



The 8th IAL Symposium Lichens in Deep Time August 1–5, 2016 Helsinki, Finland

IAL8 Abstracts

Welcome Messages, pages 3, 5

Opening Address, page 7

Abstracts of keynote lectures, pages 10–17

Abstracts of oral presentations, pages 21–82

Abstracts of poster presentations, pages 85–199



Thorsten Lumbsch
IAL President



Welcome Message The President of the International Association of Lichenology

Dear Fellow Lichenologist,

It is a great pleasure for me to welcome you to IAL8 in Helsinki on behalf of the IAL Council and the Scientific Committee of the symposium.

Since the inaugural IAL meeting in Münster in March 1986, our society has had tremendously successful and enjoyable meetings. I still remember the first meeting when, for the first time, I met a number of prestigious colleagues and – as an undergraduate student – could interact with colleagues in a relaxed atmosphere. These meetings are especially vital for students and early career scientists where they can interact with colleagues and build networks. Older scientists, like myself, can pass on essential guidance to younger scholars, while at the same time also learn from their new and bright ideas. We are confident that this 8th Symposium in Helsinki will be equally as memorable as the previous ones. Helsinki has a rich history and tradition in lichenological research and we are looking forward to this event, entitled "Lichens in Deep Time". Contributions to the symposium will reflect the latest trends in using genomic data to better understand the lichen symbiosis and the evolutionary history of its partners, have a strong part in ecological studies, address the threats imposed by rapid man-made changes occurring to the biosphere and an ever-growing interest in tropical lichens. The topics discussed at the symposium will be as diverse as the field of lichenology itself is today.

In addition to the scientific presentations and discussion, there is an opulent and exciting social program. Numerous excursions have been organized which I am confident will produce new friendships and collaborations. The scientific committee is optimistic that you will not only enjoy excellent science, but also engage in stimulating interaction with colleagues and a sense of community in one of the major capitals of lichenology.



Marko Hyvärinen,
Chairman of the Local
Organising Committee



Welcome Message from the Local Organising Committee

Dear Colleagues,

It gives me great pleasure to welcome you on behalf of the local organising committee to IAL8. We are very excited to be hosting this important conference in Helsinki. We hope to follow in the successful footsteps of the previous IAL symposia and make this event as enjoyable as the previous ones.

Four and a half years ago, right after the inspiring 7th IAL Symposium in Bangkok, we started planning the content of its successor. During our first brainstorming sessions it was decided that the motto of the congress should be "Lichens in Deep Time", referring to different timescales in evolution, ecology, and environmental change as well as in the history of lichenology. Our wide selection of sessions reflects this idea of exploring changes in lichens at different timescales and also changes in the way we perceive the very concept of a lichen. To our satisfaction this setting of sessions was well received by the lichenological community, and we now have more than 350 presentations to follow and enjoy during the congress week.

The previous IAL symposia have proven to have a significant impact on the scientific activity in the field of lichenology in hosting countries. Invigorating our long tradition in lichen research is one of the major incentives for us to host the congress. However, together with the science we also want to celebrate public outreach. The ways to communicate the value of science and present the beauty of lichen diversity are variable and some of these ways are presented during the social programme of the week as well as in the pre- and post-congress excursions organised by our collaborators in the universities of Turku and Oulu. We in the Finnish Museum of Natural History 'Luomus' are especially proud to announce the publication of the brand new book, "Lichens of Finland" that is based on the award-winning Finnish books "Suomen jäkäläopas" and "Suomen rupijäkälät".

We welcome you all, and particularly those of you, who have had to travel far to join us; we wish you all a pleasant and fruitful stay.

Tervetuloa jäkälöitymään! (Welcome to get lichenized)



Leif Schulman,
Director of the Finnish
Museum of Natural
History 'Luomus'

LUOMUS
FINNISH MUSEUM OF NATURAL HISTORY

Opening Address CEO, Finnish Museum of Natural History 'Luomus'

Dear Lichenologists,

On behalf of the Finnish Museum of Natural history 'Luomus' and the University of Helsinki, I am very pleased and happy to welcome all 300 delegates from 46 countries who have honoured us by taking part in IAL8 in Helsinki.

Lichens in Deep Time is a most suitable topic for a congress at the University of Helsinki, which has a deep tradition in lichenology. This history is reflected in the exceptionally rich lichen collections that we at Luomus are proud to keep for current and future generations of researchers. They are a part of Finland's national natural history collections, the care of which is the core duty of Luomus. In addition, Luomus is constituted to conduct research on the collections and display them to the public. These duties are intertwined in a fruitful interaction – indeed like the symbionts of a lichenized fungus – and I hope you will have some time to familiarise yourselves with and benefit from all these resources of Luomus.

I wish to express my warmest thanks to the IAL Council led by the President of the IAL, Thorsten Lumbsch and to the Local Organising Committee led by Marko Hyvärinen for their joint venture to build a platform for fascinating and informative scientific presentations. The scientific programme of the conference looks impressive and seems to address questions that have wide relevance far beyond the borders of lichenology. I hope that the exciting social programme will entail plenty of opportunities for stimulating conversations and relaxation.

I wish you a productive symposium and fruitful discussions, and hope that IAL8 will have a major impact on the international community of lichenologists.

IAL Council (2012–2016)

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KEYNOTE LECTURES



Dr. Silke Werth (Karl-Franzens-Universität Graz) has been an assistant professor (Universitätsassistentin) at the University of Graz since 2014. She has a diploma from the University of Tromsø (Norway) in lichen community ecology, and a PhD from the University of Berne (Switzerland). Her thesis on the dispersal biology and population genetics of the tree lungwort, *Lobaria pulmonaria* was awarded in 2005. As a post doc at the University of California, Los Angeles, she worked on the phylogeography of the lace lichen, *Ramalina menziesii* in coastal western North America between 2005 and 2008. She then studied the phylogeography of *Lobaria* sp. and its lichenicolous fungus *Tremella lobariacearum* in Macaronesia, and the population genetics of the endangered riparian shrub *Myricaria germanica* in Central Europe at the Swiss Federal Research Institute WSL (Switzerland). Werth was awarded a Marie Curie fellowship and two project grants by the Icelandic Research Fund to study the population genomics of the common terricolous lichen *Peltigera membranacea* at the University of Iceland. Her current research integrates traditional lichen ecology with population genetics and genomic approaches using *Peltigera membranacea* and *Lobaria pulmonaria* as study systems. She has published on population genetics and the phylogeography of lichens, including review papers on lichen population genetics and lichen biogeography. She recently coauthored a book chapter on how high-throughput sequencing can be used to study the population biology of lichens.

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Lichen population genetics in the era of high throughput sequencing

Silke Werth

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Population genetics deals with the distribution and amount of genetic variation in populations and with changes of this variation over space and time. In the past decade, population genetics has received attention in lichenized fungi and their photobionts, mostly based on neutral markers. We have learnt that each species shows unique population genetic patterns. I discuss lichens as a system for population genetic studies, highlighting how lichens differ from other types of organisms regarding some important traits that might be directly reflected in microevolutionary processes. Sessility, leptokurtic dispersal curve, dependency on specific environmental conditions, and other traits lead to the prediction that populations of lichenized fungi should be under strong natural selection. However, with most studies focusing on neutral markers, the role of natural selection may not have been recognized yet. Even so, some studies have reported environmental or climatic associations of genotypes, which might be due to selection. High throughput sequencing (HTS) has the potential to transform lichen biology and result in many important discoveries, such as finding loci under selection, unveiling intrathalline biodiversity, highlighting how genes are expressed in response to environmental cues, and revealing how important epigenetic and genomic variability are for the persistence of individuals under specific environmental conditions, including environmental stress. To make the most of HTS data, we need to work across disciplines. Also, certain questions can only be answered if we perform experiments under controlled conditions. I will show examples from ongoing work and point out some promising avenues for future research.



Prof. Bruce McCune (Oregon State University) is a professor in the Department of Botany and Plant Pathology at Oregon State University, USA, where he teaches courses in the lichenology, bryology and the analysis of ecological community data. His research interests include temperate forest epiphytes, biological soil crusts, methods for the multivariate analysis of community data, lichen ecology and the taxonomy of lichens. His research group's work on lichen ecology includes management applications. For example, the group has studied the long-term consequences of green-tree retention, how different species and functional groups of lichens are distributed in young, seemingly monotonous forests, and whether the structure of young forests can be changed to enhance the re-entry and development of old-growth-associated epiphytes. His research on analytical tools concerns how species abundance as a response variable differs from the ideal variables, how this creates problems, and how to deal effectively with them. His current research in this area focuses on species response surfaces in multidimensional predictor spaces, using methods that are open to any functional form, nonlinearities in response and interactions among predictors. He has authored or co-authored 175 peer-reviewed publications and seven books. He is the lead author for the software packages PC-ORD and HyperNiche.

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Three powerful tool sets in lichen ecology: critical issues and opportunities

Bruce McCune

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I critically examine three powerful tool sets in lichen ecology that have fostered substantial contributions and are likely to receive heavy or increasing use in the coming years. These tool sets include species distribution (or habitat) modeling, field transplant experiments, and analysis of ecological traits. For each of these tool sets I discuss the ecological questions that they address, some example contributions, and critical issues with their application. *Species distribution modeling* is an important tool set for addressing climate change effects on lichens, but the methods can be mathematically opaque, conceptually naive, divorced from the species biology, and give results with inadequate characterization of prediction error and response surfaces. *Field-based transplant experiments* have been extremely productive in lichen ecology, but we have barely begun to appreciate the temporal stability or instability of the results, as revealed by multi-year studies showing large fluctuations in growth rates from year to year. *Analysis of ecological traits* of lichens is an increasingly popular effort to link performance of different kinds of lichens under various environments and disturbance regimes in a way that transcends particular species on particular continents. While methods for analyzing ecological trait data have proliferated, including advances that allow non-linear responses to environment, definition and widespread measurement of non-trivial quantitative traits for a large number of species has been virtually stalled at the starting line.



Dr. Ward Wheeler (American Museum of Natural History) is the Curator of the Division of Invertebrate Zoology, AMNH. His research focuses on systematic theory and its application to the historical relationships among and within a number of metazoan lineages. He has developed theory and algorithms to interpret evolutionary patterns from multiple sources of phylogenetic information including anatomy, behavior, and a diversity of genomic information. Lately his research has expanded to integrate linguistic, ethnographic and genetic information of human populations. Dr. Wheeler's funding has been equally diversified with grants received from DARPA, NASA and NSF, among others. His laboratory at the AMNH reconstructs evolutionary trees to determine how metazoan taxa and their anatomy and genomes have evolved over the past 500 million years. Dr. Wheeler has built a series of high performance cluster computers to analyze these data, some of the fastest in the world for phylogenetic research. He, along with a team of researchers and graduate students, seeded the high-performance computing facility beginning with a commodity cluster some 20 years ago, built and used to analyze phylogenetic relationships among and within species of invertebrates. This technology is put to use in the American Museum's quest to link extinct lineages with the genomes, morphology, and behavior of species that survive today. Dr. Wheeler serves as Curator-in-Charge of the AMNH Science Computing Facility and professor of the Richard Guilder Graduate School. Dr. Wheeler joined the Museum in 1989 and has authored over 150 scientific publications and books, including a general textbook of systematics. He has also authored software packages (e.g. POY), and has been awarded a US patent in DNA sequence analysis.

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The new-er systematics: taking phylogenetics to the next level

Ward Wheeler

American Museum of Natural History, NY, USA

Technical, intellectual, and conceptual advances have come to historical biology at rate previously un- contemplated. This is beginning to allow systematists to approach problems and investigate phenomena long thought inscrutable. Perhaps the most powerful synthesis we will be able to make is among molecular biology, comparative anatomy, and Earth history. A new era of of exploration and investigation beckons and we will be drawn in excitement.



Prof. Markku Kulmala (University of Helsinki) is the Director of the Division of Atmospheric Sciences at the Department of Physics. He leads the Centre of Excellence in Atmospheric Science consisting of 280 physicists, meteorologists, chemists, forest scientists and biologists. Kulmala has also headed two Nordic Centres of Excellence as well as the NordForsk Graduate school. He has coordinated the European Integrated project on Aerosol Cloud Climate and Air Quality Interactions, and has participated in 36 other EU projects, most of them as a PI. His current research unit consists of 150 scientists, and he also leads a research group in Aerosol and Environmental Physics totalling 60 persons. Kulmala is a leading international expert in atmospheric aerosol science and one of the founders of 'terrestrial ecosystem meteorology'. His work covers theoretical and experimental physics, atmospheric chemistry, observational meteorology, biophysics and biosphere-aerosol-cloud-climate interactions. His main scientific goal has been to decrease scientific uncertainty about global climate change issues, particularly those related to aerosols and clouds. Kulmala has created a comprehensive research programme including continuous long-term atmospheric observation, global modelling, as well as deep theoretical and experimental investigation of atmospheric cluster and aerosol dynamics. He has published over 700 studies in geosciences, chemistry, physics and environmental studies, and has been the world's most referred geoscientist since 2011. He has also won several prizes and awards such as the Finnish Science Prize in 2003, International Aerosol Fellow Award of the International Aerosol Research Assembly in 2004, and Fuchs Award in 2010.

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Biosphere – atmosphere interactions and feedbacks

Markku Kulmala

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The Earth is facing several environmental challenges on a global scale, called "Grand Challenges". The growing population needs more fresh water, food and energy, which will affect our climate and air quality, and cause ocean acidification, loss of biodiversity and shortages of fresh water and food supplies. The Grand Challenges are the main factors controlling human well-being and security as well as the stability of future societies. Since the Grand Challenges are highly connected and interlinked, they cannot be solved separately. Therefore, the development of a framework is needed in which a multidisciplinary scientific approach has the required critical mass and which is strongly connected to fast-tracked policy making.

Concentrations of reactive gases, greenhouse gases (GHGs) and atmospheric aerosol particles are tightly connected with each other via physical, chemical and biological processes occurring in the atmosphere, biosphere and at their interface. Human and socioeconomic actions, such as emission control policies, urbanization, forest management and land use change, as well as various natural feedback mechanisms involving the biosphere and atmosphere, have substantial impacts on the complicated couplings between atmospheric aerosols, trace gases, GHG, air quality and climate. Our first quantification of the COBACC (*C*ontinental *B*iosphere-*A*erosol-*C*loud-*C*limate) feedback loop (Kulmala *et al.* 2014a) was based on continuous comprehensive observations at SMEAR II (Station for Measuring Forest Ecosystem-Atmosphere Relations) station in Hyytiälä, Finland, and showed that a 10 ppm increase in atmospheric CO₂ concentration leads to a significant (several percent) increase in both carbon sink and aerosol source. These effects operate through changes in gross primary production, volatile organic compound (VOC) emissions and secondary aerosol formation associated with atmospheric oxidation of VOCs. This feedback loop demonstrates the importance of biospheric processes on the whole climate system.

ORAL PRESENTATIONS

Lichens in the history of botany

Per Magnus Jørgensen

University of Bergen, Norway

Ever since the term lichen was coined by Theophrastos (c.300 B.C) it has been difficult to classify them. It took 2000 years before Tournefort took up Lichen as a generic name, including the hepatics. Michelius in 1729 defined the group without the bryophytes and divided it into several "genera" called Ordo. Unfortunately Linnaeus followed Tournefort placing all in one genus. However, his student Acharius devised a new taxonomy in 1803, using fruiting-bodies to divide the genus, but did not take the full consequences thereof. Later, however, Lichen was split into several genera. The greatest splitter Massalongo in the mid 1800 described numerous new genera, mainly based on spore-characters. Much debate followed. The strongest opponent William Nylander maintained that no character should be given more weight than any other. About this time Schwendener discovered another controversial fact, the so-called double nature of lichens. This was hardly reflected in the next major classification-attempt by A. Zahlbruckner in 1906. His system prevailed through that century in spite of several attempts of modernizing. In 1953 Santesson classified all foliicolous lichens in the new fungal system proposed by Nannfeldt. Gradually it was accepted that lichens are specialized fungi needing to be incorporated in the fungal system.

The early history of Canadian lichenology

Irwin Brodo¹, Stephen Clayden², Trevor Goward³

¹Canadian Museum of Nature, Ottawa, Canada, ²New Brunswick Museum, Saint John, Canada, ³Beaty Museum, University of British Columbia, Vancouver, Canada

The lichens of Canada were unknown to non-indigenous people until early explorers of the northern regions brought back samples to Europe. The history of Canadian lichenology thus begins with the early records of Joseph Banks (1766) and continues with the surveys of Dominion Botanist John Macoun and others in the late 19th and early 20th century until the 1950s with the collections of mycologist, Roy Cain. The appointment of Ivan Mackenzie Lamb at the National Museum of Canada in 1950 began a new era of lichenological activity.

William Nylander, the defender of lichen autonomy

Orvo Vitikainen

Finnish Museum of Natural History, University of Helsinki, Finland

The life and significance of William Nylander (1822–1899) is surveyed with notes on and from his extensive correspondence. William Nylander, Doctor of Medicine, was a versatile biologist – entomologist and botanist – when commencing lichenological research. In this period several new classifications of lichens were introduced, but Nylander soon presented his own 'natural' system to supersede the previous 'artificial' ones. Some of his ideas were gradually adopted by colleagues but his concepts of genera were often criticized as too broad and species concepts too narrow. Neither did his system gain general support. Nylander published profusely on lichens, the material being provided from all continents by his numerous correspondents. His intended synopsis, however, discontinued half-way in lack of funding. He in many ways promoted lichenology e.g. in the British Isles and continental Europe plus North America but his polemics and habit to dismiss the ideas of others as well as expectation of due obedience to his principles alienated many colleagues, an absolute requirement being rebuffing the 'Schwendenerian heresy' of the dual nature of lichens. This campaign Nylander eventually lost but he took as personal credit and consolation that he at least delayed the breakthrough of the new doctrine.

Discovering Australia's lichens – from seafaring collectors to a continental flora

Gintaras Kantvilas

Tasmanian Herbarium, Tasmanian Museum and Art Gallery, Sandy Bay, Australia

The discovery of Australia's lichen flora begins in the late 18th Century with the European sea-faring explorer-botanists, including Labillardière, Brown and Hooker. Their work inspired resident collectors who sent specimens to European herbaria to be studied by the leading lichenologists of the time, including Müller Argoviensis, Stirton and Nylander. Thus by the beginning of the 20th Century, many species had been described from Australia, there were several regional accounts, and a bibliography. The resurgence of lichenology in the 1960s in Europe was mirrored in Australia where Peter James played a major role. The Sydney Botanical Congress in 1981 that brought many international lichenologists to Australia was inspirational, as was David Galloway's New Zealand work. There followed a remarkably productive period of collecting and species discovery, led chiefly by Australians but aided by visitors from abroad. Today Australia boasts a continental lichen flora, an actively maintained checklist of nearly 4,000 taxa, a bibliographic index, and lichens feature prominently in national species discovery programmes. The question "Where to now for Australian lichenology?" is considered. Two critical ingredients for a positive future – comprehensive herbarium collections and a solid literature base – are well provided for, but dwindling and aging personnel pose a problem.

Amber as source of Mesozoic and Cenozoic cryptogams

Alexander Schmidt¹, Ulla Kaasalainen¹, Christina Beimforde¹, Jochen Heinrichs², Jouko Rikkinen³

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Preservation in amber is renowned for its microscopic fidelity, including cells and organelles. Although arthropods represent the majority of amber inclusions, fossil resins preserved a much wider range of organisms of past forest ecosystems, from prokaryotes to vertebrates. This variety also includes eukaryotic algae, liverworts, mosses, vascular plants, and fungi. Amber is found in hundreds of localities and it is most abundant in Cretaceous and Eocene to Miocene strata. State of the art preparation and screening methods permit access to micrometre-sized morphological and anatomical features of the fossils. Amber inclusions of cryptogams representing extant lineages have successfully been used for the dating the phylogenies of ascomycetes, bryophytes and ferns. However, lichens have been considered to be rare in amber and less than a dozen of specimens has been reported so far. Our recent screening of amber collections multiplied the fossil record of Cenozoic lichens as approximately 150 specimens were newly discovered. These fossils witness species-rich Paleogene lichen floras, and the evaluation of preserved cryptogamic communities supports the palaeoecological reconstruction of the 'amber forests'. Whereas the amber fossil record of bryophytes, ferns and fungi already extends back to the Lower Cretaceous, Mesozoic amber-preserved lichens still await discovery.

Lichens in Paleogene amber

Ulla Kaasalainen¹, Jouko Rikkinen², Alexander Schmidt¹

¹University of Göttingen, Germany, ²University of Helsinki, Finland

Amber is fossilized resin of gymnosperm and angiosperm trees. It is famous for its lifelike preservation of arthropods, plant remains, and microorganisms, and even the preservation of soft-bodied microorganisms has cellular and ultrastructural fidelity. Since many lichen species grow as epiphytes on tree trunks, also lichens occur as fossils entrapped in amber. However, only few specimens have been described so far. Our study focused on European Paleogene amber inclusions, preserved 47–23 million years before present. In addition to macromorphological features, the identification of the fossil lichens is based on ultrastructural features and on chemical analyses of organic molecules. Our results reveal a highly diverse Paleogene lichen flora, and also groups that are absent in Europe today were present. Of the modern lineages, especially family Parmeliaceae is abundantly represented as amber inclusions. The plethora of available material and application of geobiological methods permit for the first time a large-scale reconstruction of fossil lichen communities including interactions of lichens with associated fungi, arthropods, and plants. In addition, the Paleogene lichens and lichen communities can be compared to extant ones in order to track and analyze the essential evolutionary changes in community structure, photobionts, ecology, and secondary chemistry.

Lichen-associated microfungi from European Paleogene amber

Elina Kettunen¹, Alexander Schmidt², Paul Diederich³, Heinrich Grabenhorst⁴, Jouko Rikkinen¹

¹University of Helsinki, Finland, ²University of Göttingen, Germany, ³National Museum of Natural History, Luxembourg, ⁴Geological-Palaeontological Institute and Museum of the University of Hamburg, Germany

While most lichenicolous fungi are presumed to have shared a long history of evolution with their symbiotic hosts, fossil evidence of such microfungi has been lacking. However, recently we have found fossils of lichen-associated fungi from European Paleogene amber. Several fossils of filamentous darkly pigmented hyphomycetes growing on lichen thalli were found preserved in Bitterfeld and Baltic amber. The minimum age for Bitterfeld amber is 24 million years, and for Baltic amber 35 million years. Non-destructive imaging using light microscopy allowed detailed comparison with extant analogues. The fossil fungi are filamentous ascomycetes, some closely resembling extant genera *Sporidesmium* and *Taeniolella*. The lichen-associated species of these groups are saprotrophic or weakly parasitic. Our results demonstrate that diverse filamentous ascomycetes grew on lichens at least since Paleogene. As the fossils closely resemble their modern analogues, the evolutionary associations between lichen-associated microfungi and their substrate must extend back much further, most probably to the Mesozoic.

Insight into diversification of lichen-forming fungi in western North America: from the Neogene through the Quaternary

Steve Leavitt

The Field Museum, Chicago, IL, USA

Evolutionary histories of biota in western North America have been impacted by complex geological and climatic factors, including mountain building, desert formation, and wide climatic fluctuations. A variety of scenarios characterizing geobiotic change in western North America have been proposed. Generally, mountain building is thought to fall into two major periods of uplift, the Laramide uplift, ca. 70–50 Ma, and the Neogene uplift, ca. 15–2 Ma. The timing of desert formation is less clear, with some authors suggesting that the deserts existed as far back as 15 Ma while others propose that desert formation occurred as recently as 10,000 years ago. In spite of the uncertainties in reconstructing geomorphological changes in western North America, taking earth history data and models into account can offer important insight into the evolutionary history of biota occurring in this region. Here I attempt to synthesize relationships among the timing of diversification events for a number of lichen-forming fungal groups with major geological and climatic changes in western North America. I also explore the impact of Pleistocene glacial fluctuations on demographic histories for a number of common lichen-forming fungal species in western North America.

Integrative taxonomy of fungi: a review from the progress in Parmeliaceae

Ana Crespo, Pradeep K. Divakar

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The current phylogeny of Parmeliaceae (PARSYS 08, and PARSYS 14) is based on multiloci analyses and a large sampling. It is likely one of most solid phylogenetic information in fungal families. The huge collaborative effort was essential for this achievement. Such a background allowed us to answer evolutionary questions and to identify groups requiring further investigations. Specifically to: i) establish the monophyly and relations among internal clades; ii) estimate the divergence time of the taxa, suggesting correlations with climatic changes in the past; iii) reconstruct ancestral character state and range distribution, and revealing a key innovative traits responsible for lineage diversification; iv) shed a light on the evolutionary rates of tropical vs non-tropical clades and their correlation with habitat; v) expose diversification shifts at the nodes in the family; vi) uncover a high number of cryptic species; this has shown that the phenotypical features are insufficient to delimit species boundary; and vii) as a main conclusion, we propose the following operational criteria for generic circumscription in fungi: a) the genera should be monophyletic, b) it should have distinct divergence time than its closely related groups, and c) the lineage should be corroborated with ecological, geographical, or morphological features

Phylogeny and species delimitation in the lichen genus *Cetrelia*

Kristiina Mark, Tiina Randlane, Andres Saag

University of Tartu, Estonia

The genus *Cetrelia* W.L. Culb. & C.F. Culb., currently containing 18 species, is phylogenetically related to *Xanthoparmelia* and other parmelioid genera within the family Parmeliaceae. The genus is characterized by broadly lobed thalli, laminal pseudocyphellae on the upper surface, atranorin in the upper cortex and various orcinol depsides and depsidones in the medulla. Both apothecia as well as propagules of vegetative reproduction (soredia, isidia and lobules) are known in the genus. The species are traditionally described as combinations of morpho- and chemotypes, while extensive molecular studies have not been performed to evaluate the species monophyly in *Cetrelia*. A dataset of four nuclear markers (ITS, IGS, RPB1 and MCM7) were generated for 46 samples of 11 *Cetrelia* species, representing four morphotypes (out of five) and all six chemotypes. Bayesian and maximum likelihood analyses of the concatenated dataset demonstrated that a relatively well-resolved phylogeny where currently accepted, so-called morphochemical species generally appeared justified. Species of the same chemotype (e.g. *C. braunsiana*, *C. chicitae*, and *C. orientalis*) form monophyletic clades with subclades according to their morphotypes. Treatment of taxa of the same, for example, sorediate morphotype (i.e. *C. cetrarioides*, *C. chicitae*, *C. monachorum* and *C. olivetorum*) as one species is not phylogenetically acceptable.

Infrageneric classification and biogeography of the genus *Bryoria* based on phylogenetic analyses of six gene loci

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Species within the genus *Bryoria* (Parmeliaceae, Lecanoromycetes) are distributed mainly in boreal to north temperate regions of Eurasia and North America, but occur also in mountains of southeast Asia, Australasia and Africa. Here we use information on six gene regions – three nuclear protein-coding markers (Mcm7, GAPDH and Tsr1), two nuclear ribosomal markers (ITS and IGS), and a partial mitochondrial small subunit – to examine infrageneric classification and putative phylogeographic structuring of the genus. Our analyses support the monophyly of sections *Americanae*, *Divaricatae*, *Implexae* and *Tortuosae*, while section *Bryoria* is polyphyletic. Addition of gene regions generally resulted in improved support values for the nodes. Monotypic sections *Americanae* and *Tortuosae* are genetically distinct from the remaining taxa and appear as basal lineages in the genus. We discovered a clear phylogeographic pattern in some of the lineages. In section *Implexae* the species are divided into two subclades based on their geographic distribution: the first subclade appears to occur exclusively in North America while the second subclade is intercontinental. Section *Bryoria* is here provisionally divided into two sections, i.e., section *Bryoria* 1, which includes species restricted to southeast Asia and/or northwest North America, and section *Bryoria* 2, which contains mostly broadly distributed species.

Systematics of the shrubby-apotheciate corticolous species of the genus *Usnea* Adans. (Parmeliaceae) in Southern Brazil

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Usnea is a highly supported monophyletic and megadiverse cosmopolitan genus. The taxonomy of this group is considered exceptionally difficult due to the extensive morphological and chemical variability within species and a molecular approach is needed to evaluate species delimitation. Shrubby-apotheciate species are characterized by the erect-bushy thallus, the usually numerous apothecia and the absence of vegetative propagules. For the first time, we provide systematics of shrubby-apotheciate corticolous species occurring in Brazil based on integrative taxonomy approach i.e morpho-anatomical, chemical and molecular features. Newly collected and herbarium material were analyzed with standard methods used in *Usnea* systematics. Fourteen species were reported: *U. cirrosa* Motyka, *U. cladocarpa* Fée, *U. concinna* Stirt., *U. cristatula* Motyka, *U. erinacea* Vain., *U. fleigiae* sp. nov., *U. grandispora* sp. nov., *U. jamaicensis* Ach., *U. lunaria* Motyka, *U. meridionalis* Zahlbr., *U. parvula* Motyka, *U. steineri* Zahlbr., *U. subelegans* (Vain.) B. de Lesd. and *U. subparvula* sp. nov. For the molecular analyses we sequenced ITS rDNA, Mcm7 and RPB1 markers. A concatenated dataset with 55 specimens from 25 *Usnea* species were analyzed with maximum likelihood and Bayesian inferences. The three new species based on traditional characters were supported by the molecular analyzes.

The genus *Parmotrema* in New Zealand: investigating species diversity and phylogenetic relationships

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Parmotrema (Parmeliaceae) is a widespread and well-collected genus worldwide, with perhaps 350 species. Many species in the genus have been considered to be widely distributed, but use of molecular data has uncovered cryptic species. In New Zealand, seventeen species are recognised, none of them endemic and many with a cosmopolitan or pantemperate distribution. We used sequence data from the nuclear ITS and LSU regions for sample identification and to clarify whether collections from New Zealand are the same species as those recorded elsewhere. Phylogenetic analysis was carried out using RaxML on a concatenated dataset of the nuclear ITS and LSU regions allowing the best-fit model of each locus and the GTRGAMA+I model. Our results show three main conclusions: (1) Some species (*P. reticulatum*, *P. subtinctorium* and *P. tinctorum*) are indeed present in New Zealand. (2) Some collections previously attributed to species based on morphological or chemical characters do not match non-New Zealand sequence data and may represent undescribed species. (3) Collections named as *P. reticulatum* and *P. subtinctorium* fall into two separate clades in each case, again suggesting the presence of cryptic species and in the latter case one clade may belong to *P. subtinctorium* and the other *P. haitiense*.

Picking holes in traditional species delimitations: an integrative taxonomic reassessment of *Parmotrema perforatum* group (Parmeliaceae, Ascomycota)

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Accurate species delimitation is important since species are a fundamental unit in biological research. In lichenized-fungi, species delimitation has been difficult due to a lack in taxonomically important characters and due to the limits of traditional, morphology-based species concepts. We apply an integrative approach to reassess the taxonomy of the *Parmotrema perforatum* group; six closely related species divided into three species pairs, each pair comprising one apotheciate (sexual) and one sorediate (asexual) species. Each pair is further characterized by a distinct combination of secondary metabolites. Species boundaries were reexamined using an integrative approach incorporating morphological, chemical, and molecular sequence data to delimit species boundaries. Phylogenies were inferred from a seven-locus DNA sequence dataset using both concatenated gene tree and coalescent-based species tree inference methods. We employed multispecies coalescent method implemented in the program BP&P to validate candidate species. Micromorphological measurements of conidia were found to be congruent with clusters found in the phylogenetic analyses, uncovering unknown evolutionary relationships. Each approach that we applied to the *P. perforatum* group consistently recovered four of the currently circumscribed species *P. perforatum*, *P. hypotropum*, *P. subrigidum*, and *P. louisianae*, while *P. preperforatum* and *P. hypoleucinum* were consistently interpreted as conspecific.

Is it the more lichens the merrier, for open-air rock-art conservation?

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Open-air rock-art is found throughout the world and its conservation is interdisciplinary by nature, bringing in perspectives from archaeologists, conservators, geologists and biologists. Attempts to determine the conservation status of the open-air rock-art complex located in north-east Portugal, and inscribed in UNESCO's World Heritage List, have led to the development of an Intervention Urgency Scale (IUS) based on a set of variables taken from representative surfaces. The present study aims to link taxonomical and ecological knowledge about species assemblages on rock surfaces and the evaluation of biodeterioration state of associated rock-art, by assessing the relationship between local-scale patterns of lichen diversity and the IUS. A total of 205 lichens have been reported from the studied rock outcrops. A strongly reduced subset of surrogate species and species functional groups based on selected vegetative traits, accurately reproduced overall lichen species richness. When crossed with data on the IUS, a statistically significant negative correlation was found in terms of lichen species richness and current deterioration state of the engraved surfaces. The role of lichen species richness is discussed as an indicator of outcrop stability that may constitute a useful tool in rock-art condition assessment and monitoring within the study area.

Structure and form of an Atacama fog-oasis lichen community across a fog gradient

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The fog oases of the Atacama desert are a spectacular yet largely unexplored example of lichen dominated ecosystems, providing an excellent model for the study of lichen community responses to environmental gradients. Regular fogs provide the primary water input to the coastal slopes, sustaining a remarkably high diversity in the absence of rainfall. We sampled lichen communities across a 400 m altitudinal gradient, ranging from the lowest limit of lichen occurrence to the summit of the coastal range. Microclimatic sensor data supports the expectation of a strong vertical gradient in water availability, with fog frequency peaking around 600 m elevation and wetting duration around 800 m. Species diversity showed a similar distribution, ranging from 5 taxa at the lowest elevation to >35 at 700 m, with a total of 76 distinct taxa recorded. Although all growth forms were most abundant at 700 m, crustose lichens were the only growth-form to dominate at low and intermediate elevations, while fruticose forms showed a distinct bias towards higher elevation (and therefore denser fog). This trend towards greater dimensionality with increasing fog was also reflected in locally abundant crustose species, with *Follmannia orthoclada* and *Roccellina cerebriiformis* both showing strongly significant trends towards sub-fruticose habits with increasing elevation.

Effects of highly specific lichenicolous fungi on the growth of their lichen hosts

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Despite the evident ecological consequences of parasitism on ecosystems, host-parasite interactions between lichenicolous fungi and their hosts have rarely been studied from an ecological perspective. Highly specific lichenicolous fungi are considered commensalistic because they only apparently modify the lichen thallus by parasitic gall induction when the parasite reproduces. Whether these parasites impact the lichen fitness is still unknown. For the first time we examined the effects of lichenicolous fungi on their hosts growth. We conducted a growth chamber experiment using *Lobaria pulmonaria* and *Lobarina scrobiculata* with and without galls of *Plectocarpon lichenum* and *Pl. scrobiculatae*, respectively. Our results indicate that lichens with galls had significantly lower growth rates although growth patterns varied in species-specific ways. In *L. pulmonaria* both biomass and area growth were reduced in parasitized thalli, but the proportionality between area and biomass was similar to healthy thalli. By contrast, parasitized *L. scrobiculata* increased their area growth, but did not increase their biomass. Thereby, they became thinner during the experiment. Given this negative influence of *Plectocarpon* on the lichen primary metabolism, we conclude it is a parasite rather than a commensalistic fungus. Lower growth rates may influence important lichen functions such as reproduction and ultimately their population dynamics.

Spatial and substrate relationships of the functional redundancy in Mediterranean lichen communities

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Species traits determine the extinction threshold in the occurrence of species living in fragmented landscapes. Below this threshold, the rate of establishment of new populations is insufficient to compensate for local extinctions. In this work we tested whether 1) the functional redundancy of lichen communities increases across spatial scales, i.e. if lichen communities are able to compensate local loss of functional diversity over larger spatial scales and 2) if patterns of functional redundancy are comparable in epiphytic vs. epilithic communities. We collected lichen diversity data on rocks and trees in Sardinia (Italy), scaling up the information through increasing spatial levels, from sampling quadrat to landscape. Each species was assigned to a functional entity (FE), based on the interactions of 3 functional traits (growth form, photobiont type and reproductive strategy). For each sampling unit, we calculated two indices of functionality: Functional Vulnerability (FV), i.e. the risk of losing FE and Functional Over-Redundancy (FOR), i.e. the overrepresentation of FEs in terms of species richness. FV was poorly correlated with epilithic species richness, whereas it showed a negative correlation for epiphytes. FOR increased with increasing number of species until reaching a plateau, being higher in epilithic than in epiphytic lichens.

Are climatic factors or habitat variation more important for epiphytic lichen richness? A case study from redwood forests

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Redwood (*Sequoia sempervirens*) forests span six degrees of latitude in a narrow strip along California's coast. From north to south, decreasing storm frequency and intensity as well as increasing fire return intervals offer a range of moisture availability, tree architectural complexity, and stand ages that translate into variation in epiphyte community composition. In a previous study in the north, high lichen richness was associated with complex crown structure, but redwood trees in the south were not considered even though they greatly extend one end of this gradient in habitat variation. Using climbing techniques to access the crowns of large redwoods, we surveyed epiphyte richness and abundance in the southern range of redwood. Compared to the north where epiphytic vascular plants and bryophytes comprised a large proportion of the species composition, communities in the south were dominated by lichens as predicted by the similar gradient hypothesis. Surprisingly however, lichen richness in the south was equal to or may even exceed richness in the north. This result suggests that habitat variation is less important for epiphytic lichen richness than climatic factors. Less frequent and lower intensity storms in the south likely constrain epiphytic vascular plants and bryophytes which opens habitat for lichens

Lichen richness and composition in pine dominated post-fire stands: impact of region, time since fire, harvest and forest structure

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Fire has been the main factor influencing the function of boreal forests by changing stand structure and species composition. Still very little is known of stand-scale post-fire succession of lichens and its potential differences along a latitudinal gradient, particularly for assemblages on burned substrates. To study these questions, standardized lichen inventories (4 hr survey per 2 ha plot) were performed in 9 middle-boreal (Finland) and 9 hemi-boreal (Estonia) mature pine-dominated stands burned 15–21 or 9 years ago (half of the recently burned sites were clear-cut just before/after the fire). The highest total and mean numbers of species occurred in recently burned Finnish forests, while the other site types had similar species numbers. GLM modelling showed only modest regional influence on species richness. Still, within the site types, lichen assemblages differed clearly between the regions (MRPP test, NMS ordination). Forest structural variables (e.g. density of live trees and seedlings, volume of logs) shaped significantly both lichen richness and assemblages. Surprisingly, assemblages on only burned substrata followed similar patterns: there was a regional difference in composition, but not in richness, indicating that charred substrates can be easily colonized by local epiphyte species pool and the assemblages are universally influenced by environmental factors

Thallus morphology rather than cyanobiont type determines photosynthetic performance in cyanobacterial lichens (Lichinomycetes)

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Lichen photosynthesis is performed by the photobiont exclusively. It can either be a eukaryotic or a prokaryotic alga (Cyanobacteria), the later contribute photobionts to about 10% of the lichen species. The Lichinomycetes comprise lichens with cyanobacteria as photobionts and many of them specifically with the unicellular genus *Chroococcidiopsis*. This genus in turn is only reported so far as photobiont of the Lichinomycetes. We studied the CO₂-gas exchange of the isolated *Chroococcidiopsis* photobiont from *Peltula euploca* and of the intact cyanolichens *Peltula euploca*, *P. euploca* var. *sorediosa*, *P. umbilicata*, *P. tortuosa*, all from South Africa, and of *Paulia perforata* from Yemen. While the photosynthetic behavior of the isolated photobiont was identical with that of a non-lichenized species of the same genus in terms of thallus water content, we found clearly different patterns for the morphologically differing lichen species. From this we conclude that thallus morphology plays an important role for the efficiency of a lichens net primary productivity in their referring habitat. Species specific morphological characteristics thus may be either derived or determined from the niche the lichen species colonizes.

Network analyses of lichens and their contribution to theoretical studies on mutualism

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There is a growing interest in ecology to characterize networks of interactions, including fungi with their photosynthetic partners (e.g., mycorrhizae, and fungal endophytes). However, little attention has been paid to the lichen symbiosis, even though such network-based analyses are likely to yield significant insights regarding the establishment and maintenance of these interactions. Here, we analyze a lichenic network involving fungi from the genus *Peltigera* and their associated *Nostoc* cyanobacterial partners, sampled at a global scale, spanning a wide variety of habitats (boreal to tropical biomes). The constructed network is significantly anti-nested, and significantly modular, which contrasts with trends expected from theoretical, modelling studies. This discrepancy between theory and our data is likely to be explained, at least partly, by the unique biology of lichens, which is not very well represented in modelling studies (e.g., simulation studies typically assume free dispersal of species across the landscape, while dispersal limitations are known to play a role in lichen communities). Our findings are expected to fuel discussions regarding network-level patterns in mutualistic systems. Because most theoretical studies on ecological networks have been parameterized to mirror plant-animal interactions such as pollinator networks, our results on lichens may shed some new light on mutualistic networks

Taxon-free detection of cross-scale assembly processes in lichen epiphyte communities

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Lichen epiphyte assemblages are formed by multiple concurrent processes, including dispersal limitation, environmental constraints, competition, and disturbance. I generated predictions for how these processes affect variation in functional strategy along environmental gradients and evaluated whether morphological characters can be used to test hypotheses predicted by this framework. I analyzed trait distributions from lichen assemblages on 720 trees across two ecoregions in the southeastern United States. Generalized linear models found trait-environment relationships that were consistent with weak effects of water-limitation, competitive constraints and disturbance due to substrate instability. However, null models found no evidence of reduced trait dispersion arising from hypothesized constraints. A lack of evidence for trait constraints combined with overall small effects sizes and low levels of explained variance in linear models suggest either an important role for stochasticity or that morphological characters have limited utility for detecting processes structuring lichen assemblages in this habitat. I also evaluated the utility of trait-based metrics for studying community variation at different spatial scales and found that morphological traits exhibited much less variability at larger scales than diversity and abundance, which limits their ability to detect large-scale processes. Trait-based studies of lichen epiphyte community assembly may find greater success with quantitative traits

Tue 2 Aug 10.15–10.35 Room 1 • ORAL 24

Can large-scale biodiversity monitoring tell us about rare lichens? Re-evaluating the distribution and ecology of *Cladonia rei* in Alberta, Canada

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Conservation of rare species depends on accurate data as well as accurate assessments of rarity. Here we test the ability of the Alberta Biodiversity Monitoring Institute (ABMI), a non-traditional, large-scale systematic monitoring program that assesses many species from many taxa simultaneously, to improve our understanding of the ecology and distribution of *Cladonia rei* Schaerer within Alberta. Historically considered broadly distributed but imperiled in Alberta with 7 known collections at the beginning of our study, we test this understanding using 5 years of ABMI lichen samples (70,181 lichen specimens, including 27,870 *Cladonia* specimens), vascular plant data, and habitat information from 778 sites across the province. Using comparative morphology, thin layer chromatography and habitat modelling, we show that *C. rei* is common where it is present, which is almost entirely within the temperate grasslands and parklands of Alberta, and exhibits a consistent phenotype within those natural regions that differs from that documented in eastern North America and parts of Europe. While the grasslands and parklands are some of Alberta's most anthropogenically-disturbed ecosystems with a long history of agriculture and human settlement, *C. rei* consistently can be found where natural vegetation persists, often in conjunction with cattle-grazing.

