from other sea turtle species from different geographic locations across the globe. Both genera possess cuneate, heteropolar frustules, morphologically (though not necessarily genetically) resembling other gomphonemoid diatom taxa, most notably Tripterion R. W. Holmes & al. (Holmes & al. 1993), a genus described from the skin of Dall's porpoises and later found growing on other marine mammals (whales) but also on abiotic substrates (Fernandes & Sar 2009). Several inconsistencies in the current description of Tripterion have been highlighted (Fernandes & Sar, 2009, Frankovich & al. 2016) and Riaux-Gobin & al. (2017) further questioned the description of Poulinea, indicating incorrect character coding used in the cladistic analysis applied by Majewska & al. (2015) to differentiate Poulinea from Tripterion. Although Riaux-Gobin & al. (2017) noted that the small sea turtle-associated diatoms they examined showed a relatively simple morphology and a certain level of morphological variability, another two, morphologically very similar, taxa were described as Chelonicola caribeana Riaux-Gob. & al. and Tripterion societate 'societatis' Riaux-Gob. & al., the latter being almost indistinguishable from the previously described Poulinea lepidochelicola Majewska & al. The current study characterizes over 20 populations of epizoic "gomphonemoid" diatoms found on five sea turtle species inhabiting all three oceans, highlighting both the remarkable morphological plasticity found within each of these populations and the lack of morphological discontinuity among them. As diatom epibiosis on sea turtles (and other marine and freshwater animals) attracts growing attention, further new forms are expected to be discovered in on-going surveys, and it must emphasized that, especially in the case of these small-celled heteropolar specimens, new taxa should be described with extreme caution.

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Majewska R., Kociolek J. P., Thomas E. W., De Stefano M., Santoro M., Bolaños F. & van de Vijver B. 2015: Chelonicola and Poulinea, two new gomphonemoid diatom genera (*Bacillariophyta*) living on marine turtles from Costa Rica. – Phytotaxa **233**: 236–250.

Riaux-Gobin C., Witkowski A., Kociolek J. P., Ector L., Damien C. & Compère P.2017: New epizoic diatom (*Bacillariophyta*) species from sea turtles in the Eastern Caribbean and South Pacific. – Diatom Res. **32**: 109–125.

A forgotten treasure: how zoological museum collections can contribute to epizoic diatom research

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Aquatic animals, both marine and freshwater, provide unique habitats for various macro- and microorganisms, including many diatoms that seem to cope especially well with challenges posed by rapidly changing conditions related to the host's biology and behaviour. Although exploration of previously undescribed biotic marine habitats has yielded many new diatom taxa, some exhibiting traits of obligate epibionts (Holmes & al. 1993, Wetzel & al. 2012, Majewska & al. 2015), the nature of the close relationships between the host organism and its epibionts remains poorly understood. This study takes advantage of the unique resource of well-preserved aquatic vertebrate specimens (including whales, sea turtles, freshwater turtles, aquatic snakes, seabirds, and marine iguanas) provided by the Canadian Museum of Nature, the Yale Peabody Museum of Natural History, and the California Academy of Sciences. It aims to provide baseline data about epizoic diatoms from both marine and freshwater habitats, generating an advance in epibiotic diatom research and minimizing the cost and any possible environmental footprint of a similarly extensive study involving fieldwork and fresh material collection.

Selected samples of both dried and liquid-preserved specimens of aquatic animals collected from locations across the different ocean basins were analysed for their associated diatom communities. Whenever possible, a few cm² tissue sample was digested with acids to extract the diatom valves. In several cases, to avoid the destruction of the especially valuable animal tissue, samples were placed in separate beakers with distilled water and sonicated for ca. 30 minutes. Subsequently, the water with detached diatoms was collected, while the animal samples were air-dried and returned to the collection manager. Cleaned diatom frustules were examined using both light and scanning electron microscopy. Altogether 100+ samples were processed. The analysis proved that although zoological museum collections may indeed constitute an excellent source of unique and often very rich epizoic diatom material, several important limitations of such study must be considered. The advantages and disadvantages of the research approach will be critically assessed and discussed.

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Majewska R., Kociolek J. P., Thomas E. W., De Stefano M., Santoro M., Bolaños F. & van de Vijver B. 2015: Chelonicola and Poulinea, two new gomphonemoid diatom genera (*Bacillariophyta*) living on marine turtles from Costa Rica. – Phytotaxa **233**: 236–250.

Wetzel C.E., van de Vijver B., Cox E. J., Bicudo D. de C. & Ector L.2012: Tursiocola podocnemicola sp. nov., a new epizoic freshwater diatom species from the Rio Negro in the Brazilian Amazon Basin. – Diatom Res. 27: 1–8.

Molecular phylogeny and morphology of the diatom genus *Nupela* Vyverman & Compère

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The naviculoid genus *Nupela* Vyverman & Compère was described in 1991 with the type species *Nupela giluwensis* Vyverman & Compère. *Nupela* is a freshwater, oligotrophic to dystrophic genus, which possesses simple or inconspicuous raphe fissures (Vyverman & Compère 1991). One of the features of this genus was the reduction or underdevelopment of one or two branches of the raphe on one valve (Kulikovskiy & al. 2009, 2015). A distinctive morphological feature for this genus was the structure of elongate areolae. On the outer side of the valve areolae had deepening along the perimeter and closed internally by hymenes. This type of areola composition was characteristic only of the genus *Nupela* (Kulikovskiy & al. 2009; Potapova 2011, 2013). It entailed the attribution of a large number of monoraphid diatoms with this type of areola to the genus *Nupela* (Kulikovskiy & al. 2009, 2015).

It was considered that *Nupela* is closely related to *Brachysira* Kütz., because the areolae were arranged in longitudinal rows and they had the same structure on the mantle and the valve face (Vyverman & Compère 1991). This assumption was represented in the system of diatoms in Cox (2015). The phylogenetic position of *Nupela* using molecular approaches has not yet been studied. The aim of this work is the description of a new *Nupela* species from Indonesia with remarks about the phylogenetic position of the genus on the basis of molecular data.

The phylogenetic analysis (region V4 18S rDNA and partial *rbc*L gene) of the genus *Nupela* shows that the new taxon forms a separate clade, and with the low supports includes in a larger naviculoid clade with such genera as *Diadesmis* Kütz., *Luticola* D. G. Mann, *Neidium* Pfitzer, *Scoliopleura* Grunow and *Brachysira*.

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Diatoms: the third dimension

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Although any student knows that the diatom frustule comprises two types of element, valves and girdle bands, the girdle is usually ignored unless it possesses special features, such as the partecta of *Mastogloia*. Often, the diatom wall is presented and described as if it comprised only the two valves, which are treated as essentially two-dimensional entities, with an outline shape and interior pattern; the third dimension of the diatom cell is acknowledged to exist but it is rarely described and quantified unless this is unavoidable, e.g. because frustules almost always lie in girdle view. For example, the majority of SEM photographs of new taxa published in *Phytotaxa* during the last five to six years are presented in strict valve view, providing little or no information about the structure and depth of the valve mantle and girdle. This would have been disappointing to H.A. von Stosch, who wrote (1975) that the SEM "has much facilitated the observation of the diatom girdle" and that its use would help to provide descriptions of the whole frustule "instead of one part of the frustule, the valve, as do some diagnoses up to the present time."

Several questions may be asked about the girdle, such as what is it? how is it formed? and what is it for? Taking the last first, the functions of the girdle might be: to act as a functional cell wall, protect, and allow assimilation and secretion (all shared with the valves); to create intracellular space (shared with the valve and valve mantle); to allow growth (unshared); to control the size-shape trajectory during the life cycle (an interplay between girdle and valve mantle); and permit the release and uptake of cells or organelles, e.g. during sexual reproduction and auxosporulation (unshared). These functions are performed by a number of different types of girdle elements, which were identified and discussed by von Stosch (1975) – segmental, half, open and closed bands. He suggested that the girdle elements of a single theca can usually be classified into two structurally different and developmentally distinct types, termed copulae and pleurae (in addition, the modified copula adjacent to the valve was termed the valvocopula). However, while the developmental sequence is universal (girdle elements are formed strictly in order, from the valve outwards), some girdles are differentiated into either more or less than two types of element, making it impossible to make a non-arbitrary separation between two and only two types (i.e. copulae and pleurae) on the basis of morphology alone. What we still do not know, however, is whether a division can be made ontogenetically, between girdle elements that are present throughout interphase and those formed in preparation for cell division, to create the space necessary for cell division and the formation of the new valves. Indeed, the number of species in which the development of the girdle is known is still in single figures and, even though diatoms are almost ideal organisms for studying cell growth (since this occurs almost wholly in one dimension only, as in some bacteria or the fission yeast Schizosaccharomyces), documentation of when cells increase in volume during the cell cycle remains almost non-existent. There is also little understanding of whether, how, and how much the girdle deforms at cell division to create and control changes in shape.

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Variability within indicator species populations from Georgia, USA

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With human population growth and significant anthropogenic influence on aquatic habitats, it is not clear which taxa proliferating prior to industrialization were lost in specific areas. Research on aquatic microbial populations' ecology is of great interest for the conservation of aquatic ecosystems. Surface waters in the State of Georgia, USA, by law have to protect human health, fish conservation, wildlife, and other beneficial aquatic life. Wadeable streams and rivers in the State of Georgia were sampled following standard protocols by Environmental Protection Division biologists. Diatom community composition and physicochemical characteristics at each site were assessed and compared. Only diatom populations from least impacted streams were described morphologically for this research. Least-impacted streams have low to no agricultural or urban land use and no or low number on pollutants added based on the number of National Pollutant Discharge Elimination System permits in the watershed upstream of the sampling site. In addition, materials collected from the State of Georgia and the Southeastern United States from museum and national collections, prior to 1940, were examined. From each collection slide, dominant and subdominant taxa were compared with membership of current least impacted streams. It was predicted that diatom species that were able to grow at very low nutrient concentrations (prior to 1940) grew equally well when nutrients were not limiting, but the high nutrient species grew faster with nutrient increases and were limited from low nutrient habitats today. This prediction was not supported. Currently, Achnanthidium minutissimum (Kütz.) Czarn. dominated 86% of the least impacted sites. In Georgia this taxon has low TP optimum and is able to tolerate higher TN concentrations. This taxon was rare in pre-industrialization freshwater communities from the state. Those communities were dominated by representatives of the genus Eunotia Ehrenb., followed by representatives of the genera Aulacoseira Thwaites, Sellaphora Mereschk., Nupela Vyverman & Compère, and Gomphonema Ehrenb. Adaptive morphology was tested for taxa found in the 2 datasets. Based on the community comparison, in addition to nutrients, the shallowing of rivers in Georgia from navigational to wadeable might be contributing to diatom community dominated by prostate diatoms. Today, low nutrient streams support a lower species richness compared to pre-industrial streams.

Diatoms: from eutrophic indicators to mitigators

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Diatoms are highly productive, environmentally flexible, ubiquitous and diverse class of microalgae. They contribute about 20% of the total photosynthetic CO₂ fixation and 40% of the annual marine primary productivity on this planet. Moreover, they are exceedingly robust and can inhabit virtually all photic zones from the equator to arctic. Their population diversity reflects the environmental conditions of their oceanic or riverine ecosystems. This highlights their potential role as bioindicators for pollutant levels in their immediate environment. The ease of their detection and versatility across different eco-systems complements to their sensitively to many physical, chemical, and biological changes. Constructed wetlands are dynamic ecosystems with varying nutrient loads and treatment efficiencies based on vegetation. Monitoring their performance however remains a challenge for remote locations as the time lag between sampling and analysis often diminishes accuracy. In this work, we present the changes in diatom community structure of field scale constructed wetland planted with different surface and subsurface macrophytes treating real domestic wastewater at ICRISAT and explore their use as bio indicators of treatment efficiency. We compared nontaxonomical parameters like lipid globules, cell size and motility-based monitoring with physiochemical data to explore their usefulness as bio indicators. Diatoms are the most-explored species in terms of their use as indicators of pollution but their use as mitigators of pollution is not fully explored when compared with green algae. In the present study we also explore the potential of diatom dominated natural biofilms grown using real wastewater on artificial substrates in mitigation of excess nutrients and heavy metals and also study seasonal variations in diatom biofilm community structure. We also report biomass, lipid and fucoxanthin productivity of biofilms to access their potential for biofuel and biomolecule production. Changes in epiphytic and epilithic diatom communities provide evidence that diatom-based metrics had a good fit with the available physicochemical data and are useful indicators of water treatment efficiency of constructed wetlands. Diatom dominated biofilms using novel substrate resulted in efficient nutrient and heavy metal removal. This work further emphasizes the significance of diatoms not just as bio indicators of anthropogenic europhication but also as ecofriendly solution to reverse eutrophication and simultaneous generation of valuable biomass for biofuel and neutraceutical production.

The species composition and ecology of the genus *Leptocylindrus* Cleve in the Northern Adriatic Sea

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The marine diatom genus Leptocylindrus Cleve is an important component of phytoplankton blooms in coastal ecosystems worldwide. However, only little is known about the ecology and species composition of this genus in the Adriatic Sea. Although Leptocylindrus danicus Cleve and L. minimus Gran have been reported from numerous studies conducted in the Adriatic Sea, there has been neither unequivocal species identification nor focused examination of the temporal abundance of Leptocylindrus in this region. In a recent reappraisal of Leptocylindrus by Nanjappa et al. (2013), five species and one new genus were identified using both morphological and molecular methods. We here describe the temporal distribution of the genus Leptocylindrus based on 45 years of records, revealing that this diatom is a key component of the seasonal phytoplankton cycle, with highest abundance in the spring and autumn periods. Using light and scanning electron microscopy as well as genetic analysis based on the nuclear- encoded rDNA regions and environmental meta-barcoding, our study unambiguously revealed three species new for the Adriatic Sea, Leptocylindrus hargravesii Nanjappa & Zingone, Leptocylindrus convexus Nanjappa & Zingone and Leptocylindrus aporus (F. W. French & Hargraves) Nanjappa & Zingone. Making use of the steep ecological gradients that characterize the Northern Adriatic Sea, we report here on the ecological circumstances under which those species thrive and how their respective populations are globally connected. The ecology, physiology and evolution of this significant diatom genus should be further investigated to improve our knowledge of its ecological significance in marine, planktonic ecosystems.

Nanjappa D., Kooistra W. H. C. F. & Zingone A. 2013: A reappraisal of the genus *Leptocylindrus* (*Bacillariophyta*), with the addition of three species and the erection of *Tenuicylindrus* gen. nov. – J. Phycol. **49**: 917–936.

Photonic structures created by diatom frustule infilling

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Opalising diatoms - this unique mode of diatom preservation is only described at two Early Eocene localities worldwide: (I) Danish Fur Formation e.g., islands Mors and Fur (mo-clay; Lierl & Mende 1991, Böhmecke 1998) and (II) Schlieven Formation in northern Germany e.g., Greifswalder Oie island (cementstones; Böhmecke 1998, Obst & al. 2015). So far, it was postulated that the photonic properties originate from diffraction of visible light by an ordered lattice of amorphous silica nanospheres, i.e., precious opal (Lierl & Mende 1991). Here we analyse the photonic nanostructures of the common giant diatom Fenestrella antiqua (Grunow) Swatman, embedded in carbonatecemented volcanic ashes (tuffites) from the Greifswalder Oie island, Pomeranian Bay (southern Baltic Sea). The diatoms of the tuffites display different modes of preservation: pyrite and calcite steinkerns, opaline valves, diatoms within faecal pellets, and diatom valves with opalising light effects (Obst et al. 2015). Scanning electron microscopy (SEM) and energy-dispersive X-ray spectroscopy (EDS) reveal that the frustule is composed of delicate, amorphous silica wall structures and carbonate infillings. Transmission electron microscopy (TEM) shows that these infillings consist of randomly-oriented, polycrystalline calcite. Mild etching of opaline valves with hydrofluoric acid removes the amorphous silica component, exposing regularly ordered, hexagonal calcite tubes. The photonic phenomenon is still visible after this etching process. Conversely, etching with hydrochloric acid results in dissolution of the calcitic material (e.g., steinkerns and valve infillings) and a subsequent loss of photonic properties. Our results show for the first time that the regular arrangement of calcite tubes in an amorphous silica biotemplate causes the photonic properties of opalising diatoms. The unique mode of diatom preservation as precious opal can be discarded.

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Lierl H.-J. & Mende R. 1992: Edelopal-Kieselagen aus dem Moler Dänemarks. – Geschiebek. aktuell 7: 159–163.

Obst K., Ansorge J., Matting S. & Hüneke H. 2015: Early Eocene volcanic ashes on Greifswalder Oie and their depositional environment, with an overview of coeval ash-bearing deposits in northern Germany and Denmark. – Int. J. Earth Sci. **104**: 2179–2212.

Sigmoid Nitzschia species in girdle view

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Apochlorotic diatoms are model organisms useful for elucidating steps of reductive evolution in plastids (Kamikawa & al. 2017), which are seen in several groups of photosynthetic organisms. We isolated apochlorotic diatoms belonging to 6 linages from mangrove leaves in Yaeyama Archipelago. These diatoms were separately positioned as two clades in a phylogenetic tree of Nitzschia Hassall (Kamikawa & al. 2015). In one clade, diatoms showed sigmoid shape in girdle view or valve view. Conventionally, many sigmoid Nitzschia species were classified into section Sigmoideae (nomenclatural synonym of section Nitzschia) and classified into subgenus Nitzschia with those of section *Dissipatae*. This subgenus was characterized by the presence of conopea near the raphe. Close relationship between two sections was recently verified by molecular tree, which showed representatives of two sections as sister taxa, however, apochlorotic sigmoid Nitzschia made their own clade apart from Nitzschia sigmoidea (Nitzsch) W. Sm. and Nitzschia dissipata (Kütz.) Rabenh. (Carballeira & al. 2017). Although Nitzschia leucosigma W. Benecke is only described apochlorotic diatom with sigmoid girdle view, external valve face has not been observed by scanning electron microscopy (SEM) to examine the presence/absence of conopeum. In this study, we observed frustule structures of 3 sigmoid apochlorotic Nitzschia with SEM in detail and compared with those of photosynthetic Nitzschia sigmoidea and Nitzschia vermicularis (Kütz.) Hantzsch accompanied by some observations of organelle with living cells.

N. sigmoidea and *N. vermicularis* extended solid conopeum from base portions of both sides of canal raphe, but apochlorotic *Nitzschia* including *N. leucosigma* did not. *N. sigmoidea* and *N. vermicularis* had protruded raphe sternum on the raphe canal, but apochlorotic diatoms did not. Transverse sections of frustule were parallelogram or trapezoid in *N. sigmoidea*, rectangle in *N. vermicularis* and 2 apochlorotic diatoms, parallelogram in one apochlorotic diatom. Plastids of *N.* sigmoidea had many linear-oblong pyrenoids with cp-nucleoids along their sides (Mayama & al. 2004). However, cp-nucleoids showed ring-like arrangement around the plastid in *N. vermicularis*. We could not observe cp-nucleoids in apochlorotic diatoms under epifluorescence microsope. Distribution of the status of these characters are not well fit with phylogeny. Sigmoid cells of apochlorotic diatoms seem to be independently evolved from that of section *Nitzschia*.

Kamikawa R., Moog D., Zauner S., Tanifuji G., Ishida K., Miyashita H., Mayama S., Hashimoto T., Maier U. G., Archibald J. M. & Inagaki Y. 2017: A non-photosynthetic diatom reveals early steps of reductive evolution in plastids. – Mol. Biol. Evol. 34: 2355–2366.

Kamikawa R., Yubuki N., Yoshida M., Taira M., Nakamura N., Ishida K., Leander S., Miyashita E., Hashimoto T., Mayama S. & Inagaki Y. 2015: Multiple losses of photosynthesis in Nitzschia (*Bacillariophyceae*). – Phycol. Res. **63**: 19–28.

Carballeira R., Trobajo R., Leira M., Benito X., Sato S. & Mann D. G. 2017: A combined morphological and molecular approach to Nitzschia varelae sp nov., with discussion of symmetry in *Bacillariaceae*. – Eur. J. Phycol. **52**: 342–359.

Mayama S., Mayama N. & Shihira-Ishikawa I. 2004: Characterization of linear-oblong pyrenoids with cp-DNA along their sides in Nitzschia sigmoidea (*Bacillariophyceae*). – Phycol. Res. **52**: 129–139.

What are you? Non-Navicula-like species included in Navicula clade

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Navicula Bory is the largest genus among diatoms, which show wide range of morphological variation. In the past 30 years many genera were revived and newly established from *Navicula* based on the differences of valve morphology and cellular characteristics. However, many species still remain in *Navicula* despite of untypical valve morphology different from that of generic type *Navicula tripunctata* (O. F. Müll.) Bory. Recently some *Haslea* Simonsen species were transferred to *Navicula* based on molecular analysis, though they had continuous longitudinal strips on the external valve face; they seemed to be one of characteristics of the genus *Haslea* (Li & al. 2017). *Hippodonta* Lange-Bert. & al. and *Fogedia* Witkowski & al. are genera showing close relationship to *Navicula* in valve morphology. *Hippodonta capitata* (Ehrenb.) Lange-Bert. & al. was the only one *Hippodonta* species examined with molecular, showing its phylogenetic position to be a sister of *Navicula* sensu strict (Bruder & Medlin 2008).

In this study marine *Hippodonta* sp. examined with SSU rDNA and *rbcL* did not show monophyly with *H. capitata* within a large clade of *Navicula* sensu lato, in which *Fogedia densa* J. Park & al., *Navicula* cf. *diversistriata* Hust., *Navicula platyventris* F. Meister and several species with *Halsea*-like continuous longitudinal strips were included. *Navicula* cf. *diversistriata* is a heterovalvy diatom composed of radiate and parallel striae valves. These valves were also different in valve topology, striae density, and areola opening. However, it showed similarity to *Navicula* sensu stricto in early stage of valve morphogenesis, e.g. proximal extension of fimbriate polymerized silica from secondary raphe sternum. The presence of basal *Navicula* group showing untypical *Navicula* features will be discussed with the generic evolution.

Le Y., Chen X., Sun Z. & Xu K. 2017: Taxonomy and molecular phylogeny of three marine benthic species of Haslea (*Bacillariophyceae*), with transfer of two species to Navicula. – Diatom Res. **32:** 451–463.

Bruder K. & Medlin L. K. 2008: Morphological and molecular investigations of naviculoid diatoms. III. *Hippodonta* and *Navicula* s. s. – Diatom Res. **23:** 331-347.

Re-analysis of the Theriot et al. 2016 7 Gene Data Set using multiple outgroups

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Medlin (2014) tested the value of multiple outgroups in analyses of the 18S ribosomal RNA gene in recovering the three diatom Classes (Coscinodiscophyceae, Mediophyceae, Bacillariophyceae) as monophyletic groups. When certain outgroups were used (haptophytes ciliates, prasinophytes and chlorophytes), these classes were recovered as monophyletic clades with strong bootstrap support. Her analysis used the variable V4 region of the 18S rRNA gene. In the phylogenetic analysis performed by Theriot & al. (2015), an additional 6 plastid genes were added to the dataset but this dataset was used with only one outgroup, Bolidomonas Guillou & Chret.-Dinet, and did not include the V4 region of the 18S RNA gene. Their analyses recovered a grade of clades from the radial centrics into polar centrics, into araphid pennates, which themselves grade into the monophyletic raphid pennates. Theriot et al. have termed this grade of clades the structural gradation hypothesis (SGH) in contrast to the CMB hypothesis (Coscinodiscophyceae, Mediophyceae, Bacillariophyceae) of Medlin & Kaczmarska (2004). Our analysis took the 7 gene data from Theriot et al. and extracted only those species with a full complement of genes and added multiple outgroups and the V4 region of the 18S RNA gene. We recovered monophyletic, strongly supported Coscinodiscophyceae and Bacillariophyceae and Mediophyceae with 2 clades, without using any evolutionary models (codon partition scheme = CP). CP-based trees recovered grades of clades but when constrained by a tree reflecting the CMB hypothesis, a monophyletic Mediophycean clade was recovered. All trees were compared to the Theriot et al. trees, and the tree without CP (the CMB hypothesis) was significantly different and better than the Theriot & al. trees with the CP. Evidence is presented that overparamaterization of the dataset is likely the cause of the differences in the trees and why the CMB hypothesis is only recovered in analyses without any codon models.