Symbiotically dispersing lichens as photobiont nurseries

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Some degree of specificity is required for the evolution of long-lasting relationships between symbiotic organisms. Recently molecular methods have been widely used to study photobiont diversity and symbiont association patterns in cyanolichens in different ecosystems and geographical regions. Such studies have shown that mycobionts can be highly specific in their choice of cyanobionts and may only associate with a restricted selection of compatible cyanobacterial genotypes. On the other hand, some cyanobionts associate with many different fungal species, genera or even families, and can sometimes support diverse fungal communities. This presentation gives examples of both extremes and underlines the importance of symbiotic dispersal in the evolution of high reciprocal specificity between specific pairs of lichen symbionts. It also explores the interesting analogy of symbiotically reproducing lichen thalli to plant nurseries. In both photosynthetic 'cultivars' are effectively propagated and grown to usable size. Cyanobiont genotypes nursed by specific fungal hosts compare well with plant cultivars in being assemblages of photosynthetic organisms that (a) have been selected for a particular character or combination of characters, (b) are distinct, uniform and stable in those characters, and (c) when propagated by their specific host, tend to retain those characters.

Tue 2 Aug 11.18–11.36 Room 1 • ORAL 26

A panoramic path along multiple symbiotic patterns: together or not together?

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Lichen symbioses are complex, structured associations between fungi (mycobionts) and algae (photobionts). The extent to which these associations are more or less specific, is still largely unknown, and likely correlated with the dispersal mode of the partners. Variable patterns of mycobiont-photobiont associations have been detected in lichens and other algae-associated fungi. Here we present studies based on molecular and culture-dependent approaches of fungi and algae which form either well developed or loose associations. The lichen *Tephromela atra* is a geographically widespread species complex, which present a continuum of morphological diversity and different degrees of specificity towards *Trebouxia* photobionts. The fungus *Schizoxylon albescens* shows optional lichenization with algae of the genus *Coccomyxa*, occurring both as lichen and as saprobe when growing on different substrates. The species of *Lichenothelia* and *Saxomyces*, black, rock inhabiting fungi, form loose association with multiple algae. For these fungi we tested the capacity to form lichen-like relationships with algae using culture experiments. The experiments show various types of interactions with *Trebouxia* and *Coccomyxa* and shed new light on the life-style flexibility of fungi colonizing multiple ecological niches. This further suggests these fungi to be easily controlled study systems for the investigation of lichen symbiosis under lab conditions.

Diversity and biogeography of symbiotic microalgae of the lichen genus *Psoroma*

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The specific relationship between a mycobiont and a photobiont in lichens has been challenged recently. One species of mycobiont can make symbiotic partnerships with various photobiont species when they grow in geographically distant locations. In some cases, several different algal genotypes were observed in a single thallus with NGS technology. In these cases, the microalgal community was usually composed of one major species and several minor species. To investigate the genetic diversity and geographical distribution of major and minor microalgal species in the lichen genus *Psoroma*, LSU rRNA gene sequences, which were obtained with NGS sequencing, were analyzed for samples from Australia, Chile, King George Island, Falkland Islands, and Norway. The results revealed that lots of thalli contained diverse microalgal OTUs as the previous studies. Most *Psoroma* mycobionts showed preference for *Trebouxia arboricola* lineages as a major and minor microalgal partners. Some mycobiont phylogenetic lineages formed symbiotic relationship with specific microalgal OTU as a major partner unlike the other mycobiont lineages. Lichens from Norway had simpler microalgal communities than those from other geographical areas. Although some microalgal OTUs were detected from several geographical regions including Southern and Northern hemisphere, most microalgal OTUs were recovered from specific geographical regions and climates.

Global, continental, and local genetic structure in *Lobaria pulmonaria* and its photobiont *Dictyochochloropsis reticulata*

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Lobaria pulmonaria is a widespread, though regionally rare and threatened old-growth forest dependent epiphyte that is exclusively associated with the asexual green-algal photobiont *Dictyochochloropsis reticulata*. The lichen symbionts regularly co-disperse by symbiotic propagules but sexual reproduction of the fungal symbiont and photobiont switch during early stages of the thallus development may lead to new mycobiont-photobiont combinations in populations. Populations of *L. pulmonaria* were analysed from four continents and a model-based clustering method for inferring population structure using genotype data revealed a complex distribution pattern of fungal and algal gene pools and their associations at the local, continental and global level. We test how climatic and geographic variation co-vary with associations of mycobiont and photobiont gene pools.

Is a lichen an evolutionary individual?

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The fundamental unit in evolutionary theory is a population of individuals. Yet, it is not always apparent what constitutes an individual. Challenges emerge when different types of entities, considered individuals, engage in complex interactions with each other that result in new structures that may also be new individuals. While the question of individuality could be addressed from a philosophical position, we adopt, instead, a computational approach. Assuming that an evolutionary individual should be useful in making scientific predictions, we develop a theoretical framework to find the "individual" that makes accurate and timely predictions of observables of interest. We apply this framework to a dynamical simulation of populations of fungi, algae, and lichen communities interacting in an environment. We test whether or not the lichen represents a useful individual in order to predict gene frequencies. We find that depending on different ecological parameters, i.e. niche partitions and the absence/presence of a predator, the lichen may or may not be a functional individual. Interestingly, our framework reveals that new types of individuals that are not solely lichens or algae/fungi cells perform the best in terms in making accurate scientific predictions. Our results give general guidelines for addressing the question of individuality

Macroclimate and coevolutionary forces influence fungal-algal association patterns in *Protoparmelia*

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Macroclimatic and evolutionary forces influence species diversity, and species interaction patterns. In symbiotic systems, symbiont diversity and interaction strength tend to increase towards the equator. We selected the cosmopolitan genus *Protoparmelia* s.str. which is a small group of ~25 species occupying different macroclimates to assess i) symbiont diversity and association patterns in different climatic zones, and ii) coevolutionary forces shaping fungal-algal associations. Coalescent-based species delimitation approaches indicated that 23 fungal host species are associating with 19 putative algal species in *Protoparmelia* s.str. We found that one-to-one fungal-algal relationships are more common in warmer climates, whereas one-to-many (up to 5) fungal-algal relationships are most common in cooler climates. Coevolutionary analyses with PACo, ParaFit, and Jane suggest congruent fungal-algal phylogenies. We did not find any evidence for cospeciation. Host switch is a common evolutionary event in warm climates, whereas failure of the photobiont to diverge with its fungal host is a frequent event in cooler climates. We conclude that both, the environment and evolutionary forces drive fungal-algal associations in *Protoparmelia*

Diversity of lecideoid lichens in temperate forests of South America: new insights from morphological and molecular studies

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Lecidea in the broad sense, is one of the largest genera of lichenized fungi, with over 1,400 accepted species. Previous studies revealed it to be a polyphyletic artificial conglomerate composed of many different genera, whereas only about 100 species belong to *Lecidea* s. str. During the last 30 years, great progress has been made trying to split non-saxicolous *Lecidea* into more natural groups, but temperate South America (Argentina, Chile) have received little attention. Based on morphological, anatomical and chemical characters we studied the diversity of the group in southern South America. Our studies show that its diversity in the region is three times higher than previously known. We supposed that even this number represents only about half of the species present in the area. Molecular data (ITS, nuLSU, mrSSU, RPB1 and RPB2) was generated to identify the final position of some taxa. Several new species and genera were discovered, and an update of the systematics of the group is provided. Our results allow new insights into the biogeographic distribution of several autochthonous and otherwise bipolar taxa.

Molecular study of Verrucariaceae: an Icelandic perspective

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The Verrucariaceae has been intensively scrutinized lately. Several new genera have been proposed (*Hydropunctaria*, *Atla*, *Parabagliettoa*, *Wahlenbergiella*) while others have been resurrected (*Sporodictyon*, *Bagliettoa*). With the advent of molecular phylogenetics as the main framework to circumscribe genera, it has become practically impossible to recognize genera based on phenotypic "traditional" characters, which has been the foundation of taxonomy for so many years. More than 80 species belonging to Verrucariaceae have been found in Iceland, representing 16 different genera. The present study is based on more than 150 specimens of Verrucariaceae from Iceland. Five loci were sequenced viz. nrITS and nrLSU, mtSSU, RPB1 and Mcm7. Icelandic members of *Verrucaria* s. lat. belong to at least eight different clades. Our results support the presence of at least six species of *Hydropunctaria* in Iceland, and confirm that *Verrucaria* s. lat. is polyphyletic. The majority of Icelandic Verrucariaceae are saxicolous, growing on basalt. Most of the studied specimens were collected in seepages, by creeks and rivers, or on coastal cliffs and boulders. Banks and canyons of Icelandic glacier-rivers seem to house a high diversity of Verrucariaceae species, triggered by their annual and daily fluctuations. Other unique habitats include freshwater ponds under the influence of tides.

Evolution of the genus *Ochrolechia* based on a seven-marker phylogeny and a worldwide sampling

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We present a comprehensive phylogeny of the genus *Ochrolechia*, based on a worldwide sampling of more than 180 individuals representing approximately 35 species. The molecular dataset includes sequences from seven loci: ITS, nuLSU, mtSSU, RPB1, EF1, MCM7, and TSR1. Phylogenetic analyses indicate the presence of several previously unknown lineages. Many of the phylogenetic groupings are supported by morphological, chemical or biogeographic data. Only few taxa are widespread and show transoceanic distributions. Our results suggest that purely morphology-based taxonomy is misleading in *Ochrolechia*, and that revisions of the genus will include several new taxa as well as reinstatements of synonyms. This research received support from the SYNTHESYS Project (<http://www.synthesys.info>) (DE-TAF-5105).

Creating a lichen portal for world-wide lichen collections

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Many herbaria have created databases for their collections. Although institutions maintain their own portals for searching records, it quickly becomes cumbersome if one has to search multiple, separate databases for species information. Moreover, duplicates across herbaria are common; consequently, there is a need to exchange efficiently information without everyone retyping the data. In North America we have created a Consortium of North American Lichen Herbaria, which currently provides access to 80 institutions in the United States, Canada and a few in Europe. Over 2,000,000 records are available and they can be searched by individual institution or in any combination. Georeferenced specimens can be readily mapped and many images and species descriptions are accessible. For well investigated areas (e.g. the American Southwest) keys can be generated on the fly for what is known around any geographic point. The latter requires access to a character database in combination with the label information database. Let's create a world-wide lichen portal, potentially under the auspices of IAL. Someone or some group within IAL may have a better idea on how to assemble such a lichen portal, but in the meantime we could start by expanding the current system.

Lichens and global biodiversity data

Dmitry Schigel

GBIF Secretariat

Lichens are part of global biodiversity data published through Global Biodiversity Information Facility (GBIF). GBIF mediated data includes taxonomic (names and checklist) information, species occurrences in space and time, and most recently, also information on collecting events and abundances. GBIF mediated data are freely available via the Internet, enabling unique levels and scales of analyses. Global biodiversity evidence is comprised by more than 640 million records of more than 1.6 million species, collected through natural history collecting, observations, and monitoring. Over 1,400 peer-reviewed research publications cite GBIF as a source of data. Numerous lichens records are currently available through GBIF.org, including 4,970,326 occurrences of 26,259 species of Lecanoromycetes. What is the data mobilization potential and what are the unexplored data use perspectives in lichenology? How much exposing data openly would benefit the lichenology as a discipline? The nature of questions faced by lichenology increasingly calls for use of aggregated data at various temporal, spatial and taxonomic scales. In addition to supporting science, GBIF informs decisions on conservation and sustainably use of global resources. There is a strong potential in a closer collaboration between lichenology data holders and data users in biodiversity sciences, management and decision making.

Phylogeny of the family Cladoniaceae (Lecanorales, Ascomycota)

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The family Cladoniaceae (Lecanorales, Ascomycota) contains 497 species distributed in 17 genera, of which the genus *Cladonia* comprises 470 species. The taxonomy of the family is based on the morphology of the podetia or pseudopodetia and the secondary metabolites. The previous phylogenetic analyses of the family were conducted more than ten years ago, using few loci, and a new phylogeny with more extensive taxon sampling and more loci became necessary. The phylogeny of the family was reconstructed using five loci (ITS rDNA, IGS rDNA, rpb2, rpb1, efla) and 657 specimens belonging to 307 species. The family Cladoniaceae was resolved as a monophyletic. The genera *Thysanothecium* and *Notocladonia* are closely related with the genus *Cladia*. The genera *Pycnothelia*, *Carassea* and *Metus* were siblings to the genus *Cladonia*. *Cladonia* was a monophyletic genus strongly supported and *C. wainioi* was basal to the genus. Eleven well supported clades appeared inside the genus *Cladonia*. Our results show that a number of *Cladonia* species are polyphyletic. The genetic variation of the species in the main lineages of the genus *Cladonia* and the species delimitations will be discussed.

Distribution patterns of the Mediterranean Cladoniaceae

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A comparative study on the Cladoniaceae diversity in the Mediterranean Region with the results of our recent field studies, on herbarium collections and on bibliographic references related to this family in the Mediterranean countries is shown. The distribution patterns in the Mediterranean phytogeographical belts are evaluated and a scale of frequency was calculated for each of the biogeographic provinces or sectors. We are reporting 118 accepted *Cladonia* taxa and one *Pycnothelia* species in the Mediterranean Region. Many of the *Cladonia* species have a Holarctic distribution having in the Mediterranean countries the southern outposts in their European and Asian distribution (Litterski & Ahti 2004). The highest numbers of taxa occur in the western Mediterranean countries and a gradual impoverishment towards the east and the south is observed. This is related to Quaternary events, environmental conditions, substrate availability and geographical orientation of the main mountain ranges. Most of the species reach the submediterranean belt mainly related to the successional stages of the warm-temperate deciduous forest. Only few species are restricted to the widespread sclerophyllous forests of the Mediterranean Region. Three major groups following climatic patterns are observed. Financial support from the project CGL2013-41839-P, Ministry of Economy and Competitiveness, Spain.

Monster monograph of the Cladoniaceae

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The family Cladoniaceae (Lecanorales, Ascomycota) comprises 497 species in 17 genera. The genera included are *Calathaspis*, *Carassea*, *Cetradonia*, *Cladia*, *Cladonia*, *Gymnoderma*, *Heteromyces*, *Metus*, *Myelorrhiza*, *Nothocladonia*, *Pilophorus*, *Pycnothelia*, *Nothoramalea*, *Sphaerophoropsis*, *Squamella*, *Thysanothecium*, and one new genus. Synonymy, typifications, descriptions, secondary chemistry, distribution, habitats and relevant literature are given for each species. We have made special effort in treating all species level names published in connection of the listed genera. In addition, we treat all subspecies, varieties and forms that are currently in use, as well as a notable amount of those in synonymy. Many taxa are reduced to synonymy and numerous new lectotypifications are made. We have also tried to be exhaustive in giving verified distribution data (at country or province level), which has been actively collected during the past 60 years.

The lichen family Lobariaceae in the Galapagos Islands: molecular data suggest a high degree of endemism

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The degree of endemism among Galapagos lichens is considered to be much lower than among vascular plants. However, molecular phylogenetic studies in Hawaii have shown that endemism in lichen fungi can reach up to 80%. To test this, we studied Galapagos Lobariaceae using the ITS barcoding locus. Twelve species had been listed for the archipelago, none of them endemic: six of *Sticta*, three of *Pseudocyphellaria*, and one each of *Crocodia*, *Lobariella*, and *Ricasolia*. With the exception of *Lobariella pallida*, *Pseudocyphellaria argyracea*, and *Sticta dichotoma*, all other morphologically defined taxa were collected for this study. *Crocodia aurata*, *P. crocata*, *Ricasolia patinifera*, and *Sticta dichotoma* represent previously unrecognized, endemic lineages. The material of *Pseudocyphellaria dozyana* is conspecific with the Eastern North American-Caribbean taxon *P. epiflavoides*, whereas samples of *Sticta beauvoisii* and *S. carolinensis* belong to another, recently recognized pantropical species. *Sticta fuliginosa* represents two taxa, an endemic variety of the recently described *S. roseocyphellata* and a subspecies of *S. ciliata* also present in Puerto Rico. Finally, *S. weigeli* is a complex of three lineages, including *S. weigeli* s.str. and two undescribed taxa, one endemic. The nine collected taxa thus represent 11 lineages, six of them (55%) endemic.

Recent and rapid radiation of the lichen genus *Sticta* in the Western Indian Ocean islands

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In the framework of a global project on the phylogeny of *Sticta*, extensive sampling was performed on the islands of Reunion and Mauritius as well as in several parts of Madagascar (Marojejy and Amber Mountain). The aim of this study is to provide the first comprehensive molecular phylogeny of the genus in the Western Indian Ocean islands (and more specifically of a presumably local endemic lineage), and to date its local radiation. DNA sequences were obtained from 69 specimens for four loci and phylogenetic relationships were inferred using maximum likelihood and Bayesian inferences methods. We estimated divergence times using BEAST. Thirty putative species can be recognized, only five have a validly published epithet. All these species form a well-supported monophyletic group within the genus *Sticta*, and display interesting patterns of endemism: a single species is present in all islands, while the others are restricted either to Madagascar, to Reunion and Mauritius, or to Reunion only. The estimated divergence time of the radiation of this clade occurred in the upper Miocene, apparently concurrent with the emergence of Mauritius. Ancestral reconstruction was examined with LAGRANGE: an original diversification of the clade in the Mascarenes archipelago rather than in Madagascar is not excluded.

Is *Pseudocyphellaria lacerata* Degel. (Ascomycota: Lobariaceae) really in Britain?

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In the UK, a series of high-priority species for conservation action are surrounded by taxonomic uncertainty. One such case is *Pseudocyphellaria lacerata*, one of a suite of internationally important temperate rainforest taxa distributed from Macaronesia to the west coast of the UK, which is distinguished from its more common congener *P. intricata* by its isidiate rather than sorediate margin. We use a multi-locus phylogenetic approach, together with complimentary analysis of morphological, chemical and environmental data, to confirm or reject the hypothesis that *P. lacerata* in the UK is distinct from *P. intricata*. We sampled these taxa across their UK range in addition to material from the type locality of *P. lacerata* in the Azores. Out of the six markers so far tested, only ITS and RPB2 show any informative sites, separating isidiate material from the Azores plus two British sites from the remaining sorediate populations in England and Scotland. We find no evidence that *P. lacerata* in the UK is distinct from that taxon in the Azores, but that it has sequence-based and morphological discontinuities compared to the commoner *P. intricata*. *Pseudocyphellaria lacerata* in the UK has an extremely restricted distribution.

Cryptic biodiversity and symbiotic patterns of association within the trimembered section *Chloropeltigera*

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Species circumscription can impact biodiversity assessment studies, the characterization of patterns of specificity in symbiotic systems, and our understanding of evolutionary processes shaping relationships among symbiotic partners. Although widely distributed across all continents and frequently collected, species boundaries of *Peltigera* and their photobionts remain poorly understood. Members of section *Chloropeltigera* sensu Miadlikowska & Lutzoni (2000) are known to form exclusively trimembered thalli with green algae from the genus *Coccomyxa* (present in the thallus) and cyanobacteria from the genus *Nostoc* (present in external cephalodia). Previous studies relying on limited sampling have shown that this section comprised several cryptic lineages within the three currently recognized species (*Peltigera latiloba*, *P. leucophlebia*, and *P. nigripunctata*). In this study we used a world-wide sampling across the boreal biome to explore phylogenetic relationships among taxa. We sequenced seven loci for the mycobiont and performed several analyses using species discovery and validation methods to establish species boundaries. Our results suggest the presence of at least three new clades that should be recognized at the species level. We further used this phylogenetic and biogeographic framework to explore the specificity of these newly defined species and the molecular diversity of their *Coccomyxa* and *Nostoc* photobionts.

Genotype diversity of *Nostoc* symbionts of *Peltigera* species in grassland and forest habitats of Estonia

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We studied symbiont diversity of 14 *Peltigera* species in Estonian grasslands and forests. Our study locations included alvar grasslands, dunes, roadsides and coniferous forests, and represented a soil pH gradient of 3.5–7.8. Internal Transcribed Spacer (ITS) sequences of fungal symbionts and tRNA^{Leu} (UAA) intron sequences of *Nostoc* cyanobionts were amplified from a total of 180 *Peltigera* specimens collected from 43 different sites. Some *Peltigera* species (e.g. *P. canina*, *P. ponojensis*, *P. rufescens*) exhibited higher levels of photobiont diversity than others (e.g. *P. polydactylon*, *P. praetextata*, *P. malacea*). Photobiont diversity was generally higher in grasslands than in conifer forests, with little overlap in cyanobiont spectra. Furthermore, many *Nostoc* genotypes were consistently only found from either basic or acid substrates. The results indicate that some *Nostoc* symbionts of *Peltigera* may have specific habitat requirements.

A first attempt at a global phylogenetic revision of the genus *Coccocarpia* (Ascomycota: Peltigerales)

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Coccocarpia is a genus of cyanolichens with pantropical distribution. A total of 118 names have been described under it, 25 of which are currently accepted species. Ecology, biogeography and phylogeny of *Coccocarpia* species are poorly known at date. This research aims to resolve the evolutionary relationships within *Coccocarpia* focusing on Colombia, but with additional specimens from Asia and Hawaii. We revised ca. 300 specimens, 90 of them representing types, arranged in a matrix of 133 morpho-anatomic and ecological characters. Likewise, we generated sequences for the ITS (209 specimens), RPB2 (63), and mtSSU (33) and reconstructed Maximum likelihood (ML) trees with different combinations of loci. Taxa without DNA sequences were included using phylogenetic binning. Phylogenetic analysis supports monophyly of two groups proposed by Arvidsson, the stellata and the epiphylla groups. However, Arvidsson's species concept in most cases resulted to be polyphyletic. For instance, the *C. erythroxyli*, *C. palmicola* and *C. pellita* morphotypes appear in several unrelated branches in our trees. Species delimitation analysis using GMYC suggest that the ITS ML tree includes 96 different entities, which largely correlate with phenotype characters, and new characters are proposed to define species. *Coccocarpia* hence is at least four times as species-rich as currently thought.

'Dispositio Psoromatum et Pannariarum' – Version 4.0

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The title of Nylander's 157-year old study is still valid for what we are doing today. After an important review by Hue in 1902 and a series of recent studies by Jørgensen and coauthors, many challenges still remain. This is particularly the case with tripartite species and groups. We have discovered a surprising number of undescribed or misunderstood species of *Psoroma* s. str. in practically all continents, including Antarctica and Europe. One particularly interesting case is *Psoroma hypnorum*, which, based on molecular studies, developed in the Northern Hemisphere and re-migrated later to Antarctic/sub-antarctic areas. In addition to this phylogeographic study, we are also developing a large topology for *Psoroma*. The number of undescribed tripartite species in *Pannaria* s. str. is also unexpectedly high, and we are now grouping them based on renewed studies on spore and pycnidia/spermatia structures, detailed chemistry and molecular studies. The latter will integrate tripartite groups in a system along with the bipartites, which had a previous classification system in three subgenera, which did not find support in recent studies. We are developing a 5-gene topology, particularly needed for a better classification of the squamulose *Pannaria* s.l., which appear as a heterogeneous group today.

Phylogeography of the bipolar *Mastodia tessellata* (Verrucariaceae) reveals new insights into the origin of the Antarctic lichen biota

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Lichens, with 487 known species, are the most conspicuous component of the macroscopic biota in Antarctica. About 40% of them show amphitropical disjunct distributional ranges. Long-distance dispersal has been commonly invoked to explain this distribution pattern, but it is still unknown whether those species originated in or arrived to Antarctica. *Mastodia tessellata* constitutes an example of lichen-forming fungus displaying a bipolar distribution, with populations known from the north-west coast of North America in the northern Hemisphere, and Tierra de Fuego, Antarctica, Tasmania and New Zealand in the southern Hemisphere. Based on population genetics, we aim to test the hypothesis of an Antarctic origin for this organism and determine which historical processes may be responsible for the contemporary geographical distribution of alleles. Molecular data from three nuclear markers were obtained from 250 individuals. Analyses included the inference of genetic clusters based on mixture and admixture models, exploration of genealogical relationships between haplotypes, estimation of divergence times and evaluation of migration models under a Bayesian framework. Results suggest both vicariant and long-distance dispersal events as drivers of *Mastodia tessellata* evolution in space and time. Analyses carried out on its photobiont, *Prasiola borealis*, support the hypothesis of joint dispersal.

Phylogenetic structure and diversity of *Cetraria aculeata* in western Eurasia and east Africa: insights offered by microsatellite data

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Cetraria aculeata is a bipolar lichen that served as a model species to study processes of symbiotic interactions, adaptation and speciation over the last decade. The species originated in the Northern Hemisphere and dispersed through South America into the Antarctic during the Pleistocene, establishing one of its centers of diversity in the Mediterranean region. Although it has already been demonstrated, that Mediterranean haplotypes of *C. aculeata* mycobionts are similar to those from the Afroalpine mountain ranges, while Central and Northern European haplotypes differ more strongly, DNA sequence data do not sufficiently resolve the fine scale structure of both symbionts. We designed microsatellite primers for *C. aculeata* and employed data from ten loci to study the phylogeographic structure and genetic diversity of *C. aculeata* using an extensive sample across Western Eurasia and East Africa. We demonstrate, that microsatellite data offer much better resolution on genetic structure of populations with over 200 genotypes estimated in more than 700 specimens collected from 52 localities. Based on the results from Bayesian clustering we conclude that African populations are strongly genetically isolated from each other and Eurasian ones, and Eurasian populations are structured by climatic gradients from north to south.

Genomic footprints of ecotypic differentiation along an elevational cline in populations of a lichen-forming fungus

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Many fungal species occur across a variety of habitats. However, little is known about the genetic basis of environmental adaptation in fungal populations. Here we studied patterns of genome-wide differentiation and putative adaptive phenotypic diversity in the lichen-forming fungus *Lasallia pustulata* along an elevation gradient in the Mediterranean region (100 – 1,300 m a.s.l.). We detected two clearly delineated genomic groups (ecotypes) using a pooled population resequencing approach. Interestingly, the contact zone between the ecotypes coincided with the transition from Mesomediterranean to Subpratemperate climate. A total of 586 genes were significantly different in allele frequencies between the two groups. These genes were significantly enriched in gene ontology terms related to oxidative stress response, growth, and reproductive processes. Physiological experiments revealed that high-altitude lichens had a) thicker thalli, and b) significantly greater fitness at lower levels of light and higher humidity. Our results highlight the pervasive role of selection over small spatial scales. These findings corroborate previous observations that adaptation to divergent environments promotes environmental specialization and reproductive isolation among fungal populations.

Genetic variation in *Xanthomendoza fallax* and its overlap with genetic variation of its host *Quercus gambelii*

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Although some research has explored the evolutionary relationships between the fungal and algal partners that comprise the lichen symbiosis, little research addresses the potential overlapping genetic variation between lichens and their living substrates. Our research: (1) generates DNA sequence data for samples of the lichen *Xanthomendoza fallax* from branch substrates of ten genetically distinct tree clumps in Red Butte Canyon, UT; (2) correlates genetic variation between *X. fallax* and its substrate, Gambel oak (*Quercus gambelii* Nutt.), to identify phylogenetic congruence between this group of lichens and their tree hosts; and (3) reconstructs a phylogenetic tree to examine genetic structure in relation to geographic locations. Using 81 samples from 30 trees within 10 clumps of oak, fungal variation was measured with the internal transcribed spacer region of nuclear ribosomal DNA. Tree variation was captured with 101 amplified fragment length polymorphism loci. We used Mantel tests to evaluate the relationships between genetic dissimilarity matrices, and visualized the patterns of overlap in variation with NMS. MEGA was used for sequence analysis and phylogenetic reconstruction. Some correlation exists between genetic variants of trees and lichens. The phylogenetic tree showed some genetic structure, although more data are needed to elucidate intraspecific relationships

Asymmetric specialization in Myco- and Photobionts in lichen communities from Southern Patagonia

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Tierra del Fuego (Southern Patagonia) is the closest landmass to Antarctica providing the opportunity for a comparative study focusing on the diversity and specificity of myco- and photobionts within lecideoid lichen communities. Along a latitudinal gradient from Isla Navarrino in the south (S55°) to Bariloche (S41°) more than 200 lecideoid lichen species were collected, following the subantarctic climate by increasing altitude to the north. Although Antarctic lecideoid lichen species have mostly a bipolar or cosmopolite distribution, we found ten new molecular and morphologically separated species of the well described genera *Lecidea* and *Porpidia*. These highly diverse mycobionts were associated with a homogenous selection of photobionts. Network statistic revealed that mycobionts were – on average – more generalized in their associations than the photobionts that were often associated to few mycobionts only. However, the rather specialized photobionts were complemented by three strongly generalized species. This pattern is reflected in the modularity of the networks as the well-defined modules consisted of up to eight mycobionts but only two or three photobionts. The asymmetry in specialization in myco- and photobionts sheds new light on the ecology and evolution of the associations between the symbiotic partners of these lichens.

Proposal to use mating type locus (MAT) sequences to account for the interbreeding criterion in lichen species delimitation

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Conceptual considerations on the potential use of the mating type locus (MAT) in low-level phylogenetic studies of lichenized ascomycetes are discussed, in order to apply the criterion of interbreeding capability to lichen species delimitation. Reviewed species recognition methods currently used in lichenology do not take into account the interbreeding criterion, the basic premise of the Biological Species Concept and implicit component of other species concepts. The MAT locus is considered the biologically most meaningful molecular marker in terms of the interbreeding capability criterion. Several studies on non-lichenized ascomycetes demonstrate the suitability of mating type genes to resolve species aggregates. Therefore, it is advised that future infra-generic phylogenetic studies and attempts to resolve species aggregates of lichens should include examination of MAT sequences. In the past, the major obstacle for routine use of the MAT locus was its immense variability among closely related taxa, and the associated difficulties in amplifying portions of it. This obstacle has now been overcome with the advent of NGS and whole genome sequencing. Additionally, research on lichen ecology and conservation would greatly benefit, because MAT sequences that were originally generated for phylogenetic analyses can also be used to analyse the mating systems of the respective species.

The inland rainforest of western North America – An uncertain refugia for oceanic lichens in a changing world

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The rich canopy lichen communities of western North America's coastal temperate rainforests have been well documented. Less well known are the ecology and biogeography of oceanic canopy lichens in the inland temperate rainforest (ITR), an ecosystem found some 800 km from the ocean within BC's interior mountain ranges, between 50° and 54°N. Although annual precipitation in the ITR is much lower than that of coastal rainforests, summer temperature and precipitation are similar to that of the coast, with cool moist conditions enhanced by nighttime cooling and associated valley bottom fog and dew. Many toe-slope positions also receive abundant groundwater supply fed by snowmelt recharge. ITR lichens like *Nephroma occultum*, *Lobaria hallii*, *L. retigera*, *Leptogidium dendriscum*, *Sticta oroborealis*, and *S. wrightii* face an uncertain future owing to climate change and continued loss of old forests to logging. Within our 135,000 ha study area, less than 7% remains as old forests, down from more than 30% prior to the industrial logging era. Climate change predictions suggest significant increases in mean annual temperature, with warmer summers and less snowy winters predicted. Based on current understanding of lichen ecology, both trends may have significant consequences for oceanic ITR lichens.

Lichens across Antarctica: climate and performance

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Antarctica is an almost pristine continent with major gradients in environmental factors, in particular temperature and precipitation and, because of these qualities, it offers excellent opportunities to study the relationships between lichens and the environment. Lichens also show three major clines, biodiversity, cover and growth rate all declining from north to south. Possible environmental drivers will be considered including relationships between biodiversity and climate, the length of active periods and changes in growth rates. The importance of the habitat will be emphasised together with the examples of adaptation to the extreme environment. A previous suggestion that lichen growth rates may be one of the better parameters to monitor climate change will be developed using new data showing responses of lichens in the maritime Antarctic to recent climate changes. Photosynthetic performance will be analysed and the lack of apparent adaptations contrasted with the above clines. Photosynthetic performance of individual species seems not to be a major driver for lichen biodiversity and a more probable reason could be the different life strategies adopted by the lichens. This is an area of research that requires considerably more attention in the future.

Broad-scale distribution of epiphytic hair lichens correlates stronger with climate and nitrogen deposition than with forest structure

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Hair lichens are strongly influenced by forest structure at local scales, but their broad-scale distributions are less understood. This study compares the occurrence and size of *Alectoria sarmentosa*, *Bryoria* spp. and *Usnea* spp. in the lower canopy of >5000 *Picea abies* trees within the National Forest Inventory across 23 million ha forest in Sweden (55–69°N). We used logistic regression to analyse how climate, nitrogen deposition and forest variables influenced lichen occurrence. Distributions overlapped, but *Bryoria* was more northern and *Usnea* more southern. Lichen length increased towards north indicating better conditions for biomass accumulation. Logistic models had highest pseudo R² for *Bryoria* followed by *Alectoria*. Temperature and nitrogen deposition had higher explanatory power than precipitation and forest variables. Occurrence increased with stand age, particularly for *Alectoria*. Multiple logistic regression models suggest that hair lichen genera responded differently to increases in variables. Warming was negative for *Bryoria*, and for *Alectoria* and *Usnea* in warmer climates, but positive in colder climates. Nitrogen deposition was negative for *Alectoria* and *Usnea* at high deposition, but positive where deposition was low. Our analysis suggests major shifts in the broad-scale distribution of the three hair lichen genera following future changes in climate, nitrogen deposition and forest management.

Lichens and climate change: the problem of scale and non-analogue climates

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Statistical models have been widely used to compare distribution records with baseline (present-day) climatic variables. These 'bioclimatic models' are projected for baseline and future climate change scenarios, exploring risk as loss or spatial shift in suitable climate. A first criticism of this approach is the concept of climatic equilibrium. Notwithstanding efforts to address data issues such as sample size and bias, the comparison of distributional data with climate surfaces assumes the direct climatic control of a species' occurrence, rather than testing for this. A second criticism relates to forward projection of climate models, and in particular the potential extrapolation to future non-analogue environments. Criticisms were tested using a two-year growth experiment for three lichen species – *Lobaria pulmonaria*, *Sticta fuliginosa*, and *Usnea hirta* – across three climatically-contrasting botanic garden sites. Results showed that local measured growth correlated with values derived from bioclimatic models utilising 10 km (coarse-grained) distribution records. Bioclimatic modelling might be defensible in the light of a species' functional climate response. The study also asked whether annual averages for a limited number of climate variables capture the response to future non-analogue combinations of climate and irradiance. The consequences of this are discussed, with recommendations for improved model development.

Can the soil crust lichen *Psora decipiens* acclimatise to changing environments?

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Psora decipiens is a characteristic lichen of biological soil crusts (BSCs) in different biomes. Its high phenotypic plasticity may contribute to its ability to withstand environmental change. We investigated layer thicknesses related to water traits to perceive eco-physiological and morphological mechanisms that underlie the species high variability. Results highlight that highly adjusted water gain is mainly determined by changes in epinecral layer and medulla thicknesses. To investigate the lichens' potential to acclimate, we transplanted individuals across four climatically distinct sites across a European latitudinal gradient for a 2 years exposure time. The morphological analysis revealed that many samples had no remaining algal layer. *Psora decipiens* associates with various algal strains, 28s and rbcL gene analysis assessed site specific relationships and any lichen acclimation through photobiont switching. Although new growth was often determined, the algae were frequently found to have died without evidence of a new photobiont being incorporated into the thallus. ITS analysis of the fungus investigated diversity and determined that new growth were actually a part of the transplant, revealing that four distinct fungal clades exist. Our results suggest that *P. decipiens* cannot acclimatise to changing environments and the different sites are home to genetically distinct and unique populations.

Lichen functional diversity as an ecological indicator of climate change

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Climate has unequivocally changed in the recent decades impacting natural and human systems and the future foreshadows an even worse scenario. Facing these problems requires understanding and quantifying ecosystems functioning in response to change. Due to the global nature of climate change, it's also necessary to scale up from local or regional to the global level. This demands globally applicable ecological indicators and metrics able to quantify global change drivers' effects. Unlike species-related metrics, functional diversity provides the link to ecosystem functioning and has the potential to be applicable at broad spatial scales. Lichens are excellent ecological indicators of several environmental drivers and their responsiveness to climate change has already been documented. We developed a framework for the use of epiphytic lichen functional diversity as indicators of climate change. Lichen functional diversity based on simple traits performed good as indicators of climate change along spatial climate gradients in different regions of the world. This was also validated over time, confirming that lichen functional diversity can be used as an efficient ecological indicator of climate change with potential to be applied globally and to be included in the set of ecological indicators long demanded by the three UN sister conventions.

A revised Rydzak's Drought Hypothesis for a changing environment

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Air pollution is certainly a key limiting factor for the survival of lichens in urban environment, but some recent field studies underlined that water availability is also important, partially confirming what was a key point in the highly controversial Rydzak's Drought Hypothesis. This study was aimed at understanding the interplay between air pollutants and air humidity (used as a first, rough proxy of water availability) in determining (i) the lichen diversity value (LDV) of urban communities, and (ii) the physiological responses of a macrolichen transplanted to urban environments. LDV was measured in highly standardized conditions in two cities of NE Italy with different levels of pollutants along transects running parallel to or far from ditches. Healthy thalli of *Flavoparmelia caperata* were transplanted in three successive seasons to 10 sites located in two other cities of NE Italy, selected for their different climate and comparable levels of pollutants. The two data sets confirm the greater importance of meso- and microclimatic conditions with respect to the actual level of pollution, suggesting that when SO₂ is negligible, one of the key factors for the survival of lichens in urban environment is certainly water availability, from which the activation of lichen metabolism strictly depends.

Lichen response to nitrogen enrichment

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Lichens respond to nitrogen (N) pollution in two principal ways. First, high rates of N deposition frequently result in a small number of highly N tolerant species becoming increasingly represented in epiphytic communities; the relative abundance of these nitrophytic species can be used as a quantitative estimator of N pollution. Second, low rates of N enrichment modify the chemistry and physiology of lichens often without any apparent direct detriment to the species concerned. These subtle physiological changes can also be used to indicate N deposition rate; they can be induced experimentally thus demonstrating a causal link to pollution. Surface bound phosphomonoesterase (PME) activity in the heathland lichen *Cladonia portentosa* is positively correlated with N deposition and can adjust relatively rapidly to changing N load. We will present evidence that upregulation of PME activity in response to N pollution is a mechanism that might have evolved as an adaptation to exploit spatially and temporally unpredictable deposition of animal faeces in otherwise oligotrophic habitats.

Lichen-based national critical loads for nutrient nitrogen and acid deposition in forests of the United States

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Critical loads offer a scientific basis to protect ecosystem health in air resource decision-making. We derived empirical epiphytic macrolichen critical loads for nitrogen and sulfur deposition using US Forest Service lichen survey data (378 species), PRISM climate data, forest composition data, and CMAQ modeled deposition at 9,000+ sites. We calculated the deposition value associated with peak detection frequency for each species. To calculate site scores, we averaged these values for the species present, weighting by abundance. Community level surface response curves to nitrogen and sulfur deposition and 9-12 potential climate, forest structure, and location variables for the eastern and western US were modeled using non-parametric multiplicative regression. Beard and cyanolichens were most impacted by pollution and warmer, drier climates. Community-level shifts favoring tolerant over sensitive species were observed above 1.6 kg N and 0.7 kg S in the west, and 4.2 kg N and 2.5 Kg S in the east per ha/yr. We recommend US critical loads equivalent to the western values. Maintaining air quality below critical loads mitigates adverse effects on lichen diversity due to climate change, and protects the ecological roles and services provided by epiphytic macrolichens and other air-pollution sensitive biota.

Does climate modulate the effect of ammonia on lichen diversity?

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Nitrogenous compounds are currently one of the main concerns related with atmospheric pollution. The increase in their concentration results in changes on lichen diversity and composition of lichen communities. However, the interaction between climatic conditions and nitrogenous compounds has not been examined. Here we study if climate can modulate the effect of ammonia on lichen diversity, in terms of richness and community composition. Three different climatic sites from the Iberian Peninsula (north, southwest and northeast) were selected. In each site, concentration of ammonia and lichen diversity were examined along a gradient from a cow barn. Lichen diversity was surveyed according to the European norm UNE-EN 16413. Surveys were done on *Quercus* species in order to minimize differences due to tree characteristics. There was a clear relationship between ammonia and those functional groups more sensitive to this compound. Nitrophilous species were present in a great percentage when ammonia was higher, while oligotrophic showed the opposite trend. However, a different pattern was observed regarding lichen richness and diversity, increasing their values in the site with higher ammonia concentration. This site was also the most wet and coldest, showing that climate could mitigate the effect of ammonia on lichen diversity.