Medlin L. K. 2014: Evolution of the diatoms: VIII. Reexamination of the SSU-rRNA gene using multiple outgroups and a cladistic analysis of valve features. – J. Biodiv. Biopro. Dev. 1: 129. https://doi.org/10.4172/2376-0214.1000129

Theriot E. C., Ashworth M., Nakov T., Ruck E. & Jansen R. K. 2015: Dissecting signal and noise in diatom chloroplast protein encoding genes with phylogenetic information profiling. – Mol. Phyl. Evol. **89:** 28–36.

Medlin L. K. & Kaczmarska I. 2004: Evolution of the diatoms: V. Morphological and cytological support for the major clades and a taxonomic revision. – Phycologia **43**: 245–270.

Response of diatoms to abrupt changes in late Pleistocene hydrology in the Estancia Basin, USA

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Time series of diatom species from lacustrine sediments of the Estancia Basin in the southwestern United States reveal dramatic changes in lake salinity during the Last Glacial Maximum (LGM). Previous work by Allen & Anderson (2000) revealed that Pleistocene Lake Estancia, a closed-basin pluvial lake, expanded from 400-1100 km² surface area and 5 to 45 m water depth five times during the LGM, with each highstand lasting several hundred to 1000 years and transitions between lowstands and highstands occurring within decades. Highstand sediments consist of massively bedded authigenic carbonates and detrital clastics whereas lowstand sediments consist of thinly laminated gypsum sands and algal mats. Timing of highstands is constrained by radiocarbon dates on shoreline and basin center deposits. Numerical modeling showed that lowstand to highstand transitions required increases in precipitation 1.5-2 times modern values for periods of a few decades along with decreases in evaporation caused by colder LGM temperatures (Menking & al. 2004, 2015). A high-resolution study of the LGM stratigraphic section, concentrating on sediment mineralogy, revealed the cause of these brief pulses of moisture to be related to variations in the strength of the East Asian monsoon through teleconnections to precipitation in the American Southwest and showed a timing consistent with solar cycles.

Here we relate new diatom time series data to the high resolution sedimentological time series. Notable amongst results is the high abundance of centric diatom *Lindavia comta* (Kütz.) Nakov & al. at the base of the LGM stratigraphic section followed by the total disappearance of the species after 22.8 ka. Previous work by Allen & Anderson (2000) showed a rapid expansion and then disappearance of the ostracode *Cytherissa lacustris* at this same time, which they interpreted as an abrupt and extreme freshening of a previously shallow, saline Lake Estancia. Additionally, variations in the diatoms *Pseudostaurosira brevistriata* (Grunow) D. M. Williams & Round, *Caloneis schumanniana* (Grunow) Cleve, and *Diploneis smithii* (Bréb. ex W. Sm.) Cleve mirror changes in the percentage of gypsum evaporites throughout the LGM section, with *P. brevistriata* a particularly tight relationship. Fluctuations in the abundance of this species in sediments from other western US lakes were interpreted to reflect variations in littoral zone contributions to the depositional sequence (Moser & Kimball 2009), which may help explain the correlation in Lake Estancia.

Allen B. D. & Anderson R. Y. 2000: A continuous, high-resolution record of late Pleistocene climate variability from the Estancia basin, New Mexico – Geological Society of America Bulletin **112**: 1444-1458.

Menking K. M., Anderson R. Y., Shafike N. G., Syed, K. H. & Allen B. D. 2004: Wetter or colder during the Last Glacial Maximum? Revisiting the pluvial lake question in southwestern North America – Quaternary Research **62**: 280-288.

Menking K. M.: 2015: Decadal to millennial-scale solar forcing of Last Glacial Maximum climate in the Estancia Basin of central New Mexico – Quaternary Research **83**: 545-554.

Moser K. A. & Kimball J. P. 2009: A 19,000-year record of hydrologic and climatic change inferred from diatoms from Bear Lake, Utah and Idaho. – Geological Society of America Special Paper **450**: 229-246.

Molecular and morphological characterization of diatom diversity and community structure for stream biomonitoring in New Jersey, USA

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Microbial eukaryotes, including diatoms and other groups of microscopic algae possessing distinct morphological characters, have been traditionally used as water quality indicators. The limitations of morphology-based methods can lead to inconsistencies in taxon identification. Morphological plasticity, unclear boundaries among cryptic and pseudo-cryptic species, and an unknown degree of geographic variability influencing species morphology results in considerable uncertainties in environmental inferences. Next Generation Sequencing of barcode gene fragments presents an alternative, potentially more objective method to obtain diatom community data. In this pilot study, we used amplicon-based Illumina sequencing of the hypervariable v9 region of 18S rDNA to characterize microbial eukaryotic assemblages in biofilm samples from fourteen New Jersey streams, representing a gradient of high to low water quality. We also characterized the diatom assemblages from the same samples using standard morphological identification and enumeration methods. The sampling design was aimed at accessing within- and among-sites variability of assemblage structure, community response to environmental stimuli, and repeatability of each method. Diatom and green algal reads were among the most abundant in the majority of samples. Molecular survey revealed a much higher level of diatom diversity than the morphology-based method, but reproducibility of the results, expressed as relative abundance of OTUs, was stronger for the morphology-based analysis. We compare advantages and shortcomings of both approaches and discuss future strategies for combining them for bioassessment purposes.

Novel clades of intriguing Nitzschia species from marine plankton

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The paraphyletic genus *Nitzschia* Hassall comprises morphologically distinctive pennate diatoms. The principal diagnostic characters for delimitation of *Nitzschia* species include valve shape, the position of the raphe, and specific morphometrics such as size, stria density and fibula density. These often show considerable overlap between taxa, making species identification very difficult when based solely on morphology. Additionally, this genus is currently probably the largest in the diatoms (approx. 1000 species described) and occurs in fresh, brackish and marine habitats. Improving the taxonomy of *Nitzschia* species is therefore a major challenge, especially because their diversity is considerably better known in freshwaters compared to marine environments. *Nitzschia* species have been thought to be scarce in marine phytoplankton and are rarely reported; they usually adhere to surfaces and do not have morphological adaptations to planktonic existence, unlike the related genera *Pseudo-nitzschia* H. Perag. and *Fragilariopsis* Hust. However, as a result of ongoing global expeditions such as *Tara* Oceans or the Global Ocean Survey, more and more information about planktonic *Nitzschia* species is becoming available.

During a BIOTA (Bio-tracing Adriatic Water Masses) cruise conducted in March 2016 in the open waters of the South Adriatic Pit we isolated several (11) small pennate strains into cultures from net samples and fractioned seawater samples taken from range of different depths (30m, 100m, 250m, 400m). Morphological analyses comprised LM, SEM and TEM observations, which, along with specific morphometrics, allowed us to distinguish 4 different *Nitzschia* morphotypes. These findings were congruent with molecular analyses performed on *rbcL*, SSU and *psbC* genes. Two distinct clades, represented by a total of 9 strains of Adriatic *Nitzschia* species, represent new lineages in the *rbcL* tree of *Bacillariaceae*, one being sister to *Psammodictyon* D. G. Mann and one corresponding to a novel clade that is very distinct from other *Nitzschia* species sequenced so far. The remaining 3 *Nitzschia* strains corresponded to *Nitzschia* cf. *incerta* (Grunow) Perag. and two more unknown species.

"Planktonic lifestyle lovers": a story of eight new marine *Entomoneis* species

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The diatom genus Entomoneis Ehrenb. has been known as a common floristic component of marine, brackish and, to a lesser degree, freshwater habitats, with a largely unknown phylogenetic and ecological history. The genus includes diatoms with a bilobate keel elevated above the valve surface, a sigmoid canal raphe, transition between keel and valve body – so called "junction line" and numerous girdle bands. Here, we will present the recent discovery of eight morphologically diagnosable species of Entomoneis found in the marine plankton, a habitat not usually associated with a high diversity of raphid diatoms. While Entomoneis cells often occur in near-shore plankton tows, where cells from the benthos can get trapped in the water column by wave or tidal action (tychoplankton, e.g. E. alata Ehrenb., E. pulchra (J. W. Bailey) Reimer), offshore planktonic Entomoneis are reported far less frequently, and are perhaps best known from polar habitats (E. gigantea (Grunow) Nizam., E. kjellmanii (Cleve) Poulin & Cardinal). Nevertheless, all known Entomoneis species were mainly described as epipelic, epiphytic or associated with sea-ice, while Entomoneis cells from deepwaters, temperate or tropical plankton until recently have been unexplored. To a degree, the poor understanding of species diversity in Entomoneis is a result of a lack of taxonomic and phylogenetic framework against which newly recorded specimens, especially from the plankton, can be compared. In 2017 we described E. tenera from the Adriatic Sea, as a first species of this genus preferring an exclusively planktonic lifestyle (Mejdandžić & al. 2017). Subsequent research revealed six additional planktonic Entomoneis species: E. pusilla Bosak & Mejdandžić, E. gracilis Mejdandžić & Bosak, E. vilicicii Bosak & Mejdandžić, E. infula Mejdandžić & Bosak, E. adriatica Mejdandžić & Bosak and E. umbratica Mejdandžić & Bosak (Mejdandžić & al. 2018). These species were characterized by unique morphological parameters such as valve shape and torsion of cells, valvocopulae shape and perforation, striae ultrastructure and density, transition between valve body and keel and specific raphe features (fibulae in raphe canal and central and terminal raphe endings). Along with morphological parameters, phylogenetic support for monophyletic and well supported species delineation based on a three-gene phylogeny contributed to new species descriptions. Additionally, we present the description of a planktonic Entomoneis from the Adriatic Sea, new to science, that is characterized by an extremely light silification of the frustules and multiple plastids within its cells. With this in mind, future research should be focused on searching the traits that are possibly shared between raphid diatom genera that prefer planktonic lifestyle as well as further in-depth investigation of Entomoneis species regarding this underappreciated species diversity combining classical morphological and phylogenetic analyses along with global metagenomics approach.

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Organellar genome inheritance in araphid diatom Pseudostaurosira trainorii

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To reveal the evolution of endosymbiotic organelles and their control their inheritance pattern has been widely studied in various organisms. Mitochondria and chloroplasts are endosymbiotic organelles that have their own genome which are inherited typically in a non-Mendelian fashion. However, there are only two reports studying inheritance of these organelles in diatoms. We studied the inheritance of chloroplast and mitochondria genome in araphid diatom *Pseudostaurosira trainorii* E. Morales. This species possesses opposite mating types (male/female) and their sexual reproduction is easily inducible in lab. Together with the crossing experiments, we determined the inheritance pattern of chloroplast and mitochondria genome in single cells isolated from F1 strains. We designed molecular markers from chloroplast and mitochondrial genomes of *P. trainorii* in both male and female strains in that short insertion/deletion to enable us to trace parental origin of each organelle by PCR.

In chloroplasts, many isolated cells showed paternal inheritance patterns and few others showed maternal or biparental patterns, while in mitochondria, F1 cells showed either maternal or paternal inheritance patterns. However, the time to complete such uniparental inheritance was different depending on cells. Some cells showed uniparental patterns even in small auxospore while the others retained both parental mitochondria even after first mitotic division. The number of mitochondria was decreased during elongation of auxospore. These results suggested that mitochondria were eliminated selectively during auxosporulation in some F1 cells. In *P. trainorii*, both organelles were not strictly inherited biparentally nor uniparentally in F1 cells.

Diatom diversification through the lense of large sequence, fossil, trait, and diversity databases: Examining the roles of life history strategies and environmental gradients

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The rate of diversification, and its variation across lineages, through time, or in different environments, is a core question in diatom evolutionary biology. The rich diatom fossil record has taught us and will teach us much about these patterns. However, the fossil record is incomplete and biased towards marine planktonic diatoms from the Cenozoic. Phylogenies offer an alternative that can consider the entire diversity and timespan of diatom evolution while maintaining a close integration with the fossil record. We constructed a time-calibrated diatom phylogeny of 1151 species, the most-inclusive to date, and used it to test several hypotheses regarding patterns of variation in species richness across life history strategies (mode of sexual reproduction, motility) and ecological gradients (plankton-benthos, marine-freshwater). Anisogamous diatoms diversified faster than oogamous diatoms, but this increase was restricted to the nested clade of raphid diatoms with active motility in the vegetative cells. Diversification rates did not differ between planktonic and benthic lineages, but freshwater clades diversified faster than their marine counterparts. In both cases there was substantial variation within each group, indicative of the influence of other unobserved factors. Moreover, both the plankton-benthos and marine-freshwater divides were typified by strong niche conservatism: bidirectional transitions were possible, but transitions took much longer to occur than in situ speciation or extinction events. Overall, our results support that the evolution of the raphe and colonization of freshwaters are independently associated with increased species turnover. However, as the rate of colonization of freshwater is higher in the raphid clade relative to non-raphid diatoms, the observed effect of active motility could in part be due to the underlying dynamics of traversals of the salinity gradient. Our results provide the first phylogenetic examination of diversification patterns in diatoms and set the stage for comparative and integrated analyses of the rich fossil record and phylogenetic data.

Using population genomics and experimental transcriptomics to understand local adaptation by the diatom *Skeletonema marinoi* across the Baltic Sea salinity gradient

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Changing precipitation patterns and melting polar ice caps are freshening large parts of the world's oceans, resulting in changes in water stratification, convection, and nutrient availability. These changes are expected to have profound effects on the size distribution, species composition, and ultimately the primary productivity of phytoplankton communities in ocean regions diluted by freshening. Little is known about how phytoplankton will respond, both at the species and community levels, to osmotic stress, and less is known about the underlying genetic basis of the salinity stress response in most phytoplankton groups. The diatom Skeletonema marinoi Sarno & Zingone – a salinity generalist species common and locally adapted across the Baltic Sea salinity cline-is an excellent candidate to address these questions both at a deeper evolutionary timescale, via population and comparative genomic approaches, and at a contemporary timescale, through common-garden experiments. We are re-sequencing genomes of about 40 individuals per population from a dozen sites spanning the salinity and geographic range across the Baltic Sea (NE Atlantic). Patterns of nucleotide polymorphism and linkage disequilibrium across the genome will show whether adaptation to low salinity in S. marinoi required a new mutation that swept to fixation (a hard selective sweep) or whether selection acted on a variant already present either in S. marinoi or an older ancestor. A time-calibrated phylogeny of Skeletonema Grev., together with a precise estimate of when marine migrants first colonized the low-salinity Baltic Sea, will show whether the adaptive mutations predate the exposure the new selective regime, further helping distinguish between hard and soft selective sweep models. To determine the extent to which adaptation may also be driven by regulatory changes, the population genomic analyses will be augmented with gene expression data designed to measure differentially expressed genes in response to altered salinity. Overall, our approach will identify key genetic markers and gene-expression patterns associated with adaptation to altered salinity, a key environmental barrier to the distribution of microbes.

Benthic diatom taxocenes off the Crimean coast (Black Sea): analysis of diversity and taxonomic structure

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An important task for Black Sea biodiversity conservation is the assessment of the structure of benthic diatom taxocene. They have a large role in the relationship between coastal ecosystems and the increasing pollution of the shelf zone. The material for the study was sampled off the Crimean coast within the range 0.5 to 50 m depth during 1984–2016. The database of the Black Sea Bacillariophyta was compiled using both literature and our own data (Nevrova & al. 2015), whose scope included 5 regions (Caucasian, Crimean, Bulgarian, Romanian coasts and North-Western shelf). The updated inventory of the Black Sea benthic diatoms holds 1094 species and intraspecific taxa (IT), pooled into 953 species, 149 genera, 61 families, 32 orders and 3 classes (Round & al. 1990; Fourtanier & Kociolek 2011; Witkowski & al. 2009). The highest species richness of diatoms ever registered in the Black Sea was recorded near Crimea – 80.6% of the total number (882 taxa, belonging to 132 genera, 56 families, 29 orders). The families Naviculaceae, Bacillariaceae, Catenulaceae and Cocconeidaceae were most represented. The most saturated poly-species branches in the diatom hierarchical tree were formed by the genera Navicula Bory, Nitzschia Hassall, Amphora Ehrenb. ex Kütz., Cocconeis Ehrenb., Diploneis Ehrenb. ex Cleve, Fallacia Stickle, Lyrella Karaeva, Cymbella C. Agardh, Achnanthes Bory, Planothidium Round & Bukht., Caloneis Cleve and Licmophora C. Agardh. In total, 15 areas along the Crimean coast were analyzed for estimating diversity features in diatom taxocenes. Taxonomic Distinctness Indices (TaxDI), where Δ^+ is the average Distinctness and Λ^+ is the variability of Δ^+ (Warwick & Clarke 2001) were calculated. The structure of diatom taxocenes from polluted water areas in Crimea was characterized by low species richness and a large share of mono- and oligo-species branches at the family and order levels. It indicated that the species that can not withstand the high level of technogenic pollutants accumulated in the bottom sediments. Taxocenes in water areas under moderate anthropogenic impact were characterized by relatively high species richness and an equal ratio of oligo- and poly-species branches that are closed at the genus level, with presence of monospecies branches, which are converged at family or order levels of hierarchy. Taxocenes in pristine water areas was characterized by the highest species richness and the presence of taxonomic branches of various species saturation, which are closed at different hierarchical levels, with a predominance of polyspecies taxa. Following the calculation algorithm for Δ^+ and Λ^+ indices, the appearance or elimination of a large number of new closely related species has a more significant effect on the tree architecture than the appearance or elimination of new species with a distant phylogenetic relationship. In other words, when the species richness of the taxocene based on polyspecies in phylogenetically similar branches is higher, the average value of the Δ + index is lower.

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Post-mining open pit reservoirs – 'blind' spots of environmental degradation or diatom hotspots for taxonomical and ecological studies?

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Introduction: Artificial reservoirs originating from excavated mineral ores are the ecosystems of welldefined and highly specific environmental conditions. These reservoirs have stable parameters of water; thus, they may serve as excellent object for investigation of new diatom species, verification or establishing improved ecological values of diatoms. The aim of the study was the analysis of diatom diversity and the identification of characteristic species in three post-mining, open, pit water ecosystems, i.e., brine (Pełczyska), iron ore (Łęczyca) and coal ore (Bogdałów). The evaluation and verification of the ecological values with proposal of some modifications, according to the classification of Van Dam & al (1994), were conducted. Material and Methods: A total of 44 diatoms samples have been collected from benthos of the reservoirs during two following seasons. The chemical and physical parameters of water, e.g.: potassium, ferric, ferrous, calcium, chloride and carbonate ions concentration, pH, conductivity and temperature, were analyzed. The morphological evaluation was performed using a LM and SEM. For particular species, the morphological features were compared with the type material of Pinnularia krookiformis Krammer, Melosira muzzanensis F. Meister, Cyclotella woltereckii Hust. and Cyclotella pseudostelligera Hust. obtained from Friedrich-Hustedt-Zentrum für Diatomeenforschung, Institute for Polar and Marine Research, Bremerhaven, Germany. Mathematical methods were used to compare the diatom assemblages and to analyze both; the diatom diversity and the similarity between diatom taxa distribution. The Bray-Curtis similarity index was used to determine the similarity between samples from different sampling sites. To analyze the spatial relationships between diatom taxa in particular habitats the multidimensional scaling procedure (MDS), based on the Bray-Curtis similarity, was used.

Results: Diatom species from the Pełczyska athalassic ecosystem were characteristic for the brackish or marine conditions. The benthic diatoms collected in this habitat represented high morphological variability within *Chamaepinnularia krookiformis* (Krammer) Lange-Bert. & Krammer, that allowed us to establish the new species *Chamaepinnularia plinskii* Zelazna-Wieczorek & Olszynski. Moreover, the classification of halabion system of Van Dam & al (1994) for *Fragilaria famelica* (Kütz.) Lange-Bert. and *Halamphora sydowii* (Cholnoky) Levkov, was established or updated the ecological preference for salinity level. In the case of Łęczyca ecosystem, which is a complex of three shallow, iron ore, post-mining reservoirs, high morphological diversity of centric diatoms, was observed. The observation and comparison with the type material of *Melosira muzzanensis* allowed the suggestion of establishing a new *Aulacoseira* Thwaites species. The results obtained from the third ecosystem located in Bogdałów, which is post coal, ore mine reservoir, revealed the high species diversity of *Caloneis* Cleve.

Conclusions: The water reservoirs created by flooding the excavated mineral ores mines seem to be very interesting study sites from the ecological and taxonomical point of view. They can be local hotspots for new diatom species as well as the elucidation of the environmental conditions impact in the morphological differentiation of diatoms.

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Diatom biosilica – a promising alternative to synthetic silica materials in different applications

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Diatoms are small wonders of the oceans, playing a key role in the primary production, the supply of oxygen and the fixation of carbon dioxide. The special hallmark of diatoms is their cell wall of amorphous biosilica, showing a species specific patterning. Besides the importance of living diatoms as monitoring organisms and source of different nutrients (lipids, proteins, metabolites), the process of biomineralization is a main issue of biological and material research. Moreover, the biosilica itself is a promising material due to its outstanding properties like long-range ordered structure, high specific surface area, high internal pore volume, biocompatibility, high stability, and tailorable surface chemistry. We investigated the performance of biosilica in different applications like adsorption and catalysis (Jeffryes & al. 2015).

To use diatom biosilica in different applications, the first step is the generation of the material. The cultivation is performed in large scales up to 1000L. After cultivation, the diatoms are harvested and the cells are cleaned by different purification steps (SDS/EDTA, calcination). The cleaned biosilica is used as support material in different catalytic reactions. The advantageous surface chemistry leads to a strong binding of the active sites and high catalytic activities. Moreover, it could be shown that different silica structures from three diatom species have an influence of the catalyst efficiency (Fischer & al. 2016).

Diatom biosilica and replica materials can be used in the adsorption of heavy metals. I want to present the usage of pure biosilica in the adsorption of radionuclides from aqueous solution. Macroscopic batch sorption experiments and spectroscopic methods were used to reveal the sorption process. In another approach the diatom biosilica was converted into a highly porous carbon material using a nanocasting procedure. The characteristic species-specific macroporous diatom structure is retained during the process and the resulting materials exhibit a hierarchical porosity. The material achieves very high mercury adsorption capacities in combination with a rapid uptake and a good recyclability (Fischer & al 2017).

Biosilica has outstanding properties and due to its "green synthesis" it a promising alternative to synthetic silica materials.

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A training set for diatom-phosphorous quantitative reconstructions for montane to alpine lakes of the northern Alps

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The background for the presented study is a major project at the Limnological Research Station Iffeldorf, which investigates the impacts of climate change on mountain lakes in the northern Alps. Prognosis models predict rising temperatures and stronger rainfall due to global warming (Gobiet & al. 2014). We hypothesize that this fact leads to further rise of the tree line and to an intensifying of weathering and will result in an increase of the load of organic matter into the lakes. To test this we developed a training set for establishing a diatom – phosphorous transfer function, which will be presented here.

There has been increasing debate concerning the reliability and applicability of quantitative methods in paleolimnology. It has been shown that the fundamental assumptions for the application of transfer functions are rarely met (Juggins & al. 2013). Yet there exists a row of successful examples of quantitative reconstructions, especially concerning lake pH value and phosphorous content (Bennion & al. 1995, Lotter 1998). These issues will be discussed by means of the presented training set. Our lake data set comprises 45 lakes situated between 700 and 2500 m. asl. These lakes can be grouped (1) into shallow and deep lakes and (2) into waters with and without macrophyte cover. The lakes represent a phosphorous gradient from oligotrophic to mesotrophic conditions. All studied lakes are situated -at least partly- on calcareous bedrock. Therefore, they are well buffered and show stable pH values between 8 and 9.5. Additionally to diatom and hydrochemical analysis, summer water temperatures were measured and lake morphometry was surveyed. The study was funded by the German Federal Environmental Foundation.

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Diatom community composition across ecological gradients in the Eastern Cape, South Africa

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Diatoms are excellent indicators of specific impacts on water quality but are currently underutilised in South Africa. One of the reasons for this is the considerable information gap in the National Diatom Collection on diatoms of the Eastern and Western Cape Provinces. This project aimed to document the diatom species diversity of riverine habitats in the Eastern Cape Province, South Africa, and to assess diatom community composition across ecological gradients. A total of 29 sites were sampled across four seasons during 2014 and 2015. In total 36 873 individuals were identified from 84 samples and 24 rivers. A total of 215 species were identified. Community composition showed significant difference between ecoregions. The main species responsible for the identity of the different ecoregions were the following: South Eastern Coastal Belt - Eunotia minor (Kütz.) Grunow, Achnanthes oblongella Østrup, Eunotia incisa W. Greg., Frustulia saxonica Rabenh. and Eunotia flexuosa (Bréb. ex Kütz.) Kütz.; Southern Folded Mountains - Fragilaria biceps Ehrenb., Eunotia minor, Nitzschia closterium (Ehrenb.) W. Sm., Achnanthes oblongella, Gomphonema parvulum Kütz. and Planothidium frequentissimum (Lange-Bert.) Lange-Bert.; and in the Drought Corridor - Cocconeis placentula Ehrenb., Cocconeis placentula var. lineata (Ehrenb.) Van Heurck, Gomphonema parvulum, Rhopalodia gibba (Ehrenb.) O. Müll., Achnanthes oblongella, Achnanthidium minutissimum (Kütz.) Czarn. and Staurosira elliptica (Schum.) D. M. Williams & Round. Spatial patterns indicated a strong relationship between diatom community composition and pH, salinity and conductivity. With Africa expected to experience a significant increase in urbanisation, population growth and direct impacts of a globally changing climate, the use of detailed ecological information, which includes diatoms, to inform sustainable development and management of freshwater resources will become increasingly important.

Diatoms of Maloye Shchuchye Lake (Polar Ural, Russia)

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The Polar Ural is one of the most poorly studied regions of Russian Arctic. In the present time, it is characterized by glacial landforms such as cirques, U-shaped valleys, and proglacial lakes. The largest lakes in the northern part of the region are Bolshoye and Maloye Shchuchye Lakes. A 24 m long core from the Lake Maloye Shchuchye was taken in July 2009 from the depth of 31 m. The core is a subject of a multiproxy study, biological part of which includes pollen, diatoms, chironomids and ancient DNA analyses. The aim of the project is to make a reconstruction of palaeoclimate and palaeoecological conditions in Polar Ural using biological proxies from sediments of the Maloye Shchuchye Lake.

In the upper 4 m of the core that corresponds to Holocene, we found 75 diatom species from 43 genera. Benthic and planktonic-benthic diatom species prevailed (58.7% and 21% from total number of species respectively), the share of planktonic species was only 12%. However, planktonic species predominate at all horizons of the investigated Holocene part of the core. Pantocsekiella schumannii (Grunow) K. T. Kiss & Ács, P. tripartita (Håk.) K. T. Kiss & Ács, P. ocellata (Pant.) K. T. Kiss & Ács, P. rossii (Håk.) K. T. Kiss & Ács, Aulacoseira ambiqua (Grunow) Simonsen, Pliocaenicus costatus (Loginova & al.) Flower & al. dominated at different periods. Freshwater species prevailed, of which 65.3% were indifferent to salinity, 12% were halophilic and 8% halophobic. We found several mezohalobic species: Eucocconeis flexella (Kütz.) F. Meister, Navicula digitoradiata (W. Greg.) Ralfs and Stauroneis producta Grunow. With respect to pH, the alkaliphilic species were the most abundant (38.7%). We found a small number of acidophilic species (9.3%): Achnanthes didyma Hust., Eunotia bilunaris (Ehrenb.) Schaarschm. and E. praerupta Ehrenb., Fragilaria exigua Grunow, Cavinula variostriata (Krasske) D. G. Mann, Tabellaria flocculosa (Roth) Kütz., Tetracyclus emarginatus (Ehrenb.) W. Sm. Two typical reophilic species Didymosphenia geminata (Lyngb.) M. Schmidt and Hannaea arcus (Ehrenb.) R. M. Patrick were probably brought with the inflowing stream. With respect to temperature, one thermophilic species Planothidium lanceolatum (Brébisson ex Kütz.) Lange-Bert., and two species that prefer cold condition Eunotia praerupta, Tetracyclus emarginatus were found. The diatom flora was dominated by cosmopolitan species (61.3%) and includes arctic-alpine species: Eucocconeis flexella, Karayevia laterostrata (Hust.) Bukht., and Didymosphenia geminata, Hannaea arcus, Cavinula scutiformis (Grunow ex A. W. F. Schmidt) D. G. Mann & Stickle, Neidium hitchcockii (Ehrenb.) Cleve, Pinnularia nodosa (Ehrenb.) W. Sm, Tetracyclus emarginatus.

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A review on the studies of Korean marine benthic diatoms

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A comprehensive review of the Korean studies of marine benthic diatoms has been made. Of particular interests were the recent findings on the ecology and taxonomy of benthic diatoms from Korean tidal flats. Historical topics in the studies of Korean marine benthic diatoms appeared to be the assemblages, dynamics, production, and food web etc. Brief summaries of several studies related to the very topics were also presented when appropriate. While clear progresses in the understanding the true biodiversity of Korean marine benthic diatoms has been made during the last decade, there have also been clear scientific gaps between Korean and international countries in both terms of taxonomy and ecology of diatoms. It is expected that future studies would enhance the proper understanding of ecology and biodiversity of Korean marine benthic diatoms.

Phylogenomics reveals an extensive history of genome duplication in diatoms

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Diatoms are one of the most species-rich lineages of microbial eukaryotes. Similarities in clade age, species richness, and primary productivity motivate comparisons to angiosperms, whose genomes have been inordinately shaped by whole-genome duplication (WGD). WGDs have been linked to speciation, increased rates of lineage diversification, and identified as a principal driver of angiosperm evolution. We synthesized a large but scattered body of evidence that suggests polyploidy may be common in diatoms as well. We used gene counts, gene trees, and distributions of synonymous divergence to carry out a phylogenomic analysis of WGD across a diverse set of 37 diatom species. Several methods identified WGDs of varying age across diatoms. Determining the occurrence, exact number, and placement of events was greatly impacted by uncertainty in gene trees. WGDs inferred from synonymous divergence of paralogs varied depending on how redundancy in transcriptomes was assessed, gene families were assembled, and synonymous distances (Ks) were calculated. Our results highlighted a need for systematic evaluation of key methodological aspects of Ks-based approaches to WGD inference. Gene tree reconciliations supported allopolyploidy as the predominant mode of polyploid formation, with strong evidence for ancient allopolyploid events in the thalassiosiroid and pennate diatom clades. Our results suggest that WGD has played a major role in the evolution of diatom genomes. We outline challenges in reconstructing paleopolyploid events in diatoms that, together with these results, offer a framework for understanding the impact of genome duplication in a group that likely harbors substantial genomic diversity.

Are the Vistula River waters reaching the Hel Peninsula slope? Diatom data from the Gulf of Gdańsk (Southern Baltic Sea, Poland)

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The Baltic Sea is a semi-enclosed basin considered to be one of the most contaminated seas. The phosphorus and nitrogen loads have increased several times since the turn of the 19th and 20th centuries. The most important sources of biogenic salts in the Baltic Sea are river inflows. In the region of the Gulf of Gdańsk the main supplier is the Vistula River. Primarily anthropogenic activity caused by so-called cultural eutrophication such as urbanization, agriculture, soil erosion, domestic animal livestock and industrial sewage disposals leading to the degradation of water quality. Excessive use of fertilizers causes nutrient enrichment, which leads to an increase of primary production and, in consequence, reduced light transparency, oxygen depletion, changes in biochemical cycles and biological structures including the loss of biodiversity. These environmental changes are well registered in diatoms preserved in bottom sediments.

The aim of the study was to determine the impact of environmental conditions on Vistula River waters. The studied material consisted of six short (20-30 cm) sediment cores collected from the Vistula mouth and the Hel Peninsula slope. Diatom species were divided into groups according to ecological groups.

In the studied material, diatom flora was abundant and taxonomically diverse. In some intervals diatoms were not well preserved. The greatest species diversity was observed in benthic groups; however, its percentage was lower than plankton. In the region of the Vistula mouth, diatom taphocoenoses were dominated by planktic forms represented by oligohalobous indifferent Stephanodiscus parvus Stoermer & Håk., S. hantzschii Grunow and oligohalobous halophilous *Cyclotella atomus* Hust. and *C. meneghiniana* Kütz.. In addition, polysaprobous and α -mesosaprobous taxa dominated , however their abundance decreased in the second study area. In a region of the Hel Peninsula slope, marine and brackish forms were the most common. The most important components were marine species Opephora krumbeinii Witkowski & al., Pauliella taeniata (Grunow) Round & Basson, Skeletonema marinoi Sarno & Zingone, Thalassiosira levanderi Goor. Mesohalobous forms were represented by Chaetoceros Ehrenb. spp. (resting spores), C. wighamii Brightw., Cyclotella choctawhatcheeana A. K. S. Prasad, Opephora guenter-grassii (Witkowski & Lange-Bert.) Sabbe & Vyverman. In both areas, the diatom flora was dominated by eutraphentic taxa. The results of the diatom study indicate that the structure of diatoms assemblages is undoubtedly related to the distance from the Vistula mouth and different hydrodynamic conditions. Riverine taxa i.e. Stephanodiscus hantzschii, S. parvus and Aulacoseira ambigua (Grunow) Simonsen, being abundant in the vicinity of the Vistula mouth (23%, 11% and 6%, respectively) were present also in the Hel Peninsula, however with lowest frequency (0.5-4%). The frequency of halophilous species Cyclotella atomus and C. meneghiniana decreased from 28% and 25% to 1% and 9%, respectively.

Pauliella taeniata as a bioindicator of the recent environmental changes in the Gulf of Gdańsk (Poland)

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The studied material consisted of 10 sediments cores collected from different parts of the Gulf of Gdańsk in April 2014. Four of them (W9, ZP1, UP10, GG) were taken during a research cruise on board ORP Heweliusz. Six other cores (P110, BMPK10, P104, P116, M1, P1) were collected during a research cruise on board the R/V Oceania within the framework of the international project CLISED – Climate Change Impact on Ecosystem Heath – Marine Sediments Indicators. The project was funded by the Norwegian Grants in Polish - Norwegian Research Program. Cores were drilled by a Niemistö core sampler.

Cores BMPK10, ZP1, P104 were taken in the outer part of the Puck Bay, from depths of 31, 50 and 55 m, respectively. The four cores W9, P110, UP10, P116 were successively drilled from the open part of the Gulf from depths of 49, 72, 79 and 89 m. The remaining cores (M1, GG and P1), located in the Gdańsk Deep area, were taken from depths of 92, 102 and 112 m.

The diatom samples were prepared according to standard methods after Battarbee (1986). The counting method of Schrader & Gersonde (1978) was used. All identified diatoms were classified with respect to their ecological requirements (habitat, salinity tolerance, trophy and saprobity). Then the percentage of distinguished ecological groups was calculated.

In the material studied, diatom flora was abundant and taxonomically diverse. A total of 296 species, subspecies, forms and varieties belonging to 69 genera were identified. One of the most important components was the planktic species *Pauliella taeniata* (Grunow) Round & Basson, known as a taxa typical of arctoboreal zone. This is a cold water marine species noted from waters with salinity 18–35 PSU and temperature -2 to 5°C. As an oligotraphentic and oligosaprobic species, it prefers lower content of nutrients (nitrate 0.5–13.2 µmol/l and phosphate 0.06–1.3 µmol/l) and less polluted waters.

Regardless of the location, *Pauliella taeniata* were observed the most often in the uppermost part of all cores. These species were noted frequently in the Gdańsk Deep (ca 60%). In the open part of the Gulf of Gdańsk (W9) and in outer part of Puck Bay (BMPK10) it achieves ca 40% frequency. The lowest frequency was observed in the cores P1 and P104, where the percentage of this species did not exceed 12%.

Such a high frequency of *Pauliella taeniata* in the superficial sediments may be related to the trophic conditions in the Gulf of Gdańsk. Undoubtedly, the changes in the trophic status in the Gulf of Gdańsk were caused by the use of fertilizers in agriculture and progressing urbanization in the area. In the 1980s increased amounts of biogenic substances were supplied by riverine waters, mainly the Vistula River, which contributed to the progressive eutrophication in the study area. Differences in the trophy status may result from the reduction in the use of fertilizers in the 1990s. As a result, we observed a gradual improvement of the water conditions in the Gulf of Gdańsk. These changes have been very well preserved in the recent diatom flora.

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Linking the Messinian diatomaceous deposition in the Mediterranean and the latest Miocene biogenic bloom event

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During the latest Miocene, the Mediterranean experienced a dramatic oceanographic reconfiguration leading to the so-called Messinian Salinity Crisis at about 5.97 Ma. This event was preceded by an extensive diatomaceous sedimentation that reached its acme at around 7-6 Ma and was classically interpreted as a prelude to the subsequent onset of evaporitic conditions. However, the latest Miocene was globally characterized by a remarkable increase of the biosiliceous production. This suggests that the Messinian diatomaceous event in the Mediterranean may have been triggered by a combination of regional and global processes, even if these latter have been widely neglected.

Diatoms are critically dependent from the availability of dissolved silica for the synthesis of their opaline skeletons, and terrestrial biomes play a fundamental role in the control of the silica supply to oceans. In particular, grass-dominated ecosystems represent an exceptional reservoir of easily dissolvable amorphous silica, stored in the form of phytoliths and mobilized by rapid foliar turnover, grazing and wildfires.

We highlight how the late Neogene continental record strongly supports an intriguing scenario involving both the abiotic and biotic components of the Earth system and overall favorable to the silica eutrophication of the oceans, including the Mediterranean.

Revision and cladistic analysis of the genus Anorthoneis

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The genus *Anorthoneis* Grunow is a small benthic marine diatom genus belonging to the family *Cocconeidaceae* Kütz., order *Achnanthales* P. C. Silva. Araphid valves are more silicified and carry more complex ornamentations than the corresponding raphid valves. Rapheless valves show a convex profile and a monolayered or bilayered ultrastructure, whereas the raphe valves are mainly concave and always monolayered. Finally, on both valves there are functionally elaborated girdle bands, which can be particularly complex on the raphe valve. The genus *Anorthoneis* differs from *Cocconeis* Ehrenb. for having the raphe and median line eccentric on both valves. Here we present an ultrastructure-based complete revision of the diatom genus *Anorthoneis* using both light (LM) and electron microscopes (SEM). The original slides and type materials of all species belonging to the genus *Anorthoneis* have been analysed. New morphological features for the genus *Anorthoneis* on diatom frustules were revealed providing detailed observations and SEM images (i.e., rota-like vela and ligulate structures). Moreover, the phylogenetic relationships based on morphological characters among all taxa were performed via parsimony method.

The character states that describe variations of the internal and external central area tend to be homologous and to support an important first big clade which includes *A. dulcis* M. K. Hein, *A. tenuis* Hust., *A. vortex* Sterrenburg, *A. excentrica* (Donkin) Grunow, *A. hummii* Hust., *A. hyalina* Hust., *A. arthus-bertrandi* De Stefano & Pennesi, *A. eurystoma* Cleve and *A. minima* Foged. Such taxa share similarities in external and internal ultrastructure of the central areas in both raphe-sternum and sternum valves such as (i) externally and internally transversely dilated central area on both sides of the raphe-sternum valve, (ii) externally transversely dilated central area on both sides of the sternum valve, (iii) sternum valve striae parallel at the center and radiate at the apices, and (iv) areolae with hymenes in both valves.

Pinnularia Ehrenb. species from the Amazonian region (Santarém, Pará State, Brazil)

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Pinnularia is a freshwater genus and frequently associated with oligotrophic conditions with low electrolyte content and acid waters. In the last 20 years, the Pinnularia flora of the Brazilian Amazonian region has been studied by Metzeltin & Lange-Bertalot (1998, 2007) and Pereira & al. (2012, 2013, 2014, 2015, 2017). Studies in clear water environments cite 39 species described for floodplain lakes, as well as the Arapiuns and Tapajós rivers. The Verde Lake (54°56'06.9"W 02°28'43,8"S and 54°56'52.6"W 02°29'26,7") is situated in an Environmental Protection Area – EPA-Alter do Chão – about 35 km southwest from Santarém city, on the right bank of the Tapajós River. According to the classification Amazonian aquatic system, the lake is a typical clear-waters ecosystem. The study was based on a monthly sampling (beginning in July 2016 and ending in June 2017) taken on four stations in the limnetic zone of the lake collected with net (25 μ m mesh). The samples were fixed with Transeau solution. Aliquots of sample were concentrated and cleaned according to the Stoch's method. The results revealed the presence of 50 specific and infraspecific taxa. In total, 34 taxa are the first records being 24 for the Pará state and ten for the Brazilian Amazonian. As for the distribution, the highest percentage was of frequent organisms (37%), followed by sporadic (30%), rare (20%) and constants organisms (13%). Pinnularia divergens var. media Krammer, P. tumescens Metzeltin & Krammer and P. monicae Metzeltin & Lange-Bert. were the most constants taxa. The high richness of Pinnularia in the Verde Lake show that this region can be considered a diatom biodiversity hotspot.

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The marine diatoms of Kenting National Park and Taichung Port, Taiwan R.O.C.

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As a contribution to Taiwan's biodiversity (Chen & al. 2009, 2010, Pan & al. 2016, Su &al 2004, Wang & al. 2015, Wu 1999, Wu & Kow 2002, Wu & Wang 2002, 2005, 2009), diatoms were collected from marine waters at Kenting National Park, Taiwan, and at the Port of Taichung City, Taiwan andseparated into single-cell diatom cultures allowing for the identification of approximately 30 taxa of diatoms. Frustule morphology and 18S rDNA analysis were used to identify and classify diatoms species belonging to different genera, including Thalassiosira Cleve (3 species), Skeletonema Grev. (1 species), Cyclotella (Kütz.) Bréb. (1 species), Odontella C. Agardh (1 species), Rhizosolenia Brightw. (1 species), Chaetoceros Ehrenb. (2 species), Hyalosynedra D. M. Williams & Round (2 species), Psammoneis Shin. Sato & al. (2 species), Diploneis Ehrenb. (1 species), Cyclophora Castrac. (1 species), Amphora Ehrenb. ex Kütz. (5 species), Psammodictyon D. G. Mann (1 species), and Nitzschia Hassall (6 species). The determination of these diatoms at the species level was accomplished using a combination of key morphological features of evolutionary significance and molecular work using their extracted portion of the 18srDNA sequence. Following work by Medlin & Kaczmarska, the systematics of these diatoms is confirmed based on three classes of diatoms: Clade 1 Coscinodiscophyceae (radial centrics) or Clade 2 Mediophyceae (polar centrics and radial Thalassiosirales) and Bacillariophyceae (pennates). We conclude that further work is needed in applying both primary characteristics (morphology and molecular barcodes) as well as secondary characteristics (the structure of the auxospore, the Golgi body, plastids and pattern of diatom cell genesis) to correctly place and identify diatoms in general, as suggested by the work of Medlin (2016).

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Inferring salinity changes of the Río de la Plata estuary during the last 1000 years, through the study of modern and fossil diatoms

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The Río de la Plata estuary (RdIP), the second largest from South America, is a highly dynamic and productive system, which presents environmental variations related to natural and anthropogenic forcing. The objective of this work was to determine salinity-indicative modern diatom groups from the RdIP, and to infer the salinity variations of the system during the last 1000 years using such groups as modern analogues. To achieve that, the composition of diatoms from surface sediments through a salinity and a trophic gradient in the RdIP was studied, and the ecology of such species to the fossil record from sediment cores retrieved from the RdIP mud depocenter was extrapolated. Two groups of salinity-indicative modern diatoms were determined. The internal section of RdIP was dominated by *Aulacoseira* Thwaites spp., *Eunotia* Ehrenb. spp., and *Staurosirella martyi* (Hérib.) E. Morales & Manoylov. Such species are indicative of low salinity levels and high trophic conditions, associated with the riverine and estuarine regimes. The external section was dominated by *Coscinodiscus radiatus* Ehrenb., *Coscinodiscopsis commutata* (Grunow) Sar & Sunesen, *Thalassiosira* Cleve spp., *Paralia sulcata* (Ehrenb.) Cleve, *Cyclotella striata* (Kütz.) Grunow, among other marine taxa. Such species are indicative of high salinity and low trophic conditions, associated with the influence of the Southwestern Atlantic Ocean (SWAO).

Through the study of the diatom record from sediment cores of the RdIP three different regimes of salinity over the last 1000 years were inferred. Regime 1 (1000-500 cal yr BP), was dominated by the marine salinity-indicative group, suggesting a stronger influence of the South Weastern Atlantic Ocean. Regime 2 (500-80 cal yr BP), contained mostly freshwater salinity-indicative taxa, implying an influence of freshwater discharge from RdIP. Regime 3 (last 100 yr) indicates more estuarine conditions, as revealed by higher abundance of marine and marine-brackish species.

The variations in the sedimentary record can be attributed to the Medieval Climatic Anomaly (MCA) and the Little Ice Age (LIA), both of which had a significant impact on rainfall and wind patterns over the region. During the MCA a weakening of the South American summer monsoon system (SAMS) and the South Atlantic Convergence Zone (SACZ), could explain a marine-dominated diatom record. In contrast, during the LIA, a strengthening of SAMS and SACZ may have led to an expansion of the RdIP river plume to the far north, as indicated by a marked freshwater diatom signal.

How diatoms win: Life strategies of diatoms in the Northern Adriatic

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The northern Adriatic Sea is a highly structured and shallow ecosystem. It is characterized by steep, spatiotemporal ecological gradients. These characteristics allow us sampling strategies with reasonably good spatiotemporal coverage both, across longitude and latitude as well as throughout the water column. The northern Adriatic hence is particularly suited for ecological observations of phytoplankton, here we can observe its behavior and succession as it travels through a multitude of ecological conditions while climate stays a constant. Growth of phytoplankton in the area is generally controlled by light, temperature and Phosphorous limitation, while nutrient availability is governed by the river Po, the largest freshwater input into the Mediterranean. The phytoplankton of the northern Adriatic is largely dominated by diatoms. To understand the in situ performance of marine planktonic diatoms, we here present the analysis of long term monitoring data on transects across the most pronounced ecological gradients. Our results demonstrate that the phytoplankton succession and growth is mainly governed by light availability, temperature and the species capability to cope with phosphorous limitation. In situ measurements demonstrated that the expression of alkaline phosphatase activity as a tool to access the organic phosphate pool is a key reaction of the phytoplankton community to phosphorous limitation. We then analyzed key species from the northern Adriatic phytoplankton in vitro with respect to their reaction to nutrient availability and phosphorous limitation. We characterized growth curves and morphological alterations. Additionally, we characterized nutrient uptake rates, lipids profiles, chlorophyll content and the expression of alkaline phosphatase activity as a reaction to phosphorous limitation. To further compare the expressed alkaline phosphatase activity, we characterized the dynamics of its expression across growth phases as well as the kinetic parameters of the enzyme activity. Combining all our results we formulated strategies for each examined species that explain how the respective species competes within the phytoplankton community for resources. Our results support the notion that success in competition for the limiting nutrient salt (phosphorous) as well as relative performance with respect to temperature and light availability explains the succession and composition of marine phytoplankton. Our results also demonstrate a high diversity of ecological niches in marine phytoplankton ultimately explaining the resulting biodiversity. Phylogenetic analyses of our results uncovered a surprisingly low phylogenetic restraint of the analyzed physiological adaptations and further helps understanding the biodiversity paradox of planktonic ecosystems.

A new species of the genus *Eunotia* Ehrenb. for algal flora the Republic of Belarus

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We give here a brief description of the of new species of the algal flora of the Republic of Belarus (*E. fennica* (Hust.) Lange-Bertalot, *E. juettnerae* Lange-Bert. and *E. ursamaioris* Lange-Bert. & Nörpel-Schempp) which were collected within the territory of the national landscape reserve "Yelnya". "Yelnya" is the largest unique array of *Sphagnum* bog in Belarus. It is located in the north-west of the Vitebsk region.