Phosphatase activity in nitrophobic and nitrophytic lichens

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Eutrophication leads to changes in epiphytic lichen community structure whereby those species adapted to oligotrophic conditions (nitrophobes) are replaced by a small number of species that are tolerant of high nutrient loads (nitrophytes). The physiological basis of lichen adaptation to high nutrient deposition loads is poorly understood. We have measured rates of surface-bound phosphomonoesterase (PME) activity in nitrophobic and nitrophytic lichens and used a fluorescent marker (ELF 97) to locate enzyme activity in sections of lichen thalli. PME activity was higher in nitrophobic than in nitrophytic species, possibly reflecting the relative availability of nitrogen and phosphorus in their respective habitats. ELF 97 locates PME activity predominantly in the fungal tissue of the cortices consistent with a function in phosphorus scavenging from atmospheric deposits. Activity is associated with the cell lumina but is insensitive to oxygen deprivation suggesting that PME could be a membrane bound enzyme with an outward facing active site, which is independent of physiological activity. PME could be induced in both lichen photobionts and the nitrophyte *Xanthoria parietina* when grown in P-deprived axenic culture. We suggest that lower phosphorus scavenging efficiencies might be advantageous in lichens adapted to eutrophicated habitats.

Studying substrate associations of lichens with phylogenetic comparative and genomic methods

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Lichens from the order Baeomycetales s.lat. (Ostropomycetidae, Lecanoromycetes) live in close physical contact with a variety of organic and non-organic substrates. Although lichens have long been recognized to show narrow preferences for certain substrates, those are seldom placed in an evolutionary context. We studied substrate specificity using a two-step approach. First, we coded substrate affinity and ecological strategy of species and performed ancestral state reconstruction, speciation rate and character correlation analyses on a set of phylogenetic trees, to better understand consequences of different substrate associations. Informed by our phylogenetic results we sequenced, assembled and annotated the fungal genomes of selected members of Ostropomycetidae. In a comparative genomic framework we searched for signatures related to long-lasting substrate use in CAZymes and codon usage of orthologous gene sets. Our results reveal high levels of substrate-related niche conservatism with possible consequences leading to evolutionary dead ends.

A natural classification of the Lichinomycetes

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The Lichinomycetes, with ca. 350 spp., is one of the least understood lichen-forming fungal groups in the world. The species form gelatinous lichen symbioses with cyanobacteria and are often inconspicuous but ecologically important. It currently comprises one order in which four families are recognized: Gloeohpepiaceae, Heppiaceae, Lichinaceae and Peltulaceae. However, delimitation and main phylogenetic relationships between families have not been tested thoroughly using molecular data. Generic circumscription is another major challenge within the group. Main diagnostic characters are type of photobiont, thallus morphology and anatomy, ascoma ontogeny and ascus structure, but some of these characters can occasionally overlap, be ambiguous or symplesiomorphic and cannot be used to delineate natural groups. A combination of molecular, morphological and ecogeographical data is here combined to propose a well-supported systematic treatment of the Lichinomycetes. In this study, we develop a 3-gene phylogeny (mtSSU, mcm7 and RPB2) including a dataset covering a broad selection of taxa within the Lichinomycetes and study character evolution of selected traits. Based on these data we proposed here a natural classification of the group.

Phylogenetic relationships among extremotolerant rock-inhabiting fungi and their associations with algae

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Black fungi are among the most stress-tolerant eukaryotic microorganisms. Though they share morphological similarities, they often hide great genetic diversity and present multiple life-styles. *Lichenothelia* and *Saxomyces* are two genera for which insights in the ecology and phylogenetic relationships within the class Dothideomycetes have been recently revealed. Here we expanded the taxon sampling and added new taxa, from multiple habitats, to previous datasets to better resolve and support their independent identity. Environmental samples and culture isolates have been DNA-extracted and sequenced by Sanger sequencing to produce a strong multilocus phylogeny. Furthermore, the axenically isolated fungi of both *Saxomyces* and *Lichenothelia* have been used to set co-cultures with algal strains (*Trebouxia* spp. and *Coccomyxa* sp.) previously isolated from different lichen thalli. By doing this we aim at inducing possible formation of lichen-like or less organized structures and to improve our knowledge about the trophic pathways of these particularly oligotrophic fungi. Our molecular phylogeny and culture experiment show to which extent black fungi underwent convergent evolution and are related to lichenized fungi and fungi presenting different life-styles.

A revisionary synopsis of the Trypetheliaceae recognizes 15 genera and increases the number of species from 280 to 435

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We present a revisionary synopsis of the lichenized family Trypetheliaceae, based on type studies, herbarium revisions, recent collections, and DNA analyses of numerous specimens. The generic concept within the family was traditionally based on thallus development, ascoma arrangement, and ascospore septation, recognizing seven genera; however, based on phylogenetic studies, genus-level delimitations have changed considerably. Whereas genera already characterized by particular features, such as *Aptrootia*, *Architrypethelium*, *Bathelium*, and *Pseudopyrenula*, were confirmed by molecular data, the ascospore- and ascomata-based genera *Astrothelium*, *Cryptothelium*, *Laurera*, and *Trypethelium* do not represent natural groups. The bulk of the species, with variable ascoma arrangement and ascospore septation, belongs in a single genus, for which the oldest name is *Astrothelium*. Some basal groups were so far thought to belong to genera in other families, such as *Arthopyrenia* and *Mycomicrothelia*. As a consequence, 15 genera are now accepted in the family, with a total of 435 species, 130 of which are being newly described. Similar to what has been found in Graphidaceae, hamathecium inspersion, presence/absence of lichexanthone and ascospore size classes turn out to be valid species characters. We predict that hundreds of additional species are still to be discovered.

Co-occurrence of closely related genotypes in the morphologically variable script lichen (*Graphis scripta*) complex (Ascomycota: Graphidaceae)

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Graphis scripta is now considered to be a species complex, but because of the lack secondary chemistry and paucity of measurable morphological characters, species delimitation within the complex has been challenging and is thus far based on apothecium and ascospore morphology. In this study, we employed molecular and morphological data to assess phylogenetic structure and delimitation within the *G. scripta* complex. We generated sequences for four markers (mtSSU, nuLSU, RPB2, EF-1) and performed phylogenetic analyses. The resulting trees were used to determine the number of distinct lineages by applying a general mixed Yule coalescent model (GMYC). Focusing on the sites with more than three samples, we also calculated mean pairwise distance (MPD) among co-occurring samples to determine whether they are more clustered than random. Our analyses suggest up to eight putative species within the *G. scripta* complex. However, these did not correspond to the taxa that were recently distinguished based on apothecium morphology and could not be circumscribed with the morphological characters that were traditionally used in the classification of the complex. The resulting MPDs revealed that co-occurring samples are phylogenetically more clustered than expected, suggesting a strong role of local filters and local genetic divergence at the population level

Thermal acclimation in polar macro-lichens

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Many eco-physiological studies deal with the question of how the absolute rates and the balances between photosynthesis and respiration will change in response to climate. Climate models have assumed that both will rise exponentially with short-term changes in temperature. Thermal acclimation in response to temperature changes can alter this short term response, so that respiration responds much less to temperature fluctuations than anticipated. Although acclimation of respiration to temperature has been demonstrated for lichens, how fast they can respond to environmental temperature change, is unknown at present. The Antarctic Peninsula and arctic Svalbard belong to the regions of the world that had experienced relatively fast regional climate warming and, due to their relatively simple ecosystems, serve as early warning system in understanding species and ecosystem responses to climate change. Terrestrial ecosystems here are dominated by mosses and lichens. In our experimental setup we assess thermal acclimation of 4 polar macro-lichens by measuring full respiration response as well as net photosynthesis, light and water relations before and after an incubation treatment, at different temperatures. Initial results show that acclimation may be a species specific trait that can be a key process determining species distribution and fitness under rapid changing climates.

Effects of UV radiation on growth in lichens

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Lichens are normally well protected against ultraviolet (UV) radiation. They may even survive outer space conditions. The cortex of lichen thalli efficiently screen UV-B radiation. However, the effects of UV on growth in lichens has rarely been studied. In a growth chamber experiment with *Lobaria pulmonaria*, *Peltigera aphthosa* and *Cetraria islandica* the thalli exposed to UV-B had significantly lower relative growth rates (RGR) than thalli exposed to visible light only. However, maximal photosystem II efficiency (Fv/Fm) was not reduced by UV for any of the species. A field experiment was done with *L. pulmonaria* and *Lobaria virens* with three screening treatments: 1) full solar radiation, 2) full solar radiation minus UV-B and 3) full solar radiation minus UV-A and UV-B. The thalli receiving visible light without UV had much higher RGR than thalli exposed to visible light + UVA, whereas thalli exposed to full solar radiation had lowest RGR. However, there were small differences in Fv/Fm between the different UV treatments, and thalli exposed to the different UV treatments had almost similar light response curves of photosynthetic CO₂ uptake. In conclusion, in both the growth chamber and the field experiment UV reduced growth.

Patterns of symbiont distribution along altitudinal gradients suggest environmental structuring in a lichen symbiosis

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Symbiotic organisms may adapt to the abiotic environment by reshuffling genetically differentiated symbiont strains into locally adapted holobionts. To understand whether specific fungal-algal haplotype interactions are driving the adaptive dynamics of the lichen holobiont we asked whether I) distribution shifts exist along environmental gradients within a single species, and II) whether the same shift occurs in repeated gradients. We analyzed populations of *Lasallia pustulata* and its green algal photobiont *Trebouxia* along three elevational gradients (100–1700 m) in Italy and Spain. Our data show altitudinal structure in both, the fungal and algal symbionts, with a clear-cut algal switch at approximately 900 m above sea level. Model predictions of haplotype distributions indicate a shift of algal and fungal haplotype when the average temperature of the coldest month falls below 4°C. We conclude that environmental filters force functionally adapted symbiont lineages into specific interaction pairs in *L. pustulata*, and that cold tolerance limits the geographic distribution of these algal and fungal functional types.

Transition to the glassy state in the lichen *Flavoparmelia caperata* (L.) Hale: molecular mobility in relation to thallus water content

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Lichens are desiccation tolerant, but the relationship between thallus water content (TWC), cytoplasmic viscosity and metabolism are underinvestigated. As water is lost, cellular components undergo "vitrification", which is the transition from a liquid to a "rubbery" to a "glassy state", in which molecules are "frozen in structure". Here, thalli of *Flavoparmelia caperata* were dried and kept up to 45 days at various relative humidities, resulting in TWCs from 26 to 5%. Molecular mobility was measured by dynamic mechanical thermal analysis, and the enzyme-dependent violaxanthin de-epoxidation was used to study at which WC enzymatic activity ceases. Photosynthetic pigments and alpha-tocopherol, and fatty acids were measured by HPLC and GC-MS, respectively. Whereas desiccation did not affect the other metabolites studied, violaxanthin was de-epoxidised, but only at TWCs higher than 12%. At these TWCs samples were in the "rubbery" state which still has sufficient molecular mobility for enzymatic reactions. By contrast, no enzymatic activity was found below 8% TWC. In summary, vitrification and the accompanying restriction of enzyme-dependent metabolism occurs at TWC between 12 and 8%, corresponding to 35 and 55% relative humidity. Our results may help to better understand the underlying mechanisms of desiccation tolerance.

Abscisic acid and saline stress responses in symbiotic green alga *Trebouxia* sp. TR9 isolated from the lichen *Ramalina farinacea*

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Tolerance to stress in plants is a coordinated response of multiple stress-related genes, which also cross-talk with other components of stress-signaling transduction pathways. Abscisic acid (ABA) is the critical phytohormone that controls a series of downstream stress responses from saline, thermal and drought stress conditions. Although ABA role in saline stress management has been studied in land plants, little is known of its effects on lichen microalgae. In *Ramalina farinacea* thalli two *Trebouxia* -*T. jamesii*, *T. sp. TR9*- coexist and are able to withstand severe aerial abiotic stresses. From the genome of *Trebouxia* TR9, sequenced and annotated by our group, we have identified genes implicated in ABA biosynthesis and ABA-mediated responses to salt stress. We have used qRT-PCR to measure their expression levels in cultures of *Trebouxia* sp. TR9 grown under a wide range of salinity concentrations and determined the endogenous concentrations of phytohormones. Our results point to a completely different behavior in the response to saline stress between land plants and *Trebouxia* sp. TR9, with a remarkable increase in ABA biosynthetic genes expression under high salinity concentrations paired with high levels of endogenous ABA under the same conditions, revealing great resilience to ABA-mediated saline stress response. Generalitat Valenciana (PROMETEO/021/2013/GVA).

Effects of habitat fragmentation on the taxonomic, phylogenetic and functional diversity of epiphytic communities of beech forests

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Habitat fragmentation constitutes one of the major threats for biodiversity. However, knowledge on the effects of forest fragmentation on the diversity dimensions of epiphytic communities is limited. Here, we assessed the effects of forest fragmentation on the taxonomic, phylogenetic and functional diversity of lichen epiphytic communities at forest-patch and plot scales, considering fragmented beech forests in the north and in the southern limit of *Fagus* in Spain. We hypothesized that forest fragmentation decreases taxonomic, phylogenetic and functional diversity of epiphytic communities, and this effect should be stronger in the southernmost beech forests. We selected two beech forests landscapes (47 patches, 238 plots) in the Atlantic and Mediterranean regions. We recorded the presence and abundance of lichens in 952 trees, various functional traits and we built multigene phylogenetic trees. We used mixed models to assess the relationship of these variables with environmental and forest structure variables linked to habitat fragmentation. Preliminary results indicate that taxonomic diversity declined in smaller forest patches and this effect was stronger in the southern forests, suggesting that the Mediterranean climate exacerbated the negative effects of forest fragmentation. Functional and phylogenetic diversity suggest filtering processes structuring epiphytic lichen communities in the southernmost forests.

Coupling genetic and ecological niche modelling of two epiphytic lichens with contrasting dispersal modes

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Dispersal among populations is a key process which shapes species distributions and also drives genetic structure. Dispersal traits (i.e. reproductive strategy and propagule size) are thought to reflect a trade-off between dispersal ability and establishment success, with important consequences on population structure that may explain a species occurrence under different ecological scenarios. We tested evidence for this trade-off using two closely related epiphytic lichens, which differ in their reproductive mode – *N. laevigatum* (sexual spore-dispersed) and *N. parile* (asexually species dispersing both symbionts together). We compared the patterns of occurrence and genetic diversity along a bioclimatic gradient, in Scotland. As expected from their contrasting dispersal modes, we found differences in both their local occurrence and genetic diversity despite their similar biogeographic distributions within our study region. The sexually reproducing *N. laevigatum* may be limited by the presence of other asexual species which act as key photobiont facilitators, while *N. parile* was sensitive to a precipitation gradient modified by microhabitat factors. Using newly developed microsatellite markers for each species, we found that both species showed a decreasing genetic diversity under drier and sub-optimal macroclimatic conditions. Furthermore, *N. laevigatum* showed substantially higher gene and genotypic diversity than the predominantly asexual *N. parile*.

Interception of simulated N pollution by *Cladonia subtenuis*

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Lichens can regulate ecosystem processes where they are major producers in ecosystems; our work addresses how soil lichens regulate nitrogen cycling in forests. Lichens are abundant in the NJ Pinelands; because the soils have low nutrient availability, any lichen-induced effects on N availability may be important for the forest. It has been established that N-deposition occurs here and influences soil fungal and bacterial diversity. Our study asked if lichens intercept N from airborne N-deposition, preventing N enrichment of soil or groundwater. We created lysimeters, small pans filled with soil and one of 3 different cover types: no cover, lichen, or fabric (a polyester mesh which simulated the abiotic structure of lichens, but had minimal biological activity). We added 0, 5, or 50 kg N Ha⁻¹ yr⁻¹ of N-15 enriched ammonium nitrate as an aqueous spray, throughout the growing season and in the fall. We measured nitrogen enrichment of the soils, aboveground material, and water leached through the lysimeter. We found that lichen and fabric performed similarly; both were able to reduce soil and groundwater N in high N-deposition scenarios. We conclude that the abiotic structure of lichens is more critical for their role in nutrient cycling than their biological activity.

The genetic diversity of a widespread epiphytic lichen *Usnea subfloridana* (Parmeliaceae, Ascomycota) in response to alkaline dust pollution

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Long-term dust pollution, which increases the pH value of phorophyte bark, can influence species richness and composition of lichen communities. However, there is gap of knowledge whether and how dust pollution impacts the genetic diversity of lichen populations. Our study aimed to investigate the genetic variation of eight *Usnea subfloridana* populations in *Pinus sylvestris* dominated boreal forest stands with different pollution load in southern Estonia, Northern Europe. We collected and then genotyped 274 *Usnea* thalli using nine specific fungal microsatellite markers. Genetic variation was calculated and compared between populations from different habitats using GLZ analysis. The bark pH of the phorophyte (*Picea abies*) was higher (6.0–6.7) in polluted forest sites than in unpolluted forest stands (3.5–3.6), indicating the significant presence of dust pollution. Allelic richness, Shannon's information index, and genetic diversity of lichen populations were significantly higher in unpolluted forest sites than in polluted forest sites. Our results indicate that *U. subfloridana* populations from unpolluted forest sites maintain higher levels of the genetic variation, in contrast to populations from polluted forest sites. Our results imply that a decline in genetic diversity of common lichen species could be used as an additional tool to highlight the potentially threatening environmental disturbances.

Biomonitoring of atmospheric deposition from petrochemical industry in Thailand by the lichen *Parmotrema tinctorum* (Despr. ex Nyl.) Hale

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This research observed the effects of atmospheric deposition at Map Ta Phut, the largest petrochemical complex in Thailand, on the transplanted lichen *Parmotrema tinctorum* (Despr. ex Nyl.) Hale. The study could provide a precautionary measure for sustainable development. Lichen thalli from a relatively unpolluted area were transplanted to six industrial sites, one rural site and one unpolluted site. Concentrations of NO₃⁻, SO₄²⁻, Cu, Ni, Sb, V and Zn accumulated in the transplanted lichens were used to calculate pollution load indexes (PLIs). It was found that NO₃⁻ and Sb were the most prominent contaminants accumulated in the lichens at most industrial sites. Their concentrations were 2–4 times higher than those at the unpolluted site. The PLIs from the industrial sites were 1.3–2.2 and from the rural site were 1.1 times higher than the unpolluted sites. A chlorophyll fluorescence parameter Fv/Fm, the indicator of environmental stress, suggested that the areas within the vicinities of 3 km from the main industrial area were affected by air pollution. This study reaffirms the efficiency of this lichen as a bioindicator of air pollution, that need to be considered at an early stage as it could lead consequent impacts on sustainable development.

Conservation of pyrenocarpous lichens in Finland

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Research among lichen conservation, ecology and distribution has traditionally concentrated on Lecanoromycetes, which includes the majority of the currently known lichens. Pyrenocarpous lichens, i.e. species characterized by perithecioid ascoma and mostly belonging to Eurotiomycetes, have been less studied owing to their small size and poorly known taxonomy. We examined the distribution, ecology and conservation needs of pyrenocarpous lichens on a national scale in Finland by field sampling and using herbarium specimens. DNA barcodes of ITS regions were used in identification of species. The key findings are: 1) Number of species is almost 3-fold than previously known including many undescribed species, 2) The proportion of pyrenocarpous species is much higher among epilithic than among epiphytic species, 3) Many species are extremely rare and have tiny population sizes, 4) Most species occur exclusively on calcareous rocks, aquatic siliceous rocks or on trees growing on shores. We conclude that pyrenocarpous lichens depend on effective habitat conservation; particularly protection of calcareous rocks and forests affected by flooding should be emphasized. Pyrenocarpous lichens have apparently effective dispersal ability and are capable of long-distance dispersal. ITS sequencing is important in species identification and the technique needs to be improved to avoid excessive destructive sampling.

Impacts of biofuel harvest, retention forestry and prescribed burning on epiphytic lichens in boreal pine-dominated forests

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In the boreal region, intensive forestry has caused endangerment of various forest-dwelling species, including epiphytic lichens. Currently harvest of stumps and logging residues for biofuel intensifies forest use even further. However, certain management methods, such as retention forestry, are also used to counter the negative impacts of forestry. The combined effects of these practices on forest-dwelling lichens are still poorly known. We examined, for the first time, the impacts of retention forestry and prescribed burning as well as the potential influence of biofuel harvest on epiphytic lichens in pine-dominated boreal forests. The data were collected in eastern Finland, from 24 sites treated experimentally with a combination of retention-cutting and prescribed burning. Retained Scots pines, their dead wood legacies and Scots pine stumps all hosted rich lichen assemblages, including Red-Listed species and dead wood specialists. Thus, large-scale stump harvest could be a significant threat to epiphytic lichens, particularly wood-dwelling species. Retention forestry, on the other hand, has a potential to sustain lichen richness in the harvested stands. Prescribed burning decreased lichen richness at stand scale, but as it also created diverse woody habitats, it could enhance the richness on landscape scale – provided that species-rich stands are left outside burning.

The impacts of sea-level rise on coastal lichens: a case study in the Mid-Atlantic Coast Plain of eastern North America

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Large-scale assessments of global sea-level rise (SLR) have predicted significant impacts to coastal and island biodiversity. The Mid-Atlantic Coast of eastern North America is particularly threatened because the sea-level is rising four times faster than the global average. Here we use a dataset of >13,500 occurrence records for lichens in the Mid-Atlantic Coastal Plain of eastern North America to model distributions of 193 species and estimate how they will be impacted by SLR. We found that species have likely already lost an average of 32% of their distributional area to development and agriculture, and are predicted to lose an average of 12.4 and 33.7% of their distributional area with one foot and six feet of SLR, respectively. Furthermore, species reproducing with symbiotic propagules have significantly larger distributions than species that reproduce sexually with fungal spores alone, and that the sexually reproducing species are predicted to lose greater distributional area to SLR. We further examined patterns of total species diversity and found that the areas with the highest diversity overlap with areas that will likely be inundated by SLR. The workflow applied here is flexible and applicable to estimating SLR impacts worldwide and can provide essential insights for local conservation planning.

Population size of *Anzia centrifuga* and other lichen endemics of Porto Santo (Portugal)

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Due to isolation, islands are known for their high number of endemics. Often, those endemic taxa have a low population size and are vulnerable to ecosystem change. We carried out a survey of all five endemic lichens of the island of Porto Santo (Madeira, Portugal, 42 km²). 6 km² of suitable habitat for the species was searched and mapped at 100 m resolution. The main habitat for the species consisted of volcanic outcrops, mainly basalt peaks and lava flows on the slopes. All accessible areas – circa 90% of the peaks and 50% of all outcrops – were surveyed by the authors during one week as a volunteer project. The population size of *Anzia centrifuga* was estimated to be 50–100 individuals greater than 2 cm diam. It occurred only on exposed, stable, vertical, N to W facing rockfaces above 240 m, restricting the potential habitat to less than 1.0 km². *Ramalina nematodes* and *R. portosantana* occurred often abundant on most larger exposed ridges. *Ramalina confertula*, *R. erosa*, *R. jamesii* and *R. timidiana* are restricted to an area often less than 1000 m² in the surroundings of their type localities. The non-endemic *Ramalina cupularis* and *R. requienii* occurred frequently throughout rocky areas.

Colonization, identification and conservation of *Bactrospora dryina* in the forests: lessons learned with polymorphic fungus-specific microsatellite markers

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Bactrospora dryina is specifically related to old-growth coppice-with-standard and flood-plain forests, which have dramatically declined in Europe in the past decades. We developed 16 polymorphic microsatellite markers, which are specific for *B. dryina* and reliably amplify either single fruit bodies or sterile thallus. We tested the markers in 264 samples, collected on 10 trees originating from three populations in North-Eastern Switzerland. Although oak trees were mostly covered with a single, continuous *B. dryina* colony, the microsatellite markers allowed to distinguish single or multiple lichen colonizations per tree. Hierarchical AMOVA revealed a relatively high level of differentiation between the three regions. The species-specific polymorphic loci developed here can also be used to detect poorly developed, sterile thalli of *B. dryina* and will allow to quantify the recent spread of the species into restored habitats. The markers will therefore play an important role in monitoring the effectiveness of habitat improvement measures for the conservation of *B. dryina* and associated forests and riverscapes

Implication of species distribution modeling (SDM) for conservation of epiphytic lichens in forest landscapes

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Epiphytic lichens are an important component of forest biodiversity. Many of them are threatened and conservation planning therefore requires comprehensive information about their distribution over space and time. Species distribution modeling (SDM) has become a powerful instrument in conservation biology and management. However, the spatial pattern of epiphytic lichens is not only strongly related to climatic and topographic variables but also to the characteristics of the tree species on which they grow. We applied SDM techniques to test the hypothesis that habitat specialists restricted to specific habitat types and common species with a wide range of ecological preferences may respond differently to the topo-climatic and forest-structure predictors. Our results showed that forest-structure predictors significantly improved the models of rare and threatened species with specific microhabitat requirements, i.e. mainly forest lichens (*Arthonia byssacea*, *Bactrospora dryina*, *Calicium viride* and *Lobaria pulmonaria*). We recommend using high-resolution forest-structure data for robust and reliable predictions of the distribution patterns of threatened epiphytic lichens, most of which are habitat specialists. The inclusion of these data will increase the effectiveness of the field observations needed to develop a conservation strategy for threatened epiphytic lichens at national level.

Visualizing fungal communities in lichens by fluorescent in situ hybridization

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Lichens are communities of different groups of fungi, photosynthetic organisms and bacteria. Distinguishing between different fungi with light microscopy can be challenging, even when the occurrence of lichenicolous fungi is known based on molecular data. Fluorescent in situ hybridization (FISH) is a method to visualize different structures, species or specific RNA targets but has rarely been used in lichenology. We developed general protocols for FISH in lichens, accounting for cortical polysaccharide matrix and cell wall permeabilization as well as autofluorescence of different parts of thalli. We also designed specific probes for simultaneous visualization of Ascomycota and Basidiomycota.

Cyphobasidium hypogymniicola (Pucciniomycotina, Basidiomycota) is a lichenicolous fungus occurring on *Hypogymnia physodes*, one of the most common lichens in Scandinavia. *Cyphobasidium hypogymniicola* forms its sexual stage in thalline galls. We used *Cyphobasidium*-targeted FISH to reveal previously unrecognized details of the fungal teleomorph as well as a previously unknown anamorphic (yeast) state of *C. hypogymniicola* occurring on the cortical layer of apparently uninfected *H. physodes*. FISH with its many applications appears as a powerful tool for the study of communities within lichens.

Boreal endolichenic fungal community structure at local, regional, and global scales

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Lichen thalli contain abundant and diverse fungal communities that are phylogenetically distinct from the lichen mycobiont and lichenicolous fungi. These endolichenic fungi occur within thalli in close association with the photobiont. Like their close relatives, plant endophytes, endolichenic fungi cause no apparent symptoms. Here a collection of >11,000 cultures in conjunction with next-generation sequencing (NGS) from the same host tissues was used to examine endolichenic communities in (a) multiple years at one boreal forest site; (b) nine equidistant sites across a 1300 km transect from the southernmost to northernmost extent of boreal forest in Québec; and (c) seven sites distributed along the entire circumboreal belt. This study reveals previously unexplored temporal stability of endolichenic communities in a focal boreal site. Despite relatively similar biotic and abiotic conditions along a consistent circumboreal latitudinal band, the abundance, diversity, and composition of endolichenic fungal communities differed as a function of geographic location. Across the north-south extent of boreal forest in Québec, communities were largely structured by host. Overall, culture-based and NGS methods yield different richness estimates but complementary ecological patterns. Ongoing work will incorporate network analyses with fungal and bacterial symbionts and examine biotic and abiotic factors important for structuring endolichenic communities.

Intrathalline diversity of lichen-inhabiting fungi assessed by metabarcoding of ITS2 region

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Lichen-inhabiting fungi represent a large and diversified but still unknown ecological group. They can live on host thalli symptomatically, showing characteristic phenotypes and different degrees of specificity (lichenicolous fungi), or asymptotically (endolichenic fungi), detectable only through culture and molecular techniques. Here we aim at studying the whole diversity of lichen-associated fungi using a metabarcoding analysis of the internal-transcribed-spacer regions, as parts of the fungal standard barcode, comparing the results obtained by sequencing separately both the ITS1 and the ITS2 segments. In this way we also avoid the analysis of group I intron occurring in some ITS1 fragments and achieve with the ITS2 a higher resolution on species composition. We analyzed thalli with and without symptoms of fungal infection collected from Alpine lichen communities on the Koralpe Massif (Austria). The first ITS1 amplicon sequencing highlighted a great taxonomic diversity. The majority of detected OTUs represents fungi of the two main classes Dothideomycetes and Eurotiomycetes. Shared endolichenic fungal composition in the thalli varies in different lichen species and does not correlate with the symptomatic fungal infections. Metabarcoding allows the exploration of lichens as ecological niches, revealing the organization of complex symbiotic communities and potentially the presence of coherent patterns.

Evidence of multiple origin of the lichenicolous life habit in Helotiales

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The order Helotiales (Leotiomycetes) represents the largest group of inoperculate discomycetes, comprising species with diverse lifestyles, including those inhabiting fungi and lichens. Phylogenetic analyses of five DNA markers have shown that the lichenicolous life style has appeared multiple times within the order. Most genera (*Diplolaeviopsis*, *Llimoniella*, *Macroskyttea*, *Rhymbocarpus*, *Skyttea*, *Thamnogalla*, *Unguiculariopsis*) belong to the recently resurrected family Cordieritidaceae, together with the non-lichenicolous *Cordierites*, *Diplocarpa*, *Ionomidotis*, and some others. *Protounguicularia* (= *Unguiculariopsis*) *nephromatis*, a fungus inhabiting *Nephroma* species, belongs to Cordieritidaceae as well. The genera *Llimoniella*, *Rhymbocarpus* and *Unguiculariopsis*, which are morphologically highly variable within their current genus concept, also show polyphyly based on the multi-gene analysis. The asexual lichenicolous fungi from the genus *Hainesia* form a distinct clade, the affinities of which with non-lichenicolous species remaining unknown because of missing data. The helotialean species *Geltingia associata*, *Pezizella epithallina*, and *P. ucrainica* appear independently from the rest of helotialean lichenicolous species.

Exploring the microbiome of the optionally lichenized fungus *Schizoxylon albescens*

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Recent studies show that non-photosynthetic bacteria may form abundant, diverse and presumably species-specific bacterial communities in the lichen thallus. These new discoveries have challenged the traditional view of the lichen symbiosis and stressed that lichens should be viewed as mini ecosystems, where microbial communities may contribute to and facilitate the lichenization process, but where the role of the participating bacteria still is very unclear. The Stictidaceae (Ostropales, Ascomycota) contains saprotrophic, parasitic and lichenized fungi, and several species that can live either as saprotrophs or as lichens depending on the substrate they grow on, a phenomenon termed "optional lichenization". Here, we will explore the microbial communities of *Schizoxylon albescens*, which either grows as loosely lichenized on *Populus* bark or as a saprotroph on dead *Populus* branches. We will compare the microbial communities in the lichenized and saprotrophic states, using next generation sequencing data generated on the Illumina MySeq sequencer combined with microscopic studies using DNA fluorescence in situ hybridization.

Interaction networks between lichen-forming fungi and their photobionts in continental Antarctica

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Lichen-forming fungi interact with their photobionts showing different patterns, from highly specialized species to others that are able to interact with different photobiont lineages over their ranges. Most studies have so far focused on the range of photobionts interacting with a single species or with few species from the same community, genus or family. Here, we use the mutualistic interaction network framework to study all the links among lichen-forming fungi and their photobionts in 5 different localities in continental Antarctica along a latitudinal gradient from 77°S to 85°S. We analyzed a total of 756 thalli, recovering 842 interactions. GMYC, ABGD and PTP algorithms were used to delimit fungal species using the ITS as barcode. Algal ITS and *rbcL* markers were used to identify photobiont genotypes. Analyses revealed higher nestedness and modularity than null models. Fungal and algal phylogenies based on 4 (5.8, nuLSU, mtSSU, RPB2) and two (ITS and *rbcL*) markers respectively were used to test the influence of phylogeny and geography in the architecture of the recovered interaction network by means of mcmcGLMMs. Coevolutionary interactions (closely related fungi share closely related photobionts) were recovered as the main factor shaping the interaction network, with geography having a small effect.

454 amplicon pyrosequencing as an accurate tool to reveal the concealed microalgal diversity inside a single thallus

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Current literature has revealed that in lichens intrathalline coexistence of different microalgal lineages or taxa is a more common event than previously thought. In *Ramalina farinacea* our team demonstrated that *Trebouxia* sp. TR9 and *T. jamesii* were coexisting along with different populations. Moreover, physiological characterization exhibited different behavior in response to abiotic stress in these phycobionts, which seems to be the key to the intrathalline co-occurring. The majority of studies on molecular phycobiont diversity within entire thalli are based mainly on the SANGER methodology that may be underestimating the potential heterogeneity of the microalgae. The aim of this study was to design an accurate 454 pyrosequencing protocol to allow the detection of the vast number of microalgal genotypes that remain concealed when using traditional molecular techniques. A total of 41,185 raw sequences were obtained, and we were able to detect more than 35 OTUs inside a single thallus. Our results suggest that the diversity of symbiotic microalgae in lichen thalli is a more important feature than was previously thought, and should not be underestimated in phylogenetic and ecophysiological studies. (GVA, PROMETEOII/2013/021) (MIMECO, CGL2012-40058-C02-01)

Sequencing genomes of lichenized fungi: evaluating the metagenome skimming approach

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Lichen thalli represent complex multi-species communities of fungal, algal, and bacterial species. In recent years, the metagenome skimming approach has been used for in-depth genomic characterization of eukaryotic communities. This approach thus represents a promising tool for reconstructing genomes of lichen-forming fungi from metagenomic reads of uncultured thalli. However no study has so far tested accuracy and completeness of skim-based assemblies compared to assemblies based on pure culture strains of lichenized fungi. We assembled the metagenomes of *Evernia prunastri* and *Pseud-evernia furfuracea* based on metagenomic sequences derived from whole lichen thalli. We extracted fungal contigs using metagenome binning methods and performed gene prediction and functional annotation on the fungal contig subsets. We then assessed quality and completeness of the skim-based assemblies using as reference genome assemblies based on pure culture strains of the two fungal species. Our findings suggest that metagenome skimming is a viable tool to reconstruct fungal genomes from uncultured lichen thalli. However, the applicability of the method may vary from species to species. We further discuss additional assembly problems and biases related to the presence of other fungi and/or rich bacterial communities.

Genome-wide search, characterization and comparison of MAT gene families in lichen-forming fungi

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Scientific and technical advances achieved in recent years are allowing a higher speed and lower cost in whole-genome sequencing. The information obtained from the comparison of genomes can be used to predict the gene function and to establish the genomic region organization by inferring similarities in regulation. Fungal reproduction is regulated by the mating-type genes (MAT) locus, usually containing one or several idiomorphic genes. The presence of one or more idiomorphic genes in the locus is what determines the reproductive strategy in fungi including lichenized fungi (homothalium vs. heterothalium). This locus shows a high interespecific variability in Ascomycota, where only model organisms have been studied. Our main aims include (i) seeking and analyzing of MAT genes in lichen-forming fungi using whole-genome, (ii) comparing genomic architecture the MAT locus with that of non-lichenized fungi, and (iii) evaluating recombination events among MAT genes

Evolution of the ribosomal RNA cistron in the *Rhizoplaca melanophthalma* species complex

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Nuclear ribosomal DNA (nrDNA) is an important tool for inferring evolutionary relationships and investigating diversity in lichen-forming fungi. In spite of the prevalent use of ribosomal markers in fungal research, central features of ribosomal evolution are poorly known for lichenized fungi. The internal transcribed spacer (ITS) region of the nuclear ribosomal DNA has been adopted as the standard DNA barcode identification marker for fungi. However, little is known in regards to intragenomic variation in rDNA. In order to better understand evolution of nrDNA and the utility of the ITS for barcode identification of lichen-forming fungal species, we generated complete nuclear ribosomal cistron sequences from species in the *Rhizoplaca melanophthalma* species complex. Using high-throughput sequencing we document low levels of intragenomic variation in the nrDNA. In the ITS regions, the limited number of potentially polymorphic sites do not correspond to diagnostic fixed nucleotide position characters separating taxa within this species complex, supporting the role of the ITS as an effective barcoding marker. We estimated copy numbers for the rDNA cistron ranging from nine to 48 copies. We will discuss important features of rDNA evolution and their implications for studying lichen-forming fungi.

Bacterial microbiomes of lichen thalli: from observations to understanding interactions

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Amplicon sequencing data reveal that host-specific bacterial communities associate with lichen thalli. FISH/CLSM microscopy locates these communities on the surface of the thalli. A comparative metagenomic and metaproteomic analysis, visualized by Voronoi treemaps shows that bacteria encode multiple functions such as nutrient supply, especially nitrogen, phosphorous and sulfur, resistance against biotic stress factors (pathogen defense), resistance against abiotic factors, support by production of vitamins, detoxification of metabolites, and lytic functions. In essence the environmental proteomic data agree with these functions. Bacterial data can be integrated in a comprehensive model of the symbiosis as a functional multi-player network of the participants. Analysis of herbarium material also shows that bacterial communities are very stable on lichens. We hypothesize that lichen thalli – as one of the most complex structures in the fungal kingdom – evolved not only to optimize the interaction with the algal partners, but also to control benefits from the bacterial associates. To what extent partners beside the photobiont also contribute to the lichen morphogenesis now needs to be tested by experimental approaches. We also observe a certain overlap with microbiomes on different adjacent substrates/hosts and distinguish habitat specialists from generalists, which link lichen microbiomes with their environment

Secondary metabolites of lichens as potential allelochemicals

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Lichens are symbiotic organisms consisting of fungus (mycobiont) and photosynthetic partner (photobiont), which can be either algae or cyanobacteria. Ecological success of symbioses forming lichens may be, in part, explained by production of organic compounds called secondary metabolites. Lichen secondary metabolites are produced by the fungal partner and their presence is mostly restricted to the lichens themselves. Biological activities of lichen secondary metabolites were confirmed in several studies such as photoprotection, antiviral, antibacterial, antitumor, antiherbivore, antioxidant, anti-pyretic, analgetic action. Some secondary metabolites of lichens appear to have allelopathic effects on neighboring lichens, bryophytes, fungi, vascular plants, microorganisms as well as on the algal partner of lichens. However, the mechanisms of the phytotoxic effects of these compounds on plants, including its own algal partner in the lichen thalli are still not understood sufficiently. Interactions between lichens and bryophytes are still not clarified. Lichen overgrowth on bryophytes is frequently observed in nature although mosses grow faster than lichens. In the present study phytotoxic effects of secondary metabolites on cultures of the aposymbiotically grown lichen photobiont *Trebouxia erici* were evaluated. Influence of lichen extracts on growth of *Physcomitrella patens* were tested. Inhibition of protonemata, differences in cells lengths and widths were also noticed.

Mycosporine screening in fresh and historic collections of Verrucariaceae – opportunities and limitations

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Mycosporines are discussed as possible photoprotective substances or as more generalised antioxidants in various pro- and eukaryotic phyla. In lichenised fungi they are mainly found in species which are associated with cyanobacteria and could play a role as alternatives to polyphenolic metabolites. After the recent discovery of two different mycosporines in *Dermatocarpon luridum* with its Chlorophyta photobiont *Diplosphaera*, we have aimed to test how widespread mycosporines are across the family Verrucariaceae and to assess their occurrence in related taxa from contrasting habitats and different associated algae. We have first optimised a screening protocol for selected Mycosporines to work with minute quantities of fresh and herbarium material. In a second step we have studied the variation of mycosporines in a variety of samples. These results were compared with data obtained from a time series of herbarium samples of the same test species covering a period of up to 163 years of storage. Only mycosporine glutamicol is preserved well over long storage periods. Mycosporine glutaminol instead disappears completely from stored specimens after a period of only 15 years. First results show a complex pattern of Mycosporine glutaminol occurrence across the Verrucariaceae, which requires interpretation in a phylogenetic and ecological framework.

Do Secondary Metabolites Influence Lichen Community Structure?

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Lichens produce hundreds of secondary metabolites, many of which are unique to the lichen symbiosis and have established ecological significance. We focused on the role of these compounds at the community scale to potentially reveal the benefit these compounds confer to lichens. Using field data from Arctic National Parklands, Alaska, USA, we related trends in the frequency and abundance of lichen compounds with lichen community structure and environmental gradients. We created a lichen compound by species matrix from online databases and scientific literature. Using ordinations and nonparametric multiplicative regressions, we generated hilltop plots that represent the relationship of chemicals and environmental variables in species space. In 328 plots across five national parks spanning approximately 81,500 km², we found 342 macrolichen species that contained 125 known lichen compounds. A 3-dimensional ordination explained about 75% of the variation of plots in species space. Hilltop plots revealed that many compounds show strong relationships to community structure, but few environmental variables showed strong associations with community patterns.