The materials for this work are samples of algae collected from April to October 2016 and 2017 in the Yelnya Reserve from basins and streams. Together with the sampling, the hydrochemical characteristics of the water were measured. Thus the pH of the Kurganistoe and Bolshoe lakes was 3.38 and 3.81, respectively, the Yelnyanka River was 3.09. The index of the electrical conductivity of water bodies varies within 24.6 to 41.4 (μ S/cm). The technical treatment of samples and the production of permanent preparations were carried out according to a generally accepted procedure. The preparations were examined using the light microscope Axioskop 2 Plus. Representatives of the genus *Eunotia* Ehrenb. are exclusively freshwater organisms that live mainly in dystrophic and oligotrophic waters and some species live in eutrophic ecosystems. In Belarus this genus is represented by 54 species.

Eunotia fennica was found in samples of the sediment lake Kurganistoe. The length of the valves is 30-40 μ m, width 3.5-4.5 μ m, striae 18-20 in 10 μ m. *E. fennica* resemble with *E. denticulata* (Bréb. ex Kütz.) Rabenh. *E. denticulata* has broader valves (6-10 μ m) and more spaced striae (13-16 in 10 μ m). *Eunotia juettnerae* was found in samples of the sediment lake Bolshoe. The length of the valves is 51-95 μ m, width 2,8-3,5 μ m, striae 20-22 in 10 μ m. *E. juettnerae* resemble with *E. bilunaris* (Ehrenb.) Schaarschm. *E. bilunaris* has a broader valves (3.5-5.5 μ m) and more spaced striae (13-17 in 10 μ m). *Eunotia ursamaioris* was found in samples of the sediment river Yelnyanka. The length of the valves is 14-27 μ m, width 4,5-6 μ m, striae 14-16 in 10 μ m. The dominant species in the preparation, *E. ursamaioris*, resembles *E. septentrionalis* Østrup. *E. septentrionalis* differs by dorsal margins highly arched and distally deeply depressed towards the distinctly capitate ends that are abruptly deflected to the ventral side. Ecological index of the water bodies of the sphagnum bog satisfy the requirements of these species.

These findings confirm the need for further study of algal flora of the sphagnum bogs of Belarus.

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The Nagoya Protocol: implications for diatom research

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The past few decades, the implementation of molecular data in diatom focused research has become widespread. Nevertheless, in the 21^{ste} century research environment, the use of molecular data is becoming increasingly regulated and consequently any researcher accessing and using genetic material carries strict responsibilities. The most significant development in this field is the *Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization to the Convention on Biological Diversity, or in short the <i>Nagoya on 29 October 2010, is an international agreement on the biodiversity of our planet and is a supplement to the 1992 Convention on Biological Diversity.*

One of the tree objectives of the Convention on Biological Diversity is the protection of the genetic resources of all known and unknown organisms. Since molecular research is becoming increasingly important in all fields of the biosciences, in order to prevent biopiracy, it is essential that genetic resources as well as the countries or indigenous people to which they belong, receive a legal framework for protection of their genetic resources as well as the traditional knowledge associated with it. Therefore, the Nagoya Protocol aims to implement a fair and equitable sharing of benefits arising from the use of genetic resources for both commercial applications as well as fundamental research.

With this poster, we give an overview of the objectives and regulation of the Nagoya Protocol and how this will influence diatom research in the decades to come. Already today, research of almost any genetic resource is subject to the ABS regulation which implies that in order to do research, scientists are obliged to obtain the correct permits in order to collect, transport, share, do research and publish on genetic resources. Nevertheless, the ABS regulation is still unknown or unclear to the overall majority of the scientific community.

The evolutionary and biogeographical history of diatoms in Antarctica: a tale of fossils, eDNA and molecular phylogenies

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Despite increasing evidence for significant levels of endemism among various microbial groups, a comprehensive understanding of the evolution of regional microbiota and how they are shaped by tectonic and paleoclimate events remains virtually lacking. Here we combine evidence of fossil data, molecular phylogenies and next generation environmental amplicon sequencing to provide insights into the biogeographical and evolutionary history of Antarctic freshwater and terrestrial diatom biomes. We undertook detailed taxonomic inventories of fossil Antarctic diatom assemblages dating back to the Mid Miocene and dovetailed this dataset with a comprehensive assessment of the diversity and biogeography of the contemporary Antarctic flora. In addition, using cultures and eDNA, we complemented the fossil dataset with a detailed Antarctic and global inventory of the molecular diversity and phylogeny of the common cosmopolitan diatom complex Pinnularia borealis Ehrenb. as a case study for extant diatom lineages. Taken together, our data support the hypothesis of widespread but selective extinction among an ancient diatom flora, characterized by distinct Gondwana elements, in response to the Mid Miocene cooling (ca. 14 Ma) and the subsequent expansion of ice sheets, followed by the evolution of a species-poor yet highly adapted and largely endemic modern diatom flora. Climatic sorting of regional floras resulted in the current bioregionalisation patterns in the Antarctic diatom biome, which shares striking similarities with that of macroscopic organisms. In parallel, our molecular data suggest multiple colonizations of Antarctica by the P. borealis species complex during the past 20 Ma. Since the majority of the P. borealis lineages currently inhabiting Antarctica are presumed to be endemic for the region, isolation and genetic drift following colonization are hypothesised to drive in situ (allopatric) speciation. Altogether, our data suggest that historical processes, i.e. geology and climate, have been crucial in shaping the history of Antarctic microbial lineages, in similar ways as these processes affected macroorganisms.

Ecological and biogeographical drivers of diatom diversity in the Kolyma Lowland, Northeastern Siberia

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Diatoms have a considerable potential as indicators of environmental change in arctic freshwater ecosystems, but the knowledge of their diversity and distribution is still fragmentary. Although diatoms have been studied in many locations across the Arctic, the sampling efforts have been uneven and patchy. Moreover, most conclusions on arctic diatom biogeography so far have been based on records not documented by photographic evidence. The prevailing view is that majority of arctic diatoms have circumpolar or cosmopolitan distributions because of their high dispersal potential and the high connectivity of freshwater habitats in the Arctic zone. The aim of this study was to analyze composition and distributional patterns of diatoms in the Kolyma Lowland located in the northeastern part of Yakutia (Eastern Siberia, 69 N). A rich diatom flora of 520 morphospecies was found in a survey of 79 thermocarst lakes, ponds and rivers from both tundra and northern taiga zones. The most common and abundant species were those commonly reported from the Arctic: small fragilarioid taxa, Nitzschia perminuta (Grunow) Perag. species complex and Rossithidium Round & Bukht. species. Diatom assemblages in acidic polygonal bogs were typically species-poor and dominated by Eunotia Ehrenb. species, while the most diverse assemblages were found in circumneutral lakes located on the remnant Pleistocene yedoma plain. Composition of diatom assemblages was sensitive to changes in water mineralization and turbidity caused by the permafrost thaw. In addition to the circumpolar and widespread species characteristic for high-latitude and alpine regions of Eurasia and North America, the presence of diatoms with restricted longitudinal distribution ranges have been noted. Examples of species so far known only from Northern Asia include Pantocsekiella strelnikovae (Genkal & Yarushina) K. T. Kiss & al., Eunotia frigida Potapova & al., E. latitaenia H. Kobayasi & al., E. mongolica Kulikovskiy & al., E. pararepens Kulikovskiy & al., E. michaelis Metzeltin & al., a new species of Psammothidium Bukht. & Round, a new species of Genkalia Kulikovskiy & al., Krsticiella cf. subbaicalensis Kulikovskiy & al. and "Navicula" brehmii Hust. Sellaphora vekhovii (Lange-Bert. & Genkal) C. E. Wetzel & D. G. Mann, Psammothidium sacculum (J. R. Carter) Bukht., Eunotia elena Lange-Bert. are known only from the Northern Eurasia. Species with distribution limited to East Asia-North America, such as Navicula aurora Sovereign and Boreozonacola natchikae (J. B. Petersen) Lange-Bert. & al., as well as some species characteristic for mountain lakes across Eastern Siberia, such as Pliocaenicus Round & Håk. / Lindavia (F. Schütt) De Toni & Forti spp., were notably absent in the Kolyma Lowland. The history of land connections and glaciations is suggested as a potential driver of observed biogeographical patterns of arctic diatoms.

Regional diatom paleolimnology reveals widespread stressors

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Long-term records of environmental condition are critical for diagnosing region-wide anthropogenic impacts and establishing best management practices. Extending paleolimnology from single lakes to large regions should enable detection of widespread stressors such as climate change and atmospheric deposition. Using assemblage similarity analysis on diatom paleorecords from more than 100 Minnesota lakes, we characterized periods of spatially consistent assemblage changes over the last 150 years. While we expected localized stressors such as agriculture and urban development to drive assemblage reorganization in specific lakes, overarching stressors such as climate change should be discernable in the regional analysis. We hypothesized that this overarching shift would manifest as diatom assemblage reorganization from low-nutrient to higher-nutrient taxa and, more recently, species that indicate warmer atmospheric temperatures, warmer surface waters, and shifts in lake thermal structure. We specifically test whether diatom communities are stronger indicators of multiple regional stressors than other common paleolimnological proxies.

Macroevolutionary patterns in Cenozoic marine diatoms from deep-sea sediments, and their relationship with climate and marine geochemical cycles

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In the modern ocean, marine planktonic diatoms occupy a unique ecological role in the marine geochemical cycles, as the main carbon and silicon exporters to the deep sea. Many have hypothesized on their impact on a geological time scale on the Earth's climate. Thanks to fifty years of scientific deep-sea drilling with the DSDP, ODP and now IODP campaigns, a gigantic corpus of data on Cenozoic deep-sea pelagic sediments has been gathered, allowing us to test these hypotheses. Based primarily on 105,698 diatom occurrences data from the Neptune (NSB) database (Lazarus & al. 2014; Wiese & al. 2016), on a dataset of 10,832 DSDP-ODP-IODP smear slides description (Renaudie 2016), on a new database of biogenic silica geochemical measurements, and on original observations on Paleocene samples (Renaudie et al., subm.) from the Berlin-hosted Micropaleontological Reference Center (MRC) collection, we have conducted various studies during the last five years on the Cenozoic diversity and abundance patterns of marine diatoms in deep-sea sediments. We observed that the Cenozoic marine diatom history is marked by two main events of diversification and increased, worldwide abundance (at the Eocene-Oligocene transition and during the Middle Miocene), in concordance with noticeable shifts in the global weathering history (as recorded by strontium and osmium isotopes) and drops in the estimated atmospheric pCO₂, thus confirming a strong tie between diatom history and the carbon and silicon cycles. Additionally, diatom diversity during the whole Cenozoic seems primarily controlled by climatic variations (as recorded by benthic oxygen isotopes). Observations in the Paleocene also showed an unexpectedly high diversity and abundance, as well as a high survivorship of Cretaceous taxa well into the late Paleocene/early Eocene.

In a major new 4-year DAAD-funded project (set to start July 2018), we will further explore the Eocene-Oligocene diversity/abundance event using diatom and radiolarian assemblages, geochemical proxies, and ocean circulation-productivity models.

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Ecological status assessment in estuaries using diatom-based metrics: Could microphytobenthos become a new biological quality element?

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Diatoms are the basis of most of the phytobenthos assessment methods for rivers in the majority EU Member States since the Water Framework Directive (WFD) was implemented. In spite of dominating most microphytobenthic assemblages in intertidal estuarine and coastal areas, marine and brackish benthic diatoms have never been considered as viable indicators of ecological status in transitional waters. With the aim of evaluating if intertidal diatoms could potentially be used as indicators of environmental change and anthropogenic pressure in a large macrotidal estuary, three impacted sites in the Loire estuary were surveyed during spring and autumn 2016. Diatom analysis was coupled with the collection of a thorough set of physical-chemical parameters (e.g. sediment analyses, nutrients, heavy-metals, polyaromatic hydrocarbons), as well as of other biotic assemblages (e.g. meiofauna, macrofauna).

A total of 351 diatom taxa were found and belonged to 98 different genera. A species-by-species literature research allowed the description of the assemblages in terms of their ecology, namely, salinity and habitat preferences (e.g. freshwater, benthos, etc.), as well as growth-forms. Most samples were dominated by benthic, epipelic, species and there was a clear difference in diatom assemblage structure between both seasons. Multivariate analysis revealed that the linkage between the diatom and environmental datasets had a significant, if moderate correlation (i.e. $\rho = 0.41$, BIOENV routine), with the best subset of selected variables composed by temperature and salinity, which are closely related with seasonality. Moreover, when considering the seasons separately, the correlations between the biotic and abiotic datasets were not significant and differences in assemblage structure were mainly influenced by tidal height and topography (e.g. tidal creek vs mudflat) for each of the three sites. Therefore, possible anthropic pressures, such as nutrient concentration or heavy-metal and hydrocarbon content, seemed subsidiary to the natural ones. However, it should be noted that the pollutant concentrations recorded during this study were considerably lower that to the ones found in previous studies made in comparable habitats. This study highlighted the inherently difficulties of using intertidal diatoms as assessment tools in such dynamic environments, but it also provided important clues for future approaches and strategies that could allow, in the foreseeable future, the addition of benthic diatoms as valuable ecological indicators in estuarine and transitional waters.

DNA barcoding libraries for diatom biomonitoring using metabarcoding

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Water managers use diatom biomonitoring since several decades to assess rivers and lakes ecological quality. Current standardized methodologies are based on microscopic determinations, which is time consuming and prone to identification uncertainties. The use of DNA-barcoding is a way to avoid these flaws. Combining barcoding with next-generation sequencing enables collection of a large quantity of barcodes from natural samples. These barcodes are identified as certain diatom taxa by comparing the sequences to a reference barcoding library using algorithms.

During the 25th International Diatom Symposium, several authors will give presentations about this subject. Most of these presentations will highlight the importance of reference barcoding libraries because its content has an obvious impact on species detection and on the final ecological assessment of ecosystems.

During this talk, several key points about reference barcoding libraries and their use in metabarcoding studies are given. The first point will show the necessity of taxonomy curation of data coming from different sources and used to complement the reference barcoding libraries. The second point will show that, based on molecular data, the way we delimit species has an impact on the precision and stability of ecosystem assessment. The third point will be about library completeness: do the existing libraries are covering enough taxonomic diversity to have a correct ecosystem assessment, and how can we improve this coverage? Finally, a presentation of the standardization actions undertaken in Europe since 2012 and giving a framework to set up barcoding libraries will be done.

These different points will be illustrated through the open access reference library R-Syst::diatom (https://www6.inra.fr/r-syst_eng/).

New and poorly known diatoms from the Kalakuli lakes in the Pamir Mountains, Xinjiang, Western China

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In the context of an ongoing project investigating the Holocene changes in palaeoclimate and palaeoenvironment in the Pamir Mountains in Xinjiang Province, northwestern China, the diatom flora from two alpine lakes was investigated from a large set of samples including live material, sediment trap, surface-sediment and core samples. So far two species new- to-science have been formally described from these samples: *Cymbella pamirensis* Zhongyan Zhang & Rioual and *Diatoma kalakulensis* Y. Peng & al. *Cymbella pamirensis* is distinguished by its strongly dorsi-ventral triangular shape and a dorsal side semi-rhomboid (Zhang & al. 2017). *Diatoma kalakulensis* is most similar to *Diatoma tenuis* C. Agardh but can be distinguished from it by having longer valves, higher stria density, wider apical ends and the position of its rimoportula (Peng & al. 2017). In addition, we could emend the description of *Lindavia lacunarum* (Hust.) Nakov & al., a poorly known species originally described by F. Hustedt (1922) from Tajikistan and that is seldom reported (Houk & al. 2010). Among all the know species of *Lindavia* (F. Schütt) De Toni & Forti, *L. lacunarum* (Hust.) Nakov & al. is most similar to *Lindavia intermedia* (Manguin ex Kociolek & Reviers) Nakov & al. but differs by having central fultoportulae with two satellite pori.

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Paleolimnological changes over 25,000 years at Lake Nakuru (Kenya) using diatoms as a proxy

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Lake Nakuru in Kenya, located south of the equator along the East African Rift Valley, is one of the many modern, shallow saline lakes in the East African Rift System (EARS). During the African Humid Period (AHP) 15,000 to 5,000 years ago, many of these "amplifier lakes" were instead deep, freshwater lakes due to a change in earth's precession, causing increased moisture in the region. Beyond the existence of such lakes during the AHP, little is known about them, particularly regarding their internal stability/instability during the AHP, as well as the transitional speeds in and out of wet phases. Here we present the results from diatom identification for the past 25,000 years as part of a high-resolution multi-proxy study. Samples were retrieved from the upper eight meters of two duplicate, 17 meter drill cores taken by the Lake Naivasha Coring Project (LNCP) in 2004. The chronology of the cores is based on 11 AMS ¹⁴C ages measured on charcoal and two ⁴⁰Ar/³⁹Ar ages from separate tephra layers. Diatoms were used to reconstruct the water conditions of Lake Nakuru. Different taxa were used as indicators for changes in pH, alkalinity, water temperature, and water depth. In addition to its use for paleoclimate reconstruction, this study provides an in-depth look at Lake Nakuru's diatom taxa over the past 25,000 years. In addition, this study will contribute to knowledge regarding the impact of moisture changes during and along the transitions of dry-wet-dry cycles on the sensitive lake systems of the EARS. Lastly, the new record will resolve a regional data gap regarding the synchronicity of lake level changes and its associated impact on humans living in the region.

Shift in the species composition of the diatom community in the eutrophic Mauritanian coastal upwelling: Results from a multiyear sediment trap experiment (2003 – 2010)

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A multiannual, continuous sediment trap experiment was conducted at the mooring site CB_{eu} (Cape Blanc, ca. 20°N, ca. 18°W; trap depth = 1,256-1,296 m) in the high-productive Mauritanian coastal upwelling. Here we present fluxes and the species-specific composition of the diatom assemblage, and fluxes of biogenic silica (BSi, opal) and total organic carbon (TOC) for the time interval June 2003-Feb 2010. Flux ranges of studied parameters are (*i*) total diatoms = $1.2*10^8$ - $4.7*10^4$ valves m⁻² d⁻¹ (average = 5.9×10^6 valves $\pm 1.4 \times 10^7$); (*ii*) BSi = 296-0.5 mg m⁻² d⁻¹ (average = 41.1 ± 53.5 mg m⁻² d⁻¹), and (*iii*) TOC = 97-1 mg m⁻² d⁻¹ (average = 20.5 ± 17.8 mg m⁻² d⁻¹). Throughout the experiment, the overall good match of total diatom, BSi and TOC fluxes is reasonably consistent and reflects well the temporal occurrence of the main Mauritanian upwelling season. Spring and summer are the most favorable seasons for diatom production and sedimentation: out of the recorded 14 diatom maxima of different magnitude, six occurred in spring and four in summer.

The very diverse diatom community at site CB_{eu} is composed of four main assemblages: benthic, coastal upwelling, coastal planktonic and open-ocean diatoms, reflecting different productivity conditions and water masses. A striking feature of the temporal variability of the diatom populations is the persistent pattern of seasonal groups' contribution: benthic and coastal upwelling taxa dominated during the main upwelling season in spring, while open-ocean diatoms were more abundant in fall and winter, when the upper water column becomes stratified, upwelling relaxes and productivity lowers. The relative abundance of benthic diatoms strongly increased after 2006, yet their spring-summer contribution remained high until the end of the trap experiment. The occurrence of large populations of benthic diatoms at the hemipelagic CB_{eu} site is interpreted to indicate transport from shallow waters via nepheloid layers. We argue that a significant amount of valves, BSi and TOC produced in waters overlying the Banc d'Arguin and the Mauritanian shelf is effectively transported to the CB_{eu} trap in intermediate waters at the outer Mauritanian slope. The impact of the intermediate and bottom-near nepheloid layers-driven transport in the transfer of valves and bulk particulates and its potential contribution to the export of biogenic materials produced from the shelf and uppermost slope might play a significant role in hemipelagial fluxes off Mauritania.

Reassessment of centric diatoms from Austrian lakes: updating *Cyclotella* sensu lato and the *Urosolenia gracilis/longiseta* complex

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Centric diatoms are frequently dominant elements of phytoplankton in lakes of the Eastern Alps and peri-alpine areas of Austria. For the species complex of Urosolenia gracilis (H. L. Sm.) N. A. Andresen & al. and U. longiseta (O. Zacharias) Edlund & Stoermer we combined LM and SEM data from lakes in Austria and upper Italy with findings from a reservoir in central France to support future studies of ecological quality analysis for to the implementation of the EU Water Framework Directive. Within the last 10 years, we have collected samples from altogether 22 standing waters including large perialpine and alpine lakes in Upper Austria and Tyrol as well as mid-size natural and small artificial lakes situated from 400 to 1300 m altitude. The samples were peroxide or sulphuric acid treated (except for Urosolenia Round & R. M. Crawford where more gentle cleaning and CP-drying had to be applied) and sputtered with gold-paladium for classical SEM and in FE-SEM (Urosolenia). Although this is not an exhaustive list of centrics for Austria we can show morphological and ultrastructural data and ecological information for almost 30 taxa. To facilitate future work in practical ecological diatom/ phytoplankton monitoring, we will show the size spectra and characters for key taxa in analogy between LM and SEM as well as give practical comparison tables and a simple key for the identification to the major taxa. This will imply nomenclatorial changes based on recent progress achieved for species around Cyclotella sensu lato including e.g. the separation of species into the genera Lindavia (F. Schütt) De Toni & Forti (Nakov & al. 2015) and Pantocsekiella K. T. Kiss & Ács (Acs et al. 2016). The most common other genera are Aulacoseira Thwaites, Cyclostephanos Round, Discostella Houk & Klee, Stephanodiscus Ehrenb. and Urosolenia. For temperate Urosolenia- species of the thin-long growth type of the gracilis/ longiseta group we studied potential difference in the parallel descriptions of *U. gracilis* (described as *Rhizosolenia* by HL Smith 1882) and *U. longiseta* (≡ Rh. longiseta O. Zaracharias 1893). We studied these taxa from type slides from Canada and Germany and made morphological measurements which statistically significantly corresponded to recent populations from Austria and France. We will discuss the taxonomic position of both taxa in relation to each other and to other thin long Urosolenia species described within the last 10 years from tropical and subtropical areas (see e.g. Liu & al. 2015)

Ács E., Ari E., Deleba M., Dressler M., Genkal S. I., Jako E., Rimet F., Ector L. & Kiss K. T. 2016: *Pantocsekiella*, a new centric diatom genus based on morphological and genetic studies. – Fottea **16**: 56–78.

Nakov T., Guillory W.X., Julius M.L., Theriot E.C. & Alverson A.J. 2015: Towards a phylogenetic classification of species belonging to the diatom genus *Cyclotella* (*Bacillariophyceae*): Transfer of species formerly placed in *Puncticulata*, *Handmannia*, *Pliocaenicus* and *Cyclotella* to the genus *Lindavia*. – Phytotaxa **217**: 249–264.

Liu Y., Kociolek J.P. & Fan Y. 2015: *Urosolenia* and *Acanthoceras* species from Hainan Province, China. – Phytotaxa 244: 161–173.

Dissecting the role of salinity on growth rate, morphology and transcriptome response of putative osmolytes in *Cyclotella* spp.

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Salinity has been proposed as is a major impactor on diatom distribution, across the freshwater – marine boundary (Mann 1999). Even inland waters seem to have a salinity barrier in anthropogenically impacted inland hypersaline environments (Jickells 1998). Species of the genus *Cyclotella* Kütz. ex Bréb. seem to be a notable exception to the idea that salinity is a barrier to diatom dispersal (Alverson & al. 2007). This a large genus, with over 100 species, and has species which are marine, freshwater, and estuarine in distribution, with some apparently able to thrive in a full range of salinities from fresh to normal seawater, such as *C. nana* Hust. (Guillard & Hasle 1962). The whole genome of this diatom (as *Thalassiosira pseudonana* Hasle & Heimdal; see Ambrust & al. 2004) generated a wealth of insight into the latter group and even made it a subject of intense study (see Alverson & al. 2011, for systematic treatment).

Researchers have sought to determine the influence of salinity on growth rate, cell size and silicification (Roubeix & al. 2008, Schulz 1971) of *Cyclotella*. We will explore the ecophysiological and evolutionary aspects of salinity on growth rate and metabolites in species sampled across the phylogenetic tree of *Cyclotella*.

Previous studies reported great nitrogen demand in *Cyclotella meneghiniana* Kütz. due to higher osmolyte production of amino acids such as proline in response to hypersaline environments (Schobert 1974). Kettles & al. (2012) reported the change of dimethylsulphoniopropionate (DMSP), in *C. nana* cells acclimated to salinity change. DMSP is a tertiary solphunium compound, known for osmoregulatory functions, synthesized in many algae and a limited lineages of halophyte plants such as salt marsh grasses, *Spartina alterniflora* (Otte & al. 2004).

First, to evaluate the growth kinetics and morphological response of three candidate species of *Cyclotella*, multiple strains of each will be grown under two different salinity levels. Then, the biomass and dry weight of each strain under each condition will be broken down to the major constituents and we will search for the known osmolytes in algae. Once general patterns are identified, we will search for specific molecular mechanisms that may allow the adaptation of *Cyclotella* across a broad range of salinities.

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Diatoms as indicators of ecological quality in the rivers of the Basin of Mexico (Cuenca de México)

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Mexico's Basin constitutes a very important hydrographic region in the country, being one of the most densely populated areas in the world. In it, there are still many rivers that exploited by the populations that surround them, and with that, different problems arise related to the use and management of the riparian ecosystems. In this work, an ecological quality assessment was carried out in 11 rivers in the Mexico's Basin, based on the characterization of epilithic diatom communities and the recognition of the indicator value of the species, along with a physicochemical and hydromorphological analysis. These rivers responded in a general way to a gradient of longitudinal degradation head to mouth in their physicochemical and hydromorphological quality, yet, even though the headwaters of most of the rivers were found within protected areas, structures for extraction or canalization of water were recognized altering the hydromorphology of these systems. In the studied rivers, we identified 450 diatom species distributed among 80 genera. The diatom communities responded to two main environmental gradients: the increase of nutrients and the alteration of hydromorphological quality. We recognized three groups of species that responded to these, and an ecosystem quality value was assigned for each one. With this indicator value, the creation of the Diatom's Ecosystem Quality Index (DEQI) was proposed, which allowed us to evaluate the ecosystem quality of the studied sites, recognizing 11 out of 38 with good quality. These indices are proposed as an effective tool to determine and monitor the quality of the riparian ecosystems based on the study of diatom communities, for which we propose their use and calculation in future studies in the region.

The paleoceanographic evolution of the Black Sea during the Last Glacial-Holocene period as a proxy for diatom records

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A sediment core 7625-3 was recovered by R/V Meteor from 1244 m water depth off the Sakarya River mouth on SW continental margin of the Black Sea. We report analyses of diatoms, organic carbons, carbonates from this core. As identified by the previous studies, three units are present in the Black Sea Core 7625-3. The uppermost unit consists of microlaminated gray green mud containing alternations of coccolith rich and clay-organic matter rich laminae. The underlying unit is a sapropel unit that consists of laminated dark gray mud with high (3.5 wt %) organic carbon. It includes at its base a laminated and banded dark green mud with silt laminae and a relatively carbonate-rich yellowish light green aragonitic band with a high Sr content in the Black Sea and dated 9.3 cal ka BP. The Lutite unit deposited under lacustrine conditions consists of gray clayey mud. Diatom analysis in Core 7625-3 shows that the major shift from freshwater to a marine taxa occured with an influx of marine planktonic Thalassiosira Cleve and Coscinodiscus Ehrenb. diatom species. These changes occurred at 8.9 cal ka BP and gradually increased at 7.4 cal ka BP with the last marine inflow from the Mediterranean to the Black Sea. These results support that the water level of the Black Sea increased gradually in contrast to catastophically. The second increase in *Thalassiosira* and Coscinodiscus species occurred at 7.5 and 6.6 cal ka BP with a increase in high organic carbon in the base of a sapropel unit. When marine Mediterranean waters poured into the Black Sea, it caused an upwelling of the nutrient rich deep waters into the photic zone, thereby initiating high primary productivity and led to water stratification, preconditioning the basis for sapropel formation. Diatom assemblages in the lacustrine period show distinction between some cold and warm periods. It may be explained by two different mechanisms: 1) high terrigenic input to the basin during cold periods like Red Layer (16.2-14.8 cal ka BP) periods, it caused crashing of the diatoms with terrigenic sediment. 2) high carbonate deposition (such as C2 (11.9-9.3 cal ka BP) and C3 (14.8-12.9 cal ka BP) periods caused dissolution of diatoms due to alkaline conditions in lake water. The highest freshwater planktonic Stephanodiscus astraea (Ehrenb.) Grunow species in lake phase occured only during the Younger Dryas (12.9-11.9 cal ka BP) period with a mostly high organic productivity with Sea of Marmara input during that time.

Morphology, phylogeny and whole genome sequence of a hitherto undescribed scaly *Parmales* – reminiscent of pre-diatom?

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The sister lineage of diatoms is the order Parmales, comprising the parmalean algae sensu stricto (hereafter referred to as siliceous Parmales) and the bolidomonad formerly called Bolidomonas Guillou & Chret.-Dinet, now integrated into Triparma B. C. Booth & H. J. Marchant after an emended description by Ichinomiya & al. (2016). It is noteworthy that there are only 26 described species in the order *Parmales*, despite the fact that its sister lineage, diatoms, is one of the most speciose group among protists. Therefore, we have been studying this "unsuccessful" relative of diatoms to make a comparison and reveal the keys to success of diatoms in the current ecosystems. In the course of survey on the *Parmales* diversity, we encountered a hitherto undescribed *Parmales* from a sample collected from Oyashio current, Japan, and successfully established its clonal culture. Cells of the clones were considerably small, i.e. < 1μ m, only half as large as other siliceous *Parmales* described so far. As seen in the other siliceous Parmales, the cells of the clone were spherical and covered with siliceous scales, which was confirmed by the presence of a positive signal with PDMPO staining. The most striking feature of the clone was the number and topology of the scales: cells had more than 50 tiny scales partially overlapping one another, reminiscent of the pre-diatom proposed by Round and Crawford (1981), in marked contrast to the other siliceous Parmales in that plate with intricate outlines that were arranged to tightly fit next to each other allowing no overlap of the plates. All scales consisted of a disk that exhibited unfilled radiating rib networks and a central spinule occasionally extending vertically to form a long spine. Moreover, the external surface of the disk was often ornamented with small knobs. Observation of the earliest stage of the scale ontogeny revealed that the pattern centre was either the annulus or sternum, although further silica deposition to form the central spinule and spine masked the early structure and that the difference of the pattern centre was undetectable from the matured scales. In the molecular phylogeny, the Parmales clade bifurcated into a small clade containing the undescribed scaly clone along with sequences from several environmental probes, and the rest of the members including *Triparma* spp. and large numbers of environmental probes. In a draft genome of the clone, we detected a more-orless complete set of genes responsible for meiosis and formation of the flagellum. The chloroplast genome size (106 kb) of the clone was slightly smaller than that of T. laevis (117 kb) and lacked an inverted repeat region which had been found in most of the chloroplast genomes of photosynthetic organisms sequenced so far, including diatoms. Further study of this undescribed clone to better understand its features would shed new insight into the origin of diatoms.

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Cell size changes linked to life cycle may influence DA production in three *Pseudo-nitzschia* spp.

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Diatoms have a cell wall called frustule made from silica which strongly constrains their life cycle, leading to a reduction in the average cell size at each division and makes obligatory sexual reproduction. This life cycle influences population dynamics, genetic diversity and cell physiology. In the heterothallic diatom genus Pseudo-nitzschia H. Perag., several species produce a neurotoxin, domoic acid (DA), that bioaccumulates in marine food webs resulting in Amnesic Shellfish Poisoning (ASP) events. These ASP events may have negative consequences on coastal ecosystem services especially through their impact on fisheries. Different factors (nutrient limitations, growth phase...) are known to control production pattern of DA which behave as a typical secondary metabolites. The objectives of our study were to characterize Pseudo-nitzschia cell size changes during life cycle (in particular gametangia size range and initial cell size) and to explore the relationships between life cycle stages, cell size changes, growth and DA production in three Pseudo-nitzschia species: P. australis Freng., P. fraudulenta (Cleve) Hasle and P. pungens (Grunow) Hasle. To address this issue, mating experiments and batch culture experiments (with silicate or phosphate limitation) were performed with numerous strains for each species to characterize the intraspecific variability. The induction of sexuality was possible only in species-specific cell size ranges where cells acted as gametangia: 55 μm to 85 μm for *P. australis*, 29 μm to 90 μm for *P. fraudulenta* and 43 μm to 75 μm for *P. pungens*. The average size of initial cells was 144 μm, 113 μm and 164 μm for *P. australis*, P. fraudulenta and P. pungens, respectively. The growth rates during the exponential growth phase in the batch cultures were not significantly different between the three species, especially because of large intraspecific variabilities (0.15 to 0.82 day⁻¹). In all species, the growth rate was influenced both by the cell size and culture duration (time since isolation from natural populations). Our results confirm that P. australis is the most toxic of the three studied species with a maximum cellular DA (cDA) of 645 fg.cell⁻¹ associated with a very high concentration of dissolved DA (dDA, 6000 fg.cell⁻¹). *P. pungens* and *P. fraudulenta* produced respectively, 50 fg.cell⁻¹ and 5.6 fg.cell⁻¹ of cDA and 90 fg.cell⁻¹ and 10 fg.cell⁻¹ of dDA. These results show that it is essential to take into account interspecific variability in Pseudo-nitzschia monitoring for bloom dynamic studies and that intraspecific variability have to be considered when characterizing life traits of species. No influence of cell size on cDA and dDA production was noticed for P. pungens and P. fraudulenta. DA production by P. australis was largely influenced by cell size variation related to life cycle stages. P. australis gametangia were six times more toxic than smaller and larger cells not able of sexual reproduction. We have pointed out in P. australis, that physiological modifications linked to life cycle and especially the acquisition of sexual reproduction in gametangia seem to play a major role in toxin production capacity in *P. australis*. These results demonstrate that life cycle dynamics in natural populations may influence bloom toxicity.

DNA barcoding reveals a new species of the genus *Stephanodiscus* Ehrenb.

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Centric diatoms are a major part of fresh water phytoplankton communities worldwide. Within these, the genus *Stephanodiscus* Ehrenb. is one of the most diverse and common genera. However, the taxonomy of the smaller species of this genus has been problematic until today. This applies especially to the species complex around *S. minutulus* (Kütz.) Cleve & J. D. Möller and *S. parvus* Stoermer & Håk. The taxonomic situation of these taxa is subject to controversial discussion, insufficient species description and fossil type material contribute to persistent confusion. Håkansson & Kling (1990) described another morphologically similar species in this group: *S. binatus*. Following the reinvestigation of the type materials of *S. minutulus* and *S. parvus* by Houk & al. (2010), it seems that these names are often falsely applied to *S. binatus* Håk. & H. J. Kling.

We successfully established over 100 monoclonal strains of the assumed *S.minutulus/parvus/binatus* species complex from 26 European water bodies and compared them by morphological and molecular methods. For the morphometric analysis we used parameters based on SEM photographs. For the molecular analysis we used three different DNA barcoding markers nuclear (D2-D3 LSU), chloroplast (*rbcL*) and mitochondrial (*cox*1) DNA.

As a result of this screening we found that about 90% of the strains belonged to *S. binatus*, which seems to be a very common species in meso- to eutrophic water bodies in middle Europe. Notably differing in the barcoding markers, the remaining strains represent an unknown species similar to *S. binatus*. Surprisingly, we have not been able to cultivate *S. minutulus* and *S. pavus* sensu Houk (2010) so far, which implies that at least in middle Europe these species are not as common as generally assumed.

For a detailed morphometrical investigation we selected 8 strains of the unknown species as well as 3 strains of *S. binatus* and 2 strains of *Cyclostephanos invisitatus* (M. H. Hohn & Hellerman) Theriot, Stoermer & Håk. Additional 4 strains of the species *Stephanodscus hantzschii* Grunow, *Stephanodiscus neoastraea* Håk. & B. Hickel, *Cyclostephanos dubius* (Hust.) Round were included in

the molecular analysis. The new species has a flat, usually more finely structured valve face and has a higher striae density than *S. binatus*, which makes it similar to *C. invisitatus* in the light microscope. In contrast to *C. invisitatus* we found the internal openings of marginal fultoportulae, surrounded by three cowlings, typical for *Stephanodiscus*. Moreover this species has 1-2 central fultoportulae instead of only a single one, mostly distinctly visible in lightmicroscopical investigations. Although morphological characters are overlapping with those of both species mentioned, statistically the differences between some morphological features are significant.

While the morphological diagnosis seems to be difficult, the results of the molecular investigation show that these species are distinctly different. Using all three markers the distance between the new species and *S. binatus* equals the distance between *S. binatus* and *S. hantzschii*.

Houk V., Klee R. & Tanaka H. 2010: Atlas of freshwater centric diatoms. Part III. *Stephanodiscaceae* A. *Cyclotella*, *Tertiarius*, *Discostella*. – Fottea **10 suppl.**: 1–[498].

Systematics and Biodiversity: an international peer-reviewed journal

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Systematics and Biodiversity is devoted to whole-organismal biology. Numerous algal papers have been published in the journal. Systematics and Biodiversity is an international, peer-reviewed, life science journal, without page charges, which is published by Taylor & Francis for the Natural History Museum. Eight issues are published online each year, including two printed copies (four issues each). The criterion for publication is scientific merit. Systematics and Biodiversity documents the diversity of all organisms in all natural phyla, through taxonomic papers that have a broad context (not single species descriptions), while also addressing topical issues relating to biological collections, and the principles of systematics. Systematics and Biodiversity particularly emphasizes the importance of multi-disciplinary significance of systematics, with contributions which address the implications of other fields of systematics. Also, it may advance our understanding of other fields through taxonomic knowledge, especially in relation to the nature, origins, and conservation of biodiversity, at all taxonomic levels. The journal does not publish single species descriptions, monographs or applied research nor morpho-species descriptions. Taxonomic manuscripts must include modern methods such as molecular analysis and/or cladistics. The most recent Impact Factor was 2.127 and the journal ranked 15/53 or the upper 28% in the category: Biodiversity and Conservation © Thomson -Reuters JCR). The five-year Impact Factor was 2.141. The most outstanding paper is selected by the Associate Editors and Editorial Board and recognized with the Taylor and Francis Prize (£500 and a certificate). The Editor is available for individual consultation about possible manuscript ideas and/or submissions.

Niche measures and habit of diatom species are good predictors of the distribution pattern in tropical reservoirs

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The positive relationship between local abundance and regional distribution of species is one of the most investigated patterns in macroecology (see Rocha & al. 2018). This pattern is widely observed in different taxonomic groups, especially in marine and terrestrial environment of temperate regions. For tropical freshwater environments this relationship is poorly investigated. Among the mostly used hypothesis to investigate this pattern are niche position (species with low niche position are locally abundant and widely distributed) and niche breadth (species with high tolerance are able to occupy different places). Mechanism of species dispersion is able to affect this relationship, so that planktonic microorganisms would be more readily distributed than benthonic microorganisms. We presently analysed the planktonic diatom community in tropical reservoirs and tested whether niche position, niche breadth and habit of species explain this pattern. Analyses were based on the diatom community of 33 reservoirs (oligo to super-eutrophic) in southeastern Brazil. We used the Outlying Mean Index (OMI) to calculate Niche Position (NP) and Niche Breadth (NB). Species with high NP values are classified as specialists and occupy restricted niches, whereas generalist species demonstrate low NP values and are widely distributed. Beta regression models were run to predict the proportion of sites occupied by species as a function of the niche position, niche breadth and types of habit (planktonic and benthonic). All analyses were performed in Rlanguage. We found positive relationship between occupied locals and local mean abundance (pseudo-R2=0.38, p<0.001). The niche position was the main explanatory variable of the relationship NP and occupation frequency (pseudo-R2=0.54, p<0.001), with significant explicability increase when added the type of species habit (pseudo-R2=0.64, p<0.001). This result was supported by the model that had niche measures and habit of species as explanatory variables. The species with restricted distribution (high NP values and low NB values) were considered as a potential bioindicator of trophic gradient. For oligotrophic environments we highlight the following species: Achnanthidium tropicocatenatum Marquardt & al., A. exiquum (Grunow) Czarn., Fragilaria grunowii Lange-Bert. & S. Ulrich, Navicula herbstiae Metzeltin & Lange-Bert. and Nitzschia palea var. debilis (Kütz.) Grunow. For mesotrophic environments we identified five species: A. macrocephalum (Hust.) Round & Bukht., Aulacoseira pusilla (F. Meister) Tuji & Houki, Fragilaria longifusiformis Siver & al., Geissleria lateropunctata (J. H. Wallace) Potapova & D. M. Winter and Nitzschia amphibia Grunow. Finally, only Ulnaria acus (Kütz.) Aboal showed restrict distribution to eutrophic environments. Our results emphasize the niche position and types of habit as good predictors of occupation and abundance for diatom species and contribute with new metrics for diatom autoecological studies and their use in bioindication.

Rocha M. P., Bini L. M., Siqueira T., Hjort J., Grönroos M., Lindholm M., Karjalainen S.-M. & Heino J. 2018: Predicting occupancy and abundance by niche position, niche breadth and body size in stream organisms. – Oecologia **186**: 205-216.

From S to XXL in a day – Observations on diatom cell enlargement in cultures

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Size reduction is an obligatory side effect of diatom cell division. To reverse the diminution of cell volume diatoms either develop auxospores or have other ways of vegetative cell enlargement (Geitler 1932, Kaczmarska & al. 2013).

In natural populations these rejuvenating cell activities happen unfrequently and are rarely observed. But as a consequence of cell enlargement the size distribution of a diatom population will change from a bell curve to bimodal curve with two separate peaks. This situation may be misinterpreted as evidence for two coexisting species.

Cultivating diatoms provides an opportunity to observe the cardinal points of diatom life cycles. During the first two years of German Barcode of Life 2 (GBOL 2) more than one thousand diatom cell cultures were established but less than 40 cases of cell enlargement were found. A few spectacular examples are presented on this poster.

Geitler L. 1932: Der Formwechsel der pennaten Diatomeen (Kieselalgen). – Arch. Protistenk. **78:** 1–226.

Kaczmarska I., Poulíčková A., Sato S., Edlund M. B., Idei M., Watanabe T. & Mann D. G. 2013: Proposals for a terminology for diatom sexual reproduction, auxospores and resting stages. – Diatom Res. **28:** 263–294.

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Some new record diatoms from alpine lakes in the Black Sea region (Turkey)

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The works on diatoms of alpine lakes are new topic for Turkey. There are few studies about the topic. The Black Sea region is unique area because of its climate conditions, where the summer is slightly rainy, spring and autumn are rainy and winter is snowy. So, the area does not have a typical climate for the Anatolian Peninsula. In this study, the samples were collected from two high-altitude lakes (about 3400 m) and some small streams flowing into the lakes in July-2015. As a result, the genus *Genkalia* Kulikovskiy & al. and over 50 diatom taxa are "new record" for Turkish freshwater diatom flora.

The diatom distribution in the Tigris-Euphrates River System (Turkey)

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The Tigris and Euphrates Rivers originate in Southeastern Anatolia in Turkey and the catchments are the largest basins in Turkey. The aim of the study is to reveal the distribution of diatoms in the Tigris-Euphrates river catchment. For this purpose, samples were collected from 20 different flowing water bodies in 2014. They were taken by brushing from submerged stones. As a result, 153 diatoms were identified and 32 diatom taxa have "new record" status for Turkish freshwater diatom flora. Among the collected species, *Caloneis macedonica* Hust., *Craticula minusculoides* (Hust.) Lange-Bert., *Encyonema ventricosum* (C. Agardh) Grunow, *Encyonopsis cesatii* (Rabenh.) Krammer, *Gomphonema tergestinum* Fricke, *Luticola goeppertiana* (Bleisch) D.G. Mann ex Rarick & al., *Navicula cryptotenelloides* Lange-Bert., *N. erifuga* Lange-Bert., *N. kotschyi* Grunow, *N. libonensis* Schoeman, *N. reichardtiana* Lange-Bert., *Neidiomorpha binodiformis* (Krammer) Cantonati & al., *Nitzschia communis* Rabenh. and *Sellaphora seminulum* (Grunow) D. G. Mann were rarely found taxa in Turkish diatom flora.

All polluted waters are alike; but clean waters are clean in their own way

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"All happy families are alike; each unhappy family is unhappy in its own way." Tolstoy wrote about families, but he just as well could have been describing the nature of diatom assemblages.

All polluted waters are alike. A number of diatom species are indicative of human disturbances, particularly disturbances that result in increases in nutrient concentration, fine sediment load, and specific conductance. Such pollution tolerant species are generally widespread in their geographic distribution, even occurring in both polluted and clean waters. We might even say that these species *lack* a biogeographic distribution, because their distribution is controlled by water chemistry and microhabitat rather than geography or geologic history. Consequently, we expect that the distribution of this group of pollution tolerant species can be predicted by a limited set of environmental parameters (certain pH, sediment load, specific conductance, nitrogen concentration and phosphorus concentrations).

Clean waters are clean in their own way. An even larger number of diatom species occur in the absence of human disturbance in streams and lakes designated "in reference condition" or "least impacted sites". These species tend to be rare, show narrow geographic distribution or simply appear in such low abundance that it is not possible to describe their distribution and tolerance of various parameters.

In this presentation, we consider the variety of practices for assessment of biotic condition of freshwaters based on diatom species. The two observations above are at odds with the existing approaches to assessment. Are there are alternatives that might be better suited to the nature of diatom species?

Diatom diversity obtained by metabarcoding using a chloroplast and a ribosomal marker on modern and Holocene lake sediments from the Siberian treeline ecotone

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Different markers have been tested to retrieve best results in diatom richness and taxonomic resolution by environmental metabarcoding approaches. Those analyses generally depend on the specificity of the genetic marker, available references and the nature of the investigated environmental sample. Retrieving genetic diatom diversity from sediments is particularly prone to amplify non-targeted taxonomic groups because large parts of the sedimentary metagenome are composed of bacteria and archaea and only a small fraction is attributed to eukaryotes. The majority of diatom references are known from the nuclear ribosomal 18S and the chloroplast rbcL gene, as both markers have different characteristics, they will track diatom diversity differently. In this study, we investigate diatom diversity in modern and past lake sediment samples from the Siberian treeline ecotone by applying a chloroplast and a ribosomal marker gene and compare the retrieved diatom diversity in regard to taxonomic resolution, richness and turnover related to spatiotemporal environmental variations. We assessed 39 modern lakes (locations range from taiga to tundra) and 21 core samples (oldest sample 9600 years BP) from two sediment cores. The applied chloroplast marker (rbcL, 76 bp) revealed a moderate to high specificity to diatoms (45% of in silico amplified sequences and 93% of empirically obtained reads) and a moderate taxonomic resolution (43% of all diatom sequences can be unambiguously identified to species level). The ribosomal marker (18S, 140-151 bp) has minor specificity to diatoms (1.6% of in silico amplified sequences and 8.5% of empirically obtained reads) and a moderate taxonomic resolution (37% of all diatom sequences can be unambiguously identified to species level). Both markers identified 60% of all in silico amplified diatoms unambiguously to genus level. The rbcL diatom data revealed high diatom richness with in total 494 different sequence types and the composition data analyses indicate a strong relation to vegetation and water chemistry differences across the ecotone. So far, a smaller sampling set of 8 lakes for the 18S data revealed 244 different sequences types and also a change of diatom composition across the ecotone, but we still await the sequences from the entire data set to make final conclusions. However, both approaches identified unexpected high genetic diatom diversity in modern and old lake sediments, which support their application for ecological interpretations of lake environment and history.

Late Miocene palaeoenvironmental reconstruction of Gavdos Island, Greece, using fossil diatom assemblages

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The Messinian salinity crisis (MSC) occurred in the Mediterranean during the late Miocene at 5.97 (Manzi & al. 2013), when gateways connecting the Atlantic Ocean and Mediterranean Sea became progressively restricted leading to the deposition of a large volume of evaporites. The evaporative phase was preceded by a preconditioning period, the pre-MSC phase (7.1-5.97 Ma), during which diatom-rich sediments started to form at the transition between sapropelitic and marl/limestone intervals, resulting in precession-driven cyclical successions. Although many studies have been conducted on the pre-MSC, relatively few of them focused on diatoms, which are very sensitive to changes in environmental conditions and useful for reconstructing palaeoenvironments (Jordan & Stickley 2010). The aim of this study is to reconstruct the pre-MSC environment of the upper part of the Metochia section (UpMet; 6.25-5.97 Ma) on Gavdos Island based on the comparison of fossil diatom and calcareous plankton assemblages (Gennari & al., in prep.).