Acetone rinsing tolerance of *Cladonia foliacea*

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We plan to study the usnic acid production in thalli of *Cladonia foliacea* after acetone rinsing in a transplantation experiment. This species is excellent for investigations in the Hungarian steppe vegetation, where predictive data on the effect of global climate change will be gathered during future studies. To establish the optimal period for applying acetone, dry thalli were rinsed in acetone for 0.5, 1, 2, 4, 8, 16, 32, 64, 128, 256, 384, 640 and 1024 hours following methods by Solhaug and Gauslaa (2001). Secondary lichen substances were analysed by HPTLC and HPLC, the detrimental effect of acetone was tested by chlorophyll fluorescence measurement on thalli after thorough aeration and two days rehydration. The optimal duration for acetone rinsing proved to be around 1–2 days in the samples collected in summer. According to our hypothesis and preliminary results, the thalli are more sensitive to acetone rinsing in winter. Therefore the summer period – when lichens are more frequently in dry condition and therefore photosynthetically active for a shorter period – is probably more advantageous for collecting samples for transplantation experiments combined with acetone rinsing. Supported by the Hungarian Scientific Research Fund OTKA 81232, 101713, the Research Centre of Excellence 9878/2015/FEKUT.

Accumulation of metals by saxicolous *Aspicilia* species on different rock types

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Secondary metabolites are able to retain metals in thalli of lichens (Purvis et al. 1990). 'Lichen acids' differ in their affinity to metals and may determine distribution patterns of species (Hauck et al. 2009). In order to check this statement, thalli of *Aspicilia* species were collected on ultramafic serpentine and on acid rocks – granite and quartzite in the Middle and Southern Urals (Russia). Lichens and underlying rock samples were analysed by AAS. It has been shown that lichens growing on metal-rich serpentine regardless to their secondary chemistry accumulate relatively low amount of metals compared to the substrate. Some metals contained in thalli in concentrations equal or even lower than in the rock (Paukov et al. 2015). Opposite to this, the same species on granite contain much higher levels of metals than in the substrate. The most pronounced differences were found for Cu, Zn, Pb and Ni (10–20 times higher). Interestingly that absolute level of metals in lichens on serpentine and granite (except Ni) are comparable. Our results prove the statement that high affinity of secondary metabolites to metals may be an advantageous feature for lichens growing in habitats with poor availability of elements such as granite compared to serpentine.

Fri 5 Aug 12.25–12.40 Room 13 • ORAL 100

Biosynthesis of Naphthoquinones, anthraquinones and depsides in the cultured mycobiont of the Christmas wreath lichen *Herpothallon rubrocinctum* (Arthoniales)

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Quinones, in general are synthesised from very different starting substances and via different biochemical pathways. Strongly pigmented lichens, like *Herpothallon rubrocinctum* colonize sun-exposed habitats on the bark of trees in the American tropics. *Herpothallon rubrocinctum* (in the past named *Chiodecton sanguineum*) is an eye-catching lichen, because of its bright red color. Under permissive ecological conditions in a culture chamber (simulation of tropical conditions/by induction of UV radiation) the mycobiont biosynthesized the typical lichen pigments. HPLC-analyses of the *Herpothallon-rubrocinctum*-thalli showed the production of confluent and chiodectonic acids as minor substances. Additionally, an unidentified anthraquinone (reddish pigment) was detected in minor quantities. The cultured mycobiont biosynthesized chiodectonic (major) and confluent acids (minor) as expected, but also produced the chemically related rhodocladonic acid. Comparing the chromatograms/UVspectra and quantifying the metabolites of the thallus and the mycobiont it became evident that the cultured fungus had formed the metabolites in higher quantities and also β -carotene, as well as 4 different unidentified anthraquinones. Chiodectonic acid is thought to function as a radiation protectant; in combination with beta-carotene, which has been found to have an established role in cellular DNA repair (UV-damage). In the cultures intermediates and endproducts were found, elucidating essential steps in the respective pathways.

The importance of spatio-temporal photobiont patterns for phylogenetic revisions and macroevolutionary studies of lichens: a worldwide case study of *Peltigera*

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Within the framework of a worldwide revision of *Peltigera*, several thousand specimens were gathered to attempt to sequence all main partners (i.e., *Peltigera*, nrITS, nrLSU, RPB1, EFT2.1, β -tubulin, COR1b, COR3, COR16; *Nostoc*, rbcLX; and *Coccomyxa*, nrITS and rbcL). We succeeded to sequence the fungal and cyanobacterial partners for 1900 and 650 specimens, respectively. The difficulty to identify *Peltigera* species and to understand the observed phenotypic variation was due to a high number of cryptic species within phenotypically defined species. This study identified 900 unique fungal ITS haplotypes and increased the number of *Peltigera* species from 90 known species to > 170 species when using various species discovery and validation methods. Sixty *Nostoc* phylogroups were found in association with *Peltigera*. Patterns of *Peltigera* species and *Nostoc* phylogroup diversity, biogeographical distributions, and specificity towards their respective partners, greatly differ among *Peltigera* sections. The overarching trend is that nearly 85% of *Peltigera* species are specialized on one or two *Nostoc* phylogroups, whereas > 55% of *Nostoc* phylogroups associates with at least three *Peltigera* species. The number of species in sections *Peltigera* (~95 species) and *Polydactylon* (~55 species) was much higher than expected and *Nostoc* phylogroups can help delimit and identify *Peltigera* species.

From one to one hundred and eighty species: phenotypical and ecogeographical diversification in the genus *Cora* (lichenized Basidiomycota: Hygrophoraceae)

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Foliose macrolichens in the Basidiomycota genus *Cora* (Agaricales: Hygrophoraceae) were long recognized as a single species. Yet, molecular sequence data of the ITS barcoding locus have shown that *Cora* contains hundreds of species. Here we provide an updated ITS phylogeny with over 600 samples corresponding to approximately 180 taxa. Phenotypical (lobe configuration, color, soredia, cortex type, photobiont) and ecogeographical characters (substrate, distribution range) are mapped on the tree to analyze patterns of correlation with major and minor lineages and species. It is shown that phenotype and substrate ecology are highly species-specific but may vary between closely related species. Most species have a narrow geographic range, whereas a few are more widely distributed, particularly among those producing soredia. Various types of 'cryptic species', that is species with very similar phenotype, are found in the genus, forming either sister species with different ecology or subtle phenotypical differences ('semi-cryptic'), different geographic ranges ('allo-cryptic' in a phylogenetic sense), or unrelated taxa exhibiting parallelism ('pseudo-cryptic') species. Characters not previously recognized, such as papilliform hyphae in the lower medulla, are shown to be important for species recognition. Photobiont switch appears to have triggered diversification of *Cora* in the northern Andes.

Untangling *Usnea*: multi-locus concatenated and coalescent-based analyses reveal recent diversification history and clusters of mixed morphospecies in the section *Usnea*

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While the cosmopolitan genus *Usnea* (Parmeliaceae) is well known and easily recognized by the usually yellowish beard-like thallus with central cord, delimitation of many *Usnea* species is difficult due to the high variation and complexity of diagnostic characters. We assessed the monophyly of 18 species from section *Usnea* occurring in North America and Europe, including sorediate and sexually reproducing taxa with both pendent and shrubby thalli. Six nuclear markers (ITS, IGS, beta-tubulin, MCM7, RPB1 and RPB2) were sequenced for 144 samples. All analyzed loci showed weak genetic structure and short branch lengths in single-locus topologies. Concatenated, multi-locus analyses conducted in Bayesian and maximum likelihood frameworks, as well as coalescent-based species delimitation and species tree methods, recovered several distinct clades, some represented traditional morphology-based species (*Usnea cavernosa*, *U. praetervisa*, *U. silesiaca*, *U. wasmuthii*), while others formed clusters of two or more species (*Usnea florida* – *U. subfloridana*, *U. fulvoviregens* – *U. glabrescens*, *U. barbata* – *U. chaetophora* – *U. dasopoga* – *U. diplotypus*, *U. barbata* – *U. intermedia* – *U. lapponica* – *U. substerilis*). We illustrate how the utility of some traditionally used characters in *Usnea* species identification varies in the light of the genetic data.

Umbilicariaceae – trait evolution and new generic concept

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The evolution of Umbilicariaceae was reconstructed based on 640 sequences (429 new) from three independent DNA regions (ITS/5.8S/SSU, RPB2, and mtLSU) using Maximum Likelihood and Bayesian phylogenetic inference frameworks. The study included a representative fraction (presumably about 80%) of the overall species diversity of the Umbilicariaceae. The analyses resulted in the recognition of eight well supported clades, delimited by a combination of morphological and chemical traits. None of the previous classifications within Umbilicariaceae s. str. were supported by the phylogenetic analyses. Our results suggest that Umbilicariaceae s. str. has to be divided into 8 genera, 3 of which were newly erected. Patterns of evolutionary progression and functional couplings of diagnostic characters (adhesive structures, thalloconidia, apothecia and ascospores, lichenized dispersal units, secondary metabolites) will be discussed against the molecular phylogenetic tree topology. The investigation was supported by Russian Foundation of Basic Research (grant no. 14-04-00067).

Distinctive characters of *Nostoc* genomes in cyanolichens

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The complete genome sequencing and gene annotation of *Nostoc* sp. N6 from the lichen *Peltigera membranacea* and the *Nostoc* cyanobiont of the lichen *Lobaria pulmonaria* plus draft sequencing of four more lichen-associated *Nostoc* strains, together with previously available *Nostoc* genomes, allows identification of genes potentially involved in symbioses with a broad range of partners as well as genes specific to the symbiosis with lichen mycobionts. The presence of additional genes necessary for symbiotic competence is likely reflected in larger genome sizes of symbiotic *Nostoc* strains. Some of the identified genes are presumably involved in the initial recognition and in establishment of the symbiotic association, while others may confer advantage to cyanobionts during cohabitation with a mycobiont in the lichen symbiosis. The *Nostoc* genomes encode a large number of secondary products, both previously known and novel, including the trans-PKS/NRPS product nosperin. Since many phylogenetic studies have shown that *Nostoc* is a polyphyletic group that includes several lineages, this work also provides an improved molecular basis for taxonomic revision of the genus *Nostoc*.

High throughput genome sequencing of a lichen-forming fungus *Usnea hakonensis* and its photobiont *Trebouxia* sp.

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Importance of symbioses in ecosystem and evolution is now indisputable. A number of works revealed that symbioses could affect organisms at genetic level. Although lichens are considered as one of the most successful symbiotic interactions in nature, only little of their genetic characteristics are known. In this study, we sequenced genomes of a lichen-forming fungus *Usnea hakonensis* and its photobiont from a genus *Trebouxia* (*Trebouxia* sp.). Independent cultures of the fungus and the alga, isolated from the same thallus, were used to extract genomic DNA. For each symbiotic partner, a DNA library was constructed using standard Illumina protocols and paired-end sequencing was performed by Illumina HiSeq2500 platform. The sequencing from *Usnea hakonensis* resulted in 227 million 125 bp reads that were assembled into 2,454 scaffolds with the N50 value of 163 kb. The predicted genome size was 42 Mb with average coverage x590. Scaffolds longer than 2 kb were retained for further analyses in order to reveal genomic features of the lichen-forming fungus. We also determined 30 Gb of the algal DNA and the genomes of both symbiotic partners are going to be reported.

Transcriptomic analysis of the lichen photobiont *Trebouxia gelatinosa* subjected to dehydration and rehydration processes

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All the species of *Trebouxia*, the most common lichen-forming genus of aero-terrestrial green algae, are desiccation tolerant. This remarkable adaptation is, however, poorly known on its molecular bases. We applied a transcriptomic approach to investigate changes in the gene expression of *T. gelatinosa* induced by changes in the cell water status. The mRNA of three sample groups (control, dehydrated, rehydrated) was subjected to Illumina massive sequencing (2 × 100 bp), that produced a total of 243 × 10⁶ fragments. From this pool 13,648 protein-coding transcripts could be annotated and used for the subsequent gene expression analysis. During the dehydration/rehydration cycle c. 92% of the total protein-coding transcripts displayed a stable expression, suggesting that the desiccation tolerance of *T. gelatinosa* mostly relies on constitutive mechanisms. Components of the photosynthetic apparatus, the ROS-scavenging system, expansins, and Desiccation Related Proteins were those most affected by changes in the cell water status. The assembled *T. gelatinosa* transcriptome here presented is a valuable standard reference for future RNA-seq based gene expression studies and represents a new tool to investigate the mechanisms of desiccation tolerance in aero-terrestrial green algae and lichen photobionts.

The nuclear, chloroplast and mitochondrial genomes of the symbiotic microalga *Trebouxia* sp. TR9 from the lichen *Ramalina farinacea* (L.) Ach

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Previous studies in *Ramalina farinacea* populations have shown that the same two *Trebouxia* species coexist in every analysed thallus (*T. jamesii* and *Trebouxia* sp. TR9). *Trebouxia* sp. TR9 shows inducible responses against stress and has a better physiological performance than *T. jamesii*. These microalgae were selected as model organisms for studying interactions between phycobionts and mycobionts. The scarcity of genomic information about *Trebouxia* algae prompted us to generate a survey of the genomic sequences of *Trebouxia* sp. TR9 by NGS. Total DNA and RNA isolated from nine different experiments were sequenced by 454 and Solexa technologies. The assemblage of the obtained sequences from the chloroplast, mitochondrial and nuclear genomes resulted in sizes of more than 300 Kb, 70 Kb and 59 Mb, respectively. "Ab initio" gene predictions calculated 9,500 nuclear genes. Gene annotations based on RNAseq data produced 13,887 genes and 21,076 isoforms. Results showed the absence of genome reductions and suggested the existence of overlapping UTRs. This work provides for the first time the organellar genomes and the draft nuclear genome of a member belonging to the predominant lichen-forming genus of phycobionts, and may shed light on the evolutionary trends of the Trebouxiophyceae. (MINECO_CGL2012-40058-C02-01), FEDER, (GVA_PROMETE-OII/2013/021).

A little explored lichen hot spot in tropical Asia: 66 new species and 666 new records from Sri Lanka

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Tropical lichens are an extremely successful and diverse group of fungi. The combination of a topographically varied and geologically ancient landscape and repeated influxes of biota from spatially and temporally disparate biogeographic regions have resulted in a highly diverse lichen biota in Sri Lanka, including species that apparently are absent from India. For instance, Sri Lanka became one of the Graphidaceae hot spots in the world. During a lichen collecting trip made in 2015, in representative wet, dry, submontane and montane habitats on the island, 66 new species and 666 new records in many different genera were discovered. With new species described previously, Sri Lanka has become the country with the highest number of new species and new records reported per area size during the past four years. In addition, fresh material was collected of species which were hitherto only known from older type material: as a result, molecular analysis was carried out elucidating the phylogenetic positions of endemic genera, e.g. *Leightoniella*. Comparison with other recently explored areas of tropical Asia reveals Sri Lanka as a hot spot for lichen diversity in this region.

Diversity of the lichen family Graphidaceae in mangrove forest, Eastern Thailand

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Graphidaceae is the highest diversity of crustose lichens, with nearly 2,400 known species. They are typically found on barks and very occasionally on rocks or leaves. Our objective was to explore the diversity of lichen family Graphidaceae in mangrove forests in Eastern Thailand. Over 1,500 specimens were collected and identified to 48 species within 21 genera; *Carbacanthographis*, *Chapsa*, *Creographa*, *Diorygma*, *Dyplolabia*, *Fissurina*, *Glyphis*, *Graphis*, *Leiorreuma*, *Leptotrema*, *Leucodecton*, *Melanotrema*, *Nadvornikia*, *Nitidochapsa*, *Ocellularia*, *Pallidogramme*, *Phaeographis*, *Platygramme*, *Sarcographa*, *Stegobolus* and *Thelotrema*. During the identification of the materials, several species have been discovered as new record for Thailand. In addition, *Nitidochapsa siamensis* is described as new to science and five species are expected to be new species. Our results emphasized that mangrove forests had distinctive characters which were favorable for specific lichens to grow on this forest type, either new additions to the lichen biota of Thailand or even new for science.

Lichen biodiversity in tropical islands: the case of the genus *Sticta* in Puerto Rico

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Tropical islands exhibit the highest number of species and the largest proportion of endemics per unit area for many biological groups making them important hotspots for biological diversity worldwide. While biodiversity patterns and geographical distributions in insular regions are well understood for many organisms, the extent to which these patterns apply to groups like lichens remain largely unknown. Here we present a phylogenetic analysis for the lichen genus *Sticta* in Puerto Rico to determine how well the current morphology-based taxonomy agrees with phylogeny and to make inferences about the biogeographical history of this group in the island. Following a multi-locus approach, we show that species-level taxa appear dispersed within and among clades from different geographic regions suggesting that extant species assemblage was likely shaped by multiple colonization events. We found that the flora is composed of a combination of widespread and previously unrecognized endemic species and that the recognized number of species using morphology-based approaches resembles that obtained from our phylogenetic approach. We will discuss potential factors influencing the observed patterns, as well as how the case of *Sticta* in Puerto Rico provides useful insight on our understanding about lichen dispersal and evolution in ecosystems.

Drivers of lichen community composition in old growth and secondary lowland rain forests of northeast Borneo

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We have studied the epiphytic lichen communities in two of the largest remaining areas of old growth lowland rainforest in the Malaysian state of Sabah (NE Borneo), separated by extensive areas of oil palm plantations and secondary forests. We have compared the lichen communities within and between these areas with those found in logged forest fragments, following principles of the BioAssess-protocol. We found significant differences in lichen communities of old growth from those of logged forests, but also between the two old growth forest areas. Lichen communities from both old growth forest areas include a wide range of taxa significantly associated with specific features such as tree girth, bark structure and the presence of buttresses. The effects of bark pH and polyphenol content are less significant. Logged forests support fewer taxa, most of these being associated with disturbance, but relicts of "old growth" taxa can survive in low frequencies. The use of a quantitative approach, estimating frequency of each taxon in each plot, allows us to detect the scale of devastation of lichen communities in the logged forest and the shifts between lichen communities associated with a range of conditions in the old growth forest.

Phylogenetic structure of lichen metacommunities in northern and northeastern Brazil

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Analysing the phylogenetic structure of plant communities is an increasingly popular field in ecology; however, this approach has not yet been employed for lichens. Here, we analyse the phylogenetic structure of lichen metacommunities in northern and northeastern Brazil, focusing on the Amazon and the coastal Atlantic rain forest and the Caatinga, but also considering other associated ecosystems such as Brejos de Altitude, Carrasco, Cerrado, and Restinga. We assembled a data set of approximately 1,600 species for the target area and their presence or absence in the aforementioned biomes and vegetation types. Using a combination of existing and newly generated molecular sequence data, we built a supertree by combining published phylogenies of different taxa and adding taxa for which new molecular sequence data were generated. We used the software PHYLOCOM to compute various indices of phylogenetic community structure. Species richness was highest in the Atlantic rain forest, followed by the Amazon, the Caatinga, and Brejos. The Caatinga exhibited strong phylogenetic clustering, whereas the Amazon appeared phylogenetically overdispersed, which suggests stronger ecological constraints with respect to lichen colonization for the dry, deciduous Caatinga.

POSTER PRESENTATIONS

Taxonomic study of Acarosporaceae in Altay Mountains in Xinjiang, China

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Acarosporaceae classified into Acarosporales, Lecanoromycetes, Ascomycota. The largest genus in Acarosporaceae is *Acarospora*. Species of Acarosporaceae more in arid region, they are more appeared in the northeast region, Kansu, Inner Mongol, Tibet and Xinjiang. In this paper, more than 300 specimens were studied that were collected from Altay Mountains, studies on lichen family Acarosporaceae are performed using the methods of morphology, anatomy and chemistry. Five genera of Acarosporaceae are reported in this paper, and one of them is new to China, that is *Polysporina* Vězda, also 37 species of Acarosporaceae are reported, 19 species of them are new to China and one of them is new to science. Based on the anatomical study of every genus and species, we can get the result that the structure and thickness of upper cortex, degree of evenness of algal layer, the type of apothecia and the size of ascospores are important for classification. There are seven secondary natural products examined by using thin layer chromatography and chemical spot test, they are: Gyrophoric acid, Lecanoric acid, 3-hydroxygyrophoric acid, Methyl lecanorate. Rhizocarpic acid, Noristic acid, Acaronic acid.

Understanding bacterial nutrient supply in lichens from Iberian and Canarian lichen species: symbiosis sustainability and environmental stress tolerance

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Lichens are now recognized as multispecies microbial mutualisms in which heterotrophic bacteria are relevant symbionts. Metagenomic studies have proposed that these bacteria may play important roles within lichens, including nutrient supply and recycling. However, a full understanding of their metabolic potential and functions in lichen symbiosis requires studies with culturable isolates. We have characterized a collection of bacterial strains from two Parmeliaceae lichen species, *Pseudevernia furfuracea* from Mediterranean mountains and *Ramalina farinacea* from the Canary Islands. The aim was to explore and compare their nutrient provision and hydrolytic activities, along with their growth at different temperatures and pHs. Most of the strains were able to hydrolyze proteins, polysaccharides, lipids and nucleic acids, as well as fix nitrogen and solubilize phosphates and iron. These results showed that bacterial symbionts could be able to cover diverse nutritional requirements of lichen thalli as well as to recycle the older parts of thalli, favoring symbiosis sustainability. Interestingly, *P. furfuracea* associated bacteria were more active and able to grow in a wider range of temperature and pHs than those from *R. farinacea*, suggesting that lichen colonization of different biogeographical regions could be related with an increased tolerance of their bacterial partners to environmental stresses. (MINECO-CGL2012-40058-C02-01)(GV-PROMETEOII/2013/021) (University-of-Valencia-Research-Support)(VALi+d-Fellowship).

Diversity and biogeography of lichen-associated fungi

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Lichens are majorly composed of lichenized fungi and symbiotic microalgae, but other microorganisms such as bacteria and lichen-associated fungi are also important components of lichens. The presence of lichen-associated fungi has long been recognized, but fungal diversity across diverse lichen species and geographical area has rarely been studied. In this study, we analyzed lichen-associated fungal diversity from diverse lichen species collected from the Antarctic and Arctic areas based on nuclear LSU sequence information. Fungal diversity in lichens was also compared with those recovered from soil, rock, marine sediment and water samples. Fungal diversity in lichen thalli was lower than terrestrial soil, marine sediment, and endophytic environment, but higher than rock or fresh water environments. Many of the fungal OTUs in lichens were also observed in terrestrial soil, marine sediment, rocks, and plants. Fungal communities in lichens were mostly composed of Lecanoromycetes, Eurotiomycetes, and Sordariomycetes. Lichens in continental Antarctic hardly share fungal OTUs with lichens from other areas, but lichens from Chile, Falkland Island, King George Island, Svalbard, and Russia shared many of OTUs each other. It may imply that climatic condition is more important than geographical isolation for lichen-associated fungal distribution

Barcoding lichen-forming fungi using 454 pyrosequencing

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Although lichens play an important role in the ecological integrity of many vulnerable landscapes, only a minority of lichen-forming fungi have been barcoded out of the currently accepted ~18,000 species. Applying Sanger sequencing can be problematic with lichens since saprophytic, endophytic, and parasitic fungi live intimately admixed, resulting often in low-quality sequences. We opted high-throughput, long-read 454 pyrosequencing in a GS FLX+ System to barcode the full fungal Internal Transcribed Spacer region (ITS) of 100 epiphytic lichen species from Switzerland. We demonstrate the potential of pyrosequencing in DNA barcoding, in that the expected lichen fungus was successfully sequenced for all samples except one, and that the NCBI nucleotide database—currently the most complete database for lichens—can be used as a reference database in identifying common lichen fungi. Besides the expected mycobiont, many other fungi were identified within our samples, on average 11 fungal lineages per lichen sample, many of which were identified as lichen-associated (facultative parasites / lichenicolous) or plant-associated (epi- or endophytes). At the same time, several issues were encountered, including a high sequencing error rate, multiple ITS versions in a genome (incomplete concerted evolution), and in some samples the presence of mixed lichen-forming fungi (possible lichen chimeras).

Foliose lichens in Sugadaira harbor various *Nemania* lineages

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Recently endolichenic fungi (lichen endophyte) have been reported from various countries. However, their distribution patterns remain largely unknown. We collected six foliose lichen genera (*Flavoparmelia*, *Parmelia*, *Menegazzia*, *Cetrelia*, *Peltigera*, *Leptogium*) growing on bark or rock in order to obtain new knowledge of the endolichenic fungal flora in Sugadaira highlands (ca. 1300m) of central Honshu, Japan. Each lichen material was divided into segments of ca. 0.5 cm², followed by surface sterilization using the procedure of U'Ren et al. (2010). These segments were further cut to ca. 0.25 cm², then 50 segments of them were haphazardly selected and placed on the malt extract agar for three month at room temperature. A total of 163 isolates were recovered from 750 thallus segments of the fifteen lichen materials. Fungal isolates were identified to genera by morphology or ITS sequence. The most abundant genus was *Nemania* (Ascomycota, Xylariaceae) (151 isolates), and the other fungi were far less abundant. Molecular phylogenetic analysis of these *Nemania* isolates revealed that they were consisted of at least eight lineages and distributed in every materials regardless of lichen genera. Results of this study suggest that *Nemania* spp. are likely to colonize within foliose lichen thalli and probably dominant endolichenic fungi in Sugadaira.

Tangled trees? The phylogenies of Tremellomycetes and their lichen hosts

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Understanding the origin of biodiversity is one of the most exciting aims of biology. Nowadays it is assumed that coevolution between organisms that live associated, especially between parasites and their hosts, has generated a great fraction of the known biological diversity. Systems composed of lichenicolous fungi and their lichenized hosts are interesting associations to identify potential evolutionary forces driving diversification. Some species of lichen-inhabiting fungi behave as generalists, whereas others are very specific towards their hosts and are therefore considered specialists. The Tremellomycetes (Basidiomycota) belong in this second group, and their host-specificity is often a great aid to identify species. In associations involving specialists, cospeciation was in general traditionally suggested as the prevalent hypothesis to explain diversification, although this paradigm gradually lost strength. In the first study achieved on the joint evolution between lichens and lichenicolous fungi we showed that other events, in particular host switches followed by adaptation to different ecological niches, were prominent forces promoting speciation in the *Biatoropsis-Usnea* system. Here, we extend our studies to other groups of Tremellomycetes and lichenized fungi, and use cophylogenetic analysis tools to identify potential evolutionary events explaining the joint recovered phylogenies.

Buellia zoharyi populations show noticeable microalgal diversity throughout their entire range of distribution

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Buellia zoharyi Galun is a widespread lichen on sun-exposed biological soil crusts (BSC) under xeric Mediterranean bioclimatic conditions. This species was said to be highly specific to gypsum soils, but it has also been found occasionally in a great variety of basic substrata. We have selected 24 different populations covering the entire range of the species in the field, from NW Africa to the Canary Islands and to Iran. The *B. zoharyi* mycobiont was identified using ITS rADN as barcode. Phycobiont phylogenetic analyses were made using both chloroplast (LSU rDNA) and nuclear (nrDNA ITS) molecular markers. In addition, ultrastructural microscopic techniques were used to characterize each of the microalgae found. Our results evidence the presence throughout all populations of at least four different *Trebouxia* lineages. Furthermore, phycobiont coexistence events occur in all the analyzed populations, strengthened by the presence of at least three taxa of intrathalline microalgae. In conclusion, these data seem to highlight that *Trebouxia* diversity inside a single thallus could be an advantageous event under extreme environmental conditions. (MINECO, CGL2012-40058-C02-01), FEDER, (GVA, PROMETEOII/2013/021)

Do saxicolous lichen communities represent photobiont-mediated guilds?

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The general goal of the study was to verify the theory of photobiont-mediated guilds at the case of saxicolous lichen communities in central Europe. Several communities growing on various rock types in similar altitudes were explored for their photobionts using ITS rDNA sequencing (*Rhizocarpetalia geographici* on siliceous rocks; *Aspicilietalia calcareae* and *Verrucarietalia nigrescentis* on limestones and concrete; *Lecanoretum argopholis* on diabases, community with *Porpidia nadvornikiana* on serpentinites). The photobiont inventory in 90 lichen taxa revealed 20 well-supported *Trebouxia* lineages including 10 described *Trebouxia* species and 10 non-described but already known lineages. The photobionts exhibited rather clear substrate/habitat preferences – each lichen community shared only several distinct algal lineages. They formed obvious ecological assemblages – siliceous, calcareous and volcanic rock guild. Our data showed an interesting disproportion in the occurrence of core (vegetatively reproducing) and fringe (sexually reproducing) species in lichen guilds. Some algal lineages (mainly calciphilous) were not found in any core species, even in lichen communities outside their home guilds. Therefore, we speculate about the role of symbiotic propagules such as soredia and isidia as common sources of photobionts. We suppose the "photobiont rain" includes relatively high portion of free-living forms of symbiotic algae.

Phylogenetic diversity of cyanobacteria associated with the Lichinomycetes

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Cyanobacterial symbioses have evolved repeatedly in different lineages of lichen forming Fungi, among both the Ascomycota and Basidiomycota. Lichenized cyanobacteria were mostly assigned to either Chroococcales or Nostocales, with *Nostoc* being the most common genus of cyanobacteria in lichens. Within the Lichinomycetes, a wide variety of cyanobacteria belonging to different genera and orders have been identified based on morphological characters, including cell anatomy and cell division. However, symbiotic cyanobacteria cannot be reliably identified to species because many morphological characters of free-living cyanobacteria are not apparent within lichen thalli. Most molecular studies of cyanobacterial diversity in lichens have centered on *Nostoc* and very few data are available about the genetic diversity of other groups. Thus, the aim of this study is to characterize the molecular and taxonomic diversity of cyanobionts of the Lichinomycetes. To do this, we sequenced 16S and rbcLX rRNA genes for a wide sample of Lichinomycetes species and constructed phylogenetic trees. Operational taxonomic units were identified and their taxonomic affinities were studied by comparing with public databases. A wide variety of cyanobacteria belonging to Chroococcales, Chroococcidiopsidales, Nostocales, Oscillatoriales and Pleurocapsales were found. The distribution of some cyanobacterial genotypes are correlated with the mycobiont taxonomy at the genus level.

Heveochlorella (Trebouxiophyceae): a little-known algal genus outside the Trebouxiiales emerges as mayor clade of lichen photobionts in foliicolous communities

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Over half of the foliicolous lichen fungi are members of either the Gomphillaceae or Pilocarpaceae, and associate with *Trebouxia*-like green algae whose identities have never been determined. We investigated the phylogenetic affinities of these photobionts by collecting thallus samples from foliicolous communities in southwest Florida and processing them for direct sequencing, cultivation and/or TEM. Additional specimens from these two families and also from *Aspidothelium* (Thelenellaceae) were collected from various substrates globally. Sequences obtained from rbcL and nuSSU regions were subjected to Maximum Likelihood and Bayesian analyses. Analysis of 37 rbcL and 7 nuSSU algal sequences placed all photobionts within the so-called Watanabea clade. All but three of the sequences showed affinities within *Heveochlorella*, a genus recently described from tree trunks in East Asia. The photobiont chloroplast showed multiple thylakoid stacks penetrating the pyrenoid centripetally as tubules lined with pyrenoglobuli, similar to the two described species of *Heveochlorella*. We conclude that *Heveochlorella* includes algae of potentially major importance as lichen photobionts, particularly within – but not limited to – foliicolous communities in tropical and subtropical regions worldwide. The ease with which they may be cultivated on minimal media suggests their potential to thrive free-living as well as in lichen symbiosis.

Species delimitation of *Abrothallus* (Abrothallales, Dothideomycetes) growing on parmelioid lichens

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The species of the lichenicolous genus *Abrothallus* inhabit foliose and fruticose lichens from different families and orders, with 16 of them described occurring on lichens of Parmeliaceae. The multi-gene based phylogenetic analysis showed that host-specificity as a species-delimiting criterion is not uniformly applicable for the whole genus. Large monophyletic clades only occur on certain lichen-forming families, but high specialization at host species level seems to be unique of certain lineages. The widespread Parmeliaceae-group is exceptional within *Abrothallus* due to the low genetic diversity found in commonly used markers (ITS, TEF-1, RPB2) and the inconsistency between the groups recovered from molecular markers and the combination of morpho-anatomical characters used for species delimitation. This pattern may indicate on-going speciation processes and incomplete lineage sorting regarding host due to Parmeliaceae is among the youngest families within Lecanoromycetes.

Ecological factors determining local symbiont associations in *Nephroma cyanolichens*

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A range of selectivity for cyanobacterial symbionts has been demonstrated across investigated lichens, with some species apparently sharing *Nostoc* widely, and others highly selective, with little to no switching so far observed. We ask how ecological factors affect this symbiotic composition, testing climate, microsite, woodland connectivity and environmental availability of symbionts, including substrate sampling and co-occurring 'companion' cyanolichens. In the Atlantic forest of Scotland, two *Nephroma* species often co-occur, the sorediate *N. parile* and the sexually-reproducing *N. laevigatum*, and contrasting selectivity was expected in these species based on published work. Full-length rbcLX from Sanger sequences and partial sequences from Illumina metabarcoding including bryophyte mats on trees, and bare bark were compared. Using more than 300 full-length rbcLX sequences sampled from 15 sites, we found that *N. laevigatum* associates with a wide range of *Nostoc* genotypes. These genotypes are shared widely across sampled frequent companion species (*Degelia* spp., *Lobaria* spp., *Sticta* spp., and *Pannaria rubiginosa*). In contrast, *N. parile* associates with a single sequence type, otherwise rarely shared by co-occurring species. There is strong *Nostoc* genotypic association with climate, and a metabarcoding dataset sampled from bark, bryophyte mats and cyanolichens from these woodlands will also be presented and discussed.

Lichenicolous fungi growing on *Cladonia* in the Holarctic

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Cladonia is one of the most "hospitable" lichen genera for lichenicolous fungi. It currently embraces about 460 lichen species and hosts 108 species of lichenicolous fungi (ratio = 4.3), 65% of which are known only from this host genus, 20% of cladoniicolous species have been described in the past 10 years. This study is based on 690 examined specimens of lichenicolous fungi growing on *Cladonia*, mainly from the arctic and boreal vegetation zones of the Holarctic. It revealed 52 species of cladoniicolous fungi, which is about half of their known species diversity. *Neolamya ahtii* is introduced as new to science. *Abrothallus cladoniae*, *Arthonia digitatae* s. l., *Cercidospora cladoniicola* s. l., *Didymocyrtis cladoniicola*, *D. foliaceiphila*, *Hainesia longicladoniae*, *Lichenocodium aeruginosum*, *Lichenopeltella cladoniarum*, *Pezizella ucrainica*, *Polycoccum laursenii*, "Stictis" *cladoniae*, *Stigmatidium cladoniicola* and *Zwackhiomyces diderichii* are new to Asia. *Biazrovia stereocaulicola*, "Echinothecium" *cladoniae*, *Hainesia longicladoniae*, *Polycoccum microcarpum* and "Stictis" *cladoniae* are new to North America. *Biazrovia stereocaulicola*, *Merismatium coccisporum* and *Pyrenidium actinellum* s. l. are first reported on *Cladonia*. The most common in the arctic and boreal biomes are *Sphaerellothecium cladoniae*, *Lichenosticta alcorniaria*, "Taeniolella" *beschiana*, *Epicladonia sandstedei* and *Syzygospora bachmannii*. The study was partly supported by RFBR grant 14-04-01031 "Lichenicolous fungi of Northwest Caucasus".

Potential horizontal gene transfer (HGT) of Desiccation Related Proteins in the lichen photobiont *Trebouxia gelatinosa*

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Desiccation Related Proteins (DRPs), firstly described in desiccation tolerant plants, are present also in several unrelated bacterial and algal groups. Although their role is still unknown, their presence seems to confer an increased desiccation tolerance in some extremophile bacteria, including the *Deinococcus/Thermus* phylum. In this study we describe our findings on the DRPs present in the transcriptome of *Trebouxia gelatinosa*, a member of the most common lichen-forming genus of green algae. Thirteen sequences were classified as DRPs: they are characterized by a c.170 aa long ferritin-like domain (PF13668), followed by one or two domains of unknown function. This gene family has undergone relevant expansion in *T. gelatinosa*: in the majority of green algae DRPs are present in few copies or they are completely absent. Further, their diversification finds no parallelism in other desiccation tolerant organisms investigated so far. Bayesian phylogenetic inference pointed out that DRPs of green algae are unlikely to be orthologous to those found in Embryophyta. Conversely, they share an unexpected sequence similarity to DRPs found in bacteria. This result led us to consider a bacterial origin for *Trebouxia* DRP genes, which may have ancestrally been acquired by horizontal gene transfer (HGT) from lichen-associated bacteria.

Characterization and role of a novel class of peroxidase-like enzymes from lichenized fungi

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In our earlier work, we demonstrated that the oxidases tyrosinase and laccase occur widely in lichens from the Peltigerales. Recently, we discovered the presence of another oxidoreductase, a heme peroxidase, in the Peltigeralean "jelly lichens" *Leptogium* and *Collema*. A survey showed that a range of lichens can display significant peroxidase activity. While the catalytic properties of the enzymes resemble dye-decolorizing peroxidases, to our surprise their sequences do not resemble those of any other known peroxidase. The N-terminal sequence contains the "nitrobindin" domain reported to be present in other proteins, and we therefore propose the name nitrobindin peroxidases. Phylogenetically, the enzymes probably originated in the eubacteria, as they lack introns and a eukaryotic signal peptide. In addition to lichens, blast searches reveal the presence of homologous genes in free-living ascomycetes and some bacteria. The role of the peroxidases in lichen biology remains uncertain. It seems likely that the enzymes have both pro- and antioxidant activities. We suggest that the peroxidases are involved in the radical-based degradation of complex macromolecules. Such degradation may allow the lichen some saprotrophic existence. However, the enzymes may also act as a classic scavengers of hydrogen peroxide.

A phylogenomic examination of the diversification of black fruited *Caloplacas* in Eurasia (*Pyrenodesmia*, Teloschistaceae)

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The lichen genus *Pyrenodesmia* in the strict sense comprises a phylogenetically coherent group of species within the wider genus *Caloplaca*, sharing the lack of anthraquinones and the presence of dark brown to black acetone insoluble pigments as diagnostic characters. The taxon is widespread across geographic regions, especially in the Northern Hemisphere. But it shows exceptionally high morphological and genetic diversity in the Mediterranean and Irano-Turanian regions of Eurasia. Previous studies have found a striking lack of congruence between phylogenetic reconstructions and morphology-based species concepts. Under the current paradigm of phylogenetic species delimitation, this incongruence would be solved by proposing new taxa based on the estimated phylogeny. These 'cryptic' species concepts are often narrow and dataset-dependent. Moreover, they may overlook both the permeability of species boundaries, and whether the phylogeny represents the history of the genomic regions that contribute to reproductive isolation or local adaptation. One solution to these limitations is to develop phylogenies using large portions of the genome. In this study, we present the first phylogenomic study on the *Pyrenodesmia* group using genomes and metagenomes sequenced from nine closely related specimens, and propose a framework to study phylogenetic divergence based on genes located in different regions of the genome.

De novo assembly and characterization of mycobiont and co-culture transcriptomes of *Usnea rubrotincta* using RNA-seq

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Lichens produce characteristic secondary metabolites known as lichen substances. However, these unique compounds tend not to be synthesized by cultured lichen mycobionts, suggesting the regulatory mechanisms to activate their secondary metabolism during symbiosis. To identify the regulated genes, RNA sequencing (RNA-seq) analyses for two different secondary metabolic states of mycobiont cultures and a symbiotic state of co-culture were performed for *Usnea rubrotincta*. High-quality paired-end reads processed with three programs were used for a *de novo* assembly with the Trinity program to generate 110,225 contigs, eventually. Of these, 46,054 contigs (about 42%) were functionally annotated by the Blast2GO program and were found to include 187 contigs for polyketide synthase (PKS) and 886 contigs for cytochrome P450. Between the mycobiont culture without secondary metabolites in natural thalli, such as salazinic acid and norstictic acid, and the co-cultures with these compounds, differentially expressed transcripts with high fold-change values were identified. Among 1,466 differentially expressed transcripts, two and eleven transcripts for PKS and P450 were found to be upregulated, respectively, suggesting that these genes might be involved in the fungal secondary metabolism in the symbiotic interaction with algal partners.

An unexplored aspect of lichen biology: karyotypic variability and polyploidization – potential implications for speciation, mating systems and reproductive modes

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Lichenology has arrived in the era of whole genome sequencing and genomics. However, there is still a huge gap of fundamental knowledge pertaining to "classic" genomic research in lichens. Hardly anything seems to be known regarding the possible number of chromosome set copies (ploidy levels) or the number of different chromosomes per haploid chromosome set in complete genomes of different lichen species. This conceptual work reviews the current knowledge about chromosome counts, karyotypes and ploidy levels in lichens and non-lichenized ascomycetes, in which the haploid phase is commonly said to dominate throughout most of the life-cycle. Only very few examples of classic, microscopical karyotypification studies exist for lichenized ascomycetes, and modern electrophoretic karyotypification has (apparently) never been applied to lichen mycobionts. Based on various examples of other organismal groups (e.g. plants, other fungi and animals), it appears not unlikely, that polyploidization might play an important evolutionary role that has not received any consideration by lichenologists so far. Faulty ascosporeogenesis seems to be a very plausible source for abnormal chromosome numbers. Some potential implications are discussed: (i) Evolution of asexual species through triploidy or aneuploidy, (ii) Formation of hybrid-species through allopolyploidization, (iii) Transition from heterothallism (outcrossing) to homothallism (self-fertility) through autopolyploidization

Recombination and horizontal gene transfer in mitochondrial genomes of the genus *Rhizoplaca* (Lecanoraceae)

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Recombination and horizontal gene transfer (HGT) in mitochondrial DNA (mtDNA) is increasingly recognized as an important evolutionary process in eukaryotic evolution. In contrast to metazoans where mitochondrial recombination and HGT play a negligible role, frequent and massive HGT is common in plant mitochondrial genomes and highly recombinogenic and dynamic mtDNAs have also been documented in yeast. With the increasing recognition of the role of mitochondrial recombination and HGT in some fungi, it is important to evaluate the prevalence of mitochondrial HGT in other fungal lineages, including lichen-forming Ascomycetes. With only two published mt genomes of lichen-forming fungi to date, general patterns of mt genome evolution are largely unknown. To provide crucial insight into mt genome evolution in these fungi, we sequenced and annotated over thirty complete genomes representing ten *Rhizoplaca* (Lecanoraceae) species. We find a general pattern of consistent gene content and syntenic gene order, in addition to a unidirectional transcription of genes. Differences in genome size were largely due to variation in the number of introns in three genes. Most strikingly, we find evidence of rampant recombination and potential HGT in *Rhizoplaca* mt genomes. We discuss the implications of our findings on understanding mt genome evolution in lichenized fungi.

Extensive mitogenome rearrangement within the Peltigerinae (lichenized Ascomycetes): comparison between *Ricasolia amplissima* and *Peltigera membranacea*

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Mitochondrial genomes vary extensively in size and gene order among fungal lineages. So far, the mitogenomes of only two lichen-forming fungi (two species of *Peltigera*) are assembled. These are completely syntenous but differ in their intron content. The aim of the present study was to assess architectural stability of the chromosome between lichen forming fungi at the interfamilial level. We assembled the mitochondrial genome of *Ricasolia amplissima* (Peltigerales: Lobariaceae), and compared its organization with that of *Peltigera membranacea* (Peltigerales: Peltigeraceae). Whereas gene content between these two species is similar, their relative gene order is substantially different, which may suggest that massive gene rearrangements may occur in the mitogenomes of lichenized Ascomycetes at a relatively shallow phylogenetic depth. Additionally our study offers the opportunity of designing new molecular markers for studying phylogenetic relationships within the suborder Peltigerinae.

Patterns of symbiotic associations among *Peltigera* and *Nostoc* partners along a 1200 km South-North transect crossing the circumboreal belt

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To deepen our understanding of evolution of symbiotic systems, patterns of association between *Peltigera* and its cyanobacterial counterpart, *Nostoc*, were analyzed along a South-North transect spanning the entire boreal belt (1200 km) in Québec, Canada. To analyze these associations at both a local and biome scale, lichens were collected from nine equidistantly distributed localities along this transect, using three quadrats separated by 4 km at each locality. The nuclear ITS of the mycobiont as well as the rbcLX of the cyanobiont partner were sequenced for 90 specimens from sections *Peltidea* and *Polydactylon*. Eight *Peltigera* species were found to associate with only five *Nostoc* phylogroups. Some *Peltigera* were present along the entire transect while others were restricted to certain localities, suggesting that distribution patterns can be shaped by climatic factors. All mycobiont species show a high degree of specialization with their cyanobionts, whereas some cyanobionts associate with many *Peltigera* species. Overall, *Nostoc* phylogroups had narrower distributions across latitudes compared to their *Peltigera* mycobionts. The distribution of highly specific *Peltigera* species was locally restricted when a cyanobiont partner had a limited distribution. However, less specific *Peltigera* species could extend their cross-latitude distributions by switching to a different locally adapted *Nostoc* phylogroup.

Candidates of ribitol transporter gene obtained from *Ramalina conduplicans*

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Although it was known that characteristic carbon such as ribitol were utilized in lichen for a long time, the carbon transport mechanisms including transporters are poorly understood up to date. It is hypothesized that diversity and evolution of lichen were promoted due to acquired characteristic and high affinity carbon transporters. Therefore, this study was conducted to obtain candidates of ribitol transporter genes in lichen mycobiont, for the first time. It was confirmed that *Ramalina conduplicans* isolated from photobiont could grow by utilizing ribitol as an only carbon source. This result suggests *R. conduplicans* have a certain transporter carrying ribitol on its transmembrane. Degenerate PCR and RACE methods revealed the candidates of ribitol transporter gene in *R. conduplicans*. Because the obtained sequence had high homology with ribitol transporter genes in species of other Ascomycota, it was suggested that ribitol transporter genes would be widely conserved in Ascomycota. However, diversity and affinity level of these genes have been unclear. Therefore, finding of these genes is the first step for the elucidation of lichen specific carbon transport system, and possibly disclose the reason why lichen could be one of the most diversified fungi.

Ontogenetic development in axenic conditions of some Parmeliaceae lichen-forming fungal taxa

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In spite of successful culture experiments of lichen-forming fungi, little is known about their ontogenetic development and the culture conditions for most mycobionts are unknown. In order to investigate the possibility of producing in vitro axenic mycobionts, a culturing study was carried out using ascospores of different lichen-forming fungal taxa of the family Parmeliaceae. The chosen specimens were *Parmelia saxatilis*, *Parmelina tiliacea*, *Platismatia glauca*, *Xanthoparmelia tinctoria*, *Arctoparmelia centrifuga* and *Usnea ghattensis*. Early stages of productivity and germination were tested in Basal Bold medium (BBM) without additional carbon source and growth was evaluated on different enrichment culture media: 2% glucose BBM (2G-BBM), LiLly and Barnett medium with 3% glucose (3G-BBM), 0.2% glucose malt-yeast extract and corn meal agar (CMA). Sample of all species studied grew successfully in the four enrichment media. However, the productivity and germination were significantly different between species. Moreover, large variability of sizes and shapes found in the colonies within the same species provides new insights into the importance of the nutrients on morphogenesis.

Morpho-chemical variability of *Xanthoparmelia* (Vain.) Hale at the local scale: unexpected patterns and edaphic influence

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The variability of yellow-green *Xanthoparmelia* at the local scale has been poorly investigated, neither through traditional approaches on morphology and chemistry, nor with advanced chemical characterization or molecular markers. In this work, two sets of 24 thalli were sampled on two approx. 2500 m² rock outcrops in NW-Italy. Secondary metabolites were examined by spot-tests and TLC, together with morphological characters traditionally used for species delimitation. Thirty-one morpho-chemotypes were recognized, several of which were unexpected in the variability reported for Europe and showed metabolites with Rf values unreported for *Xanthoparmelia*. Secondary metabolites were also identified and quantified by HPLC-DAD-ESI-MS₂ and UPLC-HDR-DAD, confirming the presence of unknown depsidones and unreported metabolite combinations. Only some metabolites displayed a presence/absence behaviour, while others showed a rather continuous variability, with some concentrations below the TLC detection limit. Multivariate analysis of morphological and UPLC data defined four isidiate and three non-isidiate morpho-chemotype clusters, only partially related to phylogenetic lineages based on ITS1-5.8S-ITS2 and beta-tubulin sequences. Metabolic variability of non-isidiate types was significantly related to macro- and micronutrient contents in thalli, as quantified by XRF-spectroscopy. Such finding suggests that environmental influence contributes to complicate the *Xanthoparmelia* variability patterns and should be considered in the taxonomical debate.

Updated *Usnea* species from Mexico: distribution and floristic affinities

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The updated study of the genus *Usnea* in Mexico revealed a total of 66 species. A data base of their occurrence (presence/absence) by biomes and biogeographic provinces was compiled to study their distribution, abundance, and floristic affinities. Five biomes were considered: humid tropical forest, humid mountain forest, temperate forest, tropical seasonally forests and xerophytic scrubland, as well as nine biogeographic provinces: California (Cal), Baja California (BC), del Cabo (C), Northwestern Coastal Plain (NWCP), Sierra Madre Occidental (SMOC), Sierra Madre Oriental (SMOR), Neovolcanic Belt (NB), Sierra Madre del Sur (SMS), and Transisthmian Mountains (TM). The highest relative species richness was examined primarily in the temperate forests (47%) and secondarily in the humid mountain forests (28%); next in the xerophytic scrubland (12%) and the lowest number of species was found in the humid tropical and seasonally dry forests (6.5% in both biomes). Most species (77%) grow at elevations higher than 1200 m in NB, SMOR, SMS, and SMOC provinces, followed by the TM (12%), and last BC, CAL, C and NWCP add together 11%. Given Mexico's location between the Nearctic and the Neotropical realms, different types of elements: cosmopolitan, boreal/temperate, neotropical, pantropical, and endemic are recognized among its *Usnea* species.

Elucidation of species in the genus *Usnea* (Parmeliaceae, lichenized Ascomycota) in eastern Asia using ITS rDNA

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Taxonomy of the genus *Usnea* is one of the most difficult problems in lichenology. The species concept of the genus defined by morphology and chemistry should be objectively evaluated with molecular data to avoid further confusions. Sequences of the ITS rDNA regions were successfully obtained from 839 samples collected mainly from Japan and Taiwan but also from South East Asia, Far East and central Russia, and USA (vouchers are housed in TNS). Among the species from eastern Asia, the following species are genetically supported: e.g. *U. aciculifera*, *U. baileyi*, *U. bicolorata*, *U. bismolliuscula*, *U. dasaea*, *U. dasopoga*, *U. diffracta*, *U. dorogawensis*, *U. esperantiana*, *U. flavocardia*, *U. hakonensis*, *U. lapponica*, *U. longissima*, *U. merrillii*, *U. mutabilis*, *U. nidifica*, *U. pangiana*, *U. pectinata*, *U. praetervisa*, *U. pycnoclada*, *U. roseola*, *U. rubrotincta*, *U. sinensis*, and *U. trichodeoides*. However, there are still many species, which should be taxonomically re-examined because they appear as polyphyletic in the phylogenetic tree. Both possibilities of inadequate/wrong species concept or low resolution of DNA analysis could be considered. Problematic species are seen especially in sorediate inflated species (e.g. *U. cornuta* and *U. fragilesceus*) and species pairs (e.g. *U. florida* – *U. subfloridana* and *U. glabrata* – *U. orientalis*) respectively.

Species of the genus *Xanthoparmelia* (parmeloid lichens) as model systems for molecular and chemical investigations

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The genus *Xanthoparmelia* has been revised several times due to molecular data sets and extended phylogenetic analyses. New species have been described and new combinations have been included into a wider generic concept. Species of the genus *Xanthoparmelia* have been identified first morphologically, later on the basis of chemotaxonomic characters. They are widely distributed in the Southern hemisphere with an outstandingly diverse chemosyndromic variation. In this study we report investigations employed with common species growing in semiarid habitats of southeastern Australia, e.g., *Xanthoparmelia substrigosa*, *X. filarszkyana*, *X. hypoprotocetrarica*. Mycobiont-cultures were performed as an attractive alternative to the extraction of naturally grown thalli. In case studies, selected species of *Xanthoparmelia* were cultured under optimized culture conditions. We achieved the production of one particular polyketide and even the production of a predictable pattern of polyketides, depending upon the investigated lichen chemotypes. Variations in chemistry of *Xanthoparmelia* models were found to mirror physiological and ecological fluctuations in the environment. The study further addresses the detection of PKS genes that control the formation of polyketide-type compounds. The repeatable and in vitro production of lichen metabolites in fungal cell cultures has already become a milestone elucidating the architecture and function of PKS genes.

Diversity and distribution of some genera in the family Parmeliaceae in Russia

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In this study, the distribution and diversity of ten genera in the family Parmeliaceae were examined using morphological, anatomical and chemical methods. More than 2500 specimens deposited in various Russian herbaria were studied. Preliminary data showed that the genus *Hypogymnia* includes 26 species, seven of which have been collected in the Russian Far East during the last 15 years. The species includes the recently described *H. papilliformis*, for instance. The genus *Myeolochroa* includes ten species, most of which are confined to the south of the Far East. Two species from the Western Sayan are described as new to science (*M. sibirica* and *M. sayanensis*). The genus *Parmelia* is represented by 19 species in Russia. These include the following newly described species: *P. asiatica*, *P. barrenoae*, *P. discordans*, *P. ernstiae*, *P. pinnatifida*, *P. serrana* and *P. submontana*. The genus *Nipponoparmelia* contains four species, including *N. perplicata*, which is known only from the Shikotan Island (Sakhalin Region) in Russia. The genus *Hypotrachyna* is represented by four species in Russia. Two species were found from the genus *Bryocaulon*, while the genera *Everniastrum*, *Oropogon*, *Usnocetraria* and *Remotrachyna* were each represented by only one species. The record of *Remotrachyna koyanensis* is based on the literature data only.

Chemosystematics and evolution of Icelandic cetrarioid lichens (Parmeliaceae) and the *Cetraria islandica* species complex

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Traditional medicinal uses of several cetrarioid lichens, especially the lichen *Cetraria islandica*, have intrigued us to investigate their bio- and chemo-diversity and to test if phylogeny provides any insights in selection for medicinal plants. In total 102 Icelandic cetrarioid lichen specimens representing 13 lichen taxa of 6 genera (i.e. *Cetraria*, *Tuckermannopsis*, *Vulpicida*, *Cetrariella*, *Flavocetraria*, *Melanelia*) were incorporated into phylogenetic analysis, based on six genetic markers (i.e. fungal nr ITS, nr LSU, MCM7 and mtSSU as well as algal nr ITS, ACTIN). Lichen metabolomic profiles correlated well with phylogeny of lichenized fungi, and the distribution of selected bioactive lichen acids (i.e. protolicheterinic acid and usnic acid) was also mapped on the phylogeny of lichenized fungi, where the phylogeny proposed that the biosynthesis of aliphatic lichen acids is facilitated in lineages lacking or producing less depsidones and dibenzofurans, and that the production of usnic acid does not follow the phylogeny but rather seems to have a convergent evolution pattern. In addition, a re-visit to the secondary chemistry of the *Cetraria islandica* species complex rendered it again to re-consider the species boundaries between *C. islandica* and *C. ericetorum*.

The diversity of the genus *Anzia* (Parmeliaceae, Lecanoromycetes) in the Paleogene of Europe

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Amber, fossilized tree resin, is famous for its lifelike preservation of various organisms. Only relatively few lichen fossils have been described so far, but among them is *Anzia electra* from Eocene Baltic amber. *Anzia* is a lichen genus with over 30 extant species that mainly occur in subtropical to tropical mountains. The genus is completely missing from today's Europe, with the closest current observations from Madeira Islands. *Anzia* is easily recognizable based on a specific cushion-like structure called spongiostratum that only exists in *Anzia* and in the closely related genus *Pannoparmelia*. Our fossil material comprises over 30 *Anzia* inclusions in Baltic and Bitterfeld ambers, which have been preserved for at least 47 to 23 million years, respectively. There is remarkable morphological variation among the fossils, and in addition to *A. electra*, we were able to identify several distinct fossil *Anzia* species. Some of them have morphologically similar counterparts among the extant *Anzia* species, while some others possess rather unique habits. Based on our fossil material we show that *Anzia* was a relatively common and highly diverse lichen genus in the Paleogene of Europe.

Fossil evidence of lichen grazing from Paleogene amber

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Amber is fossilized tree resin and famous for its lifelike preservation of arthropods, plant remains, and microorganisms. A piece of Paleogene Bitterfeld amber (23-24 million years minimum age) includes a fossilized lichen with marks of grazing and faecal pellets. Light microscopy and scanning electron microscopy (SEM) were used to study the specimen. Additionally, in order to identify the source(s) of the feeding marks and faecal pellets, an actuo-paleontological experiment was designed using extant lichens and known lichen grazers including mites, collembolans, psocopterans, coleopterans, and gastropods. The morphological characters of the fossil lichen, especially the structure of the lower side pseudocortex, suggest an affiliation to the extant genus *Phyllopsora*. Based on the results of our grazing experiment and published data we identified gastropods and/or mites as the most likely grazers of the fossil lichen.

Calicioid fungi and the reconstruction of the 'Baltic amber forest'

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The common notion that Baltic amber derives from tropical or subtropical forests has recently been questioned based on the evaluation of plant inclusions from this amber deposit which rather suggest warm-temperate forests as source ecosystems. We aimed to provide independent data from ecologically specific fungi and lichens that hint to climate and forest structure. Screening of major Baltic amber collections revealed that calicioid fungi transect were diverse and probably abundant in the source forests of the Baltic amber. The polyphyletic group of calicioid fungi can be highly specific to certain forest types and climatic conditions, and the extant forms exhibit high selectivity in their microhabitat preferences. Furthermore, their abundance and diversity in modern forest ecosystems is climate and habitat dependent. As the group has a wide extant distribution and it dates back at least to the Eocene it can provide valuable information about forest conditions, past and present. The assemblage of calicioid fungi from Baltic amber most closely resembles those found in modern transitional mixed conifer forests along a across major temperate to warm-temperate forest types. Moderate humidity and semi-open forests with open-edge habitats are required to accommodate the diversity of these fungi from Eocene Baltic amber.

Influence of the Irish cryptogamist Ellen Hutchins (1785–1815) on research by her cousin, Thomas Taylor (1786–1848)

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Ellen Hutchins was 29 years old when she died in 1815, yet she had excelled as a collector of cryptogams. Although born to a wealthy family in southwest Ireland, Ellen did not marry and so she cared for her invalid brother and mother. While rehabilitating in Dublin from an early illness, Ellen was encouraged to study botany by her doctor, Whitley Stokes. Taking this knowledge back to Bantry Bay, Ellen supplied specimens of Lusitanian flora to English taxonomists including Dawson Turner and William Hooker. Ellen became a watercolourist to provide botanical illustrations. Her cousin Thomas Taylor, visited Ballylickey House, where Ellen lived. Thomas had been born in India but, as the eldest son, he was sent home to school in Ireland. He trained as a doctor but his interests in botany and natural science developed. Thomas became a significant lichen taxonomist of the early 19th century from his home at Dunkerron, Co. Kerry. His herbarium incorporated Ellen Hutchins' lichen collections. The Taylor Herbarium is in the Farlow Herbarium, Harvard. It was purchased after Thomas died while treating patients during the Irish Famine. Ellen Hutchins' 200th anniversary was marked in August 2015 by a festival to celebrate her life's work.

Local harnessing and commercialization of lichens in Tehuacán-Cuicatlán, Mexico

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Lichens have had cultural significance since the dawn of humanity, being used as edibles, medicine, poisons, and for dyeing and ornamental uses. Currently they still are used around the world; however in Mexico there is no research that addresses the local harnessing of lichens. An ethnolichenological study was conducted in Tehuacán-Cuicatlán, region with an extraordinary biocultural wealth. Two hundred and twenty interviews in six markets and 11 locations were applied. The specimens were collected during expeditions guided by locals and in the markets the lichens were exchanged for money or corn. One hundred and fifteen taxa were documented, mainly for medicinal and/or ornamental uses, the genus *Usnea* stands out with 34 species. Medicinal lichens are utilized to relieve ailments of the respiratory and urinary tracts, as well as skin lesions; while ornamental ones are employed as decorations in religious holidays. It is concluded that lichens are an important resource for the mestizos and indigenous people (Nahua, Cuicatec, Popoloc and Mazatec) in extreme poverty, since they use them to treat deadly diseases like pertussis and to complement their income. Unfortunately, lichens and traditional practices associated with them are threatened by transculturation and environmental degradation.

Lichens of the Salvador's collection: emerging from obscurity 300 years later

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The herbarium Salvador was part of the naturalistic cabinet belonging to the Salvador family, a dynasty of apothecaries settled in Barcelona. The collection started being gathered in early 18th century and was accessible until the middle of 19th century. The herbarium compiled around 5000 specimens, representing almost half of the complete collection. It was composed mostly by vascular plants, but several sheets included cryptogams. Among them, 30 were identified as lichens. Recently, the finding of part of the naturalistic collection has afforded new material, mainly stones, which were colonized by lichens. The revision of samples containing lichens has provided a list of 49 taxa. The samples present in the herbarium were labelled according to pre-Linnaean nomenclature. Lately, a revision carried in early 19th century emended nomenclature of several specimens' labels following Linnaean rules. The importance of those old and well-preserved herbaria lays out on knowing changes in geographical distribution of species. Unfortunately, most of the samples lack location, making it difficult to find out the provenance of them. According to available documents, the 26% of samples were collected in the north east of the Iberian Peninsula. At least one species with known location, *Usnea articulata*, has disappeared.

The rich history of lichenizing in the Chic-Choc Mountains, Québec, Canada

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The Chic-Choc Mountain Range (Chic-Chocs) on the Gaspé Peninsula in eastern Québec is part of the northernmost region of the Appalachian Mountains in continental North America. Formed ca. 480 million years ago, the Chic-Chocs have eroded over time and the summits of many peaks are now large plateaus (up to 9 km in length). Plateaus above ~1000 m have arctic-alpine environments that are hypothesized to have been nunataks during the Wisconsin glaciation. These conditions combined with a coastal influence and regionally uncommon substrata, such as amphibolite and serpentine rock, have contributed to a rich lichen biota with many disjunct populations, which have attracted lichenologists for over a century. A historical review of lichen collecting in the Chic-Chocs will be presented. This mountain range has been visited by lichenologists almost every decade since 1882 and specimens have been reviewed by specialists across the globe. The results from these collectors will also be presented. The lichen biota of the Chic-Chocs includes 570 lichen and allied fungi species, 15 species that reach their southern limit in eastern North America, and 6 species that are not known to occur for over 1000 km to the north.

The type collections of August von Krempelhuber (1813–1882) in Munich (M)

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Krempelhuber was a forester by profession and one of the outstanding German lichenologists of the 19th century. At the beginning of his career, he collected lichens mainly in his Bavarian home country, but later he concentrated on extra-European collections. During his life, he described around 580 new taxa, nearly 400 of them on species level. Many of them stand the test of time and are still accepted. After his death, his herbarium was partly sold to C. Eggerth (1861–1888) from Vienna but was soon after the early death of the buyer donated to Vienna University herbarium (WU). This part of the herbarium consists of published exsiccata and most of the European collections. The extra-European collections as well as an important part of the European specimens were bought by the Bavarian state and are now in Botanische Staatssammlung München. We found many more type collections over the last years. It can be estimated, that all types of exotic taxa described by Krempelhuber but also many European specimens are available in M. During our general search for lichen types at M, we also found nearly 30 collections marked as "new" by Krempelhuber often with accompanying notes and drawings but apparently unpublished.

Identification of lichenous and lichenicolous diaspora in the atmosphere of Madrid (Spain) using Next-Generation Sequencing

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Lichens play a major role in the ecosystems. In the cities, lichens contribute to support biodiversity of micro- and macroorganisms and are useful as bioindicators of air pollution and environmental changes. Although we know that lichen diaspora (spores and vegetative propagules) can travel by the wind and colonize faraway areas, the species richness and abundance of lichen diaspora presented in the air is still scarcely known. We combine the use of Hirst-type volumetric aerobiological trap with the analyses from Next-Generation DNA Sequencing (NGS). The molecular marker analysed was the ITS2 of the rDNA. The samples were collected during one week in two different sites of Madrid (Spain). Sampling was repeated once for each season during a year. The preliminary results obtained for fungal identification show an interesting diversity of species of different taxonomic groups. This diversity varies among seasons of the year. We are analysing the dispersal strategies of the species and comparing the species record with the regional checklists of the Madrid province, bordering regions and whole Iberian Peninsula. Altogether, our preliminary results show that aerobiological techniques in combination with NGS analyses are a promising tool for the study of different subjects as ecology, biogeography or biological conservation. This study was funded by the Community of Madrid, Spain, under the AIRBIOTA-CM Program (S2013/MAE-2874).

How diverse and how local are the lichens in the Amazon?

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Lichen diversity is often thought to be highest in arctic or alpine regions, but the diversity in the tropics is higher, with up to 175 species occurring on one tree and nearly 100 on one leaf. Even though the country has only low mountains, Brazil is the country with the highest lichen diversity on earth. Currently 4000 species are known, a number that has risen with 100–200/year in recent years (half of them new to science). We did field work in Rondônia and Amapá, two states at the western and the eastern edge of the Amazon. In each, 300–400 species were identified. Some are widely distributed, but a real Amazonian lichen element could be detected. We already described 100 new species from Rondônia, mainly Arthoniales, Graphidaceae, *Opegrapha*, Pyrenulaceae, and Trypetheliaceae, that is c. 7 species per fieldwork day. A few dozen of these have already been found in other places, mainly in Amapá. But the collections from Amapá contain another 30+ new species. All published estimates about numbers of still undescribed species seem to be underestimations.

Towards a checklist of the lichens of the Alps

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The Alps are one of the largest continuous natural areas in Europe, stretching approximately 1,200 kilometres across eight countries, and including fourteen national parks. The Alpine Convention emphasizes the importance of this area and encourages transnational research and conservation projects. Lichens as unique models of fungal symbioses with macroscopically recognizable, light-exposed individuals are important colonizers of rock, soil and plant material, and they are a dominant symbiotic life form of higher altitudes in the Alps. National checklists or catalogues exist for Austria, France, Germany, Italy, Slovenia and Switzerland. The compilation of a catalogue of the lichenized fungi of the Alps is a long overdue task and will enable us to compare, for instance, the genera or species diversity of the Alps with those of other mountain systems of the world. We have summarized the abundant but scattered baseline information on lichen biodiversity in the Alps, which will lead to a transnational inventory of all lichen taxa (c. 3,000), including data on their horizontal and vertical distribution and their ecology. This information will be of use for experts, decision-makers, and citizen scientists.

Epiphytic lichens at ZBS (Moscow Region)

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Zvenigorod Biological Station of Moscow State University (ZBS MSU; 715.4 ha) is situated not far from Moscow (Russia). The main part of the territory is covered with aged forest. So the last years were rich in fallen trees. This sad phenomenon allowed study of trees all trunk long. The most common trees are *Acer platanoides*, *Betula pendula*, *Picea abies*, *Pinus sylvestris*, *Populus tremula*, *Salix alba*, *S. fragilis*. 32 macrolichen species are found on the bark in total (foliose – 20, fruticose – 12). The greatest number of species are typical for *Salix* and *Populus*. *Hypogymnia physodes* and *Parmelia sulcata* could be found on every tree. Lichen's abundance increases monotonically to the upper branches. The area of birch trunk occupied by lichens at 10 m high is about 30%, but at 25 m it is more than 70%. Lichen society complex changes great with height and many species one can find only above 10 m.

Spatial distribution of the churchyard lichen *Xanthoria calcicola* at the rim of its northern distribution

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We made an attempted total field survey of *Xanthoria calcicola* within a continuous 5500 km² area in southern and western Scania, Sweden. A Bayesian Inference of a Gaussian Field through a Gaussian Markov Random Field representation was applied. This GMRF approximates residual spatial structure as a latent multivariate Normal distribution with a Matérn covariance. Samples from all populations were collected and the genetic variability was investigated applying total ITS. The lichen occurred at 125 localities with abundance varying from 1 to 8800 thalli per site. Preliminary results show a major gradient with declining probability of occurrence from the coastal areas in the S and W to the interior in the NE. This gradient is largely explained by the distribution of wall types with suboptimal dry walls dominating at churchyards in the NE. When habitat quality is accounted for, the probability of occurrence still varies greatly within the area suggesting an effect of dispersal. This hypothesis is strengthened by marked differences in probability of occurrence of the most frequent ITS haplotypes in different parts of the study area. We conclude that the spatial pattern of *Xanthoria calcicola* of today is a result of independent colonization events and dispersal from various beachheads.

Species composition comparisons at climatically distinct areas in Antarctica reveal correlation of photobiont choice and ecological amplitude of lichens

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Previously, there was a lot of speculation about how photobiont specificity influences the lichen's capability to grow even in the climatically most extreme areas of the world. Based on earlier findings we follow the hypothesis that photobiont choice combined with low photobiont specificity will influence the lichen's ecological amplitude and constitutes the decisive factor for a successful colonization of climatically extreme regions. To provide empirical evidence for this hypothesis we focused on sample collections from two of the southernmost collection areas of the world. The sampling sites differ significantly in the prevailing climatic conditions (defined by recent climate interpolations by our working group) but both areas are populated by an overlapping pool of lecideoid lichens with *Trebouxia* as photobiont. By comparing species distribution and mycobiont-photobiont associations we found that the photobiont pool perfectly reflects the climatic properties of the different habitats. The data show that species evenness is strongly decreased in the harsher areas with a high share of the endemic photobiont T. URa1, which was not found in the significantly, but slightly milder sampling area. These findings clearly support that certain mycobiont-photobiont associations are correlating with climatic factors with a competitive advantage for lichens with low photobiont specificity.

The importance of vanadium-based nitrogen fixation in boreal cyanolichens: a case study using *Peltigera aphthosa* (L.) Willd. s. l.

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Cyanolichens from the genus *Peltigera* are abundant in high latitude ecosystems where they are key contributors to the nitrogen (N) cycle thanks to their cyanobionts nitrogenase (Nase) enzymes. While Nases exists as three isoenzymes: the molybdenum (Mo) Nase, the vanadium (V) Nase and the iron (Fe) Nase, only the Mo-Nase is thought to have ecological relevance in unmanaged ecosystems. However, genetic and biogeochemical evidences tend to question this assumption for peltigerean cyanolichens. In this study, we used genetic, metallomics, and isotopic characterization methods to investigate the importance of alternative N fixation in thalli of the tri-membered *Peltigera aphthosa* collected from several areas of the northern hemisphere (Eastern and Western Canada, Sweden and Russia). We report that the V-Nase genes are present, that the V in *P. aphthosa* demonstrate all the characteristics of a metal of critical importance to N fixation, and that its acquisition by *P. aphthosa* is controlled by the Mo available to the cyanobiont. We also show that alternative Nase activity in *P. aphthosa* may account for as much as half of the total Nase activity. These results highlight the role of alternative N fixation in boreal cyanolichens, with strong implication for the N cycle in high latitude ecosystems.

Effect of soil moisture on the percolation of lichen substances from *Cladonia verticillaris* (Raddi) Fr. in quartzarenic neosol from Brazil.

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Cladonia verticillaris (Raddi) Fr. is a lichen species that grows on sandy soil of tablelands coexisting with savannah-like vegetation in Brazil. This species produces different lichen phenolics that are leached to the soil by the rainwater and exhibit several biological activities that could affect the habitat. The effect of soil moisture in the retention and percolation of proteins, protocetraric acid (PRO) and fumarprotocetraric acid (FUM), the main phenolics produced from *C. verticillaris*, was analyzed in this work. Proteins were retained in dry soil but they percolated when the soil was water-saturated. FUM was strongly retained in this kind of acidic soils and transformed into PRO by spontaneous hydrolysis when the soil moisture increased. This study demonstrates that proteins, PRO and FUM that were effectively leached to the soil, retained, transformed or percolated to deeper soil layers depending on the amount of previous rainfall. This fact must be taken into account in order to consider the biological effects of these substances on the vegetation of coastal tableland Brazil.

Influence of barbatic acid on sandy soils and vegetation growth from Brazilian Northeast

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About 180 millions hectares of Brazilian area are occupied by savannah-like vegetation where the occurrence of Cladoniaceae is common. This study focused on how *C. salzmännii*, lichen species known for the production of barbatic acid, change soil biological processes in savannah-tropical ecosystem. Soil analysis, measurements arbuscular mycorrhizal colonization (AMF) and growth of *Genipa americana* were analyzed. Samples of soil were collected under pillows of *C. salzmännii* thalli or in open spaces without lichen. *G. americana* seedlings were grown under greenhouse conditions, the experiment was done in a factorial randomized design of 4 treatments: control, lichen, lichen +AMF and AMF. Through TLC assays it was detected in the soil the presence of barbatic acid which influenced on soil chemical and physical characteristics. AMF and number of spores were higher in lichen covered soil. The inoculated plants either with lichens+AMF presented higher growth parameters, as well as a higher number of spores. The results could indicate that the lichens substances are capable of provide the association between plants and AMF, that is one of the most important symbioses on earth, linking the root and the soil system. This arrangement will improve a positive feedback loop establishes between lichen-AMF and vascular plant.

Dispersal in epiphytic lichens; the answers are blowing in the wind

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The dispersal ecology of lichenized fungi is challenging because of the microscopic size of reproductive propagules. A good understanding of dispersal is critical to conservation biology however, particularly in the case of epiphytic lichens which occur as patch tracking metapopulations. Uncertainties become even more pronounced with the current emphasis on ecosystem function and services which promotes a landscape approach to addressing conservation issues, e.g. if species are able to frequently disperse over long distances, the management consequences at one site can be traded off against another, alternately, the implications of management activity must be considered for the individual site only. Existing literature is largely based on a single species, *Lobaria pulmonaria*, and draws on a variety of methods to infer a dispersal kernel for its combined sexual and asexual propagules. The results are conflicting however, some concluding frequent long distance dispersal over many kilometers, others concluding a steep decay rate over distances of up to 50 m. Here the results of a novel study combining spore trapping with genetic methods are used to infer dispersal distances for a suite of 6 sexual and asexual epiphytic lichen species. The implications for species ecology, land management and response to global change are discussed.

Celebrating lichens and their uses

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This poster demonstrates the air-pollution sensitivity of lichens and their value to humans, wildlife, and forests. Because lichens are often unfamiliar to policy and decision-makers tasked to protect or improve air quality, our goal is to 'put a face' on lichens and their roles—and to illustrate various species and their association with wildlife and ecological services that we as humans value. We hope to add dimension to the rationale for protecting species that may require cleaner air than that which directly protects human health. At the same time, we hope that our audience will discover in the poster illustration, text, and photographs something new to appreciate of the beauty, complexity, and vulnerability of lichens and their associated wildlife and ecosystems, or be intrigued by their remarkable pharmaceutical properties, environmental monitoring uses, and traditional uses.

Towards taxonomy, phylogeography and ecology of *Solenopsora* species (Leprocaulaceae) – elements with a strong link to Mediterranean-type ecosystems

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Mediterranean ecosystems are well-known for high species richness, which has been triggered by the interplay among various environmental and bioclimatic factors. Despite a lot of data on evolution and ecology of Mediterranean biota, little is known about symbiotic systems like lichens. We analysed material from all the Mediterranean area, together with specimens from North America and Australia, aiming at investigating: 1) phylogenetic position of the genus *Solenopsora* within Leprocaulales, proper delimitation of which is needed (nrITS, Mcm7, PKS sequence data); 2) phylogeography of *S. candidans* (nrITS and β -tubuline sequences), and 3) species ecology (by mean of ecological niche modelling). Preliminary analyses of phylogeographic dataset suggest several centres of genetic diversity, mostly in the Mediterranean area. Two larger groups of ubiquitous, and more ancestral ribotypes occur across Europe. Certain accessions of *S. candidans* from Turkey and Morocco are more closely related, forming a well delimited lineage, which is clearly distinct from the rest of the material. Unexpectedly, samples from Pannonia are heterogeneous. This might indicate that Pannonia has represented an important connection between centres of species distribution in the Mediterranean, and in the Western Carpathians, representing northern periphery of distribution range, where few rare ribotypes were also revealed.

Mapping lichens in western Arctic Alaska using new species proxies and high-resolution remote imagery

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Mapping lichens at a landscape scale has received increased recent interest due to fears that terricolous lichen mats, primary winter caribou forage, may be decreasing across the arctic and boreal zones. However, previous efforts have produced taxonomically coarse, total lichen cover maps or have covered relatively small spatial extents. Here we attempt to map lichens of differing colors as species proxies across northwestern Alaska to produce the finest taxonomic and spatial-grained lichen maps covering the largest spatial extent to date. Lichen community sampling in five western Alaskan National Parks and Preserves from 2002-2012 generated 328 FIA-style 34.7 m radius plots on which species-level macrolichen community structure and abundance was estimated. Species were coded by color and lichen cover was aggregated by plot as the sum of the cover of each species in a color group. Ten different lichen color groupings were used for modeling. Reflectance signatures of each plot were extracted from a mid-summer Landsat composite (circa 2000-2010). Lichen color group cover was regressed against plot reflectance plus additional abiotic predictors in two different data mining algorithms. In the best models, reflectance, elevation and heat load explained about 40% of brown and grey lichen cover.

Blowing in the wind: Genetic and population assessment of diverse vagrant lichen patch

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Vagrancy in lichens is an uncommon but widely distributed phenomenon occurring primarily in windy, open habitats where thalli grow unattached to a substrate. Vagrancy usually occurs only in a few species per site and vagrant lichens rarely cover much area. We describe a large, dense and species-rich patch of vagrant lichens in the coastal Atacama desert. Our study goals were to 1) assess whether there were multiple source populations of a few vagrant species using molecular data and 2) describe the size of the vagrant lichen patch and the density of thalli for several species. We mapped the patch using a GPS and measured the density of lichen thalli by belt transect. We also generated 21 nITS sequences for two abundant species. We found five different vagrant lichen species (putative *Xanthoparmelia* sp., *Santessonia cervicornis*, *Ramalina* sp., *Niebla* sp., *Rocellina* sp.) in the 0.87 km² patch. Density of thalli between species ranged across six orders of magnitude, from 0.0009 thalli/m² for the putative *Xanthoparmelia* sp. up to 650 thalli/m² for *Niebla* sp. The *Ramalina* sp. population had higher genetic variability than the *Niebla* sp. Genetic analyses indicated both vagrant *Niebla* and *Ramalina* species are undescribed taxa.

Samur forest – the unique habitat for epiphytic lichens in the East Caucasus (Dagestan, Russia)

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Samur forest is the only Russian subtropical Liana forest situated in the lowland at the western shore of the Caspian Sea. Its territory of 11200 ha is protected. Dominant tree species are *Carpinus betulus* and *Quercus robur*. We have explored virgin and old-growth core of the forest and also some marginal sites with a coastal shrub vegetation. We have recorded about 116 species of epiphytic (and epixylic) lichens and allied non-lichenized fungi, but only 20% are macrolichens. Our record list includes new species and genera for Dagestan and Caucasus Mts. Some species are new to Russia, e.g. *Agonimia borysthenica* and *Lecanographa lyncea*. We consider some of our records as rare and endangered lichens indicating old-growth lowland forest remnants, e.g. *Arthonia byssacea*, *Arthothelium spectabile*, *Bactrospora dryina*, *Caloplaca lucifuga*, *Gyalecta truncigena*, *Lecanographa lyncea*, *Pachnolepia pruinata*, *Pyrenula chlorospila*. Coastal shrub vegetation harbours a specific complex of species with e.g. *Athallia skii*, *Caloplaca ulcerosa*, *Lecanora hagenii*, and *Lecanora sambuci*.

To study of lichens of the Nordautlandet (Svalbard)

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Nordautlandet is the northernmost and hard-to-reach island in the Svalbard archipelago. We collected lichens in 2010-12 in Kinnvika Bay (Murchisonfjorden), Innvika Bay and Lusegrasvika Bay (Duvfjorden). To date 284 lichen species including 70 reported for the first time are treated from Nordautlandet. 71 species including 30 species recorded for the first time were found in the surrounding area of Kinnvika Bay. 104 lichen species were collected for the first time in the Innvika Bay, 111 in the Lusegrasvika Bay (Duvfjorden). *Baeomyces rufus* (Huds.) Rebent, *Bilimbia lobulata* (Sommerf.) Hafellner & Coppins, *Dacampia hookeri* (Borrer) Massal., *Lecanora cenisia* Ach., *Lobothallia alphioplaca* (Wahlenb.) Hafellner, *Rhizocarpon eupetraeum* (Nyl.) Arnold. and in addition 24 species are rare on Svalbard. *Caloplaca magni-filii* Poelt. is the interested parasitic lichen on the thallus *Miriquidica nigroleprosa* (Vain.) Hertel & Rambold. It was previously noted from Svalbard only in literature, the specimens was not found. We detected it in the Lusegrasvika Bay.

Current knowledge on lichens of the Leningrad region and St. Petersburg (North-Western European Russia)

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Current knowledge about lichens of the Leningrad region (LR) and St. Petersburg is based on considerable amount of data (ca 70000 records), including field data, publications (ca 300), herbarium collections (ca 15000 records) and archival materials amassed over the past 250 years. In total 1034 species (914 lichenized, 90 lichenicolous and 30 saprobic fungi) are known from the area. Of them, 564 species were recorded in St. Petersburg. Western part of LR is clearly richer in species than eastern: 904 taxa were found in the west, while only 637 species in the east. Altogether 171 (17%) species are known from the only locality. The territories to the north and west from LR have quite rich and well-investigated lichen floras: 959 species are known from the southern part of Republic of Karelia, 1166 from Estonia, more than 1300 from southern Finland. Known lichen diversity of southern and eastern neighbours is lower due to less active investigations and high anthropogenic pressure: 356, 299, ca 280 taxa are known from Novgorod, Pskov and Vologda regions respectively. Nowadays the lichens of LR are quite well-studied and we don't expect the number of species to increase significantly, but the lichenicolous fungi definitely are not enough investigated.

Sectorial land snail damage to the lichen *Argopsis friesiana* could be explained by metabolite profiles

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Notodiscus hookeri is the only native land snail of the sub-Antarctic, present in Crozet Archipelago, which feed exclusively on lichens. To improve our understanding of lichen-snail trophic interactions, the tripartite lichen *Argopsis friesiana* was selected. The snail occurs sympatrically with *A. friesiana*. The profiling and quantification of the major secondary metabolites in the whole lichen were investigated by LC-DAD-MS. Two main compounds were identified, the depside atranorin (8.2 mg.g⁻¹ dry mass (DM)) and the depsidone argopsin. Besides, the screening of primary metabolites was carried out to determine which compounds could be useful for the snail energetic demands. In cultivation, *N. hookeri* were fed with fructified thalli of *A. friesiana*. Snails ate the podetia cortex and phyllocladia but they avoided apothecia. This sectorial damage of the lichen by the snail suggested a differential distribution of the metabolites. Therefore, new profiling of secondary compounds was performed by Direct Analysis in Real Time – Mass Spectroscopy (DART-MS) on each morphological part of the lichen (phyllocladia, apothecia, podetia and cephalodia). The identification and distribution of secondary metabolites, fatty acids, amino acids and carbohydrates should help us to determine whether metabolites affect snail feeding choice and which of them could be implied.