Diatoms were divided into five groups based on their general ecological preferences. Those representing the continental slope, which are associated with upwelling, were the most common (Thalassionema (H. Perag. & Perag.) Perag. spp. and Rhizosolenia Brightw. spp.) and increased upward in the section (up to 95%), followed by the diatoms associated with the continental outer shelf (Chaetoceros Ehrenb.), which benefit from both runoff and upwelling. Minor percentages of inner shelf species that are more straightforwardly related to river runoff are recorded in the lower part of several diatomite beds. During the 6.25-5.97 Ma interval, the sediments of the UpMet section were deposited between the slope and the continental outer shelf. During diatomite deposition, diatoms prevalently benefit from upwelling; peaks of magnetic susceptibility and species of the calcareous nannofossil Sphenolithus and droughs of Reticulofenestra minuta indicate increased runoff during sapropel deposition. The presence of inner shelf diatom resting spores at the base of the diatomites can be a carry-over signal of the sapropels. Runoff maxima coinciding with sapropel deposition suggest their correlation with insolation maxima, which, based on the climatic model and observations on Plio-Pleistocene sapropels, would trigger maxima of North African monsoon activity and Nile outflow. The results of this study were compared with five previously studied sites (Porcuna, Sorbas, Basilicoi, Falconara, Pissouri) in the Mediterranean region. Thalassionema spp. were dominant at all 6 sites, so it is likely that upwelling occurred around the Mediterranean basin. Of the six study areas, the Gavdos Island sediments may have been deposited closest to the continental shelf, while those of Porcuna were in a more distal setting.

Manzi V., Gennari R., Hilgen F., Krijgsman W., Lugli S., Roveri M. & Sierro F. J., 2013: Age refinement of the Messinian salinity crisis onset in the Mediterranean. – Terra Nova **25:** 315–322.

Jordan R. W. & Stickley C. E. 2010: Diatoms as indicators of paleoceanographic events. – Pp. 423–453 in Smol J. P. & Stoermer E. F. (ed.), The Diatoms: Applications for the Environmental and Earth Sciences, 2nd Edition. – Cambridge: Cambridge University Press.

The diatom plankton algae in the oxbow lakes of the National Park "Pripyatsky" (Belarus)

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We present the results of a planktonic diatom study in 13 oxbow lakes located in the National Park «Pripyatsky» (Belarus): in floodplain lakes of the Pripyat' River (8 lakes, with total mineralization from 136 to 442,8 mg/L, pH from 6.0 to 7.28) and in non-flowing oxbow lakes of high floodplain or the first terrace (5 lakes, total mineralization below 50 mg/l, pH from 5.96 to 6.09). Sediment plankton samples were collected in July, 2015, simultaneously with the temperature and pH water measurements. Permanent slides of diatom algae were prepared too. Identification was done by means of light microscopes Axiostar and Axioscop (Carl Zeiss).

Altogether, 170 species and intraspecific taxa (3 classes, 14 orders, 27 families, 56 genera) and 12 up to now unidentified taxa were identified: in floodplain lakes – 151 species and an intraspecific taxon, 10 taxa of open nomenclature; in non-flowing oxbow lakes of high floodplains or the first terrace – 98 species and intraspecific taxa, 6 taxa of open nomenclature. Both groups had 79 species and intraspecific taxa in common (46.5% of total). The following species were encountered: *Cyclostephanos dubius* (Hust.) Round and *Aulacoseira ambigua* (Grunow) Simonsen (all 13 lakes), *Stephanodiscus minutulus* (Kütz.) Cleve & Möller and *Cocconeis placentula* Ehrenb. var. *placentula* (12), *Cyclotella meneghiniana* Kütz. and *Cocconeis euglypta* Ehrenb. (11 lakes).

In floodplain lakes, 72 species of diatom algae were encountered (47.7% for this group and 42.3% of total). 50 specific species (69.4% of total) were found only in one lake, and 14 species (20% of total) in 3–7 lakes. The genus Amphora Ehrenb. ex Kütz. and the abundance of species within the Cymbellaceae family (15 species compared to 2 in the lakes of the other group) were specific to this group. The species Amphora pediculus (Kütz.) Grunow (7 lakes) and A. ovalis (Kütz.) Kütz. (4 lakes), A. copulata (Kütz.) Schoeman & R. E. M. Archibald (5 lakes) are indifferent to alkaline and mineralization, the last one is halophile. In 3–5 floodplain oxbow lakes specific species were: Cocconeis pediculus (5 lakes), Navicula menisculus (4 lakes), Staurosirella berolinensis (3 lakes), Staurosira binodis (3 lakes), Rhoicosphenia abbreviata (3 lakes), Gomphonema olivaceum (3 lakes), Nitzschia recta (3 lakes), N. sigmoidea (3 lakes). In lakes of the high floodplain and above-floodplain terrace 19 species of diatoms algae were found (19.4 % for this group and 11.2 % of total in oxbow lakes). Only in one lake there were 17 species (about 90 % of total). The species Epithemia turgida (indifferent, alkalifil, typical for meso-eutrophic reservoirs) was found in 3 lakes; Tabellaria flocculosa (halophobe and acidophilus) - in 2 lakes. Thus, the flora of diatoms in studied lakes has features of originality at the level of families, genera and species. The most complete characterization of the species composition in investigated lakes water bodies were considered in previous our publications (Mikheyeva & al., 2016, Mikheeva et al. 2017). In these work the comparative floristic analysis of diatom floras of two groups of lakes by taxonomic and ecological indicators is given too. We plan to continue studying diverse water bodies of the National Park "Pripyatsky", in order to assess in future other diatom species and floristic diversity of this region.

Mikheyeva T. M., Svirid A. A., Khursevich G. K. & al. 2016: Vodorosli planktona vodoemov i vodotokov Natsionalnogo parka "Pripyatskii" [Algae of plankton of water bodies and watercourses of the National Park "Pripyatsky"]. – Mikheyeva T. M. (ed.). – Minsk (in Russ.).

Mikheeva T. M., Lukyanova E. V. & Svirid A. A. 2017: Structure and quantitative phytoplankton development in lakes water bodies of the National Park "Pripyatsky". – J. Belarus. State Univ. Biol. 2017 (1): –97 (in Russ.).

Bioindication values of diatoms as a tool for assessing the human pressure in urban streams

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Urbanisation directly affects the ecological status of rivers. Their natural flow is often regulated and, as a result, the habitat conditions are disturbed leading to the modification of entire ecosystems. The aim of the study included qualitative and quantitative analyses of diatom assemblages in stream phytobenthos, the evaluation of human impact, and stream transformation based on patterns recognized with a Kohonen artificial neural network and Principal Component Analysis, and the determination of the ecological status of the streams using five diatom indices, such as: IO, IPS, GDI, IBD, TDI. The biological methods revealed the influence of anthropogenic transformations on the ecological status of the studied streams. The Kohonen artificial neural network analysis grouped the study sites into two main clusters. The analysis revealed a clear separation of the studied sites into those of low and poor ecological status resulting from strong anthropogenic pressure and those in which good and moderate ecological status was from one side a natural phenomenon, but also in some studied streams an artificial one, resulting from the adaptation of diatom assemblages to specific hydromorphological conditions of transformed streams. In the last case the main factor shaping diatom assemblages was the level of hydromorphological transformations caused by humans. In the case of the studied urban streams, the sites with heavy morphological transformations had good and moderate ecological status, in contrast to the upper sites that were located upstream from the stream sections hydrologically transformed and which had a bad ecological status. The hydromorphological transformations of stream beds modifying the structure of diatom assemblages may cause the phenomenon of seemingly good ecological status of ecosystems; thus, the conclusions from biological assessment based on such modified assemblages may be incorrect.

The significance of OTU sequence similarity threshold as a proxy for taxonomic resolution in diatom-based bioassessment: a case study on the rivers of Mayotte (France, Indian Ocean)

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Diatom-based indices are widely used for bioassessment of aquatic habitats. The implementation of DNA-metabarcoding and High Throughput Sequencing (HTS) in biomonitoring enables the rapid analysis of high quantity of environmental sequencing data (Leese & al. 2016). The method uses different approaches to give biological meaning to sequences detected in environmental samples. *De novo* clustering groups sequences into Operational Taxonomic Units (OTUs) based on a pre-defined sequence similarity threshold (SST). OTUs are then generally assigned to taxonomy using reference sequences. A common problem however, is the incompleteness of reference libraries resulting in loss of biological information. Additionally, the selection of SST is somehow arbitrary and few studies analyzed its relevance.

In our study, we developed an index based on the ecological profile of OTUs (Idx_{OTU}) without taxonomic assignment. Our aim was to study the effect of the SST on Idx_{OTU} from different aspects: (i) number of OTUs; (ii) performance of Idx_{OTU} via correlations between index values and the environmental gradient; (iii) Discrimination power and stability.

90 biofilm samples together with their supporting physical and chemical parameters were collected from 51 river sites on Mayotte Island (France) for HTS and further analyzes. The marker (*rbcL*) and the primers were chosen to target diatoms. Hierarchical clustering was carried out at 20 SST (80– 99%) and the Idx_{OTU} was developed and tested at each level using a training (75%) and test (25) dataset that were randomly selected. Idx_{OTU} is based on the weighted average equation used for diatom indices (Zelina & Marvan 1961). The pressure gradient was defined with CCA analyzes on parameters related to nutrient and organic pollution (Tapolczai & al. 2017).

The Idx_{OTU} showed significant correlations with the pressure gradient at all SST. Nevertheless, this efficiency reached a plateau at 91% SST that is below the currently considered species-level delimitation for diatoms (95-97%). We showed an important trade-off between index stability (more stable for coarse resolution) and discrimination power along the pressure gradient (better discrimination for finer resolution) that may set a challenge for water managers when deciding which tool to develop for routine bioassessment with metabarcoding.

- Tapolczai K., Bouchez A., Stenger-Kovács C., Padisák J. & Rimet F. 2017: Taxonomy- or trait-based ecological assessment for tropical rivers? Case study on benthic diatoms in Mayotte island (France, Indian Ocean). – Sci. Total Environm. 607–608: 1293–1303.
- Leese F., Altermatt F., Bouchez A., Ekrem T. & al. 2016: DNAqua-Net: Developing new genetic tools for bioassessment and monitoring of aquatic ecosystems in Europe. Res. Ideas Outcomes e2: 11321.

Zelinka M. & Marvan P. 1961: Zur Präzisierung der biologischen Klassifikation der Reinheit fließender Gewässer. – Arch. Hydrobiol. **57:** 389–407.

Stephanodiscus – evidence for recent speciation and dispersal

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The diatom genus *Stephanodiscus* Ehrenb. shows repeated patterns of recent speciation events. Evidence from this comes from molecular, morphological and paleontological evidence in the *S. niagarae* Ehrenb. complex (Theriot 1987, Theriot 1992, Theriot & al. 2006), and molecular and morphological evidence in other groups of *Stephanodiscus* species including *S. minutulus* (Kütz.) Cleve & Möller and several close relatives (particularly *S.* cf. *jamsranii* Edlund & al., *S. meyeri* Genkal & Popovsk.), and *S. hantzschii* Grunow and *S. binderanus* (Kütz.) Willi Krieg. In each case, molecular evolution in genes typically used in diatom systematics, including common bar-code genes, has been outpaced by morphological evolution (Theriot & al. submitted) and physiological evolution (Theriot & Jones 2009).

We will illustrate that a common thread in each of these clusters of species is that there is one plesiomorphic nominal species (based on a phylogenetic interpretation of morphology), and at least one apomorphic species. In the case of the *S. niagarae* Ehrenb. complex, this pattern has already been shown to be consistent with speciation by (ecological) peripheral isolation by examining the distribution of apomorphy in the context of environmental parameters (Theriot 1992). Corroborative evidence comes from a paleolimnological study of the evolution of *S. yellowstonensis* E. C. Ther. & Stoermer from *S. niagarae* in Yellowstone Lake sediments which revealed that morphological changed tracked climate-driven changes in the lake.

Here we examine the correlation between apomorphy and the environment, and ecological distribution of *S. minutulus*, *S.* cf. *jamsranii*, *S. meyeri*, *S. hantzschii*, and *S. binderanus*, to generate a hypothesis about speciation and later dispersal of these species.

Theriot E. 1987: Principal component analysis and taxonomic interpretation of environmentally related variation in silicification in Stephanodiscus (*Bacillariophyceae*). – Brit. Phycol. J. **22**: 359–374.

Theriot E., Fritz S. C., Whitlock C. & Conley D. J. 2006: Late Quaternary rapid morphological evolution of an endemic diatom in Yellowstone Lake, Wyoming. – Paleobiology **32**: 38-54.

Theriot E. C. 1992: Clusters, species concepts, and morphological evolution of diatoms. – Systematic Biology **41**: 141-157.

Theriot E. C. & Jones B. 2009: The morphology, physiology and taxonomy of two small Stephanodiscus species in Yellowstone and Jackson Lake, Wyoming, USA. Nova Hedwigia Beih. **135**: 275-293.

Theriot E. C., Nakov T., Brady M. C., Goertzen L. R. & Likhoshway Y. (submitted). Evidence for a recent origin and rapid divergence of the modern Stephanodiscus Ehrenb. (*Bacillariophyta: Thalassiosirales*) flora: Morphological evolution outpaces barcode gene evolution. Protist.

Diatom assemblage responses to environmental change during the Holocene from a mountain lake (Prášilské jezero, Czech Republic)

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Mountain lake sediments are invaluable recorders of environmental change. Here, we present the thorough paleolimnological analysis of glacial lake in the Bohemian Forest, which aims to supplement our knowledge about paleoenvironmental development of Prášilské jezero (49.07519°N, 13.39976°E), Central Europe.

Diatom analysis was conducted as a part of the multi-proxy study (pollen, plant macrofossils, chironomids, charcoal, sediment geochemistry). Specifically, diatom analysis will be used to reconstruct pH and trophic state of the lake basin to determine timing and behaviour of major shifts in the lacustrine ecosystem. Diatom valve concentration, relative abundances of species and the stomatocyst-to-diatom ratio were examined in order to observe diatom assemblage development in detail.

Preliminary results show two distinct shifts in diatom species composition in the Holocene record. The first shift corresponded to an erosional event in association with the 8.2 ky cal. BP event. The second shift was accompanied by the establishment of *Asterionella ralfsii* W. Sm. around 4 ky cal. BP and corresponded with the decline of quillworts (*Isoëtes*). This suggests substantial changes of the water chemistry, most likely the pH decline, weakened the population of quillworts.

These results affirmed that the diatom record in Prášilské jezero was able to elucidate the factors affecting changes in lacustrine ecosystem, specifically the changing abundance of quillworts. Further diatom analysis may potentially explain the cause of quillworts' extinction in constituent basins from the Bohemian Forest.

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Diatom community response to climate change during the interglacial/glacial cycle MIS 11-10 in ancient Lake Ohrid

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Past climate change, especially interglacial periods are a focus for paleoecological research due to their potential contribution to understand the biota response to future climate change. Marine Isotope Stage, MIS 11 (ca. 425–365 ka) is a phase of low eccentricity and regarded as closest analogue to the Holocene. Here, we analyze the paleolimnological record of MIS 11 and 10 (365–335 ka) preserved in a long sediment sequence (584 m; ca. 1.9 Ma) from Lake Ohrid (Macedonia/Albania). We focus on diatom response to environmental and limnological changes driven by climatic forcing. Diatom assemblages are dominated by planktonic species mostly from the genus Cyclotella Kütz. ex Bréb. One of the dominant species is Cyclotella cavitata Tofilovska & al., a fossil taxon with no analogue in the modern flora. Due to its comparable size and ultrastructural features with hypolimnetic Cyclotella fottii Hust. it is assumed that it has similar ecology. At the beginning of MIS 11 (452–417 ka), the presence of hypolimnetic *C. cavitata* and mesotrophic Stephanodiscus transylvanicus Pant. indicate high temperatures and high nutrient availability. In the succeeding period (417–410 ka), the higher relative abundance of facultative planktonic taxa, together with the appearance of the epilimnetic Cyclotella ocellata Pant.and Cyclotella minuscula (Jurilj) Cvetkoska are indicative of higher precipitation and nutrient input. This suggests that this period was warmer and more humid compared to the previous interval. In the following period (410-400 ka), the highest relative abundances of C. cavitata and C. fottii are indicative of strongest stratification of the lake, leading to the conclusion this was the warmest period in this stage, which is in correlation with the global record (LR04). In the next period (400–377 ka) the fluctuating relative abundance of C. cavitata and C. fottii, C. ocellata and C. minuscula is indicative of colder climate conditions during winter months. However, the light availability and the temperature during the summer periods were still sufficient to support growth of the hypolimnetic taxa. The gradual transition from warmer climate conditions at the end of MIS 11 (377–365 ka) to colder climates is indicated by the higher abundance of Asterionella formosa Hassall, a species that thrives in more turbid conditions in the lake ecosystems. MIS 10 (365–335) is marked by the dominance of C. ocellata and C. minuscula. Contrary to the existing data, which indicate that C. ocellata and C. minuscula are associated with warm conditions in Lake Ohrid, especially during the late Holocene, our data reveals correlation of these taxa with cold periods. In MIS 10, the low temperature and nutrient input in the epilimnion supported the growth of these taxa, while the turbid conditions and low light availability suppressed the growth of hypolimnetic community. The glacial conditions unable forming of stratification in the lake and reduced the populations of C. fottii and C. cavitata. The higher relative abundance of C. ocellata and C. minuscula during the late Holocene is most likely due to the anthropogenic impact. The consistent eutrophication, especially the direct input of nutrients in the epilimnion, prevailed in the temperature influence.

Biogeography of living silicoflagellates off the Japan Sea coast during summer 2016

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Living silicoflagellates have been studied around the Japanese coast for many years (e.g., Shitanaka 1983, Nishioka 1986), but most recently by Abe & al. (2015), who investigated the living silicoflagellate and ebridian assemblages inside and outside the Seto Inland Sea. This latter study revealed that thicker skeletons were associated with the Seto Inland Sea, while thinner skeletons were present in the Kuroshio. The main species were *Dictyocha stapedia* Haeckel, *Octactis pulchra* J. Schiller and *Stephanocha* (formerly *Distephanus* Stöhr) *speculum* (Ehrenb.) McCartney & R. W. Jord. During a recent cruise of the T/S Nagasaki-maru of Nagasaki University (August-September 2016), about 1-10 liters of seawater were collected every 3 hours from a water depth of 3 m while the ship steamed ca. 1,500 km in the Japan Sea from Nagasaki in southwestern Japan to Hakodate in northeastern Japan. The water samples were then filtered and the plankton examined with a light microscope.

The following results were obtained: (1) In addition to the ebridian, *Ebria tripartita*, there were five taxa of silicoflagellates, i.e., *D. stapedia*, *D. aculeata* Ehrenb., *D.* sp. cf. *subclinata* Bukry, *O. pulchra* and *Stephanocha speculum*; (2) the warm water species *D. stapedia* and *O. pulchra* were present from Nagasaki to the Shimane Peninsula, but further north (from Shimane to northeastern Tohoku) they disappeared, before reappearing near the Hakodate coast; (3) *Dictyocha* sp. cf. *subclinata* was the most abundant species in Maizuru Bay and Wakasa Bay (central Japan) with a maximum population of over 2,500 individuals/liter, and including many double skeletons and aberrant skeletal forms, the latter either lacking a bar, with four struts making a central peak or lacking a strut and so the remaining struts make a Y-shape structure as in *Corbisema* Hanna; (4) the cold water species *Stephanocha speculum* appeared in the north from southern Tsugaru Strait to Hakodate Bay. Three biogeographic boundaries could be recognized based on the coastal silicoflagellate composition in the Japan Sea; from southwestern to northeastern Japan they are the Kanmon Strait (the boundary between Kyushu and Honshu Island), the Noto Peninsula (including Toyama Bay), and the Tsugaru Strait.

Abe K., McCartney K., Narita H. & Jordan, R. W. 2015: Silicoflagellates and ebridians from the Seto Inland Sea and Kuroshio, including the description of *Octactis pulchra* var. *takahashii* var. nov. – J. Nannopl. Res. **35:** 111–128.

Nishioka J. 1986: On the mechanism of red tide due to silicoflagellates, *Dictyocha fibula* Ehr. in Maizuru Bay. – Bull. Kyoto Ocean Fish. Sci. **10**: 41–53 (in Japanese with English abstract).

Shitanaka M. 1983: Silicoflagellate remains in the sediments of Lake Hiruga, Fukui, Japan. – Bull. Mizunami Fossil Mus. 10: 171–180 (in Japanese with English abstract).

Are endemic diatoms the origin of cosmopolitan diatoms?

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Praestephanos suzukii (Tuji & Kociolek) Tuji is an endemic diatom from Lake Biwa, an ancient lake in Japan. Since *Stephanodiscus suzukii* Tuji & Kociolek and *Stephanodiscus triporus* Genkal & G. V. Kuzmin share several unique characteristics and make a monophyletic clade in molecular analysis, Tuji & al. (2014) included both of them in *Praestephanos* Tuji & M. Julius, which was newly described based on *S. suzukii*.

The evolution of *P. suzukii* has been studied by Kuwae & al. (2007) and Saito-Kato & al. (2015) based on two long cores from L. Biwa for 400ka or 300ka. From the cores, Saito-Kato & al. (2015) newly described two *Stephanodiscus* taxa, but they should belong to the genus *Praestephanos* (Tuji & Ohtsuka in press). *Praestephanos triporus* (Genkal & G. V. Kuzmin) Tuji & J.-S. Ki (as *Stephanodiscus vestibulis* Håk. & al.) was estimated as an anchor species of *P. suzukii* (Saito-Kato et al. 2015). *P. triporus* is phylogenetically very close to *P. suzukii*, and the speciation era between both taxon is estimated to be 0.45 – 0.7 Ma (Tuji & Ohtsuka in press).

Recently a *Praestephanos* taxon, which should be an ancestor species of *P. suzukii*, was found from the Ayama Formation at Kamimasugi, Konan-town, Koka (3.1 Ma). A similar taxon is also known from the Iga Formation (3.4-3.2 Ma; Tanaka & Nagumo 2014) and the Kameyama Formation, Tokai Group (4.0-3.6 Ma; Hattori & al. 2017).

Since these ancestor species are only known from the Kobiwako Group and the nearby Tokai Group in West-Central Japan, *P. suzukii* likely evolved in this area. Since these fossil records are clearly older than the speciation era between *P. suzukii* and *P. triporus*, *P. suzukii* cannot evolve from *P. triporus*. More likely, cosmopolitan *P. triporus* evolved from endemic *P. suzukii* or its ancestor species.

Hattori K., Ohtsuka T., Domitsu H. & Satoguchi Y. 2017: Morphology of a diatom species similar to *Praestephanos suzukii* from Kameyama Formation, Tokai Group. – Diatom **33:** 38. (in Japanese).

Kuwae M, Yoshikawa S. & Tsugeki N. K. 2007: Long-term species and morphological changes for Stephanodiscus in Lake Biwa for the last 400 ka. – Diatom, 23: 71–81 (in Japanese with English abstract).

- Saito-Kato M., Tanimura Y., Mori S. & Julius M. L. 2015: Morphological evolution of *Stephanodiscus* (*Bacillariophyta*) in Lake Biwa from a 300 ka fossil record. J. Micropal. **34(2):** 165–179.
- Tanaka H. & Nagumo N. 2014: Stephanodiscus sp. from Iga Formation, Kobiwako Group. Diatom 30: 227 (in Japanese).
- Tuji A., Mohri Y., Ki J. S., Jung S. W. & Julius M. L. 2014: Phylogeny of *Praestephanos* gen. nov. (*Thalassiosirales*, *Bacillariophyceae*) based on *Stephanodiscus suzukii*, and related freshwater thalassiosiroid diatoms. – Plankt. Benth. Res. 9: 132–140.

Tuji A. & Ohtsuka, T. (in press.): Topic 1 Fossil diatoms from Lake Biwa and their phylogeny. Lake Biwa. – Springer.

The Shenzhen Code: what's in it for diatoms?

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The International Code of Nomenclature for algae, fungi, and plants provides the rules and recommendations for naming these organisms, including diatoms, both non-fossil and fossil. The *Code's* authority derives from international consensus – a tradition among its users that its rules are to be followed – and an explicit acceptance of those rules at an International Botanical Congress, which is held every six years. The newly published *Shenzhen Code* (Turland & al. 2018) results from the 19th International Botanical Congress, held in Shenzhen, China in July 2017. It is actually the endpoint of a multi-year process involving publishing proposals to amend the previous edition, an annotated synopsis of those proposals, a guiding vote by *Code* users, discussion and decisions on proposals at the Nomenclature Section of the Shenzhen Congress, and months of meticulous work by the Editorial Committee to incorporate those decisions into the new edition of the *Code*. One of the most extreme changes in the *Shenzhen Code* is its new "Chapter F", which gathers together those provisions that apply *solely* to organisms treated as fungi. Chapter F can be modified only by an International Mycological Congress, whereas the rest of the *Code*, which is relevant to diatomists, can be modified only by an International Botanical Congress.

Division III of the *Shenzhen Code* contains detailed provisions on governance of the *Code*, e.g. how is the *Code* amended, how are names conserved or rejected, and how do the Nomenclature Section of an International Botanical Congress and the Permanent Nomenclature Committees operate. Prior to the *Shenzhen Code*, much of this information was buried in numerous reports of Congresses and Committees or was unpublished, held in the files or memories of individuals. Its inclusion in Division III makes the governance of the *Code* more transparent.

The *Shenzhen Code* includes a new framework for the mandatory registration of new names and other nomenclatural acts for algae and plants, although the registration itself is not yet a requirement for valid publication of such names – and cannot become so before the next International Botanical Congress in Rio de Janeiro, Brazil in 2023.

Numerous other, smaller changes to the *Code* were made in Shenzhen, and a selection of the more important items is discussed, with emphasis on rules that are relevant to the naming of diatoms. The Editorial Committee has invested considerable effort in providing full bibliographic references in the 100s of Examples of the *Code*. In previous editions, names were usually cited with their author(s) and year of publication when the full references could be found in a nomenclatural index. While more and more names can nowadays be found in such indexes, it was thought that the *Code* would be more user-friendly if it was more self-contained with respect to references.

Other editorial changes to the *Code* include Article 60, on orthography (i.e. spelling), being restructured to make the sequence of rules more logical and to remove "back-door rules" in which Recommendations were made mandatory through Articles. Appendix I, concerning the names of hybrids, has been added to the main text, as "Chapter H". The remaining seven Appendices, containing lists of conserved, protected, and rejected names, suppressed works, and binding decisions on valid publication and homonyms, are separately published, currently in a continuously updated, open-access online database at http://botany.si.edu/references/codes/props/index.cfm.

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Diatom taxa from the class *Coscinodiscophyceae* Round & Crawford at Vileyskoe Reservoir

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We studied the diatom flora of the Vileyskoe Reservoir, an artificial accumulative reservoir, which is supplying water to the city of Minsk. The area of the Vileyskoe Reservoir is 64.6 km², the greatest depth is 13 m, the average is 3.7 m, the volume is 238 million m^3 . The total mineralization is 280-320 mg/l. The oxygen content in winter is 2-8 mg/l, in summer – 8-15 mg/l. The reservoir is characterized by a low content of organic substances and an average degree of anthropogenic transformation (Encyclopedia 1983). The characteristics of materials and methods of investigation were considered in previous publications (Turskaya 2010). As a result of studies of 45 samples of plankton, microphytobenthos and periphyton, collected in the summer of 2008, 175 species and intraspecific taxa of diatoms were identified by light microscopy. The Coscinodiscophyceae class is represented by 2 orders, 2 families, and 4 genera containing 11 species and 1 variety (6.7% of the total number of diatoms encountered). In the studied phytocenoses the species composition is almost identical. Cyclotella ocellata Pantocsek is found only in plankton samples collected at coastal stations at a depth of 4.5 m, with an abundance of 9.9 % on the Davydova scale (Davydova 1985). Handmannia bodanica (Eulenst. ex Grunow) Kociolek & Khursevich was absent in plankton samples, but was detected in one sample of microphytobenthos (depth 5.4 m) and one sample of periphyton (pondweed, depth 0.2 m). According to ecological characteristics, these species are planktonic, indifferent to halobity and pH (Barinova 2006). In all phytocenoses Aulacoseira granulata (Ehrenb.) Simonsen dominated: from 23.0% in periphyton to 34.0% in microphytobenthos and 35.8% in plankton. Aulacoseira ambigua (Grunow) Simonsen dominated in plankton (44.4%) and microphytobenthos (38.2%), in the samples of periphyton it is a subdominant (5.8%). These diatoms are indifferent to mineralization, alkaliphilic, planktonic cosmopolites. In plankton and microphytobenthos, the dominant complexes also include the Holarctic Stephanodiscus rotula (Kütz.) Hendey (up to 30.1%) and the boreal Cyclostephanos dubius (Hust.) Round (up to 27.9%) planktonic, alkalibiontic, indifferent to mineralization species. In periphyton these species are less than 5 %. In the samples of microphytobenthos, to the group of dominants are also alkaliphilic Stephanodiscus minutulus (Kütz.) Cleve & Möller (10.2%) and indifferent to pH Aulacoseira granulata var. angustissima (O. Müller) Simonsen (24.4%) – planktonic, alkalibiontic, indifferent to mineralization. In the studied samples of plankton, these species are subdominants; in the samples of the periphyton they were found only once. The dominant complexes of plankton and microphytobenthos concerning the presence of centric diatoms are similar consisting of planktonic, alkaliphilic cosmopolitan species indifferent to salinity, with a small proportion of alkalibiontic species.

Turskaya S. A. 2010: Diatoms of the northeastern part of the Vileyskoe reservoir, Vesnik VDU, 2010, 6(60): 60-64 (in Russian).

Barinova S. S., Medvedeva L. A., Anissimova O. V. 2006: Diversity of algal indicators in environmental assessment, Israel, Pilies Studio, pp. 498 (in Russian).

Davydova N. N. 1985: Diatoms – indicators of environmental conditions of water basins in the Holocene. L. – Nauka, (in Russian).

[[]Encyclopedia] 1983:Encyclopedia of the Belarusian nature. – Belarus, Minsk, Vol.1 (in Belarusian).

Developing alternative diatom enumeration methods to build better predictive bioassessment models

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Diatoms are routinely sampled in biological assessments of water quality, but the method traditionally used to characterize diatom communities does not adequately capture species richness for use in assessment applications. The traditional enumeration method of 300-600-cell fixed counts characterizes the relative abundance only of dominant taxa, making it inadequate for common bioassessment applications such as observed/expected (O/E) models, which rely on species richness. We analyzed the nature of diatom communities in reference sites of varying diversity using a measure of counting efficiency, which revealed 600-cell fixed counts did not consistently characterize high diversity sites compared to low diversity sites. To address this problem, we compared the fixed count method to a stratified method, which captures both abundance and richness, and a timed presence method, which captures richness for O/E models. The stratified and timed presence methods captured greater species richness compared to fixed counts. We then built O/E models using data collected with both the fixed and timed presence methods. The timed presence method produced more sensitive and precise models than the fixed method and better assigned test sites as reference or heavily impaired, though it struggled to discriminate between intermediately impaired sites. A timed presence method could thus improve measurements of stream health while expediting analyses and saving money.

The morphology and taxonomy of Miocene-Quaternary *Proboscia* spp.

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The marine diatom genus Proboscia Sundström is common in outcrop and deep-sea core sediments of Late Cretaceous to the recent age, particularly in temperate to polar regions. The genus is morphologically diverse, containing about 100 species, most of which remain undescribed, with two distinct evolutionary lineages (that can be referred to as the 'barboi' and 'alata' lineages) evolving around the Eocene-Oligocene boundary from a much older 'cretacea' lineage. Here, we describe morphological changes that occurred within the 'barboi' lineage during the late Miocene to Quaternary in the northern hemisphere. In the late Miocene the Proboscia assemblage was dominated by *P. barboi* (Brun) R. W. Jord. & Priddle, which is characterised by having an extremely long and curved proboscis, large polar spinulae (one of which is directed 90° to the proboscis) and pores running down the lateral sides of the proboscis (Jordan & Saito 1999). In the Quaternary, the Proboscia assemblage is dominated by P. curvirostris (Jousé) R. W. Jord. & Priddle, which is characterised by having a more curved proboscis with an elbow spine on the point of maximum curvature (Loseva 1994). Between the stratigraphic ranges of these two species is a set of transitional forms with additional features; (i) swollen probosces, (ii) ridges on the basal portion of the proboscis, (iii) one very long polar spinula or (iv) with two distally-directed polar spinulae. These forms may represent distinct species since they occur in restricted time intervals, and their appearance and/or disappearance may be related to climatic changes that were happening on regional and global scales. A survey of Pliocene and Quaternary Proboscia spp. from the Southern Ocean revealed that a P. barboi-like taxon and forms with swollen probosces existed in the early Pliocene, but there were no subsequent forms with elbow spines or ridged probosces. Of the living *Proboscia* spp., only *P*. subarctica K. Takah. & al. has similar features to the 'barboi' lineage (Takahashi & al. 1994), suggesting that this lineage became extinct in the Southern Ocean during the Pliocene or early Quaternary.

Jordan R. W. & Saito M. 1999: The genus *Proboscia* from the *Thalassiosira yabei* Zone (Middle-Late Miocene) sediments of Hokkaido, Japan. – Pp. 565–580 in: Mayama S., Idei M. & Koizumi I. (ed.), 14th International Diatom Symposium. – Koenigstein: Koeltz Scientific Books.

Loseva E. 1999: Are both *Rhizosolenia curvirostris* Jousé and *R. barboi* Brun found in Pleistocene sediments of northeastern Europe? – Pp. 55–61 in: Kociolek J. P. (ed.), Proceedings of the 11th International Diatom Symposium. – San Francisco: California Academy of Sciences.

Takahashi K., Jordan R. W. & Priddle J. 1994: The diatom genus Proboscia in subarctic waters. – Diatom Res. 9: 411–428.

Morphological variability of Alveolophora species from type material

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It is known that some fossil taxa are important stratigraphic markers, but it difficult to identify due to the lack of clear boundaries between species and the lack of clear diagnostic features (Jousé 1952). Therefore, obtaining knowledge about the limits of morphological variability of species and studying their typical characteristics from the point of view of the modern understanding of valve ultrastructure is very valuable. This makes it possible to clearly describe the distinctive features that define a species, as well as reducing taxonomic errors and helping in identifying redundant taxa. Our detailed studies of the valve morphology of some *Alveolophora* Moisseeva & Nevretdinova species revealed a wide variability in *A. robusta* (Khurs.) Usoltseva & Khurs., *A. bradburyi* Usoltseva & al., *A. nevadica* Usoltseva & al. and *A. americana* Usoltseva & al. species. This enabled us to get a broader view of the diagnostic features of this genus and to discuss its similarity with *Aulacoseira* Thwaites (Usoltseva & Khursevich 2013, Usoltseva & al. 2013).

The main objective of this investigation was to establish the degree of morphological variability in *A. areolata* Moisseeva, *A. bifaria* Nevretdinova & Moisseeva and *A. jouseana* (Moisseeva) Moisseeva from the type material using scanning electron microscopy. Based on the new morphological variability data, diagnostic descriptions for these taxa have been expanded.

New morphological features of *A. areolata* – rimoportulae on the valve face and separating valves without spines - were shown. High variability was found in all morphological characters of *A. bifaria* and *A. jouseana*. One of the main characteristics of the *Alveolophora* genus is the presence of alveolae or pseudoalveolae. The alveolae are open chamber with a hole of different shape, whereas the pseudoalveolae does not have a hole and it is completely open. The lateral partitions between them are costae (Moiseeva & Nevretdinova 1990). Analysis of the morphological variability of a range of valves showed that in *A. bifaria* and *A. jouseana* valves with well–defined alveolae, pseudoalveolae, microalveolae (closed microcamera) or without alveolae were found. Previously, in the descriptions of these species only valves with well–defined alveolae were considered (Moisseeva & Nevretdinova 1990). The costae are longitudinal and transverse. Only one species of *Alveolophora* in Asia – *A. bifaria* – has transverse costae. This feature brings this species closer to other species, e.g. *A. bradburyi*, *A. nevadica* and *A. americana* from the Miocene sediments of North America (Usoltseva, Kociolek, Khursevich, 2013). The presence of costae on the inner side of the valve is an ancient feature and does not occur in modern species of *Aulacoseiraceae*. The absence of alveolae and costae suggest a close association of this genus with *Aulacoseira*.

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Aulacoseira sp. found from proboscidean bone of Deinotherium sp. in Finland

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Recently, a new diatom species was found from a proboscidean bone discovered in southern Finland (Salonen & al. 2017). In this work, morphological analysis of the bone, and pollen and diatom analyses from sediment contained in the marrow cavity were carried out. A Miocene age for the bone was determined based on presence of the diatom genus Alveolophora Moisseeva & Nevretdinova, indicating a minimum age of 5 Ma, and based on the earliest appearance of proboscideans outside Africa, setting a maximum age of 19 Ma. The pollen assemblage was a rich in spores of shoreline pteridophytes, while the diatom assemblage also was consistent with a shoreline freshwater environment, suggesting that the bone was deposited post-mortem Miocene sediments which do not currently exist in southern Finland or in the near vicinity. In this work, diatoms were investigated by light microscopy. The most common diatom species were (mero)planktonic Alveolophora sp. and Aulacoseira granulata (Ehrenb.) Simonsen, covering about 90% of the total diatom sum. Other species identified at species level were planktonic species Cyclotella stelligera Cleve & Grunow, and benthic species Cocconeis pediculus Ehrenb. and Nitzschia amphibia Grunow. Here we have re-examined the diatom sample by scanning electron microscope (SEM). The SEM pictures suggest that the species actually is fossil Aulacoseira Thwaites sp. The species has micropseudoalveoli which feature we can see both in Alveolophora (Usoltseva & al. 2013) and in Aulacoseira Thwaites species (Usoltseva & Tsoy 2010). In the description of Aulacoseira sp.: Frustules form filamentous chains. Valves are cylindrical, 10-28 µm in diameter and 5-11 µm height. Areolae are located on the entire valve face. Areolae on the mantle are circle, with velum cribrum, situated in straight rows. Sometimes 2 double rows can be seen on some valves. All valves are connected by pointed spines of different lengths (1.3–6.5 μ m). An elongated separation spine exists in every 2-6th spine. The collar is narrow, thin-ribbed at the edge. Valve walls are very thick. Ringleiste is deep. 1-2 rimoportulae are located near the ringleiste. External openings of rimoportulae are small, round, and open in the area of the first areolar row. Some valves have micro-pseudoalveolae. We compared our Aulacoseira sp. to Aulacoseira helianthus J. Mohan & J. R. Stone (found from the Late Pliocene sediments from Ethiopia) because these species seem to have many morphological similarities, e.g. the valve height, areolar structure of valve face and mantle, form of separating spines. However, the species differ from each other by rimoportulae, thick walls of the valves, deep ringleiste and micro-pseudoalveoli. Hence, we suggest that the species found from the bone is a new fossil Aulacoseira species.

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Usoltseva M. V., Kociolek J. P. & Khursevich G. K. 2013: Three new species of *Alveolophora* (*Aulacoseiraceae*,

Bacillariophyceae) from Miocene deposits in western North America. – Phycologia 52: 109–117.
 Usoltseva M. V. & Tsoy I. B. 2010: Elliptical species of the freshwater genus Aulacoseira in Miocene sediments from Yamato Rise (Sea of Japan). – Diatom Res. 25: 397–415.

Salonen J. S., Saarinen J., Miettinen A., Hirvas H., Usoltseva M., Fortelius M. & Sorsa M. 2016: The northernmost discovery of a Miocene proboscidean bone in Europe. – Palaeogeogr. Palaeoclimatol. Palaeoecol. **454**: 202–211.

Mohan J., Stone J. R. & Christopher J. C. 2016: Three novel species of *Bacillariophyta* (Diatoms) belonging to *Aulacoseira* and *Lindavia* from the Pliocene Hadar Formation, Afar Depression of Ethiopia. – Phytotaxa **272**: 235–247.

A new epizoic Olifantiella species found on loggerhead sea turtles

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The marine genus *Olifantiella* Riaux-Gob. & Compère was only recently described from the coral sands of Réunion Island (Riaux-Gobin & Compère 2009), characterized by a so-called buciniportula, a raised internal tubular process, opening externally by a small funnel-shaped slit or pore. Other discriminating features include a naviculoid valve outline, rather small valve dimensions, parallel striae composed of one transapically

elongated areola, a rather simple raphe structure with short distal fissures and only weakly deflected proximal endings and a typically raised siliceous nodule between the two internal proximal raphe endings. So far, only nine taxa were described in the genus *Olifantiella*, most of them only found in the tropical regions of the Indo-Pacific basin (Riaux-Gob. & Compère 2009, Riaux-Gobin & Al-Handal 2012, Riaux-Gobin 2015). Recently, a new *Olifantiella* was described from a temperate environment, the Port of Antwerp in Belgium (Van de Vijver & al. 2016).

During a survey of the epizoic diatom flora on carapaces of loggerhead sea turtles (*Caretta caretta*) from the Adriatic Sea, a relatively large population of an unknown *Olifantiella* species was observed. Comparison with all other *Olifantiella* species, based on detailed LM and SEM observations, indicated that it should be separated as a new species. The new species is characterized in having a slender, elongated valve outline with parallel margins and clearly protracted, rostrate apices. Internally, a clear buciniportula can be observed. Several smaller, more sturdy valves were likewise observed showing a more lanceolate outline with shorter, rostrate apices; however it is unclear at the present whether they represent yet another separate species.

The poster illustrates the morphology of a new species and discusses its similarities and differences with all other *Olifantiella* species worldwide.

Riaux-Gobin C. & Compère P. 2009: Olifantiella mascarenica gen. & sp. nov., a new genus of pennate diatom from Réunion Island, exhibiting a remarkable internal process. – Phycol. Res. **57:** 178–185.

Riaux-Gobin C. & Al-Handal, A. Y. 2012: New species in the marine diatom genus Olifantiella (*Bacillariophyta, Biraphidineae*) from Rodrigues Island (Western Indian Ocean) – Fottea **12**: 199–217.

Riaux-Gobin C. 2015: The elusive genus Olifantiella (*Bacillariophyta*): South Pacific assemblage and Indo-Pacific biogeography. – Bot. Mar. **58:** 251–266.

Van de Vijver B., Mertens A. & van Dam H. 2016: Olifantiella elisabethiana, a new raphid diatom species (*Bacillariophyta*) observed in the Port of Antwerp (Belgium). – Phytotaxa **261:** 251–259.

What do we know about the genus Orthoseira?

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The centric genus *Orthoseira* was originally described by Thwaites in 1848 based on *Melosira americana* Kütz. Today, only a handful of species, typical to terrestrial habitats, have been included or described in *Orthoseira*. Species are characterized by their rather large valves, usually connected by well-developed marginal linking spines, a high valve mantle and large areolae. The most striking feature is the presence of several carinoportulae in the valve center.

The type material of *M. americana* unfortunately did not contain any centric diatoms, making it impossible to determine in more detail the morphology of *M. americana* and *Orthoseira*. However, in the original description and illustration of *M. americana* (Kützing 1844), the presence of carinoportulae is not mentioned. Since all actually known *Orthoseira* species possess very conspicuous carinoportulae, well visible even in low LM magnification, it is unlikely that they can remain in the genus *Orthoseira*.

Several months after the description of *Orthoseira* by Thwaites, Ehrenberg (1848) described three related genera (*Liparogyra* Ehrenb., *Porocyclia* Ehrenb. and *Stephanosira* Ehrenb.) showing all large carinoportula in the central area. The three genera were separated based on minor morphological details, now regularly seen in some of the known *Orthoseira* species.

The present lecture tries to unravel the history of *Orthoseira* and the three Ehrenberg genera in an attempt to determine which genus is the most suitable for the species actually placed in the genus *Orthoseira*. The outcome of this study should resolve the ongoing controversy about the correct identity of the genus *Orthoseira* and all species currently ascribed to it and will be published in the near future.

Ehrenberg, C. G. 1848: Über eigenthümliche auf den Bäumen des Urwaldes in Süd-Amerika zahlreich lebende

mikroskopische oft kieselschalige Organismen. –Ber. Bekanntm. Verh. Königl. Preuss. Akad. Wiss. Berlin **1848**: 213–220. Kützing, F. T. 1844: – Die kieselschaligen Bacillarien oder Diatomeen. – Nordhausen: W. Köhne.

Thwaites G. H. K. 1848: Further observations on the *Diatomaceae* with descriptions of new genera and species. – Ann. Mag. Nat. Hist., ser. 2. 1: 161–172.

Limiting similarity and environmental filtering under drought stress in streams, a case study on diatoms

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Environmental filters are operating on the traits of species rather than on species themselves, which is why trait composition could more efficiently explain ecosystem functioning than species richness. Based on diatom trait composition, the applicability of the concept of "limiting similarity and environmental filtering" was studied in ephemeral streams. We examined whether the divergence or convergence of traits can influence the functioning of this type of streams. The main question was: Which mechanism has the strongest influence on the diatom community structure under drought stress? We studied the "effect size", which is the value of the distance of the trait composition, of observed samples when compared to the null distribution. This effect size value can be used to compare "drought-affected" to "perennial" streams. Diatom samples were collected from small- and medium-sized lowland streams in the Hungarian Lowland Region between 2007 and 2015 from the beginning of April to the end of October (i.e. the vegetation period). Summers and autumns were extremely dry during the 2011-2014 periods. Many rivers and streams dried out during the fall sampling period. These watercourses were considered as "drought-affected" streams. Diatom data collected from these streams in 2010, which was an extremely wet year in Hungary, were used as data representative of "perennial" watercourses as well as data from streams that were not dried over the course of the 2007 - 2015 period. We found that the divergence and convergence of traits in diatom assemblages is different in "drought-affected" and "perennial" streams.

Freshwater quality assessment using diatom DNA metabarcoding: progress and prospects in French river monitoring networks

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DNA-metabarcoding of benthic diatoms has shown its potential for water quality assessment. Several optimizations have been proposed now for major steps of the workflow: taxonomic resolution of DNA barcodes, efficiency of DNA extraction methods, completion of barcode reference database, and use of correction factor to obtain taxa quantification equivalent to microscopy. Placed end-toend, those improvements make the DNA-metabarcoding approach a viable alternative to the morphological approach (microscopy) for quality assessment of rivers in monitoring networks. We set up this bioassessment-innovative approach, using the diatom *rbcL* barcode, at the scale of river monitoring networks in Mayotte Island and France. The DNA-metabarcoding approach proved to be faster and cheaper than the classical one. Molecular-based quality index values were highly correlated to morphological based indices were increased by the completion of the reference database and the use of correction factors. Those results confirm the potential of DNA-metabarcoding for bioassessment, but also raised questions about the need of standardization and harmonization prior its implementation into biomonitoring campaigns.

- Kermarrec, L., Franc A., Rimet F., Chaumeil P., Frigerio J.-M., Humbert J. & Bouchez A. 2014: A next-generation sequencing approach to river biomonitoring using benthic diatoms. Freshwater Sci. **33**: 349–363.
- Rimet F., Abarca N., Bouchez A., Kusber W.-H., Jahn R., Kahlert M., Keck F., Kelly M. G., Mann D. G., Piuz A., Trobajo R., Tapolczai K., Vasselon V. & Zimmermann J. 2018: The potential of High-Throughput Sequencing (HTS) of natural samples as a source of primary taxonomic information for reference libraries of diatom barcodes. – Fottea **18**: 37–54.
- Vasselon V., Bouchez A., Rimet F., Jacquet S., Trobajo R., Corniquel M., Tapolczai K. & Domaizon I. 2018: Avoiding quantification bias in metabarcoding: Application of a cell biovolume correction factor in diatom molecular biomonitoring. Methods in Ecology and Evolution (in press).

Vasselon V., Domaizon I., Rimet F., Kahlert M. & Bouchez A. 2017: Application of high-throughput sequencing (HTS) metabarcoding to diatom biomonitoring: Do DNA extraction methods matter? – Freshwater Sci. **36**: 162–177.