Lichens in the American Mid-Atlantic Coastal Plain: diversity and discovery of an overlooked biodiversity hotspot

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The Mid-Atlantic Coastal Plain of eastern North America is a vast region of low-lying ecosystems that extends along the Atlantic Coast from New Jersey to Florida. It hosts remarkable ecological and biological diversity, including iconic endemic species such as the Venus Flytrap (*Dionaea muscipula*) and globally unique ecosystems such as pocosins (elevated peatlands). Despite its close proximity to major American cities with museums and universities that have long employed lichen specialists, the region was virtually unexplored for lichens until we began an intensive inventory four years ago. Now, having completed an inventory of the entire region, spanning >200 sites and collecting >17,000 vouchers, we present the results of our work. In addition to new species discoveries reminiscent of the golden age of natural history exploration, our results are a sobering picture for the future of lichen biodiversity. While we document two previously overlooked biodiversity hotspots, and shed considerable new light on lichen biogeography, these results must be placed in the context of the drastic changes projected to occur in the future due to sea-level rise, global climate change, and continued trends of habitat degradation and destruction.

The phytosociological classifications of the pine forests versus the epiphytic lichen patterns

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The study is a first attempt a completely quantitative description of the lichen biota (including, e.g. biomass) in clearly defined series of forest communities: dry, fresh, wet and boggy Scots pine forest. The study addressed the following key question: does each forest syntaxon has its own unique lichen biota? This problem is regularly highlighted, e.g. in the Project CRYPTO (Collective researches on the role of cryptogamous plants in the forest communities of the Białowieża National Park, Poland). The experimental plots were established in pine stands in three classes: 1-40 years, 41-80 years and 81-100 years. Techniques for estimating lichen biomass have traditionally required destructive harvesting. In this study the several of models have been developed to estimates biomass from cover and height measurement of lichen thalli. These surveys have been carried out from 2003 to 2015 with direct monitoring. The abundance of crustose lichens significantly decreased with age stand, foliose lichen abundance was greatest in intermediate aged stands, whereas squamulose lichens, cyanolichens and bryophytes abundance significantly increased with age stand. The forest structure variable, the air quality but not the phytosociological belonging of the forests influencing the diversity and the biomass of the lichen communities in managed pine forests of Poland.

The growth rate of *Verrucaria nigrescens* in a Mediterranean climate: a tool for lichenometric purposes.

Esteve Llop

Universitat de Barcelona, Spain

The use of saxicolous species for lichenometry has been profusely applied in non calcareous stones, where the main target species has been *Rhizocarpon geographicum*. However, few surveys have been carried on calcareous stone. Additionally, each survey has focused in different species. The lack of well established growth rates does not provide a good tool for being applied in lichenometric studies on calcareous stones. This study has been conducted in *Verrucaria nigrescens*, a widespread species in the Mediterranean region growing in calcareous stones, which are the main substrate in most of archaeological sites. The study was carried in the island of Malta, with a Mediterranean climate. Several localities, whose date of building was known, were examined for the target species. The data has provided a growth rate of *V. nigrescens* of 0.85 mm/year on average. This result provides a tool for estimating the age of archaeological heritage in the island, as most of it became excavated during the 19th century. The availability of *V. nigrescens* in the entire Mediterranean region would expand the use of this species for lichenometric purposes. As well as to refine the growth rate including more data from different areas within the region.

Sterile crustose lichens, an important component of lichen biota in forests – a case study of Białowieża Forest (NE Poland)

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Sterile crustose lichens have always been much neglected in lichen inventories. However since the use of thin layer chromatography, knowledge of their taxonomy and distribution has increased significantly during the last few decades. In Poland the first studies with the use of TLC were carried out in the late 1990s. Since that time more and more sterile crustose lichens have been listed in lichenological papers. In this presentation we show how the inclusion of these species influences our knowledge on the lichen diversity of different forest ecosystems. In 2014–2015 we conducted studies in Białowieża National Park. Similar studies were carried out 25 years earlier in the same area and using the same sampling method. The more recent research revealed 60% more species than previously reported, most of which represent sterile crustose lichens. The highest number of such species was found in broad-leaved forests. The species show no special preference for one community, but only a few occurred in all communities. The research leading to these results has received funding from the Polish-Norwegian Research Programme operated by the National Centre for Research and Development under the Norwegian Financial Mechanism 2009-2014 (Project Contract No Pol-Nor/196829/87/2013).

The reproductive ecology of *Icmadophila splachnirima*

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The rare, terricolous Australasian endemic *Icmadophila splachnirima* reproduces via apothecia and soralia, which are usually mutually exclusive. Some aspects of its reproduction were examined. Micro-environmental effects on reproduction: The hypothesis that a switch from sexual to vegetative reproduction occurs due to micro-environmental conditions was tested. Reciprocal transplants and measurements of lipid hydroperoxide levels as stress marker support the idea that micro-site conditions are more stressful for sorediate and sterile thalli than for fertile and esorediate thalli. Moisture regime rather than light conditions seems to affect the reproductive mode. Mating system: The MAT locus was characterised using degenerate and inverse PCR. Mating type screening revealed the presence of only one of both idiomorphs in each thalline tissue sample, indicating that the species is heterothallic, i.e. not self-fertile. Population genetics: Fungal and algal ITS sequences were used to examine gene flow between populations, and to assess the relative importance of sexual versus vegetative propagules. Very little variability was observed in fungal sequences, yet differentiation of regional subpopulations was found. Almost every sample has a unique algal genotype. Results suggests that fungal gene flow still occurs among the very disjunct known localities, and that long distance dispersal occurs via ascospores rather than soredia.

A novel method to assess ecogeographical boundaries in niche modeling using the example of *Usnea longissima* (lichenized Ascomycota: Parmeliaceae)

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Ecological niche modeling predicts the preferred niche for a species and its geographical distribution, the so-called theoretical niche, based on georeferenced occurrence data and environmental grid data. There are certain practical limitations to this approach, including the accuracy of taxonomic identifications, the precision of geocoordinates, and the completeness of environmental grid data; the validity of the AUC (area under the curve) statistics to test model performance is also sometimes discussed. However, here we focus on a different problem: the distinction of the theoretical and the realized niche. Usually, a species occupies only a portion of the predicted niche range, the theoretical niche, due to dispersal limitations based on ecogeographical barriers or because of its particular evolutionary history. Since these aspects cannot be assessed with current niche modeling approaches, we present a novel method to visualize ecogeographic barriers using Principal Component Analysis (PCA) of environmental grid variables, setting the theoretical optimal grid for a given species to zero. We illustrate this approach with the example of *Usnea longissima*, a charismatic macrolichen long believed to be cosmopolitan in distribution but actually restricted to the Northern Hemisphere.

Strongly underestimated lichen diversity of Central European old-growth forests: the new generation of field research

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Lichen biodiversity surveys of forests are largely incomplete due to a low sampling effort, spatially random collecting, underestimating of microlichens, omitting of taxonomically difficult taxa, a time/person availability etc. The interpretation of biodiversity data is generally constrained by the lack of reasonably comparable datasets (e.g. different sizes of studied areas). We have developed a new method of lichen inventories which captures most of the real diversity and enables to compare number of localities. The method is based on an exhaustive survey of 1 ha plots in diversity hot spots. The field work is done by a team of competing lichenologists, followed by a detailed samples identification including chemical and molecular methods. Our results show much higher number of recorded species than from any other field research. Examples of this survey from the Ukrainian Carpathians and the Czech Republic are presented. Except for the surprisingly high lichen diversity in Central European forests, we search for the undescribed diversity (i.e. new species). Although the region belongs to one of the best explored in the world, many new crustose lichens stay undescribed. Most of them belong to sterile or very small crusts, a part is quite conspicuous, but rare or very locally distributed.

Ecology and life-history variation of *Lobaria* species in Mediterranean forests: insights from an integrative approach

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Effective conservation strategies rely on a thorough understanding of the life histories and ecology of threatened species. Here, we conducted various population-scale studies to understand the ecology, life-histories and functioning of the threatened lichens *Lobaria pulmonaria* and *Lobarina scrobiculata* in Mediterranean forests. We analyzed the environmental and species-specific factors driving growth, reproductive strategy, vital rates (survival and recruitment) and physiological performance of the species in contrasting habitats (beech vs oak in *L. pulmonaria*; rocks vs trees in *L. scrobiculata*). Both species showed contrasting patterns of growth and population dynamics likely due to contrasting functional traits. The cephalolichen *L. pulmonaria* grew faster, started to reproduce at a larger size and recruited faster than its cyanolichen relative. Microhabitat heterogeneity and life stage significantly influenced growth rates. At the intraspecific level, each species showed habitat-specific demographic and physiological responses. Consistent with life-history theory predictions, both species started to reproduce at smaller sizes but with higher reproductive allocation in the habitats where the species grew significantly slower. These results highlight the effects of environmental and species-specific factors on the species ability to respond to environmental changes. This integrative approach is essential to develop strategies for *Lobaria* conservation in Mediterranean forests.

Molecular clues on eco-physiological response of lichens to nitrogen

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Lichens are one of the most sensitive components of the ecosystems to nitrogen stress and one of the most effective biomonitoring tools. Therefore, the relationship between lichens and reactive nitrogen has been extensively studied in recent decades. However, while the effects of increased nitrogen availability on lichen vegetation at the ecological level are well known, the response of the individual symbionts is far from being fully explained, despite recent developments in physiological approaches. "Omics" technologies represent a powerful means to explore the roles, relationships, and cascade reactions that molecules undergo, but very few studies exist using this approach in lichens and, so far, none investigating nitrogen effects. Results of a proteomic analysis conducted on the species *Cladonia portentosa* exposed for 6 months to different forms and concentrations of nitrogen will be presented. These findings show how at the molecular level different nitrogen forms affect different metabolic pathways in the photobiont (mainly energy production) and the mycobiont (mainly protein synthesis machinery), thus contributing to explain previous eco-physiological observations. Possible mechanisms contributing to nitrogen tolerance in the nitrophilous species *Xanthoria parietina* will be also discussed. Acknowledgements: European Union Seventh Framework Programme n° [301785]; ExpeER project; Fundação para a Ciência e a Tecnologia

Poster session I, Ground floor lobby • POSTER 69

Lichens-indicators of the old-growth and undisturbed forests in the zonal gradient on of the Central Russia territory

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Using long term field research (1986–2015) as well as fond materials analysis there were several expansion patterns found for the indicator species of the old-growth and undisturbed forests in different zone divisions of the Central Russia. For the south-taiga subzone there are 111 such species from 49 genera. Twenty nine species and 6 genera from this list (*Dendrosticta*, *Hypotrachyna*, *Protopannaria*, *Parmeliella*, *Punctelia*, *Vahliella*) don't overcome the north border of coniferous-broadleaved forests subzone (CBFz). In the broadleaved forests subzone (BFSz) there are already 85 species and 18 genera disappearing (besides earlier *Alectoria*, *Cheiromycina*, *Gyalecta*, *Heterodermia*, *Lecanactis*, *Lobaria*, *Lopadium*, *Menegazzia*, *Nephroma*, *Ramboldia*, *Schismatomma*, *Thelotrema*). In the forest-steppe zone (FSZ) 92 species and 20 genera are disappearing (besides mentioned, *Microcalicium*, *Sclerophora*). It's possible that the reason for this effect might be the change of the climatic conditions, although the anthropogenic press (especially, deforestation) also plays a great role in the restriction of lichen-indicator's distribution. This is shown by single findings in separate well-preserved of the FSZ forest parts of *Evernia divaricata*, *Icmadophyla ericetorum*, *Pertusaria pertusa*, *Phlyctis agelae*, which aren't yet found in BFSz. Finding of *Hertelidea botryosa* in the BFSz is very interesting while in the CBSz this species hasn't been found yet.

Poster session I, Ground floor lobby • POSTER 71

The lichen *Thamnolia vermicularis*, a lonely fungus with many green friends

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The cosmopolitan, alpine and arctic lichen *Thamnolia vermicularis* represents one example of a successful colonizer. Nevertheless, the assumed lichen spreading biology by fragments and the fact that its fungal partner seems to completely lack sexual reproduction the species huge geographic range is puzzling. We were able to confirm the species asexuality by sequencing the genomes and transcriptome of the fungal partner, and investigating the distribution of mating types in natural populations. The architecture of the fungal genome shows that it harbors mating-type idiomorphs consistent with a heterothallic mating system. When screening a sample of 218 individuals from natural populations of *T. vermicularis*, we find only one of the mating types suggesting that sexual reproduction is constrained by the existence of a single mating type in natural populations. Even if fragment dispersal as holobiont can be advantageous in the short term, asexual lineages are considered evolutionary dead-ends. We hypothesize that the lichenized fungus of *T. vermicularis* adapts to a changing environment by associating with different algal genotypes, which are shared in the different localities with other lichen species. Using NGS sequencing data we discovered that on Iceland, it shares the photobiont with two other genetically distant lichenized fungal species of *Cetraria*.

Lichen communities under microclimate gradient along a tree trunk in the dry evergreen forest, Thailand

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Distribution of lichen in tropical forests is influenced by microclimate under the canopy. Climate change could possibly lead to changes in community structures and ecosystems. This study explored lichen distribution along a tree trunk in a dry evergreen forest. It provided information on the influences of microclimate on species existence, which is essential for further conservation. Quadrates of 20 × 60 cm encompassed 12 subplots were placed along the trunk at the canopy, mid trunk and tree-base facing the East aspect. A total of 284 thalli were discovered, consisting of 26 species. The canopy, mid trunk, and tree base hosted 16, 8 and 7 species of lichens, covering 56%, 65% and 85% of the quadrat areas respectively. Only 1 taxa inhabited all three levels, and 3 species occupied two levels. Thirteen species restricted to only the canopy, whereas the mid trunk and the base had 4 and 3 species-specific levels. Important value index (IVI) revealed that Sterile soredia 2, Sterile nonpropagule 3, Sterile soredia 3, *Pyrenula aspistea*, and *Graphis furcata* dominated the tree trunk. Lichens producing isidia colonized only the canopy, whereas those that produce soredia settled at all levels.

High photobiont diversity in the common European soil crust lichen *Psora decipiens*

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To get insights into function and strategies of a successful establishment of lichens on biological soil crusts, the genetic diversity of the green algal photobionts of *Psora decipiens* was studied as part of the SCIN-project (Soil Crust InterNational). Lichen samples were collected from four different sites along latitudinal and altitudinal gradients in Europe (Tabernas/Spain; Hochtorn-Großglockner/Austria; Gyngelvar/Sweden; Ruine Homburg/Germany). The genetic identification of chlorobionts was carried out using the nuclear marker (nrITS) and a chloroplast marker (psbL-J). *Psora decipiens* was associated with several different species of *Trebouxia* and *Asterochloris*, although previously described to only have *Asterochloris* sp. as photobiont. The phylogenetic analyses revealed a high diversity with 17 well supported clades. Most of the photobiont species appeared to be cosmopolitan, but five clades were unevenly distributed between the sampling sites with only *Trebouxia* being found in the warm and dry Spanish habitats and combinations of *Trebouxia* and *Asterochloris* in the cooler and more humid habitats. The wide range of chlorobiont species might contribute to the observed domination of *P. decipiens* at all four research sites of the SCIN project which range from a desert in Spain to an alpine site in the Alps of Austria.

Diversity of lichens along a new world latitudinal gradient

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One phenomenon that has long been observed, but the mechanism of which has long been debated, is the latitudinal gradient in biological diversity. Many taxa, including flowering plants, mammals and amphibians, have been demonstrated to follow this pattern. Fungal groups have been, until recently, neglected, and their biogeography is controversial given their often-cryptic diversity. While some small-scale studies of the lichen latitudinal diversity gradient have been conducted with mixed results, no large-scale investigation combining currently existing collection data with a systematic field sampling approach, has been attempted. Here I present work from my dissertation on the diversity of lichenized fungi along a New World latitudinal gradient, combining herbarium specimen data with lichens collected from four sites from 10 degrees to 42 degrees North, as part of a larger gradient study from -39 degrees South to 61 degrees North. I compare species richness and species accumulation curves for these four sites, and compare this to herbarium collection data from these locations. I also investigate the functional diversity of lichens at these four locations, and begin to determine potential drivers of lichen diversity along this latitudinal gradient

Photobiont partners extend range and Hutchinsonian niche space of mycobionts in *Lasallia pustulata*

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Symbiont shuffling in mutualistic associations is an expected mechanism that could mediate the impact of ongoing climate change on the geographic and ecological distribution of holobionts. For instance, diversity in host-symbiont pairings at the sub-species level has been related to functional variation in response to environmental change in reef-building corals and their photosynthetic symbionts. In the same way, plasticity in mycobiont-photobiont interactions may explain the broad ecological niches of many lichen-forming fungi. Here we test this hypothesis at a broad geographic scale. We examine the population genetic structure of *Lasallia pustulata* holobionts throughout their European distribution range, based on sequences of MCM7 (mycobiont) and ITS rDNA (photobiont). We show that occurrence probabilities of specific mycobiont-photobiont interactions are linked to climatic niches. Quantification of niche extent and geographical overlap of haplotypes based on (i) species distribution modeling and (ii) construction of Hutchinsonian climatic hypervolumes revealed that combinations of fungal-algal interactions change at the sub-species level along latitudinal temperature gradients and in Mediterranean climate zones. We discuss our results in the light of symbiont polymorphism and partner shuffling as potential mechanisms of environmental adaptation and niche expansion in lichens.

Vanadium dependent nitrogen fixation in cyanobacteria and lichens

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Availability of fixed nitrogen is essential for primary production. In many arctic and subarctic habitats characterized by dominance of cryptogams, including mosses, lichens and biocrusts, cyanobacteria are the principal providers of biologically fixed nitrogen via the enzyme nitrogenase. Most biological fixation is carried out by molybdenum-dependent enzymes (Nif), but recently vanadium-dependent nitrogenase (Vnf) has also been found in cyanobacteria associated with lichens and mosses. The Vnf system is widespread in lichens and mosses in Iceland. We ask what drives the selection of this alternative nitrogenase system. We have found that the frequency of the Vnf system in the cyanolichen *Peltigera membranacea* is high in low temperature habitats. We have also measured the relative contribution of the Vnf system via ¹⁵N/¹⁴N isotope ratios. Our findings indicate that the relative contribution of the Vnf system to nitrogen fixation in *P. membranacea* is greater in highland low temperature habitats than in more temperate coastal habitats. We also have indications that the Vnf system contributes substantially to nitrogen fixation in samples of biocrust from the Icelandic highlands. The biocrust consists mainly of the liverwort *Anthelia juratzkana* in addition to various fungi, bacteria and cyanobacteria. We are currently running metagenome studies on the biocrust.

Evaluation the effects of biological soil crusts on soil properties in Kiyamaki Wildlife Refuge rangelands, NW Iran

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Biological Soil Crusts (BSCs) have significant influence on primary ecosystem processes, and have been introduced as ecosystem engineers in drylands. In this study, the effect of BSCs on soil properties in Kiyamaki Wildlife Refuge was investigated. Soil sampling were carried out in locations with and without BSCs, at depths of 0-5 and 5-15 cm, with 3 replications. Laboratory and field tests were done, and collected data were analyzed by independent t-test. The results showed that BSCs affected soil properties investigated in this study and resulted in an increase in soil stability, soil moisture, available water content, infiltration rate, hydraulic conductivity, as well as an increase in carbon and nitrogen, electrical conductivity and availability of nutrients in soil. Improvement of soil properties occurred mainly in 0-5 cm depth. In 0-5 cm depths, amount of organic carbon and total nitrogen was 1.14 and 0.13 percent in soil with BSCs and 0.74 and 0.09 percent in soil without BSCs, respectively. BSCs improved microbial community population, soil respiration and microbial biomass carbon and nitrogen. The soil respiration rates in crusted and non-crusted soils in 0-5 cm depths were 0.349 and 0.225 mg CO₂ g⁻¹ soil 24 h⁻¹, respectively.

The influence of forest area on the lichen species richness and their frequency on *Carpinus betulus* in NE Poland

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The fragmentation of woodlands causes a serious threat to numerous epiphytic lichen species, including habitat specialists, which prefer old trees. Research was conducted in 540 micro-plots on 60–130 year old *Carpinus betulus* trees in the three types of managed oak-linden-hornbeam forests in north-eastern Poland: large (are more than 20,000 ha), medium (2000–2500 ha) and small forests (150–250 ha). During the study 64 lichen species, of which 27 are red-listed in the country, have been recorded on bark of older hornbeams. The numbers of all recorded species, including red-listed lichens, were higher on 100–130 year old hornbeams occurring in large, compact forest (in comparison to the hornbeams in the same age group in the isolated medium and small forests. A similar difference was found in respect to younger, 60–79 and 80–100 year old hornbeams occurring in all three types of forests. Lists of species and their frequency are presented. The project was funded by the National Science Centre in Poland under a Decision No. DEC–2013/11/N/NZ9/04686.

Effect of lichen compounds produced by *Cladia aggregata* on the germination of leaf lettuce

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We conducted a preliminary study and experiments to examine whether the secondary metabolites of lichens can act as allelopathic agents in the field. In this study, we analyzed water-soluble compounds extracted from soil and from *Cladia aggregata* growing on the soil using HPLC. The HPLC results showed the presence of a peak corresponding to that of barbatic acid suggesting the possibility of barbatic acid, a lichen secondary metabolite leaching into the soil where *C. aggregata* grows. Next, water-soluble compounds were extracted from *C. aggregata* by autoclaving, and a germination experiment was conducted using the leaf lettuce. An eight-fold concentrated extract significantly inhibited radicle and hypocotyl growth. Upon treatment with the 16-fold concentrated extract, we observed substantial inhibition effects, including a considerable drop in the germination rate, and the termination of germination processes at the early stages of germination. The results suggested that the leached-out compounds (lichen secondary metabolites) from *C. aggregata* could function as allelopathic agents.

Post-fire recovery of epiphytic lichen cover in pine forests of Southern Karelia (Karelia Republic, Russia)

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Post-fire recovery of epiphytic lichen cover has been studied in pine forests of Southern Karelia over the past 17 years. Altogether 31 sample plots (25×25 m) in green-moss pine forests were studied by direct observation and by constructing spatiotemporal series of forest communities, with the last fire from 4 to 206 years ago. The work is based on 8334 descriptions of epiphytic lichen cover made on 525 pine trees using vertical frame 10×20 cm. Recovery of the main characteristics of epiphytic cover (total cover and number of species) after a fire at the community level has been observed in 20–30 years after the fire at the base of the trunk and in 40–50 years – at a height of 130 cm from the ground. The formation of epiphytic cover has been quicker on trunks of trees which had been burning than on trees grown after the fire: the delay is about 60–100 years. The form and rate of post-fire recovery of epiphytic cover depend on the tree age. Stationary state occurring at a certain time after the fire has been observed at the community level only, and is supported by the presence of different-quality substrate within the community.

Freshwater habitats in the Valdivian temperate rainforest biome - an overlooked hotspot of endemics?

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Temperate rainforests host an exuberant luxury of lichens, most visible in their often spectacular epiphyte vegetation. Exposed habitats for saxicolous lichens instead are naturally rare in these dense and dark forests and often confined to isolated outcrops, short stretches of smaller streambeds close to rapids and waterfalls or along the banks of larger rivers. Species records from these communities are few and no attempt to describe community structures has been made before in temperate South America. In this study community structure and the role of endemic taxa in streams and rivers in northwestern Patagonia were assessed and compared with data from similar habitats in other parts of the world. Species inventories were obtained by targeted searches along 10–50 m long stretches of streams and rivers. Frequency data for individual species were assembled following a half randomized transect sampling strategy. For selected taxa a DNA barcoding approach was applied to assist morphology based identification and recognition of cryptic or semi-cryptic species. Freshwater lichen communities at the study sites were characterized by a high frequency of Trapeliaceae and Lichinaceae, the family Verrucariaceae instead is comparatively weakly represented. Many of the dominating species appear to be endemic to Patagonia or temperate South America.

Epiphytic lichens in differently aged and climatic *Pinus sylvestris* plantations in Belarus

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The study of epiphytic lichen communities in south-eastern Belarus deals to state how lichen species composition relates to both microclimate of habitat and pine forest age. To address this, fieldwork was carried out in 2011–2013 on 30 sample plots within 12 types of pine forest ranging by age and humidity. Only lichen species on Scots pine tree trunks were included in the analysis which employed the Sørensen-Dice index to describe differences in species composition. Altogether, 84 species of lichens and lichenicolous fungi have been recorded in the study, the occurrence and frequency of many of these varying according to the age of pine stand. It was found that maturing (80–100 years old) and mature (110–130 years old) pine forests have a similar lichen species composition, with Sørensen-Dice indices ranging from 0.63 to 0.86. Sample plots in young (20–40 years old) and middle-aged (50–70 years old) pine forests form separate clusters; all these with no apparent differences in humidity. Microclimate of habitats do not indicate similarity of lichen community structure, except for the most fertile *Oxalis acetosella*-type pine forest which has the most specific lichen flora with a Sørensen-Dice index of 0.44.

Analysis of the distribution of saprophytic lichen communities in Tumur peak national nature reserve in Xinjiang, China

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In order to evaluate the saprophytic lichen species diversity and its distribution patterns in coniferous forest in Tumur peak National Natural Reserve in Xinjiang, China, saprophytic lichens were sampled from 75 plots of five representative altitudes between 2200 m to 3200 m. Saprophytic lichens diversity was evaluated using α -diversity, measured as species richness per plot. Detrended correspondence analysis (DCA) and cluster analysis (CA) were used to classification of lichen communities. Pattern of lichen species distribution in relation to environmental variables were determined using canonical correspondence analysis (CCA). As the result show that, there are 41 saprophytic lichen species belong to 21 genera and 12 families. The CCA revealed that the considerable variation in lichen community composition can be explained by several environmental variables associated vary with forest stand structural complexity, temperature, moisture and canopy density. The highest diversity of the saprophytic lichen species in large diameter trees. The lichen cover increased with increasing stand age, humidity and light, but decreased with increasing altitude.

Epiphytic lichen distribution in nemoral forests along the longitudinal gradient

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Nemoral forests with little human impact in boreo-nemoral vegetation zone comprise rich lichen diversity. The present study was performed in nemoral forests of Latvia and Russia. Despite to historical forest land management (e.g. forest cutting for agricultural purposes) still semi-natural forest patches with relatively high biodiversity exists in Latvia and epiphytic lichens represents an important part of these forests. Similar forest patches, but in larger scale exists also in Russia. Latvia and Russia represents west – east gradient of vegetation and also differences in epiphytic lichen diversity were expected. Our hypothesis is, that lichen species diversity reflects more west-east gradient, than specific ecological conditions in particular forest stand in Latvia and Russia.

The Northern Caucasus is a Key Lichen Biodiversity Area in Russia

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Data on the lichen flora diversity of the Northern Caucasus have been collected in the framework of the project "North Caucasian Lichen Flora" (NCLF) (grant RFBR no 15-29-02396). The Caucasus Mountains are one of the world's biodiversity hotspots as well as one of the richest regions of Russia. About only 1100 species have been mentioned for NC in the first Russian lichen checklist (2010). As a result of intensive studies in latest years, the number of known species has increased by more 500 new species. At present, about 1650 species (including allied non-lichenized fungi) are recorded in NCLF. On the basis of comparative biogeographic analysis has been shows the contribution of NCLF in the Russian lichen flora diversity and the some Russian regions. NCLF includes about 43% of the Russian LF (3800 spp.) and of most species of the LF of the southern and middle parts of the European Russia, Southern Ural and Western Siberia (more 75% of species). NC is represented by about 300 species absent in other Russian regions. However, the total LF diversity and distribution of many species in NC are still insufficiently known. Therefore, extensive field researches in various regions of NC are very necessary.

Diversity, distribution and species specificity in Antarctic lecideoid lichens correlated to newly generated climate zones

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The Antarctic continent with its most extreme climate conditions provides an environment where only the hardest organisms can survive. However, the mechanisms that connect climate and life's diversity in Antarctica are still poorly understood owing to limited climate data and taxon sampling in many areas of the continent. The current study investigates the role of climatological factors (temperature and humidity) driving lichen diversity, distribution and species specificity in Antarctica using saxicolous lecideoid lichens as a model system. The mycobionts of these lichens are associated with several *Trebouxia* species as photobionts. Even so, the various mycobiont species show different patterns of distribution, genetic diversity and phylogenetic relationships to their photobionts. To demonstrate the correlations of distribution patterns and species specificity Antarctic climate zones were generated by combining twelve zones based on annual mean temperature with six zones predicated on annual precipitation. Molecular investigations show a wide range of species specificity from the mycobionts to their photobionts. It varies from very low as the widespread *Lecidea cancriformis* with the ability to choose different *Trebouxia* species available all over the continent to highly specific as *Lecidella greenii* which is restricted to only one *Trebouxia* species which merely occurs in milder habitats.

Modern studies of lichenicolous fungi of the Caucasus

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Lichenicolous fungi of the Caucasus long remained poorly known. Recent studies revealed there are 192 species (Zhurbenko & Otte 2012, Zhurbenko & Kobzeva 2014, Urbanavichus & Urbanavichene 2014), which is still far from no less than 460 species of these fungi known in the Alps. Probably significant gaps remain in such genera as *Cercidospora*, *Dactylospora*, *Pronectria*, *Stigmidium* and *Tremella*. Regional geographical novelty (75% of species new to the region) was much higher than in comparable studies in Europe, e. g. 25% in Italy (Brackel 2011), 5% in Austria (Hafellner et al. 2004), 13% in Germany (Brackel 2010) or 32% in Svalbard (Zhurbenko & Brackel 2013). However, the taxonomic novelty (3% of species new to science) was at the same level as in the other parts of the Holarctic, e. g. 3% in Germany (Brackel 2009), 5% in Spain (Etayo 2010), 3% in Svalbard (Zhurbenko & Brackel 2013), 6% in Japan (Zhurbenko et al. 2015) or 3% in North America (Diederich 2003), but much lower than in the Neotropics, e. g. 38% in Columbia (Etayo 2002), 18% in Peru (Etayo 2010) or 32% in Chile (Etayo & Sancho 2008). The study was supported by RFBR grant 14-04-01031 "Lichenicolous fungi of Northwest Caucasus".

Lichenicolous mycobiota of the Russian Arctic

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More than 250 species of lichenicolous fungi (LF) from 85 genera are registered in the Russian Arctic on approximately 20% of species and 40% of genera of its lichen biota. The most spacious LF genera are *Stigmidium*, *Arthonia* and *Dactylospora*. The most common LF species are *Dactylospora deminuta*, *Lichenocodium lecanorae* and *Lichenostigma alpinum*. The most "hospitable" lichen genera are *Peltigera*, *Cladonia* and *Lecanora*, 80% of LF species are confined to a specific host genus. Correlation between specialization of LF species and degree of immersion of their fruit bodies into host tissues was not detected. Just 8% of the LF species are strong pathogens, 7% induce galls. Lichenicolous Index of the Russian Arctic is equal to 0.2. Compared to more southern holarctic regions its lichenicolous mycobiota has higher positions in the generic spectra of e. g. *Dactylospora*, *Cercidospora* and *Muellerella*, and lower of e. g. *Capronia*, *Opegrapha*, *Plectocarpon* and *Tremella*. 60% of the Russian Arctic LF species are known only from the Holarctic. 25% of them have arctic-alpine distribution. Existence of LF endemic to the Arctic is doubtful. Just half of ca. 750 LF species reported on lichens growing in the Arctic and elsewhere have been found in the Arctic itself.

Diversity and habitat preferences of the *Peltigera canina* species complex in Estonia

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The widespread lichen genus *Peltigera* (Peltigeraceae, lichenized Ascomycota) includes many terricolous and muscicolous species. The *Peltigera canina* species complex (section *Peltigera*) is one well-defined lineage within the genus that included several poorly known and undescribed species. We studied the species diversity and habitat preferences of these lichens in Estonia by sampling a spectrum of habitats (alvars, dunes, roadsides and forests). The fungal ITS (internal transcribed spacer) gene from 137 *Peltigera* specimens was sequenced to determine species identities and to study phylogenetic relations. On the basis of this material we found six described species (*P. canina*, *P. extenuata*, *P. didactyla*, *P. ponojensis*, *P. rufescens*, *P. praetextata*) and several undescribed species (*P. "neocanina"*, *P. "neorufescens"*, *P. "fuscoponojensis"*) or cryptic species from our study sites. *Peltigera "neorufescens"* characteristically grows on basic soil in alvar grasslands and other open calcareous habitats. Also, *P. ponojensis* and *P. "fuscoponojensis"* prefer basic soil and commonly grow on eutrophic roadsides. *P. canina*, *P. extenuata* and *P. didactyla* are most frequent on dunes and forest habitats, while *P. praetextata* is found exclusively on mossy tree trunks and stones.

The genus *Lobariella* (Lobariaceae) in Colombia: Further new species revealed through ITS barcoding

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The genus *Lobariella* was introduced as a segregate of *Lobaria*, distinguished by the pseudocyphellae and/or maculae on the upper surface. For a long time believed to continue only five species, a molecular phylogenetic revision published in 2013 distinguished 26 species, a more than 5-fold increase. ITS barcoding of collections made subsequently in tropical America and Hawaii has added further eleven species, for a total of 37 taxa now distinguished. We present an updated ITS phylogeny of the genus and discuss phenotypic species delimitation using selected examples.

The lichen family Lobariaceae in New Zealand: Assessing traditional species concepts using the ITS barcoding locus

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The New Zealand lichen biota is among the best known in the Southern Hemisphere, mainly due to the work of the late David Galloway. At the time of Galloway's treatment in 2007, the taxonomy of New Zealand Lobariaceae was considered to be well-known, with five species of *Lobaria*, 47 of *Pseudocyphellaria*, and 14 of *Sticta*. Generic reassessment increased the number of genera to six, with 67 species, adding the segregates *Crocodia*, *Podostictina*, and *Yarrumia*, plus one further species in *Pseudocyphellaria* s.str. Among the listed taxa were the presumably widespread *Crocodia aurata*, *P. argyracea*, *P. crocata*, *P. intricata*, *Sticta fuliginosa*, *S. limbata*, and *S. weigeli*. We present an updated molecular phylogenetic classification of New Zealand Lobariaceae. The *P. crocata* morphotype represents seven taxa, including the known species *P. maculata* and *P. neglecta*, as well as four newly recognized lineages and the cyanomorph of the only green-algal species in the clade, *P. carpoloma*. All sequenced material of *P. argyracea* represents the cyanomorph of *P. lividofusca*. We confirm that the subcosmopolitan *Crocodia aurata*, *Sticta fuliginosa*, and *S. limbata* are indeed present in New Zealand. The stalked, green-algal *Sticta* species, apparent indicators of good forest health, are shown to contain two unrecognized taxa.

When your partner shapes your look: ITS analysis of symbionts in *Dendriocaulon intricatum* and *Ricasolia quercizans*

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Dendriocaulon is widely recognized as a form group of fruticose bipartite symbiotic associations formed by fungi typically developing foliose tripartite thalli with a green alga and *Nostoc*. Two species of *Dendriocaulon* have been identified in North America: *D. umhausense* and *D. intricatum*. *Dendriocaulon umhausense* is widely accepted as the free-living form of the cephalodia of *Ricasolia amplissima* that may grow into shrubby outgrowths on the green thallus. *Dendriocaulon intricatum* is a dendriocauloid cyanomorph from Eastern North America, but the corresponding chloromorph has still to be identified. Phylogenetic inferences of sequences of the internal transcribed spacer (ITS) regions of the nuclear rDNA sampled for several thalli of *Dendriocaulon* from North America, and all members of *Ricasolia* reveals that *D. intricatum* and *R. quercizans* share the same mycobiont. *Ricasolia ravenelii*, the only species of *Ricasolia* known to develop dendriocauloid outgrowths, albeit in southeastern North America, does not match any of the sampled *Dendriocaulon* populations. Therefore, the free-living *Dendriocaulon* form in Eastern North America is considered to be developed solely by the endemic *R. quercizans*, and primarily towards the edge of the geographic distribution of the chloromorph. The name, *D. intricatum* should be treated as the taxonomic synonym of *R. quercizans*.

Photobiont association patterns in *Pectenium plumbeum*

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In order to reestablish the lichen symbiosis fungal spores must first germinate and then associate with a compatible photobiont. We studied ascospore germination and photobiont association in the cyanolichen *Pectenium plumbeum* (Pannariaceae, Peltigerales) in temperate and Mediterranean oak forests of Spain. Germination tests were made with ascospores from 444 apothecia. Not a single ascospore germinated within the two month trial (with 32 different treatments). Then 192 isolates of the *Nostoc* photobiont were obtained from 24 *Pectenium* thalli. While 82% of isolates were still alive after six months on the growth medium, none had grown nor produced motile hormogonia. In order to determine the genotype identity of the *Nostoc* cyanobionts we obtained tRNA^{Leu}(UAA) intron sequences from 30 *P. plumbeum* thalli from one population. We also sequenced *Nostoc* cyanobionts of 40 specimens of other cyanolichen species from the same habitat and 62 *Nostoc* free-living colonies cultured from bark samples. The results indicated that *P. plumbeum* shares *Nostoc* genotypes with two other cyanolichen species. Only one of them reproduces asexually via small thallus fragments and is suspected to facilitate the establishment of *P. plumbeum* by dispersing appropriate cyanobionts into new habitats.

Four new species in the lichen genus *Sticta* from Macaronesia

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In the framework of a global project on the flagship lichen genus *Sticta*, extensive sampling has been conducted in Macaronesia, more precisely in the Canary Islands and the Azores. Four species new to science have been discovered. *Sticta* sp. 1 belongs to the fuliginosa morphotype and is widespread (known from British Columbia, China and the Canary Islands) but very rare. The other three new species (*S.* sp. 2-4) belong to the weigeli morphotype, are all endemic to the Azores and closely related to species from the Neotropics; the three species are very rare and restricted to remnants of natural laurisilva. The phylogenetic position of each species within the genus is inferred from molecular data (4-loci) using maximum likelihood and Bayesian inferences methods.

The genus *Solorina* in the Czech Republic

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Three species of the genus *Solorina* were historically recorded in the Czech Republic – *S. crocea*, *S. saccata* and *S. spongiosa*. While the first mentioned is now missing from the country, *S. saccata* and *S. spongiosa* are rarely found with several localities in the country. The number of localities of both species have significantly diminished comparing to historical records (almost identically as *Peltigera* species with green alga as photobiont). Several sites with presence of *S. saccata* are established for long term monitoring of the species.

The effects of copper stress on the ultrastructural, biochemical and physiological characteristics of *Ramalina sinensis* and *Peltigera rufescens*

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The study aimed at investigating the effect of copper on selected physiological and biochemical parameters (soluble sugar, proteins, free proline, chlorophyll, cell membrane damage and antioxidant enzyme POD, SOD, CAT activities) and ultrastructural changes in the lichens *Ramalina sinensis* and *Peltigera rufescens*. Physiological measurements showed *R. sinensis* was much more sensitive to the copper stress than *P. rufescens*. The decreased vitality and distinct damages in the cell structure of *R. sinensis* photobionts were observed with the increased copper concentrations, but less changes in *P. rufescens* photobionts vitality and not any damages in the structure were detected even in the highest copper treatment. Mycobiont, the main body of the lichen thallus, might try to adapt stress conditions by increasing the amounts of osmolytes, activating the antioxidant protective enzymes and releasing of K⁺ from the cells under copper stress. Lichenized fungi might provide better protections to their symbiotic partner- photobionts by trying to adapt the stress condition or changing their surrounding environments within the limited ranges. Because of the different response of the lichen mycobionts to copper stress, *Nostoc* photobionts of *P. rufescens* were more tolerant than green-algal photobionts of *R. sinensis* to higher copper stress.

Glass formation in three lichens and their separated symbionts

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Upon water removal, solutes can undergo "vitrification", which is the transition from a liquid to a glassy state. Desiccation tolerant life-forms, such as lichens, are capable of surviving vitrification. The glassy state restricts molecular mobility, slowing down chemical reactions, and enzyme activity ceases. Thus, deteriorative processes are reduced, helping to maintain viability in the dry state. Vitrification depends upon the composition of the matrix, water content and temperature. Glasses have been extensively studied in microorganisms and seeds because of their relevance to food quality and seed conservation, have hardly been studied in photosynthetic tissues and so far, have never been studied in lichens. Here, we studied glass transition in silicagel-dried samples of *Lobaria pulmonaria*, *Flavoparmelia caperata* and *Xanthoria parietina* (and their isolated symbionts) by Dynamic Mechanical Thermal Analysis (DMTA). According to the glass transition interval determined by DMTA lichens present lower molecular mobility than their isolated photobionts, at ambient temperature ranges of 10–20°C. The potential significance of the findings for lichens is discussed.

Wavelength-dependent photoinhibition of drought-tolerant photosynthetic organisms in continental Antarctica

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All photosynthetic organisms have a risk of photoinhibition especially the damage directly connects to the availability of living in severe environments limiting photosynthetic active period. In this study, we evaluated the wavelength dependent photoinhibition in *Umbilicaria decussata* (lichen), *Ceratodon purpureus* (bryophyte) and *Prasiola crispa* (alga) harvested from a study site in East Antarctica, at ambient light conditions by calculating their reaction factors, k_{pi} , using a large spectrograph. It revealed that lichen showed high resistance sufficient to avoid photo-damage under the summer condition. The bryophyte was only sensitive to UV-B rays. Hydrated *P. crispa* was highly sensitive to photoinhibition especially in the UV spectrum, however the reaction constants of dehydrated samples were one-tenth that of the hydrated samples. *P. crispa* need to pay large cost for recovering from photoinhibition to adapted to conditions in continental Antarctica than the lichen and bryophyte. The different photoinhibition physiological features were found to be correlated to the different habitat in continental Antarctica.