Zimmermann J., Glöckner G., Jahn R., Enke N. & Gemeinholzer B. 2015: Metabarcoding vs. morphological identification to assess diatom diversity in environmental studies. – Molec. Ecol. Resources **15**: 526–542.

Role of historical factors in diatom biogeography of the geologically ancient Vindhya and recent Himalaya (Indian subcontinent)

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The diatom flora was examined in some west Himalayan and Vindhyan Highland rivers to understand the biogeography of diatoms in the Indian subcontinent because the Himalayas are geologically recent while Vindhya are ancient. Examination of the Vindhya and Himalaya flora shows high similarity at genera level but low similarity at species level. This suggests floral exchanges among the Vindhya and Himalaya in the historical past. After the Himalayan uplift, initial exchange was facilitated between these regions by the Gangetic Drainage (GD) owing to narrow Plains. With the widening of the Plains it could serve as a potential barrier for further exchanges through GD. Isolation after glaciations led to speciation in each region leading to low similarity at species level. It is proposed that the development of the flora of these highlands can be attributed to four major historical events in the Indian subcontinent; a) colonization of the newly formed Himalayan rivers by the Vindhya (Peninsular) elements in the absence of present day wide Gangetic Plains, b) creation of barrier due to widening of the Gangetic Plains, and subsequent speciation in the Himalaya, c) southward dispersal of the Palearctic elements and Himalayan flora during repeated glaciations and d) retreat of the Himalayan flora during post glaciations, subsequent climatic changes, isolation and speciation in the Vindhya and Himalaya.

How do newly-described diatom species affect biomonitoring? – An example of *Gomphonema paratergestinum* vs. *G. tergestinum*

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Over the past decade a great number of new diatom taxa have been described, as well as many redefinitions and delimitations of taxa from different species complexes. The reasons for the constant increase in the number of described diatom taxa are numerous: unexplored habitats, improved light microscope resolution and digital cameras with accompanying softwares, scanning electron microscopy, and molecular studies. For most of the newly-described species, only morphological characteristics are known. What about their ecological preferences?

OMNIDIA is a widely-used software for evaluation of ecological status of water bodies based on diatoms. The database from the first version of the software up to today has grown from 2035 to more than 23.000 diatom taxa. However, for the most newly-described taxa there are no indicator values.

In our study, we evaluated the ecological status at six sites in Lakes Ohrid and Prespa, respectively, based on different biological quality elements (diatoms, macrozoobenthos and macrophytes) as well as water chemistry. In two out of six sites in lake Ohrid, and five out of six sites in lake Prespa, *Gomphonema paratergestinum* Levkov & al. was a dominant or subdominant species (33.5-69.66% in Ohrid Lake and 9.95-65.34 % in Prespa Lake). In the OMNIDIA software, there currently are no indicator values for *G. paratergestinum*. However, the very similar species *G. tergestinum* (Grunow) Fricke has well known indictor values. *G. paratergestinum* resembles *G. tergestinum* with respect to some morphological characteristics (e.g. valve outline), but can be differentiated by the stria density. Both species were present in Lakes Ohrid and Prespa, however, with dominance by *G.*

paratergestinum. Based on the diatoms recorded at a site, OMNIDIA calculates diatom index values. How could *G. paratergestinum* with abundances up to 69.66% influence diatom indices? If we "experiment" and substitute *G. paratergestinum* with *G. tergestinum*, the obtained diatom index values indicated a completely different ecological quality class.

Every newly-described species is important since it increases our knowledge about diversity, biogeography and distribution of diatoms. However, there still is a gap between taxonomy and biomonitoring. How can we overcome this problem? According to the International Code of Nomenclature for algae, fungi, and plants no note or suggestion regarding ecology or ecological preferences of a species is required for description. Perhaps a possible solution could be that in the description of the species, ecological data, such as pH, conductivity, total phosphorus, concentrations of different anions etc. should be included. Scientists today could join forces to review material and species collected by Kützing, Ehrenberg, Grunow, Van Heurck, Cleve etc. In the same way, ecological data of newly-described species could be assembled and their indicator values calculated.

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Lake Kinneret (Israel): Lake-level reconstruction for the Holocene based on the Plankton/Benthos-ratio –An appropriate method?

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Diatoms are abundant, diverse and sensitive to a wide range of environmental parameters, and are often well preserved in lake sediment records. Fossil diatoms have often been used to reconstruct past lake-level shifts, e.g. by using the plankton/benthos (P/B)-ratio, which is based on the simple assumption that the variability in the P/B-ratio can be interpreted as a response to varying basin morphology as lake level fluctuates (Jones & al. 2013). As a lake shallows, benthic habitats may increasingly disperse into regions that were previously inhabited by planktonic diatoms living in a deeper water column, thereby changing the P/B-ratio. To use diatom habitat groups as an indicator for lake-level shifts, it is important that each diatom species (included in the analysis) can be classified clearly to the planktonic or benthic life habit.

Twenty-seven sediment samples were collected from across the surface area of Lake Kinneret (Israel), covering a range of different water depths and habitat areas. Our results show that the composition of modern diatom assemblages can be linked statistically to varying water depth. A logarithmic relationship between the P/B-ratio and water depth was determined and used to recalculate lake-level variations during the Holocene based on a fossil diatom record from Lake Kinneret (Vossel & al., in review). The estimated lake-level reconstruction fits well with the fragmentary absolute lake-level record based on paleo-shoreline data (Hazan & al. 2005) and seems to correlate with known Holocene climate shifts in the Southern Levant.

The usage of the P/B-ratio as an appropriate tool for reconstructing lake-level shifts in Lake Kinneret was applied further by three-dimensional modeling of the lake's morphometry. This allows the calculation of the lake volume, planar and basin surface areas, which are the critical components of a conceptual model of how planktonic and benthic habitat areas might have changed with changing lake levels (Stone & Fritz 2004).

Hazan N., Stein M., Agnon A., Marco S., Nadel D., Negendank J. F. W., Schwab M. J. & Neev D. 2005: The late Quaternary limnological history of Lake Kinneret (Sea of Galilee), Israel. – Quatern. Res. **63**: 60–77.

Jones T. D, Lawson I. T., Reed J. M., Wilson G. P., Leng M. J., Gierga M., Bernasconi S. M., Smittenberg R. H., Hajdas I., Bryant C. L. & Tzedakis P. C. 2013: Diatom-inferred late Pleistocene and Holocene palaeolimnological changes in the Ioannina basin, northwest Greece. – J. Paleolimnol. 49: 185–204.

Stone J. R. & Fritz S. C. 2004: Three-dimensional modeling of lacustrine diatom habitat areas: Improving paleolimnological interpretation of planktic : benthic ratios. – Limnol. Oceanogr. **49:** 1540–1548.

Vossel H., Roeser P., Litt T. & Reed J. M. (in review) Lake Kinneret (Israel): New insights into Holocene regional palaeoclimate variability based on high resolution multi-proxy analysis. – Holocene.

Diatom names, diatom taxa and diatom herbaria as sources of discovery

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In an early version of possible 'Session Topics' for this Symposium, Integrative Taxonomy was suggested. It didn't make the final cut but it might be instructive to get an idea of what it's supposed to be. According to the original description, "'Integrative taxonomy' is defined as the science that aims to delimit the units of life's diversity from multiple and complementary perspectives (phylogeography, comparative morphology, population genetics, ecology, development, behaviour, etc.)" (Dayrat 2005). That's a lot of information. This might be contrasted with another effort, captured most recently in a document entitled "A DNA based diatom metabarcoding approach for Water Framework Directive classification of rivers" (Kelly & al. 2018). Amongst other things, this is based on getting a DNA barcode for each species, so that "...a defined DNA sequence of a specified marker gene becomes a unique 'tag' or DNA barcode for a particular organism". These two ideas – integrative taxonomy and DNA barcoding – might appear compatible or might appear to clash: the first asks for endless amounts of data (as well as requiring particular theoretical stances, e.g., phylogeography), the second asks for just a tiny little bit of exclusive data (e.g., from the rbcL gene). What, then, is to become of the poor individual(s) left with diatom collections to work on? The usual answer – a mistaken judgement in my view – is that collections have types, and types are the yardstick of taxonomy, the court of last resort when it comes to knowing what something really is, what it should be called - as the DNA report above notes, data can be linked to "Linnaean taxonomy". Is that it? Is that all? I intend to address this subject – collections and their potential – from a fresh perspective, using data from three of Rabenhorst's exsiccatae: Die Algen Sachsens (1848–1882), Die Bacillarien Sachsens (1848–1852) and Totius Terrarum Orbis (1871). The reason for this choice is that the first of these three sets is reasonably well-known and available, the second two sets less so, but all three serve to illustrate the main aspects of what I understand as the empirical basis of comparative biology (taxonomy, systematics) in contrast to the vagaries of evolutionary biology ('Integrative Taxonomy') or the panacea offered by metabarcoding for mass ecological surveys.

Dayrat B. 2005: Towards integrative taxonomy. – Biol. J. Linn. Soc. 85: 407–415.

Rabenhorst L. 1848—1882: *Die Algen Sachsens*...Decades I-C, numbers 1-1000. Dresden, Leipzig. (Rabenhorst, Heinrich) [1848-1860] ... [continued as] ... *Die Algen Europa's* ... Decades I-CIX, numbers 1-1600 (or 1001-2600). Dresden [1861-1882].

Rabenhorst L. 1849—1852: *Die Bacillarien Sachsens* ... Fascicles 1-VII, numbers 1-70, tabulae 1-5. Dresden, Leipzig. Rabenhorst, L. 1871. *Totius Terrarum Orbis*. Semi-Centuries I—II, numbers 1—100. – Dresden.

Kelly M., Boonham N., Juggins S., Killie P., Mann D. G., Pass D., Sapp M., Sato S. & Glover R. H. 2018: A DNA based diatom metabarcoding approach for Water Framework Directive classification of rivers. – Environmental Agency.

DiaCurv: curvature analysis application in diatom research

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DiaCurv is a software application that calculates curvature (the inverse radius of a curve by identifying the chord (length) and the sagitta (length) from a mid-point of an object or part of an object (Bixby & Zeek 2010; Wishkerman & Hamilton 2017). Different taxa from the genera Cymbella C. Agardh and Luticola D. G. Mann, with good size diminution series, were selected to validate curvature metrics for shape evaluations in taxonomy. The dorsal ventral curvature of Cymbella makes species within this genus a natural choice for comparison. In contrast, the lanceolate and elliptic-lanceolate to rhombic forms of species within Luticola are more problematic. Machinelearning techniques (principal component analysis (PCA) and linear discriminant analysis (LDA)) were used to evaluate the curvature metrics for distinguishing diatom taxa. Selected taxa (C. aspera (Ehrenb.) H. Perag., C. cymbiformis C. Agardh, C. diversa Krammer, C. excisa Kütz., C. japonica Reichelt, C. neogena (Grunow) Krammer, C. neuquina Freng., C. parva (W. Sm.) Kirchn., C. saxicola J. Bílý & Marvan, C. tumidula Grunow) were identified by valve curvature, except when valve shape was not a distinguishing character for the species. With the lanceolate and elliptic-lanceolate shapes of Luticola, curvature was effective in separating the linear-lanceolate forms (e.g., L. australomutica Van de Vijver, L. goeppertiana (Bleisch) D. G. Mann ex J. Rarick & al., L. murrayi (West & G. S. West) D. G. Mann, L. saprophila Levkov & al.), and some broadly lanceolate forms (L. crozetensis Van de Vijver & al., L. subcrozetensis Van de Vijver & al.) but not elliptic-lanceolate forms within the same size range (e.g., L. katkae Van de Vijver & Zidarova, L. pseudocharcotii Levkov & al., L. yellowstonensis Levkov & al.). The experimental results indicated that LDA was more suitable for distinguishing taxa. Valve shapes which are circular, or centrally constricted or with polar differentiation or 3D in complexity may not be appropriate for curvature analysis unless specific parts (regions) of the valve are selected. The merits of this approach, or any other type of shape analysis, are that the subjective interpretation of shape differences between taxa is removed or reduced. The software and associated R scripts are free in order to provide the users with the possibilities to identify and apply curvature analysis in various aspects of diatom studies (e.g., taxonomy, ecology and biotechnology).

Wishkerman A. & Hamilton P. B. 2017: DiaCurv: a value-based curvature analysis application in diatom taxonomy. – Diatom Res. **32:** 351–358.

Bixby R. J. & Zeek E. C. 2010: A simple method for calculating valve curvature. – Proc. Acad. Nat. Sci. Philadelphia 160: 73– 81.

Diatom Assemblages of the Jemez River, New Mexico, USA

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We investigated diatom communities in the Jemez River, New Mexico for bioprospecting purposes, to characterize the diatom community structure, and to develop an algal trait database for the Jemez River. The Jemez is characterized by multiple hot springs, many of which contain naturally occurring arsenic. In order to determine if there were diatom flora unique to these sites, or if diatom bioindicators could be identified, we collected samples along a gradient that included several sites with multiple hot spring input. Samples were collected above and below the hot springs at each site; the control site was a downstream location not influenced by hot springs. Samples were collected from the Jemez River at Soda Dam, in the river at Jemez Springs, and downstream at the Spanish Queen National Recreation Site in November 2016. Flow rate, temperature, pH, dissolved oxygen, conductivity, salinity, turbidity, and total dissolved solids were measured in the field at each site, and water samples were collected for anion and cation analysis. A modified syringe was used to sample stream surface sediments for chlorophyll a and algal analysis. Diatom samples were analyzed and identified to the lowest taxonomic level. Relative abundances were determined for all taxa. Multivariate analyses were used to identify diatom community assemblage characteristics, and the physical and chemical factors contributing to diatom community structure.

All about the marine and sea ice diatom Nitzschia lecointei

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Nitzschia lecointei van Heurck 1909 can be found in high densities in sea ice and is also abundant in shallow benthic ecosystems. Due to its ecological relevance and importance to the sea ice ecosystem, this species was chosen as model organism for studying sea ice algal ecophysiology under climate change.

N. lecointei was isolated from sea ice in the Amundsen sea January 2011 and was kept in f/2 medium at -1.5°C at the University of Gothenburg. In a series of experiments, we tested short-term and long-term acclimation to elevated pCO_2 , synergism between elevated pCO_2 and temperature, and effects of increased temperature in 9 weeks darkness. Variables tested included e.g. growth, photosynthetic activity, concentration and composition of photosynthetic pigments, oxygen productivity, concentration and composition of fatty acids, bacterial biomass, external carbonic anhydrase activity and oxidative stress. Not all variables were measured in all experiments.

Generally, in terms of growth N. lecointei seems quite tolerant to changes in pH and pCO₂, probably due to the fact that this species grows in an environment with large seasonal variations in the carbonate system. However, increased pCO_2 resulted in physiological changes that may have important ecological consequences, such as cellular stoichiometry. For instance, we observed changes in carbon metabolism, fatty acid content and composition that did not affect the growth rate. When the experimental period was increased (194 days, ca. 60 asexual generations), we observed a small reduction in growth at 960 μ atm pCO2 after 147 days. Carbon metabolism was significantly affected, resulting in higher cellular release of dissolved organic carbon. When studying the synergism between temperature (-1.8 and 2.5°C) and pCO2 (390 and 960 µatm), synergism was detected in growth rate and acyl lipid fatty acid content. Carbon enrichment only promoted (3 %) growth rate closer to the optimal growth, but not at the control temperature $(-1.8^{\circ}C)$. Optimal growth rate was observed around 5°C in a separate experiment. The total content of fatty acids was reduced at elevated pCO2, but only at the control temperature. PUFAs were reduced at high pCO2. When combining increased temperature and different salinity conditions, the growth rate was higher at 3°C than at -1.8°C. Salinity 10 clearly limited growth rate and the highest growth rates were found at salinity 20 and 35. In another experiment, high and low temperatures together with treatments simulating ice formation and melting conditions were studied. Here, the highest levels of oxidative stress were found in low temperature and ice melting treatments, respectively. With respect to 9 weeks in the dark, cell numbers were higher at -1.5°C compared to 3°C, but when retrieved to light conditions, after one week higher cell numbers were observed at 3°C versus -1.5°C. Furthermore, cell numbers were lower when acetate was added to the dark treatments but not in glucose and glutamate treatments.

Although *N. lecointei* seem quite tolerant to environmental stress, effects of climate change may be different depending on ocean warming scenario or season, resulting in reduced food quality for higher trophic levels. Synergy between temperature and other stress factors may be particularly important in polar areas since a narrow thermal window generally limits cold-water organisms.

Intraspecific variations of Thalassiosira pseudonana isolates from the East China Sea

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Thalassiosira pseudonana Hasle & Heimdal is the first diatom whose genome was sequenced and has become one of the best-known model organisms for studies on topics ranging wide disciplines, such as evolution, biogeochemical cycles, metabolism, origination, etc. For a cosmopolitan species like T. pseudonana, intraspecific variations play a key role in responses to environmental factors, which determines its ecological significance, as well as its biochemical material compositions, which determines its application values, if any. Two T. pseudonana strains, namely GUH005 and XSWG, were isolated from coastal East China Sea (ECS) in Zhejiang province, China. Taxonomy was done by methods of electron microscopy observation and molecular identification. Composition and variation of fatty acids during different growth phases were also comparatively studied in these two strains. The results showed that while molecular information, morphology and pattern of areola on the valve indicated that these two strains were identical T. pseudonana, intraspecific differences existed, in particular in, marginal fultoportulae structure. Strain GUH005 had 11 short tube-like fultoportulae, while strain XSWG had 7 fultoportulae. Futhermore, XSWG was larger than GUH005; its bottom of the fultoportulae was wider than its tip, which made the fultoportulaes showing not the tube-like but a trapezoidal shape. According to the fatty acid profiles of these two strains,. C14:0 and C16:0 were the dominant saturated fatty acids, and C16:1(n-7) was the dominant unsaturated fatty acid in both strains; a total of 20 fatty acids were detected. Ratios of unsaturated to saturated acids were 1 and 1.2 in XSWG and GUH005 respectively. With the comparatively higher content of unsaturated fatty acids, strain GUH005 may have relatively higher potential in adaptation to low temperature compared to XSWG. When the two strains were grown under the same conditions, changes in fatty acid composition in the cultures were different: While most of the fatty acids in both strains had similar variation characteristics during growth phases, fatty acids C14:0, C16:0 and C16:1(n-7) increased continuously in GUH005 from beginning to the end of stationary phase, while there was no significant difference in strain XSWG during the whole growth phase.

Armbrust E. V. & al. 2004: The genome of the diatom *Thalassiosira pseudonana*: Ecology, evolution, and metabolism. – Science **306**: 79–86.

German Barcode of Life² (GBOL²) – Diatom eDNA Metabarcoding in the Context of the EU Water Framework Directive (EU WFD)

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The GBOL²-Project, funded by the German Federal Ministry of Education and Research (BMBF) is the second project phase of GBOL running from 2016-2018. It focuses on the extension of the thitherto erected DNA barcode reference library to integrate all frequent, common and indicator organisms, those in the Council Directive 92/43/EEC on the Conservation of Natural Habitats and of Wild Fauna/Flora (FFH) and the German Red Lists, as well as health-relevant and invasive organisms as well as agricultural pests.

One of the project parts located at the Botanic Garden and Botanical Museum, Freie Universität Berlin, is focussing on compiling a diatom DNA barcode reference library, as diatoms are very important bioindicator organisms implemented within the EU WFD.

Hitherto, no concerted strategy for the molecular registration of diatom species exists in Germany, and the quality as well as the taxonomical validation of the deposited diatom sequences in the International Nucleotide Sequence Database Collaboration (INSDC) are often not adequate. Therefore, it is planned to DNA barcode the 400 most important indicator species of the 1700 species expected to live in German limnic waters.

For all processed taxa the DNA barcodes and all correlated information will be publicly available. The DNA stocks will be deposited in the BGBM DNA Bank connected to taxonomically validated voucher specimens deposited at Herbarium Berolinense (B) following specific standardised procedures. As a best practice use case for documenting and displaying environmental and eDNA data, the diatom DNA barcode reference library will use the EDIT platform for cybertaxonomy and provides the possibility to assign environmental sequences gained from eDNA metabarcoding to the taxonomically validated reference sequences in the database as well as providing the platform MetBaN for the complete automation of the eDNA metabarcoding data evaluation. Both are crucial prerequisites for developing a sequenced-based time and cost efficient method to analyse the diatom community composition in environmental samples via eDNA metabarcoding for water quality assessments and bio-indication.

In addition all samples and vouchers will be made available through the GGBN Data Portal (http://www.ggbn.org).

Distribution and diversity of diatom assemblages in the sediments of Turgoyak Lake (Southern Ural, Russia)

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Lake sediment sequences provide an informative historical record of changes in lake ecosystems and their surrounding areas. Reconstruction of past environment is usually based on chemical information from sediments or microfossils. Diatoms are generally used to infer environmental changes. The main aim of the study was to reconstruct changes in lake ecosystem using diatom complexes from *lake sediments* from Southern Ural, Russia. The Turgoyak Lake (N 55°09'; E 60°05) is located in the Chelyabinsk Region (the South Ural Mountains, Russia). Lake Turgoyak was investigated and sampled during the KFU expedition in July 2017. The 560 cm-long lake sediment core covers the time from 27000 cal years BP to the present-day. The technical treatment of sediment samples for diatom analysis was performed using the standard water bath method (Battarbee 1986). Where possible, a minimum of 300 diatom valves were counted in each sample using a Zeiss AXIO Scope.A1 light microscope at 1000x magnification. According to preliminary results, the fossil diatom flora from Lake Turgoyak consists of 48 species that belong to 31 genera. The spectra are dominated by planktonic, oligotrophic and alkalinophilous to neutrophilous forms. The species-rich genera include Amphora Ehrenb. ex Kütz., Tabellaria (Ehrenb.) Kütz., Diploneis (Ehrenb.) Cleve, Navicula Bory, Staurosirella D. M. Williams & Round, Gomphonema Ehrenb., Cymbopleura (Krammer) Krammer, Cymbella C. Agardh and Cavinula D. G. Mann & Stickle. At the same time, the presence of centric diatoms Ellerbeckia arenaria (D. Moore ex Ralfs) R. M. Crawford indicates the well-developed littoral vegetation, probably with an inclusion of separate species of mosses. The presence of representatives of the genus Campylodiscus Ehrenb. ex Kütz. spp. reveals the high degree of water transparency in the lake.

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Seasonal diatom variability of Yunlong Lake — a case study based on sediment trap records

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Seasonal patterns of diatom succession can provide an important reference for paleolimnological interpretations, and lakes in the monsoon region, with distinct seasonal variations, are well-suited for this type of study. Yunlong Lake, a subtropical alpine lake in southwest China, was selected for a sediment trap diatom study during the interval from September 2013 to August 2015. Combining the results with the analyses of meteorological records, water temperature monitoring and monthly water chemistry sampling, we made the following conclusions. First, the whole-year normal growth pattern of both tychoplanktonic and euplanktonic diatom species, as well as the overall high abundance of benthic species, reflects the unusually strong mixing characteristics of the lake, which is ensured by the entire upper 7-m of the water body throughout the year. Second, we found a biannual warm-cold season diatom response pattern which was mainly controlled by water temperature. The warm season was from May to November, with an overall higher water temperature, and the representative species were Aulacoseira granulata (Ehrenb.) Simonsen and Achnanthes catenata J. Bílý & Marvan; and the cold season was from December to April, with a lower water temperature and stronger turbulent mixing, which induced the blooming of species such as Cyclotella asterocostata B. Q. Lin & al., Cyclotella balatonis Pant. and Aulacoseira ambigua (Grunow) Simonsen. Third, changes in the concentration of silica also influence the succession of diatom assemblages, causing planktonic species to bloom in the sequence of A. ambigua - C. asterocostata -Cyclotella stelligera Cleve & Grunow - C. balatonis - Cyclotella pseudostelligera Hust. during the first cold season. This indicates that smaller-sized diatom species are more successful in obtaining nutrients. Fourth, there were interannual differences in the diatom assemblages, especially in the abundance of C. balatonis and the occurrence of Asterionella formosa Hassall during the second cold season, which was probably related to the significantly increased lake trophic status in the second year.

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