Poster session I, Ground floor lobby • POSTER 100

Prediction of active period of the lichen and other photoautotrophs growing in Antarctica, by physiological study and micro-meteorological observation

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Some of lichens, bryophyte and algae are successful organisms in continental Antarctica. Their brilliant resistance against the stressful condition has been known but their ecological feature hasn't been clear because the year-round observation is easily blocked for the severe climate. Recently, monitoring the ecosystem is required because of large effect of climate change. This study aimed to clarify their annual ecological behavior under Antarctic environment from the micro-meteorological monitoring of habitats and physiological study. We set up the micro-meteorological monitoring system at the observing site in Langhovde of East Antarctica. We observed habitats of *Umbilicaria decussata* (lichen), *Ceratodon purpureus* (bryophyte) and *Prasiola crispa* (alga), and the monitoring items were temperature, humidity and PAR (photosynthetic active radiation). The micro-meteorological data revealed large difference in their photosynthesis environments. The lichen was exposed to high irradiation over summer season but other two samples were put in dark condition till the mid summer because of the snow. It was predicted that the lichen could photosynthetic activity during the early summer and dried up till mid summer season. And the bryophyte and green-algae started photosynthesis the end of December. It was thought the different active periods were attributed to their different physiological features.

Functional analysis of thioredoxin from the desert lichen-forming fungus, *Endocarpon pusillum* Hedwig, reveals its role in stress tolerance

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Endocarpon pusillum is a lichen-forming fungus with an outstanding stress resistance property closely related to its antioxidant system. In this study, thioredoxin (Trx), one of the main components of antioxidant defense systems in *E. pusillum* (EpTrx), was characterized and analyzed both in transgenic yeasts and in vitro. Our analyses identified that the heterologous expression of EpTrx in the yeast *Pichia pastoris* significantly enhanced its resistance to osmotic and oxidative stresses. Assays in vitro showed EpTrx acted as a disulfide reductase as well as a molecular chaperone by assembling into various polymeric structures. Upon exposure to heat-shock stress, EpTrx exhibited weaker disulfide reductase activity but stronger chaperone activity, which coincided with the switching of the protein complexes from low molecular weight forms to high molecular weight complexes. Specifically, we found that Cys31 near but not at the active site was crucial in promoting the structural and functional transitions, most likely by accelerating the formation of intermolecular disulfide. And transgenic *Saccharomyces cerevisiae* harboring the native EpTrx exhibited stronger tolerance to oxidative, osmotic and high temperature stresses than the corresponding yeast strain containing the mutant EpTrx (C31S). Our results provide the first molecular evidence on how Trx influences stress response in lichen-forming fungi.

Poster session I, Ground floor lobby • POSTER 102

Environment factors influencing structure of lichen communities on cobbles in the Negev desert

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We studied the lichen diversity on cobbles at 13 stations located within four aspects of a second order drainage basin near Sede Boqer at the Negev desert. The hydrological rain, dew, and dust were measured at these stations over two years. The measurements showed that slopes differed both in moisture conditions, and in the amount of dust deposition due to the wind regime in the drainage basin. To evaluate the relationships between the environment factors and the lichen community structure, 10 cobbles were randomly collected from each station and examined for their species composition, cover, and growth form. Our research showed that wetness duration after the dew and rain influenced the covers of most epilithic and some endolithic species, while the amount of precipitation (dew and rain) influenced the covers of only two epilithic species. The dust deposition influenced the most lichen species only in wet habitats. In arid habitats, an insignificant dust impact was noted on the covers of five endolithic species. The data imply that annual wetness duration rather than the amount of precipitation and dust may explain the structure of lichen communities.

The monotypic *Leightoniella* recollected and placed in a new position

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The monotypic genus *Leightoniella* was described by Henssen (1965), based on 19th century material collected in Sri Lanka by Thwaites and described as *Pterygium zeylanense* by Leighton. It was assigned to the Collemataceae. It was subsequently reported only once, from Australia. During field work in Sri Lanka in 2015, specimens were recollected by the first author, in several localities. The fresh material has ascospores with a thick gel layer with pointed, asymmetrical tips, unlike Collemataceae ascospores, but resembling some Pannariaceae. DNA sequence data place *Leightoniella* firmly in the Pannariaceae, close to *Physma* and *Lepidocollema*. The affinities of the genus have remained obscure because it is gelatinous and lacks rhizines or felt on its lower surface, which were characters of the Collemataceae rather than the Pannariaceae.

Molecular systematics of the *Arthrorhaphis alpina* — *A. citrinella* species complex

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Arthrorhaphis Th. Fr. is a small genus of lichenised or lichen parasitic ascomycetes comprising ca. 11 species and subspecific taxa worldwide. The genus occurs mainly in temperate to arctic-alpine regions of the Northern Hemisphere. Three species, *A. alpina*, *A. citrinella* and *A. grisea*, have their distributions extending into the Southern Hemisphere, and *A. citrinella* var. *catolechiooides* is only known from Australasia. *Arthrorhaphis alpina* and *A. citrinella* show considerable morphological variability at the world level that is presently not well understood. In this study, we investigate the genetic structure of the *A. alpina* — *A. citrinella* species complex based on newly generated mitochondrial (mtSSU) and nuclear (nLSU, RPB1 and ITS2) DNA sequences, and ML and Bayesian methods of phylogenetic tree reconstruction. Preliminary results conform to the species concepts currently accepted in the genus and show all taxa with finally autonomous lichenised thallus to be closely related. Genetically distinct clades being correlated with morphology and/or geographical distribution are present both in *A. alpina* and *A. citrinella*. *Arthrorhaphis alpina* var. *jungens* and *A. vacillans* are recovered as sisters within *A. alpina* s.lat.

Photobiont diversity in cyanolichens of the *Dictyonema* clade (Hygrophoraceae: Basidiomycota)

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The *Dictyonema* clade is the largest lineage of basidiolichens, with five genera and hundreds of species, many still undescribed. Its photobiont is *Rhizonema*, a recently recognized clade of cyanobacteria. Here, we studied the phylogenetic diversity of this cyanobacterial clade, its geographical distribution, and its mycobiont relationships, and tested whether *Rhizonema* is entirely lichenized. Our dataset consisted of 560 specimens representing over 200 basidiolichens in the *Dictyonema* clade, with additional 21 ascolichens, and seven free-living cyanobacteria. We sequenced two genetic markers, rbcLX and 16S rDNA. All sampled lichens contained *Rhizonema* as photobiont, while all free-living samples represented other genera of cyanobacteria. The data indicate two lineages of *Rhizonema*, with 47 haplotypes of 16S, most representing the widely distributed species, *R. interruptum*. We plotted 16S data into a fungal ITS tree to observe haplotype diversity across different species and genera of the *Dictyonema* clade. A strong signal suggests that a second undescribed species of *Rhizonema* is predominantly associated with fungal species belonging to an Andean clade of *Cora*. Overall, our results show that the diversity of photobionts is far lower than that of the mycobionts in the studied material, a view that lends further support to the hypothesis of photobiont domestication and sharing.

Heterodermia Trevis. in Colombia: New Insights into generic divisions within *Heterodermia* sensu lato

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Heterodermia Trevis. was treated as a separate genus for almost 100 years, before Kurokawa in 1962 included it in *Anaptychia* Körb.; nevertheless, *Heterodermia* was reinstated shortly after, informally maintaining the infrageneric groups distinguished by Kurokawa. In a recent work, Kalb et al. proposed to recognize these groups formally, describing *Leucodermia* and *Polyblastidium* as new genera, supported mainly by secondary chemistry and ascospore types. As part of a revision of the genus *Heterodermia* in Colombia, we were able to test this new classification with a molecular phylogeny using the fungal ITS barcoding locus, with over 240 sequences including many Colombian samples and all sequences deposited in Genbank and UNITE (cross-validation). The data set corresponded to over 65 species, which were identified by comparison with type material. Our results suggest that the five genera proposed to be recognized by Kalb et al. are supported (*Heterodermia* s.str., *Leucodermia*, *Polyblastidium*, the *H. comosa* group, and the *H. obscurata* group). The *H. obscurata* group was supported as sister to *Heterodermia* s.str, both closely related to *Polyblastidium* and the *H. comosa* group, sister of *Leucodermia*. Following these results, we also propose the use of the tribe *Heterodermieae* proposed earlier by Trevisan.

LikArmor: a project to identify lichens in the west of France (Armorica)

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Likarmor is an interactive key very similar to the remarkable tool developed by Rambold et al. (li-aslight.lias.net) but focusing on the lichens of the North-West region of France. The application is based on the Intkey software of Open-Delta package (ALA) provided on Windows, Linux and Macintosh platforms and includes chemical, ecological, anatomical characters and numerous illustrations to make identification easier. Our objective (similar to the Navkey applet of the LIAS Light project) is to design a tool which could be freely used by non-experts and specialized scientists interested in lichens of Armorica. We intend to integrate information from local herbaria such as H. Des Abbayes and LJC. Massé, kept at the University of Rennes along with precise chemical data to be actualized by the lichen chemistry team in Rennes. This work was undertaken on the basis of data compiled in the "Catalogue des lichens de France" recently published by Claude Roux et al. Such an exhaustive compendium with more than 1300 lichenized fungus taxa (inland and seashore species) is an attempt to encourage confident use of this tool to identify lichens encountered in this area.

Species of lichenicolous fungi as new in Central and Southeast Europe

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The intensity of collecting lichenicolous fungi has largely increased in Hungary during the last decade. Several localities were visited also in the Balkans. According to recent identifications more than 20 species are new for Hungary related to the species recorded in the online "Revised checklist of the Hungarian lichen-forming and lichenicolous fungi" by Lőkös and Farkas (2009). The group of formerly 56 lichenicolous species belonging to 39 genera is now represented up to 80 species. Our preliminary studies seem to justify that the diversity of (semi)natural steppe areas is much higher than anthropogenic, degraded habitats investigating species of lichenicolous fungi. It is due most probably to the unique climate, habitat and host populations. Further species are new to various countries or larger areas within Central and Southeast Europe. Several new records show that these organisms are undercollected and a careful research is necessary in the field. Supported by the Hungarian Scientific Research Fund OTKA 81232 and the Research Centre of Excellence 9878/2015/FEKUT.

Bacidia s. str. (Lecanorales, Ascomycota) in Russian Far East

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The genus *Bacidia* is widely distributed around the world. More than 60 species are described worldwide, while for Russia approximately 25 species are reported. This number is constantly changing, as some regions are still poorly investigated. Furthermore, because of their small size and inconspicuous appearance they are not yet collected sufficiently in most parts of Russia. The aim of the present study is to investigate the diversity of *Bacidia* s. str. in Far East of Russia. The material was collected in the western slope of the Sikhote-Alin and Bolshekhekhtsirsky Nature Reserve in August-September 2013. Seven species of *Bacidia* s. str. were found based on morphological analysis: *Bacidia arceutina* (Ach.) Arnold, *B. fraxinea* Lönnr., *B. friesiana* (Hepp) Körb., *B. rubella* (Hoffm.) A. Massal., *B. laurocerasi* (Delise ex Duby) Zahlbr., *B. polychroa* (Th.Fr.) Körb. and *B. suffusa* (Fr.) A. Schneid. Molecular studies using the ITS nrDNA region helped to delimit doubtful species. Further studies including additional material will complete our knowledge on this genus and their diversity in Far East.

Australian lichen type digitization and barcoding

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Type specimens are very valuable to taxonomists. Most herbaria have rather old collections, with type specimens more than 50–100 years old. Working with these ancient types is difficult, as they are fragile, often lack precise locality data and are not amenable to DNA sequencing. In the lichen collection of the Australian National Herbarium (CANB), there are 632 types of lichens: 548 of them (87%) were collected after 1980. It is quite exceptional for a herbarium to host such a recent collection of type material. Because it is possible to obtain good DNA extractions from a relatively small amount of material for recent specimens, we decided to attempt to provide a molecular barcode (the fungal marker ITS) for about 150 specimens collected after 2000. These 150 specimens were first digitized, then specimens with enough material were selected for DNA extractions. Various extraction protocols were used depending on the taxonomic group. The image data will be made available through the a public web interface and the molecular barcode will be published and made available in GenBank as part of the RefSeq Targeted Loci (RTL) database.

Miriquidica – yet another non-monophyletic lichen genus rich in cryptic species

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Miriquidica Hertel & Rambold comprises about 30 saxicolous, mainly alpine species worldwide. The genus was originally delimited by the presence of miriquidic acid in most of the species and by asci of the "Lecanora-type". The species are often difficult to identify without chemical and microscopical investigations. Although they are common rock lichens in some regions, many *Miriquidica* species remain poorly understood. We have collected *Miriquidica* extensively throughout Fennoscandia, over wide climatic, geographical and ecological gradients. We studied this, and additional material of available *Miriquidica* species and presumed close relatives, using TLC, microscopy, and multi-locus DNA-sequencing. We used maximum likelihood and Bayesian phylogenetic methods on alignments containing multiple accessions of most species. We have discovered several new species, many of them so-called cryptic. As such, *Miriquidica* falls into line of crustose lichens showing a high degree of cryptic speciation. Our results show that *Miriquidica*, as currently circumscribed is polyphyletic, i.e. some species are extraneous in the genus. After their transfer from *Miriquidica*, the genus remains paraphyletic, with species of *Protoparmelia*, *Lecanora*, *Lecidea* s.lat., and *Myochroidea* nested. We describe several new species and recombine others, in order to end up with a more natural circumscription of *Miriquidica*.

Excipulum Structure of *Opegrapha*, *Alyxoria* and *Zwackhia*

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On the basis of molecular results, several *Opegrapha* species have been assigned to other genera. The aim of this study was to investigate if there are differences in excipulum structure between *Alyxoria*, *Opegrapha* s. str. and *Zwackhia*. Microscopic examination of the excipulum of *Alyxoria culmigena*, *A. ochrocheila*, *A. varia*, *Opegrapha vulgata* (type species of *Opegrapha*), *Zwackhia soreidiifera* and *Z. viridis* was performed on 3–5 µm thick frozen sections. Small portions of the ascomata were frozen in water and cut with a freezing microtome. The sections were incubated with NaOCl (Klorin 1:10), and the progressive dissolution of the dark excipulum pigmentation was photographed continuously using a light microscope. Maximum dissolution time was about 50 minutes. A computer generated contrast enhancement of the hyphal walls was made with Adobe Photoshop. The molecular-based distinction between the genera *Alyxoria* and *Zwackhia* is supported by morphological differences. The excipulum hyphae of *Alyxoria* originate from the hypothecium while in *Zwackhia* they apparently originate from a layer below the hypothecium. Thus, our results indicate that excipulum structures can be used to distinguish these genera. For the morphological differentiation of *Opegrapha vulgata* and *Alyxoria* spp. more investigation is required.

On uncertain species of the genus *Ramalina* from Yakutia (North East Russia)

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Lichen species of the genus *Ramalina* of Yakutia have been revised based on the herbarium material (LE, SASY). Standard morphological, anatomical and chemical (HPLC) examinations were made in the laboratory. It was shown that one species of *Ramalina* found in the deltas of Lena and Kolyma rivers in the arctic zone of Yakutia corresponds well with the similar samples from Canadian Arctic (Delta of Mackenzie river). The examined specimens were previously determined as *Ramalina fraxinea* (L.) Ach., *R. fastigiata* (Pers.) Ach., *R. sinensis* Jatta and *Ramalina dilacerata* (Hoffm.) Hoffm. Further investigations in the herbarium of Helsinki University (H-Nyl, H-Ach) have shown that all these samples correspond to the original materials of *Ramalina fraxinea* var. *caliciformis* Nyl. and *Ramalina fraxinea* f. *tuberculata* Ach. (H-Ach 1841) described from Central Europe. The anatomical and morphological characters and ecology of this species are not the same as typical *R. fraxinea* (L.) Ach. The characters distinguishing these taxa are discussed.

Molecular phylogenetics and taxonomy of the lichen family Ramalinaceae

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The Ramalinaceae is a family of lichenized ascomycetes in the order Lecanorales. The family is globally distributed and comprises around 50 genera and 1000 species with considerable morphological variation. Generic boundaries of the Ramalinaceae were historically based primarily on growth form, ascospore septation, and ecological preferences. Recent molecular systematic investigations of subgroups indicate that the current taxonomy is at odds with evolutionary relationships. Tropical members of the family remain particularly understudied, including the large genus *Phyllopsora*. In the present study, we aim to identify clades in the Ramalinaceae that are supported by multiple sources of data (i.e. integrative taxonomy), and to revise the taxonomy accordingly. We have collected multi-locus DNA sequence data for genera or species that: (a) are currently included in the family, (b) have once been included but are now moved to other families, or (c) show striking morphological similarities with the Ramalinaceae despite being classified elsewhere. Our preliminary results corroborate that current taxonomy is in strong need of revisionary work. In particular, morphologically convergent evolution seems to be prominent in tropical members of the family. Based on our preliminary molecular phylogenetic hypothesis, we anticipate re-circumscriptions at several taxonomic levels in the Ramalinaceae.

Micarea submilliaria (Nyl.) Coppins new to Russia and Asia from Transbaikal Region

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Micarea submilliaria (Nyl.) Coppins was found during the expeditions to the Transbaikal Region in 2013-14. This species recorded for the first time from Russia and Asia. Russian specimens were growing on the soil with mosses in mountain tundra. World distribution. Europe: Poland, Finland, Norway, Sweden, Austria, Czech Republic, United Kingdom, Spain, Slovakia. Specimens examined: Russia, Kodar Ridge, Zolotoy brookvalley, 56°55'57" N, 117°36'51" E, alt. 1857 m, rocks near the waterfall with *Salix arctica* – *Rhododendron aureum* tundra, 6.VII.2013, TLC: alectorialic acid; 56°56'04.5" N, 117°37'17.8" E, alt. 1680 m, lichen – shrub tundra on north-western slope, 6.VII.2013; Sredniy Sakukan valley, 56°56'28.2" N, 117°36'55.3" E, alt. 1686 m, *Salix* sp. – herb-green moss community with creek on the right bank, 18.VI.2014; source of the Sredniy Sakukan river, 56°56'55.7" N, 117°38'02.0" E, alt. 1993 m, *Rhododendron aureum* – lichen tundra with large boulders, 56°57'59" N, 117°37'60" E, alt. 1925 m, 16.VI.2014; Tsarskiy Tron peak, shaded gorge with *Cetraria* tundra, 18.VI.2014. We are grateful to Dr. Zdeněk Palice (Institute of Botany CAS, Czech Republic), for the revision of the first specimens in the list; Dr. M.P. Andreev (BIN RAS, Russia) for the joint work in the expeditions. This work supported by the Russian Foundation for Basic Research (grants № 16-04-01488, 15-04-05971, 14-04-01411).

DNA barcoding of lichens, including biosystematics studies of the genera *Cladonia*, *Placynthium* and *Solenopsora*

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This project is a collaboration between the Masaryk University (Brno, Czech Republic) and the Norwegian University of Science and Technology (NTNU, Trondheim, Norway); and other institutions provided additional taxonomic expertise. During the project, we have DNA-barcoded at least 100 lichen species from Scandinavia and Central-Europe. This is the first attempt to DNA-barcode lichens in the Czech Republic. We use the barcode region (nrITS) to identify species complexes for further, more in depth investigations of species boundaries using a multi-locus phylogenetic approach. Our main focus is on the red-fruited *Cladonia* (Cocciferae, Cladoniaceae), the "lobate" *Placynthium* (Placynthiaceae), and *Solenopsora* (Leprocaulaceae). Several workshops have been organized in Norway and the Czech Republic, including excursions to Norwegian boreal rainforests and various biotopes in the western Carpathians (Slovakia). Knowledge transfer and international collaboration are important aspects of the project. The project is funded by Norway Grant (NF-CZ07-ICP-3-2102015)

Molecular systematics of the lichen genus *Ramalina* (Ramalinaceae) with an emphasis on the *Ramalina siliquosa* complex

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Lichens of the *Ramalina siliquosa* species complex dominate seashore cliffs in Europe, but their taxonomy has been vigorously debated for over a century. On most cliffs, they exhibit a bewildering zonation of chemotypes that resembles the classic zonation of organisms that occupy the littoral zone below. Do the chemotypes represent separate species, or infraspecific variation? To better understand the systematics of this group, sequences from three nuclear loci (ITS, RPB1 and RPB2) were obtained for 52 samples from the UK, Denmark, France and Iceland, including all major chemotypes. Maximum likelihood analysis of these sequences together with sequences from 20 other *Ramalina* species reveals that the complex comprises two phylogenetic species, each including multiple chemotypes. These two species correspond to the currently accepted taxonomy, i.e. *Ramalina cuspidata* and *Ramalina siliquosa*. A few of the samples do not fit this taxonomy due to incongruence of their medullary chemistry with their ITS sequence. Other results include close relationships between the following pairs of species: *R. almquistii* with *R. dilacerata*; *R. americana* with *R. intermedia*; and *R. farinacea* with *R. subfarinacea*. New chemotypes are reported for *R. culbersoniorum*. There is also a strongly supported clade of *Ramalina* species from the southeastern USA and Mexico.

Two new species and new records in the genus *Arthonia* from South Korea

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Arthonia zelkoviana Lee & Hur and *A. coreana* Lee & Hur are described as new species from South Korea. These new species are in the group of *A. punctiformis* Ach., so called the *Euarthonia* tribe in the subsection *Endoleuca*, based on the key characteristics of colorless or bright hypothecium and multi-cellular spores. *Arthonia zelkoviana* has white, epiphloedal thallus, brownish black, epruinose ascomata with a margin of bark tissue, and smaller ascospores in comparing with *A. punctiformis*. Particularly, *A. zelkoviana* consists of a green alga and this characteristic differs from other related *Arthonia* species such as *A. punctiformis*, *A. pinastri* Anzi and *A. glaucella* Nyl. Although *A. zelkoviana* is similar to *A. dispersa* (Schr.) Nyl. in white color of thallus, blackish ascomata and presence of a green photobiont, *A. zelkoviana* differs from the latter in 3-septation of ascospores and bigger size of them. *Arthonia coreana* has dull brownish, hypophloedal thallus without bleaching, and rounded or curved big ascomata in comparing with *A. punctiformis*. Especially, *A. coreana* represents only 4-septation of ascospores and the 4-septation is a distinctive characteristic differing from other *Arthonia* species. As new records, *Arthonia glaucella* and *A. pinastri* are new to Asia.

The lichen family Gomphillaceae in Brazil, with an assessment of its phylogenetic classification

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Ascomycota has the highest number of species within the kingdom Fungi, with about one third of these species being lichenized. A particular group of lichenized fungi are those that dwell on leaves of vascular plants, the so-called foliicolous lichens. Gomphillaceae is the most species-rich family of foliicolous lichens, but also contains species growing on other substrata, such as bark, rocks, and soil. Despite that the family features many morphological peculiarities, in particular its conidiomata, the hyphophores, the genus-level classification of Gomphillaceae remains unresolved. This study revises the diversity of foliicolous lichens in the main Brazilian biomes, with emphasis on Gomphillaceae, and makes a first attempt at assembling a molecular phylogeny using the mitochondrial small subunit rDNA marker (mtSSU), based on new collections made in areas of Caatinga Forest, Atlantic forest and Amazon forest. The relationships between the major biomes present in Brazil and the diversity and composition of foliicolous lichens and Gomphillaceae were also analyzed, suggesting that foliicolous taxa are most diverse in Amazon and Atlantic rain forest, whereas corticolous taxa, e.g. in the genus *Gyalideopsis*, are particularly diverse in the Cerrado.

Taxonomic study of *Aspicilia intermutans* and related species

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A poorly known saxicolous lichen *Aspicilia dominiana* (Megasporeaceae) has been described from the Czech Republic and it is recently known only from a few diabasic localities in this country. Morphologically similar species, which I have examined, are *A. intermutans* occurring especially in the Mediterranean and *A. epiglypta* occurring mostly in the north part of Europe. The main aim of this study was to find out if *A. dominiana* is a well defined species or if it is one of the above species. Additionally, I tried to describe the genetic variability of *A. intermutans* within its European distribution and to find out the phylogenetic position within Megasporeaceae. After the revision of herbarium material based on microscopic and chemical characteristics, I have found out that the taxon *A. dominiana* is identical with *A. intermutans*. The compliance of these taxa has been confirmed by molecular data from the sequencing of three genes nrITS, nrLSU and mtSSU. Therefore I propose to synonymize these two taxa. According to phylogenetic trees, *A. intermutans* is not closely related to any other species included in my analysis and it forms a new separate group with a high bootstrap support in Megasporeaceae.

A molecular-genetic reassessment of the phylogeny of the lichen genus *Icmadophila* Trevis

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Sequences of the Internal Transcribed Spacer region (ITS), Large Subunit of nuclear and mitochondrial ribosomal DNA were generated for all five species currently placed in *Icmadophila*, and additional members of Icmadophilaceae. Results strongly indicate that *Icmadophila* consists of only three species: the type *I. ericetorum* plus *I. aversa* and *I. japonica*. For *I. splachnirima* the genus *Knightiella* Müll. Arg. needs to be resurrected, and *I. eucalypti* belongs in a genus of its own, for which the new genus *Knightiellastrum* is proposed. A second species of *Knightiellastrum* from Queensland, Australia, is described.

Discovery of ascomata in the *Siphula decumbens* group, and its placement in a separate genus

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Fertile specimens of *Siphula decumbens* and *Siphula fastigiata* were discovered for the first time at several New Zealand localities. Apothecial characters concur with the earlier placement of these species in the family Icmadophilaceae. Molecular-genetic comparison of DNA extracts from thalline and apothecial tissues excludes the possibility that the ascomata belong to a lichenicolous fungus. Apothecial characters of *S. decumbens* and *S. fastigiata* are indistinguishable. Initial genetic comparison of samples of both taxa from New Zealand and Tasmania supports the hypothesis that both belong to the same species with two chemotypes (containing thamnolic acid or baeomycesic and squamaric acids), analogous to what is found in *Thamnolia vermicularis*. The generic position of the *Siphula decumbens* group is revised. The placement of this group in a separate new genus is proposed, based on its remote position in molecular phylogenetic analyses relative to *Siphula ceratites*, the generitype. Apart from the presence of ascocarps, the new generic segregate differs from *Siphula* s. str. by its flattened lobes, the presence of well-developed root-like rhizines and the lack of a true cortex.

PhyloKey: A novel method to rapidly and reliably identify species in complex, species-rich genera

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Foliose macrolichens in the Basidiomycota genus *Cora* (Agaricales: Hygrophoraceae) were long recognized as a single species, *Cora pavonia* (or *Dictyonema glabratum*). Molecular sequence data of the ITS barcoding locus have shown that *Cora* contains hundreds of species, with approximately 100 formally recognized, over 180 delimited phylogenetically, and over 450 predicted to exist. The paucity of phenotypic characters, some of which are best observed in the field, poses a challenge to correct species identification using traditional keys, due to the high likelihood of misidentifications. Interactive keys partly mitigate this problem, but there is not objective measure of the reliability of identification results. Here, we present a novel identification method, named PhyloKey, based on the technique of morphology-based phylogenetic binning. The method uses a molecular reference tree and a set of phenotypic characters for each species, including substrate ecology and geographic distribution. Specimens to be identified are then scored for phenotypic character states and subjected to phylogenetic binning, which for each sample will result in placement in particular clades, with associated bootstrap support. While the observation of phenotypic characters is similar to other identification methods, the phylogenetic binning is comparatively fast and immediately provides a measure of confidence of the results.

The classification of lichen fungi: Assessment of completeness and updated statistics on class-, order-, family- and genus-level species richness

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The past two decades have seen dramatic changes in the classification of fungi, including lichenized forms. Although fungal classifications are periodically updated in various outlets, including printed publications, such as the 2007 AFTOL paper, and online classification sites, such as the Outline of the Ascomycota and the recent Syllabus (Part Ascomycota), presently no updated classification exists that focuses on lichenized fungi in both the Ascomycota and Basidiomycota. We close this gap by assembling a classification of all lichen fungi down to genus level, for a periodically updated series in *The Bryologist*. The classification is accompanied by a cartoon tree of the higher fungi highlighting orders that include lichenized lineages. We also provide updated statistics on species numbers of lichenized fungi at the class, order, family, and genus level, to offer a consistent reference for citations of species richness in various contexts.

Conserved genomic collinearity in Pezizomycotina to develop broadly applicable fast-evolving markers to resolve species complexes: a case study in *Peltigera*

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Highly variable regions that are homologous and can be amplified across broad taxonomic groups provide ideal markers for comparative studies of populations and species complexes. Fast evolving intergenic spacers in syntenic regions of genomes, where collinearity (loci in the same order on the same chromosome) is conserved, have these characteristics. We conducted a synteny analysis on genomes from different classes within Pezizomycotina and screened for Collinear Orthologous Regions (COR). As a proof of concept, we selected three promising highly variable intergenic spacer regions of about 600-1200 bp that we named COR1b, COR3 and COR16. The flanking genes of the intergenic spacer COR3 and COR16 are conserved and syntenic in several genomes across Lecanoromycetes and Eurotiomycetes. Flanking genes of COR16 are also conserved and syntenic in one lichinomycete genome, i.e., across three fungal classes, while COR1b might be specific to the genus *Peltigera*. We developed *Peltigera*-specific primers for these three new loci and compared the phylogenetic resolution and internodal support brought by these markers inside *Peltigera*. We show that each COR locus provides a better resolution than widely used loci such as ITS and β -tubulin. We delimited species across the genus based on an 8-locus dataset comprising these three new markers.

Molecular analyses uncover the phylogenetic position of the lichenized hyphomycetous genus *Cheiromycina*

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The genus *Cheiromycina* represents one of the few genera of lichenized hyphomycetes for which no sexual reproductive stages are known. The genus includes corticolous (eventually lignicolous) species which have been described from boreal to temperate regions of Europe. *Cheiromycina* is characterized by a non-corticated thallus containing chlorococcoid photobiont, nearly immersed in the bark and presenting powdery unpigmented sporodochia. In the type species *C. flabelliformis*, and the species *C. petri*, the multicellular conidia are peculiarly dichotomously branched. As the phylogenetic relationships of lichenized hyphomycetes are still largely unknown, in this work we set out to explore the phylogenetic placement of *Cheiromycina*. The two species *C. flabelliformis* and *C. petri* were considered and molecular data were obtained for three loci (nuSSU, nuLSU and mtSSU) from fresh specimens collected in different countries. A preliminary sequence identity analysis by blast search in GenBank reveals that they both are recognized within Lecanoromycetes. The phylogenetic placement and relationships with closely related taxa are here discussed.

Preliminary checklist of the lichens from Ningxia of Northwest of China

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Although lichens are an important vegetation feature in Ningxia of Northwest of China, there has been no attempt to compile a local list of lichen species. The currently known lichen flora was determined by a number of surveys conducted by the author since 2010, supplemented by detailed literature survey. Within the 800 samples collected, 109 lichen taxa are recognized, six taxa are new records for China.

The lichen genus *Arthothelium* in South Korea

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The first investigation of the lichen genus *Arthothelium* on the South Korea is presented. *Arthothelium* is close to *Arthonia* based on ascospore septation as muriform to transversely septate. *Arthothelium* has largely been studied in India and Europe while Asia countries including Korea are still unexplored. *Arthothelium* is a crustose lichen immersed and developed in the uppermost bark layers, ascomata irregular or round, surface level with thallus, 8-spored and muriform. We reported one known species of *A. ruanum* and 2 new records of *A. atro-olivaceum* and *A. indicum* in Korea. *Arthothelium ruanum* is most dominant species among them and *Arthothelium* is widely distributed in South Korea. Phylogenetic analysis of Korean *Arthothelium* was conducted using three molecular loci (mtSSU, nuLSU and RPB2). Morphological descriptions and artificial key of Korean *Arthothelium* are given in the present study.

Relationships between crustose and vagrant species of *Circinaria*

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The name *Aspicilia* "desertorum" was used for crustose forms of *Circinaria* but it is currently considered illegitimate. Five forms and varieties of this species were described by K. Mereschkowsky. He suggested that crusts and vagrant thalli represented different species; however some researchers merge them into a single species, which vary as a result of microclimatic conditions. The identity of crustose forms and their affinity to erratic or vagrant *Circinaria* are still uncertain. Specimens of crustose and dwarf-fruticose *Circinaria* from Urals, Altai and Kazakhstan were studied morphologically and genetically (ITS and mtSSU) and were compared with previous data on crustose, erratic and vagrant species. Crustose specimens vary in thalline morphology and conidial length. *Circinaria* with long conidia appeared to be related to *C. affinis*, while specimens with short conidia either clustered into groups related to other short-conidial species such as "Aspicilia" *transbaicalica* s.l., *C. fruticulosa* and *C. gyrosa*, or formed separate clades. Our preliminary data suggest that some *Circinaria* crusts represent separate species, while others are "neotenic" stages of erratic or vagrant species. The study is partly supported by RFBR (project 15-04-05971).

Phylogenetic placement of the lichenicolous genus *Epicladonia*

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The anamorphic genus of lichenicolous fungi *Epicladonia* comprises four species, three of which are known to grow on *Cladonia* and one on *Pleopsidium* (Hawkworth 1981, Ihlen & Wedin 2005). Up to date the phylogenetic relationships of this genus of lichenicolous fungi, included in Ascomycota, are unknown (Lawrey & Diederich 2015). The aims of this study were: 1) to determine the phylogenetic position of *Epicladonia* within Ascomycota, 2) to test the monophyly of the genus *Epicladonia* and the relationships between its species. A phylogenetic analysis was carried out based on four loci: LSU rDNA, SSU rDNA, mtSSU and ITS rDNA. In this analysis, the three species that have the genus *Cladonia* as a host were included: *E. sanstedei* (the generic type species), *E. stenospora* and *E. simplex*. The analyses revealed that the genus is polyphyletic. *Epicladonia stenospora* and *E. simplex* formed a well supported clade within the order Lecanorales (Lecanoromycetes), while *E. sanstedei* was placed within the class Leotiomycetes. The three species studied were resolved as monophyletic.

Two new species in the *Micarea prasina* group in Europe, supported by morphological, chemical and molecular data

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Detailed morphological and chemical studies informed by molecular inferences with mtSSU as a marker unveiled two new species of *Micarea* in Europe: *M. herbarum* sp. nov. from the Netherlands and Poland and *M. meridionalis* sp. nov. from Portugal and Italy. Both belong to the core group of the genus, namely the *M. prasina* group. Description of both species and detailed photographs are presented, as well as a phylogenetic tree of the genus *Micarea* including several new accessions.

The genus *Bunodophoron* (Sphaerophoraceae, Lecanoromycetes) in the Neotropics

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Bunodophoron has been studied in several areas of the southern hemisphere, including the Tropics. However, neotropical species of *Bunodophoron* (*B. melanocarpum* and *B. formosanum*) are not well known. The aim of this study was to look at the delimitation of species of *Bunodophoron* in the Neotropics, where the genus occur growing on the ground in the paramos, and as epiphytes in the upper mountain rainforests. The species delimitation study utilized molecular phylogenetic analysis of three molecular markers, morphology and chemistry. We based the study on fresh material collected in different regions from Colombia and Ecuador; Antioquia, Boyacá, Caldas, Cauca, Cundinamarca, Huila, Nariño, Risaralda, Tolima and Valle del Cauca, together with additional samples from other neotropical areas. These results suggest that, in the Neotropics, *Bunodophoron* includes at least five species, which will be discussed and illustrated on the poster.

Phylogenetical study of selected taxa in *Physconia muscigena* (Ach.) Poelt group

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The principal goal of our study is to find if ecologically and chemically different populations of lichens in the *Physconia muscigena* (Ach.) Poelt group belong to several species or a single one. This study focused on the molecular and chemical investigations of mostly European and Canadian populations. We used sequence data from three genes (ITS rDNA, mtSSU rDNA and EF 1 α) for the reconstruction of phylogenetic trees. We investigate phylogenetic relationships among the closely related species *P. muscigena*, *P. bayeri*, *P. rossica*, and *P. isidiomuscigena*. Also, we want to detect any possible geographical or ecological trends among chemotypes and haplotypes. As an additional goal we checked the recent localities of *P. muscigena* in the Czech Republic for valorizing its conservation status. Preliminary results show that: 1) Sequenced data of ITS rDNA and EF 1 α showed high intraspecific variability in *P. muscigena* samples; 2) The genetic variability correlate neither with geographical distribution nor thallus chemistry; 3) The most useful marker is EF 1 α , but amplification from herbarium specimens is very problematic; 4) *Physconia muscigena* has only three recent localities in Czech Republic.

Chaenotheca species inhabiting fruitbodies of *Trichaptum* spp. (Hymenochaetales)

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Chaenotheca specimens found to grow on fruitbodies of *Trichaptum abietinum* and *T. fuscoviolaceum* in Estonia are externally similar to wood-dwelling *C. brunneola*. We analysed their rDNA ITS sequences plus five morpho-anatomical and pigmentation characters, and compared those with the characters of *C. brunneola* and of recently described *C. balsamconensis* which also inhabits *Trichaptum* fruitbodies. The obtained sequences, including those from *C. balsamconensis*, formed a supported clade distinct from the *C. brunneola* as well as from the rest of 18 analysed *Chaenotheca* species. The *Trichaptum*-clade included two lineages, one of them corresponded to *C. balsamconensis*. The morphological character that differentiated wood-inhabiting *C. brunneola* and Estonian *Trichaptum*-inhabiting specimens was the length of the stalks being somewhat shorter in *Trichaptum*-dwelling specimens. Considering that the genus *Trichaptum* is widespread in Europe, we expect that *Chaenotheca* sp. growing on them is frequent and widespread also.

Using the fungal DNA barcode to locate taxonomic problems – an example from *Rhizocarpon*

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Rhizocarpon DC. is a cosmopolitan genus growing mainly on siliceous rock, with a centre of diversity in the boreal to arctic/alpine zones of the Northern Hemisphere. Among c. 350 described species, c. 125 are currently accepted, c. 175 regarded as well-established synonyms, and c. 50 as being of unknown status. Several species are based on subtle morphological or anatomical differences, and species delimitations based on more objective characters are desirable. In cooperation with the Norwegian Barcode of Life (NorBOL) project, which aims at 'DNA barcoding' all Norwegian lichens, we work towards obtaining a set of ITS sequences of all currently accepted *Rhizocarpon* species. The fungal DNA barcode marker (ITS) has been readily obtainable, even from material some decades old, and provides good resolution at the species level in *Rhizocarpon*. We have so far produced c. 250 ITS sequences of 50 species. We use ITS sequence clusters to identify cases of non-monophyly or 'cryptic species' for more in depth studies, such as coalescent-based species delimitation using multiple unlinked genetic loci. Preliminary results show that previously suspected heterogeneity is largely corroborated, e.g. in the *R. badioatrum* complex, but also that unexpected genetic heterogeneity is frequent, e.g. in *R. eupetraeum* and *R. geminatum*.

Synergy of Phylogeny and Chemotaxonomy in *Lobaria* species from Sabah

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Lichens of the genus *Lobaria* were sampled from three mountains in the state of Sabah (Malaysia / NE Borneo). Specimens were identified by morphological features, chemical characters and molecular barcoding with two markers (ITS, mtSSU). Detailed chemical profiling was carried out based on 1) Thin Layer Chromatography, 2) High Performance Liquid Chromatography, and 3) LCMS IT TOF MS. Our collections confirm the chemical distinction between the *Ricasolia* complex and the *L. pulmonaria* group. Detailed results will be presented as high resolution MS data. DNA barcoding revealed difficulties in the naming of Sabahan *Lobaria*, due to the presence of undescribed taxa particularly within the *L. retigera* group. Resolution and support of ITS and mtSSU based phylogenies were good for some of the taxa within the *Lobaria retigera* group and *L. discolor* but insufficient for a clade which included our *L. isidiophora* collections. Our results provide evidence for the need for DNA-barcoding in studies of chemical variation in SE-Asian *Lobaria* to avoid confusion of currently undescribed new species with established taxa, but also shows limitations of ITS and mtSSU data alone. Published data on chemical variation in *Lobaria* species need to be revised in light of results based on specimens that are DNA-barcoded.

Two new species of the lichen genus *Buellia* (Caliciaceae) from Japan

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The cosmopolitan genus *Buellia* De Not. with ca. 400 species, is generally characterized by crustose thallus, lecidein apothecia with black disc, dark pigmentation of hypothecium and brown septate ascospores. Our recent investigation on corticolous species of *Buellia* s.l. in Japan revealed the occurrence of two new species, *Buellia* sp1 and sp2. These two species share common morphological (whitish, smooth to rimose thallus; adnate apothecia; flat, epruinose disc; dispersa-type proper exciple; numerous ascospores per ascus; *Buellia*-type ascospores) and chemical (presence of fumarprotocetraric acid and atranorin) characters. They are clearly distinguishable from the previously described species by ascospores number and metabolites. They differ from each other in the number of ascospores per ascus and character of asci. *Buellia* sp1 has 20–64 ascospores within an ascus while *Buellia* sp2 produces 8–36, and only the latter has brownish "overmatured asci". A phylogenetic analysis based on nrDNA ITS region confirms that they should be recognised as two different species. The phylogenetic tree further suggests that they are closely related to each other and also have a relationship with *B. erubescens*, *B. griseovirens* and *B. subdisciformis* with high bootstrap values.

Species-delimitations in the *Toninia sedifolia* group

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Toninia sedifolia is a well-known and widely distributed lichen occurring in all continents except Antarctica. It is an important element in biological soil crusts and one of the components in the classic "Bunte Erdflechtengesellschaft" (the community of colored soil lichens), and frequently figures in surveys and other investigations. The species is morphologically variable and there are about a dozen synonymous epithets at the species level. Timdal taxonomically revised the genus *Toninia* in 1991, but the species concepts have not been tested by means of molecular methods. In this project, we investigate the variation in *Toninia sedifolia* and closely related species using morphology, chemistry and DNA sequence data from three genetic markers (nuITS + partial nuLSU rDNA, mtSSU rDNA and MCM7). The results show that the current concept of *Toninia sedifolia* needs to be revised and we recognize at least two distinct species occurring in Europe. Several other species recognized by Timdal but often overlooked and perhaps not widely recognized, e.g. *T. physaroides* and *T. opuntioides* are, although morphologically similar to *T. sedifolia*, clearly distinct species.

Revisional study on the genus *Cryptothecia*, Arthoniaceae from South Korea

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Arthoniaceae is one of the least explored lichen groups in South Korea. Although main genera such as *Arthonia* and *Arthothelium* have been studied, *Cryptothecia* as a minor group was much less surveyed and only one species is recorded. The members of *Cryptothecia* usually grow on rough bark in shade and moist subtropical forest. Generally, the substrata are mainly bark, wood and leaf, while in rare cases it also inhabits rock. *Cryptothecia subnidulans* Stirt. was collected in Jeju Island, South Korea, which is well known for its subtropical climate. Interestingly, one specimen (*Cryptothecia* cf. *scripta*) collected in Namcheon Valley, South Korea in 2015 represents characteristics similar to *Cryptothecia scripta* in morphology and chemistry. In specific, *Cryptothecia* cf. *scripta* has thallus crustose, adnate in the substratum, cortex absent, dull greenish grey, often byssoid, isidia-like structure absent, soredia absent, globose granules spread on the thallus, thallus lacking well-developed ascomata, and well-developed prothallus present. Chemically it contains gyrophoric acid. Although above features correspond to *C. scripta*, *Cryptothecia* cf. *scripta* grows on rock. This lichen will be clarified by phylogenetic analysis employing DNA sequence data of mtSSU and RPB2, in comparing with other *Cryptothecia* species collected from other countries in Southeast Asia.

A new corticolous species of the genus *Megaspora* from Armenia

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The genus *Megaspora* has two accepted species, occurring in arctic-alpine and in temperate to Mediterranean regions. The type species *M. verrucosa* is cosmopolitan, but the second species, *M. rimisorediata*, is only known from South West Asia (Iran and Armenia). The genus is special in the family Megasporaceae because the species are not saxicolous but corticolous or muscicolous. During the international lichenological excursion to Armenia in 2015 we collected a conspicuous, sorediate crustose lichen on the bark of *Juniperus polycarpos* trees in Armenia. In the field we did not observe ascomata and its affinities were unclear. Back in the lab under the dissecting microscope, small immersed apothecia were found on the thallus, with a greenish hymenium and large, thin-walled ascospores, which suggest that it is a further corticolous member of the Megasporaceae. A molecular analysis based on nrITS sequences is being done, after preliminary results suggested that the putative new species is clustered within the *Megaspora* clade as sister species to *M. rimisorediata*. The center of diversity of the genus *Megaspora* appears to be in Armenia, where all three known species occur.

Phytogeographical analysis of the Georgian Cladoniaceae

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The knowledge on the diversity of the lichen family Cladoniaceae in Georgia was compiled from the dispersed records in floristic studies (Inashvili & Batsatsashvili 2010) and through updating the identifications of the largest herbarium collection in Tbilisi (TBI). This contribution summarizes the results of our study of 1273 specimens housed at TBI and some new collections made together in the field in 2015 along the Greater Caucasus Range in Georgia. A comprehensive list of 41 species of the family and a short phytogeographical analysis is presented. Georgia is included in the Caucasian and the Euxine Provinces of the Eurosiberian Region and it is an important biological crossroads region in the temperate zone of the Northern Hemisphere showing great geological and climatic contrasts (Nakhutsrishvili 2013). Most of the species grow in the Greater Caucasus Range, while the Lesser Caucasus Range shows an important impoverishment. Within the analyzed species approximately one third are distributed in the West Caucasian Subprovince, while a second third are restricted to the East Caucasian Subprovince; the rest being indifferent as to the phytogeographic position. Financial support from the project CGL2013-41839-P, Ministry of Economy and Competitiveness, Spain.

Synopsis of the genus *Cladonia* in Greece

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In the framework of the project with the Cladoniaceae family in the Mediterranean area of Eurasia, a Grecian synopsis of the genus *Cladonia* is presented. Although there are many poorly explored areas, with the bibliographic examination of diverse floristic publications (Abbot 2009, Sipman & Ahti 2011, Linda in Arkadia 2013) and the results of new collections made in the field in 2015 along the NE of Greece (E of Macedonia and Thrace) the distributional areas of 21 species is enlarged. *C. conista*, *C. dimorpha*, *C. subturgida* and *C. subulata* are new records to Greece getting up to 42 recognized species. Also there were found several chemotypes in *C. furcata*, *C. rangiformis* and *C. symphycarpa*. *Cladonia borealis*, *C. cariosa*, *C. ciliata*, *C. coccifera*, *C. crispata* var. *ceptrariiformis*, *C. floerkeana*, *C. graeca*, *C. parasitica*, *C. phyllophora*, *C. prolifica*, *C. rei* and *C. squamosa* are very rare encountered and have a preferential northern distribution, mainly outside the mediterranean climate areas, while *C. fimbriata*, *C. foliacea*, *C. furcata*, *C. pocillum*, *C. pyxidata* and *C. rangiformis* are the commonest species and widely distributed. Financial support from the project CGL2013-41839-P, Ministry of Economy and Competitiveness, Spain.

New results on the genus *Cladonia* in Hungary

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Hungary is located in the Pannonian Basin of the Carpathian-Pannonian Subprovince (Rivas-Martínez 2005) of the Eurosiberian Region, and it is surrounded by higher mountain ranges of the Alps, the Dinarics and the Carpathians, which determine important climate variations in the country. The knowledge of the Hungarian Cladoniaceae was compiled by Verseghy (1994) and shows 44 *Cladonia* and one *Pycnothelia* species. After the results of new collections made together in the field in 2015 along the southwestern part of Hungary, the list is enlarged with *C. cervicornis*, *C. grayi* and *C. humilis*, which are new records to Hungary. The secondary metabolism of 274 samples of 24 species was studied. Different chemotypes in *C. furcata* and *C. rangiformis* were found. Financial support from the project CGL2013-41839-P, Ministry of Economy and Competitiveness, Spain.

The diagnostic characteristics are highly homoplasious used in *Cladonia gracilis* and *Cladonia cornuta*

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The genus *Cladonia*, more than 400 species hitherto have been documented, was traditionally classified into 7 taxonomic sections by morphology. However, the taxonomical classification is not well accord with that of molecular phylogenetic research. The genus has high morphological diversity, yet there has not been a coherent agreement on the delimitation of species. The *Cladonia gracilis* group and allies in the section *Cladonia* show an extreme phenotypic variety. *Cladonia gracilis* and *Cladonia cornuta* which are members of the *C. gracilis* group have been identified by variable characteristics. This study deals with the taxonomic problem between *C. gracilis* and *C. cornuta* by confirming the consistent phenotypic characteristics again with molecular phylogeny at species level. About 150 specimen were analyzed by 36 morphological and chemical characteristics using the DNA sequences with three loci (ITS rDNA, mtSSU and LSU rDNA). Specimen were collected from various regions covering bipolar areas and Korea. Phenotypic data were analyzed with several statistical methods. The study indicates that the homogeneous clade did not form in these species at species level. The results show no clear distinction between the two species in terms of phenotypic characteristics. The characteristics used for classical diagnosis may be highly homoplasious.

Towards a Red List of lichens in Spain and Portugal

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Many species of lichen-forming fungi are currently threatened by habitat loss, pollution, and climate change. Red Lists represent an important tool for conservation strategies of species and their habitats. To date, no Red List of these organisms is available in Spain and Portugal. Recently, the Spanish Lichen Society (SEL) launched an initiative to develop the first Red List of lichen-forming and lichenicolous fungi in Spain and Portugal (including Balearic and Canary Islands in the former, and Azores and Madeira archipelagos in the later). Twenty five lichenologists are so far involved in the working group. Using the Checklist of the Iberian Peninsula as well as regional inventories for the Canary Islands and Azores as starting point, 288 species have been proposed as candidates for evaluation (217 for Spain and 71 for Portugal). During the first year, 114 species (Spain: 82, Portugal: 32) have been chosen to be documented and evaluated according to IUCN criteria. Species considered extinct, occurring in highly declining habitats and endemics will be prioritised. Examples of the first documented species and the workflow used in this initiative are provided.

Searching for rare and overlooked lichens in Britain

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The UK is perhaps the best-studied country in the world for its lichens, but we still have much to learn. The British Lichen Society recording scheme has a database of around 1.5 million occurrence records, and one of its many benefits is the ability to analyse data to support conservation activities. In partnership with the BLS, Kew is organising a series of targeted surveys for rare lichens and fungi, funded by the Esmée Fairbairn Foundation. The aim is to resurvey known populations of species currently considered to have very restricted distributions, to establish their current status. Additionally, searches will be made for new sites, guided by enhanced knowledge of the original populations. We currently have a target list of around 30 species of lichens and lichenicolous fungi, distributed throughout the entire nation. Examples include taxa possibly extinct in the UK such as *Melanelixia subargentifera*, and the lichen parasite *Dacampia rhizocarpicola* that is known globally only as a single collection that now contains only one and a half perithecia. An early success is *Lichenochora epifulgens* (a parasite of *Gyalolechia fulgens*) which is now known from a much larger population in Cornwall in addition to its original site in Pembrokeshire.

Epiphytic Lichen Conservation in Armenia

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Armenia is located in the Southern Caucasus, which is globally recognized as a biodiversity "hotspot". Currently 612 taxa of lichenized and lichenicolous fungi are known from Armenia. The total cover of the forests of Armenia is estimated at about 7–8 % of the total area. Unfortunately, the conservation of epiphytic lichens is not included in the forest management plans and key habitats such as old-growth stands are often actively managed for timber. Our research aimed at an inventory of the epiphytic lichen diversity of protected forest areas and the evaluation of the conservation status of several taxa for inclusion in the Red Book of Armenia, a valuable tool for preserving biodiversity outside of protected areas. Its precursor, the Red Book of the USSR, lists only 3 lichen species from Armenia. Currently, the Red Book of Armenia does not include threatened species of lichens. We have assessed 16 epiphytic lichen species, *Acrocordia cavata*, *Anaptychia roemeri*, *Bacidia polychroa*, *Buellia erubescens*, *Gyalecta truncigena*, *Leptogium hildenbrandii*, *Megaspora rimisorediata*, *Melaspilea urceolata*, *Nephroma parile*, *Ochrolechia pallescens*, *Pertusaria constricta*, *Pertusaria trachythallina*, *Ramalina panizzei*, *Tornabea scutellifera*, *Usnea florida*, *Teloschistes chrysophthalmus*, and propose these for inclusion in the upcoming edition of the Red Book of Armenia.

How to explain to local stakeholders that forest habitats colonized by *Lobaria* need protection?

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Lobaria pulmonaria has suffered a general decline throughout Europe due to air pollution and intensive forest management in the past. Currently it is red-listed in several European countries. Recently, a large population of *L. pulmonaria* (hundreds of fertile thalli) has been depleted and endangered by wood cutting in an oak wood stand in Central Italy. The stand – a local hotspot, is a core area for numerous other rare lichens. In parallel with the progress of the cutting, meanwhile saving as much material as possible, we estimated the overall distribution of the population, impact of cutting on biodiversity loss, depletion of biomass and loss of fertile thalli, whose development requires more than 30 years in habitats under stable ecological conditions. We believe that studying the damage endured by the ecological continuity of this population will contribute to enhance future protection practices. Actually, in order to mitigate the damage in unprotected forests, the sensitivity of owners, education and training of wood cutters, verification of logging by the forest national service can all contribute to responsive and responsible forest management at local level. However, to finally prevent similar situations, *L. pulmonaria* should be formally recognized as protected species also in Italy.

Ignored crown jewels: Diversity and red-listed species of lichens and bryophytes on trees

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Tree crowns typically cover the vast majority of the surface area of trees, but they are rarely considered in diversity surveys of epiphytic bryophytes and lichens. We assessed the number of bryophyte and lichen species on stems and in crowns of 80 sycamore trees at six sites in the Northern Alps. The total number of species detected per tree ranged from 25 to 67 for lichens and from 13 to 60 for bryophytes. At the tree level, over 60% of lichen species and 30% of bryophyte species were recorded only in the crown. Considering all sampled trees together, 34% of lichen species, compared to only 4% of bryophyte species, were never recorded on the stem. Twenty-nine out of 39 red-listed lichen species and five out of 10 red-listed bryophyte species were more frequent in crowns. Our findings highlight the importance of tree crowns for species richness and their importance as habitat of red-listed species of epiphytic lichens and bryophytes. The study demonstrates that tree crowns need to be considered in research on these species, especially in biodiversity surveys and in conservation tasks involving lichens.

New lichen and moss garden in the heart of Helsinki

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Cryptogams have received little attention in living collections of botanic gardens with the exception of traditional Japanese moss gardens. We designed one of the world's first lichen and moss garden in the middle of Kaisaniemi botanic garden in Helsinki in order to demonstrate ecology and taxonomy of lichens and mosses growing on different substrata. Moreover, pilot experiments on ex situ conservation of cryptogams are carried out. In connection with the actual garden there is a trail displaying spontaneous lichen and moss flora growing in the area. The lichen garden includes two separate sub-gardens with contrasting exposure to sunlight, whereas the moss area is shady as a whole. Cryptogams growing on stones, wood and soil are brought to the garden from several locations in Southern Finland. Both calcareous and siliceous rocks are included to support higher diversity of epilithic species. Including lichens and bryophytes into living collections of botanic gardens is a way to emphasize their role in nature and improve the general knowledge of these often overlooked groups. The lichen and moss garden is constructed in 2016 and will be inaugurated in August. We expect this special garden to have high possibilities in fulfilling its scientific and educational aims.

Lichen conservation in Latvia: present state and problems

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Though lichens make one of the poorly studied organism groups in Latvia, over 40 species are employed as indicators of biodiversity-rich habitats. Most of these lichens are protected by law in the country, though data on their distribution and ecology are very sparse. Red lists in Latvia consist of 3 parts with different impact on lichen conservation: Red Data Book (RDB) and two official legislative lists (LL). RDB species list is meant only for publicizing decreasing biodiversity and promoting conservation issues among wider public, meanwhile LL deal with implementation of the actual conservation. Latvian LL is not actualized frequently enough; therefore some recently re-found extremely vulnerable species (e.g. *Lobaria amplissima*) are left out of protection system. Several entire genera are included in LL with some including also not threatened species (e.g. *Collema*) and species with different ecological requirements which adds confusion to the conservation system. Therefore main tasks for the closest future are following: 1) harmonization of the existing Latvian Red lists; 2) detailed analysis of all known lichen distribution data and comparison with distribution in Estonia and Lithuania; 3) increased efforts in obtaining new data on species distribution.

Geosites of Lithuania as refuges for lichen diversity

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Lithuanian lichen flora is notoriously poor in rock-dwellers: of 752 species of lichens and allied fungi, known at present in the country, only 144 are mostly confined to stone substrata. Five glaciations in Lithuania left behind moraine tills, erratic boulders and boulder fields that are protected as natural monuments. Outcrops and quarries of Devonian dolomites and gypsum, Permian limestones and Jurassic sandstones are sparse in Lithuania and many are protected, too. A part of geosites is influenced by agriculture, or is overgrown and shaded, therefore not suitable for lichens. Hence the scarcity of rock-inhabiting species in Lithuanian lichen flora and the reason why eight saxicolous lichens (some not uncommon in nearby countries) are included into the Red Data Book of the country. Protection of the rare saxicolous lichens generally coincides well with protection measures for the geosites. Though conservation conflicts arise even when protecting different species or groups of biota, not to mention conservation of bio- versus geo-diversity, most of the measures for the geoheritage protection in Lithuania are also suitable for saxicolous lichens. In such sites, protection status and measures should be negotiated by bio- and geoscientists, and such concerted efforts may improve legal basis for bio- and geo-diversity protection.

Tropical lichens and edible fungi from the temperate forest of Huitzilac, Morelos, part of the Biological Corridor Chichinautzin, Mexico

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The Biological Corridor Chichinautzin is a natural protected area, including the national parks of Lagunas de Zempoala and Tepozteco. The corridor is of vital importance for the water supply, for species conservation and for non-timber products that support the economy of the people living in the area. The principal goal of this study was to inventory the species composition of lichens and edible fungi from the temperate forest of Huitzilac, Morelos Mexico. Sampling was opportunistic and non-quantitative, on all available substrates. Preliminary results revealed 50 species of lichens and 23 species of edible fungi. The lichens belonged to eight families and 24 genera. Parmeliaceae had the highest number of species, including *Melanohalea mexicana*, an endemic species for Mexico. On the other hand, edible fungi belonged to six families and 15 genera. Agaricaceae had the highest number of species, including threatened species such as *Morchella conica*, *M. angusticeps* and *Boletus edulis*, species with special protection status like *Cantharellus cibarius* and species with special permission to be collected like *Amanita caesarea*. Our results show that the Biological Corridor Chichinautzin harbors species important to the conservation of the ecosystem and the traditional knowledge.

Growth model of *Parmotrema tinctorum* in the dry dipterocarp forest, Thailand

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The lichen *Parmotrema tinctorum* is widely distributed in Thailand, with potential to be utilized for several purposes. Dry dipterocarp forest (DDF) is one the favorite habitats for this lichen. This study aimed to develop a growth model and construct a growth curve of *P. tinctorum* that enable us to estimate age, growth rate and lifespan during thallus development. Expansions of fifty five thalli with diameters ranged from 1.51 – 17.5 cm were measured every season during July 2013 – April 2015 in the DDF at Khao Yai National Park, Thailand. It showed that this lichen had the highest growth rate during rainy season. Growth model was developed from the growth rate of each thallus size, and the growth curve was developed from a Non-linear regression equation. It illustrated that the thallus achieved the highest growth rate, or log phase, when thallus diameters were 5-30 cm. As such, it could be estimated that the age of the 32 cm largest thallus, observed in this study, is approximately 50 years old. However, the growth models of this lichen in different ecosystems need further specific monitoring to improve information regarding the influence of environmental factors over life and development of the living entity.

Growth rates of *Parmotrema tinctorum* on different artificial substrates and aspect orientation in Thailand

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The lichen *Parmotrema tinctorum* has been used for biomonitoring of air pollution and silk dying in Thailand. Enhancing its production is necessary to sustainably utilize this lichen. This study observed the growth of *P. tinctorum* transplanted on different artificial substrates and aspect orientation. Transplantation of 360 thallus fragments were performed on white plastic screens (WS) and black plastic nets (BN), oriented toward the East (E), the West (W) and horizontally (H) in a secondary forest. Microclimates of the three aspects were measured. After a year, the average growth rates of thalli on the BN in all aspects were 4.4 times higher than those on the WS. The growth rates of lichen on three aspects over the BN averaged 7.83 mm/yr, ranged from 6.55–9.95 mm/yr, whereas those on the WS were only 1.76 and 0.84–2.98 mm/yr. The East facing thalli on both substrates had the highest growth rates, and those on the horizontal had the lowest rates. However, thallus growth rates on the H, W and E over the BN were 7.8, 4.8 and 3.3 times higher than those over the WS. Differences in microclimate and mesh size of the substrates were the main causes of variation in thallus growth.

Rare saxicolous lichen communities in Lithuania

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The lichens of rocks in Lithuania is somewhat understudied and the phytosociology of the epilithic communities is completely unknown. The natural epilithic lichen flora is predominantly acidophilous. The most diverse siliceous rock-inhabiting species are found on moraine boulders, which are included into the Geosites database of the Lithuanian Geological Survey and are protected under various conservation regimes. Present study of saxicolous lichens and their communities was performed in 2014–2015 in Šaukliai Geological Reserve – one of the largest boulder fields in Lithuania. The aim of the research was to study saxicolous lichens communities on granite boulders, to describe their structure, to evaluate their ecological and sociological links and to determine threats to the rare species and communities. Communities were studied on 21 boulders following Wirth (1972). During the field studies ecological variables were recorded: rock size and position above soil level, exposure, boulder diameter and rock type. Three associations with dominant species of lichens that are rare and threatened in Lithuania were determined. These associations include five lichen species that are included in Lithuanian Red Data Book: *Lasallia pustulata*, *Rhizocarpon viridiatrum*, *Umbilicaria deusta*, *Umbilicaria polyphylla*, *Xanthoparmelia mougeotii*.

Conservation project: Protection of red list species of lichens in endangered habitats in Upper Austria

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Several common lichen species disappeared or became extinct in the last 50 years due to air pollution, destruction of habitats and impact of intensive agriculture. Especially, at the colline and sub-montane zones of Austria in former times abundant lichens like *Anaptychia ciliaris* vanished in most regions. Also, lichens from the montane zone like *Lobaria pulmonaria* and *Nephroma resupinatum*, are disappearing from continually and well observed habitats. The heterogeneous landscape in Upper Austria (Austria) provides three different main types. 1) The 'Mühlviertel' in the north on the Bohemian Mass, shaped by granite boulders in colline and high montane zones; 2) The broad valley of the river Danube and adjacent Alpine foothills in the center and 3) in the south the montane and subalpine areas of the northern rim of the Alps. The hotspots of the most endangered species which were found in surprisingly high diversity and good condition are remote areas at the 'Mühlviertel' and unsettled, humid heads of valleys in the Alps. These retreat areas will be protected by an ongoing conservation project, initiated and funded by the provincial government of Upper Austria and is unique in its extensive achievement in Central Europe.

Lichens diversity of Zagros oak forests in west of Iran at risk

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The unique Zagros Mountains forest-steppe ecoregion is located primarily in west Iran. In recent years, dust storm as natural phenomena has taken on new dimensions in Zagros Oak forests and has changed from a local problem to a national issue in Iran. Epiphytic lichens respond sensitively to ambient air pollution. The diversity of epiphytic lichens in the Zagros Oak forests still remains unknown. Such special lichens diversity is now under threats of heavy dust storm. Dust storm increase eutrophication and nitrogen-polluted environments. Recent lichenological observation in the Zagros oak forests confirm high eutrophication in tree trunks. In many localities in Ilam province, tree trunks bear no epiphytic lichen communities which could possibly colonize such substrate in normal condition. In some tree trunks we discovered some dead thalli of macrolichens. It seems that the volume of dust coating layer on bark of oak trees reach over thickness of the microepiphytic lichens such as *Caloplaca polycarpoides* or *Lecanora hagenii* or even completely cover *Phyconia* sp. Such lichen species are hidden by dust coating layer. The lichen loss of oak trees possibly is the result of dust coating layer and ambient air pollution. Lichens become overdose or passing the threshold of eutrophication.

From local to global: knowledge transfer of Swiss lichen distribution data for conservation and research

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The SwissLichens data base (National Data and Information Centre for Swiss Lichens) contains more than 120,000 georeferenced and validated records of lichen localities in Switzerland from various origins (voluntarily provided data from naturalists, public data from the Red List Program, biodiversity surveys, research projects, museum collections). Dynamically generated distribution maps and graphs describing ecological requirements at species level as well as information about their protection status and conservation needs are published on the homepage of SwissLichens (www.swisslichens.ch). More detailed information about specimens and collections is provided by the Swiss Portal of the Global Biodiversity Information (www.gbif.ch). To facilitate the planning of conservation actions, occurrence records from the SwissLichens data bases are served to the Swiss Virtual Data Centre (VDC). VDC provides controlled access to the raw data of all national data centres (Info Species network, www.info-species.ch) by a web based, interactive map tool to Swiss authorities. To support the documentation of the global diversity and promote species conservation at international level, species occurrence data from the Swiss national data centres are transferred to GBIF international (www.gbif.org). Individual data requests for research is highly appreciated! The Info Species data use agreement guarantees a targeted and transparent policy on data use.

First results obtained in a study of the Asian population of *Erioderma pedicellatum*

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The Asiatic population of *Erioderma pedicellatum* (Hue) P. M. Jørg. was found in 2009 in primeval oceanic spruce forests of Kronotsky Nature Reserve, Kamchatka, Russian Federation. Kamchatka is the fourth location of this species, which is listed as globally critically endangered. During the last six years several eruptions of volcano Kizimen, located in the near vicinities of the location of *E. pedicellatum*, have been recorded. In 2015, monitoring data were collected from the same sites as in 2009. Despite the ash emission, the boreal felt lichen survived. In total, 21 sample plots (20 × 20 m) were studied and more than 600 thalli of *E. pedicellatum* were found on 14 plots among these. Probably, the Asiatic population of *E. pedicellatum* is the most abundant in the world. The healthy state of the population is confirmed by a large number of fertile and juvenile thalli. In 2013, a substantial part of the *E. pedicellatum* population was discovered outside the Kronotsky Reserve in the vicinities of Lazo on Nikolka volcano slopes. This is the most threatened part of the population because of forest management. It is necessary to study this part of the population and to protect the whole population.

How much taxonomic expertise is necessary for prioritizing areas of lowland rainforest sites as habitats for lichens in northeast Borneo?

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The number of experienced field lichenologists in biodiversity-rich tropical countries is far too low and the challenges from still un-described and cryptic taxa too large, to allow the desirable species or even genus level assessment of lichen communities in tropical forests everywhere where it is needed. We have tested differences of the results between an assessment of lichen richness in natural and selectively logged forests, when the assessments are based on either a genus level identification or an approach based on functional groups and using characters that can all be observed in the field. Our results show that the separation of lichen communities from natural and disturbed forests in NE Borneo can be achieved in a reliable manner without the need for the identification for any named taxa. The decrease of diversity of functional groups is accurately mirroring the loss of genetic diversity at the generic level. Our simplified methodology allows a quick and reliable assessment of sites with unaltered, disturbed or regenerating lowland rainforests of NE Borneo by local people with a basic training in lichen morphology. This first stage assessment can then be followed up by more detailed inventories of the top sites by specialized lichenologists.

Taxonomic study of lichens from the Sino-Himalaya region—The genus "*Lethariella*"

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The Chinese "Hongxuecha" lichen grows in the alpine region of Himalaya area, between 3600 – 4700 m elev., it is one of ethnic medicine in this region, and is used to treat disease such as hypertension, local people usually drink it as tea. "Hongxuecha" lichen was elevated to genus by Krog in 1976, named as *Lethariella* (Motyka) Krog. 7 species have been previously reported from this region, chemical compound was used as the key factor to distinguish species. But after recent studies, various chemo-type of the same species were found in different environment, thus, 7 species were synonymized into 2 species based on combination of morphological and chemical characters: *L. cladonioides* and *L. zahlbruckneri*. After the intervention of molecular techniques (phylogenetic analysis using ITS, nrLSU and nrSSU), this genus has been revised again, combing with morphological, chemical and biogeographical characters, new boundaries between species and genus are found. The definition of species and even genus might be changed. With the increasing use of this medicine, the collection speed is much faster than its nature growth rate from its habitat. It is urgent to study this genus, promote the protection policy and explore the use of this lichen resource properly.

Changes in lichen and bryophyte communities on Scots pines along an alkaline dust pollution gradient

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Dust pollution causes significant damage of local environment and endangers human health. Bioindication provides information about polluted areas that are not covered with direct measurements. Our study aimed to investigate epiphytic lichens and bryophytes in relation to long-term dust pollution, and presents new insights into the bioindicators of dust pollution. We simultaneously recorded the species richness and cover of both cryptogamic groups using line cover method, and measured the bark pH of phorophytes (*Pinus sylvestris*) in 32 sample plots in the vicinity of limestone quarries (up to 3 km) in Estonia, northern Europe. The bark pH decreased gradually with increasing distance from quarries. We recorded the drastic changes in natural epiphytic communities, resulting in diversified artificial communities near the pollution source; the distance over 2000 m from the quarries was sufficient to re-establish the normal acidity of the bark and natural communities of both cryptogams. The cover of lichens and number of bryophytes are more promising indicators of environmental conditions than individual species occurrence. We suggest additional bioindicator species of dust pollution on pines (e.g. *Lecidella elaeochroma*, *Alyxoria varia*). Dust pollution revealed a 'parapositive' impact on cryptogamic communities, suggesting that quarrying might temporarily contribute to distribution of locally rare species.

Preliminary investigation of elemental compositions in the particles on *Parmotrema tinctorum* collected around the Fukushima Dai-ichi Nuclear Power Plant

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A plenty of various radionuclides was released into the atmosphere by the Fukushima Dai-ichi Nuclear Power Plant (FDNPP) accident. The local radioactive contaminations (i.e. radioactive plume's trajectory) around the FDNPP were caused by the releasing radionuclides from each reactor, meteorological and geographical conditions, etc. In order to clarify the contamination characteristics of the plume's trajectory, we focused on lichen samples that are well known organism to retain radionuclides for a long period. A field investigation was carried out around the FDNPP on January 2016. *Parmotrema tinctorum*, a common species at the area, growing on trunks of trees was collected around the FDNPP. The fragments of lichen thalli were analyzed by the scanning electron microscope coupled with energy dispersive X-ray spectrometer (SEM-EDS). Heavy metal particles were detected on the surface of *P. tinctorum*. They might originate from reactors of the FDNPP because they contain anthropogenic elements such as, (Fe, Zn), (Cd, Zn), (Zr, Ti), (Fe, Zn, Cr), (Ti, Fe, Ce), (Fe, Ti, Cr, Ni), (Fe, Cr, Zn, Cd), etc. Further data of the elemental composition in particles on lichen samples would be helpful to discuss the differences among the radioactive plume's trajectories from each reactor.

The "Adotta un Monumento (Adopt a Monument)" project of the Italian lichen society

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The Working Group for Biology of the Italian Lichen Society, with the support of the High Institute for Conservation and Restoration (ISCR, Rome), has established a network of collaboration with the local offices pertaining to the Italian Ministry of Cultural Heritage and Activities (MiBAC) devoted to the preservation, management and enhancement of Cultural Heritage (CH). With the "Adotta un Monumento (Adopt a Monument)" project, a series of Italian sites of artistic-historical-archaeological interest have become the object of investigations on (i) the lichen communities characterizing the stone CH in different bio-climatic areas, (ii) the lichen-deterioration/protection of different lithologies, and (iii) different strategies against the lichen colonization. In this work, the main needs declared by the local ministerial offices with regard to lichenological issues are analyzed. Experiments to compare different chemical and physical approaches against lichens to support cleaning procedures, which turned to be the main reason of interest of CH managers, are illustrated, together with preliminary results. Other methodological approaches shared by the different research groups to satisfy diagnostic queries are also illustrated and purposed for a wider networking agreement.

Species-specific lichen sensitivity to biocides and application solvents used on the stone cultural heritage

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The application of biocides is still the most widely adopted approach to support the mechanical removal of lichens from outdoor stone surfaces. In this work, carried out in the archaeological Roman site of Industria (NW-Italy), we examined if three lichen species [*Candelariella vitellina* (Hoffm.)Müll.Arg., *Protoparmeliopsis muralis* (Schreb.)M.Choisy, *Verrucaria nigrescens* Pers.] were similarly affected in the PSII photochemistry of their photobiont partner -as a marker of the whole symbiotic vitality- by six commercial biocides differing for active principles and application solvents. The biocides, prepared following the distributor's recommendations, were applied by brush and with a cellulose poultice on moistened thalli, their solvents (acetone, white-spirit, water) being also separately tested. Chlorophyll a measurements were taken one week before, and 1, 20 and 180 days after the treatments. The species were variously affected by the biocides, the application method also influencing their efficacy. In most cases, a relative decrease rather than the zeroing of photosynthetic parameters was detected, and a vitality recovery was recognized. The efficacy of organic solvents alone was sometimes remarkable. Although repeated applications are often recommended, which may likely improve the killing effect, the detected differences in the specific sensitivity seem worth of consideration to interpret frequently reported recolonization phenomena.

A Celtic script – reading our "ruin" stones. Threats to lichen diversity at Irish archaeological and heritage sites

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Over 60% of the c. 1300 lichen species recorded in Ireland are saxicolous. Each species selects preferred habitats, niches and geological contexts, depending on eco-physiological requirements for life, e.g. pH, hydration, dust deposition, temperature range, interstitial soil and rock geochemistry. Case studies from Ireland are presented from 12 sites - with contrasting habitats from coastal to inland, low-land to mountain, urban to rural, calcareous to siliceous, in order to demonstrate lichen species variation with habitat on and into the rock surfaces of national monuments. Distinctive weathering effects of rock and stone are caused by factors such as urban or rural air pollution, salt-laden coastal winds, bird perches, rock-falls and aspect. The dominant species on many Irish monuments is Ivy (*Hedera helix*). This plant is now rampant in a wide range of habitats, particularly on the walls of towns, medieval castles and ecclesiastical sites. At an advanced stage of cover, the lichen biodiversity of a monument is compromised and reduced. Our study highlights multiple threats to lichen biodiversity and recent losses due to Ivy and collapse of monuments in Ireland. Proposals are made for lichen conservation on megaliths, medieval and more recent stone structures of archaeological and heritage interest.

Composition of species and functional traits of ground layer lichens on calcified and decalcified dunes of Estonia

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Species-rich lichen biota can be found on European coastal and inland sand dunes. However, it is increasingly affected by natural succession as well as by anthropogenic disturbances. We studied epigeic lichens, general environmental variables and anthropogenic disturbances in 33 study plots of Estonian calcified and decalcified dunes. Multivariate analysis (DCA, pCCA) was performed to examine gradients in species composition and to relate variation in species data to environmental factors. In addition, we used redundancy analysis (RDA) to relate variation in species' traits composition to environmental factors. We found 73 epigeic lichen species, including several rare and red-listed lichens. Soil pH was the most essential environmental variable for determining species composition and species' traits composition. For example, lichens with cyanobacterium as the main photobiont preferred calcified dunes. Forest closeness and cover of bare soil also significantly influenced the composition of lichen species. To conserve the lichen-rich sand dunes it is necessary to regularly remove shrubs and trees and to protect the dune habitats from building activity and from overtrampling in recreational areas.

Lichens on decaying Norway spruce in managed and old-growth forests

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Dramatic decrease of dead wood is among the main reasons for the endangerment of forest lichen species in Finland. However, ecology of many of the species living on decaying wood is still insufficiently known. Research among lichens has traditionally concentrated on macrolichens because they are easier to identify. Majority of lichens living solely on decaying wood are, however, crustose lichens. We investigated ecology and distribution of lichens on decaying spruce logs in 14 coniferous boreal forests, half of which were old-growth and the other half recently managed. We examined how habitat, stage of decay, and the location of the tree affect species occurrence. We also compared species composition and richness between old-growth and managed forests. Morphological, anatomical chemical and molecular characters were used for species identification. Our preliminary results show that on landscape scale crustose lichens are more species rich in natural than managed forests. Macrolichens growing on decaying spruce logs, however, are not significantly affected by forest management practices. Eight new species to Finland, one of which is new to Fennoscandia, were discovered. In addition several new records of rare and deficiently known species are reported.

Will climate warming exceed lethal photosynthetic temperature thresholds of lichens in a southern African arid region?

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Predicted elevated temperatures and a shift from a winter to summer rainfall pattern associated with global warming could result in the exposure of hydrated lichens during summer to more numerous temperature extremes that exceed their thermal thresholds. This hypothesis was tested by measuring lethal temperature thresholds under laboratory and natural conditions for four epilithic lichen species (*Xanthoparmelia austro-africana*, *X. hyporhytida*, *Xanthoparmelia* sp., *Xanthomaculina hottentotta*) occurring on quartz gravel substrates at a hot arid inland site two epigeous lichen species (*Teloschistes capensis*, *Ramalina* sp.) occurring on gypsum-rich topsoil at a warm humid coastal site. Extrapolated lethal temperatures for photosynthetic quantum yield under laboratory conditions were up to 4°C higher for lichens from a dry inland site than those from humid coastal site. Lethal temperatures extrapolated for photosynthetic quantum yield at a saturating photosynthetic photon flux density of $\geq 11,000$ $\mu\text{mol photons m}^{-2} \text{s}^{-1}$ under natural conditions were up to 6°C higher for lichens from the dry inland site than the more humid coastal site. It is concluded that only under atypical conditions of lichen exposure in a hydrated state to temperature extremes at high midday solar irradiances during summer could lethal photosynthetic thresholds in sensitive lichen species be potentially exceeded.

Lichens *Flavoparmelia caperata* and *Parmelia sulcata* – bioindicators of oil refinery air pollution in Slavonski Brod, Croatia

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Using lichens as bioindicators provides a superior spatial resolution and a multi-pollutant/multi-effect approach compared to existing data(bases) used for air quality modelling. The city of Slavonski Brod is the most polluted site in Croatia due to air pollution from the oil refinery situated across the border in Bosnia and Hercegovina. Reports from monitoring stations indicate high content of sulphur dioxide, hydrogen sulphide, fine particles (PM_{2.5}), etc. In this study, two lichens, *Flavoparmelia caperata* and *Parmelia sulcata*, were collected at 20 sites in 20 km radius from the refinery, to investigate its effect on air quality. Quantum yield of photosynthesis, chlorophylls, carotenoids, nitrogen and sulphur content were evaluated in the collected samples. Investigated lichens were not found at two sites closest to the refinery, confirming the strong effect of industrial pollution. Significant differences among measured parameters were detected between lichens collected at different sites. Generally, highest values were recorded at sites within the city, which are also closest to the refinery, while the lowest were recorded in forests outside the city. Further investigations, which include measuring heavy metal content and secondary metabolites and utilization of transplants, are planned on the same sites to enhance our knowledge of using lichens as bioindicators.

Adapting an American method for determining air quality in the European floodplain forest (Motovun Forest, Croatia)

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Lichens are one of the most common biomonitors of air pollution, resulting in developed standardized methods for assessing lichen diversity in order to determine air quality. As a part of an environmental survey of Motovun Forest (Croatia), we conducted biomonitoring of air quality using lichens. Motovun Forest stretches along the valley of the River Mirna and is one of the last Mediterranean floodplain forests called "longoze". Due to high air humidity, the tree trunks are mostly covered in moss so it was impossible to use the European standard for biomonitoring with lichens, which defines that not more than 20% of the trunk can be covered by other epiphytes. Therefore, we adapted the Forest Health Monitoring – lichen community method developed in USA, which defines using all macrolichens in a defined radius, and combined results from this community method with indices from ITAL-IC database. The best results were obtained using poleophoby index, were the results indicated that the forest has great air quality, except in a vicinity of mineral spring rich in sulphur. Although further evaluation is still needed, the developed method could be a possible solution for European humid forests where it is not possible to use the European standard.

Recovery of epiphytic lichen communities after reduction of the copper smelter emissions in the Middle Urals (Russia)

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Epiphytic lichen communities were studied near a large copper smelter functioning since 1940s and causing a severe degradation of adjacent forest ecosystems. Studies carried out in 1995–97 revealed a decrease in species diversity up to the formation of lichen desert in the immediate vicinity of the smelter. Sharp reduce in emissions in the 2000s led to the beginning of forest restoration. In 2014–15, the lichen desert was recolonized, mostly by pollution-resistant lichen species as well as species of intermediate sensitivity but with high colonizing potential (e.g. *Hypogymnia physodes*, *Tuckermannopsis sepincola*). Others species of intermediate sensitivity also significantly expanded their ranges. However, highly sensitive *Bryoria*, *Evernia* and *Usnea* species still occur only in background plots. To understand whether the current conditions in the former lichen desert suit for lichen survival, soredia and adult thalli of *H. physodes* and *Evernia mesomorpha* were transplanted there from a background site. After 3 months, survival of soredia of both species near the smelter was significantly reduced as compared to the background zone, though adult thalli did not show any signs of damage. Thus, vegetative diaspores seem to be a critical stage limiting lichen recolonization of formerly polluted areas. The study is supported by RFBR (project 15-04-06828).

Biogeochemical characteristics of epiphytic lichens, mosses, bark and topsoil in Vilnius city (Lithuania)

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Total concentrations of 29 elements were investigated in lichens (*Phaeophyscia orbicularis*), mosses (*Orthotrichum affine*), bark (*Acer platanoides* and *Tilia cordata*) and topsoil collected in the vicinity of 58 preschools in Vilnius city (Lithuania). Energy Dispersive X-ray Fluorescence (EDXRF) was employed to determine contents of the elements in unwashed biological samples and in topsoil. Concentrations of potentially harmful elements (PHE) – As, Ba, Cr, Cu, Mn, Mo, Ni, Pb and Zn were compared in the studied objects. Highest concentrations of As, Ba, Cr, Mn, Ni, Pb and Zn were found in soil, of Cu – in lichens, of Mo – in mosses. Concentration ranges and standard deviations for all elements were high. Element concentration ranges in the investigated objects were as follows: for lichens – Mn>Zn>Ba>Cu>Pb>Cr>Ni>Mo>As, for mosses – Mn>Zn>Ba>Cu>Pb>Cr>Ni>Mo>As, for bark – Mn>Zn>Ba>Cu>Pb>Ni>Cr>Mo>As, for topsoil – Ba>Mn>Zn>Pb>Cr>Cu>Ni>As>Mo. To distinguish impact of soil-derived dust on biological samples, concentrations of PHE were compared against the concentrations of reference lithogenic elements Al and Ti. In lichens, positive correlation ($p<0.001$) was found for Ba, Zn, Cr, Cu, in mosses – for Ba and Cr, in bark – for Cr, Ba, Cu, Mo, Ni.

Effect of Cu on the fluorescence of the Cu-hyperaccumulator lichen *Stereocaulon sorediiferum*

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Metal-hyperaccumulator lichens contain metals of the order of 100–1000 ppm in dry weight; they can be used for biomonitoring. Lichen substances emit fluorescence under UV irradiation and these concentrations are affected by metal pollution. Hence, the fluorescence spectroscopy of lichens should be useful for monitoring metal pollution. To understand the relationship between the fluorescence of metal-hyperaccumulator lichen and metal pollution, we examined the effect of Cu on the fluorescence of Cu-hyperaccumulator lichen *Stereocaulon sorediiferum* with different Cu concentrations. The lichen samples of *S. sorediiferum* containing different concentrations of Cu were prepared, and their fluorescence spectra were measured. Metal concentrations including Cu in the lichen samples were determined by induced coupled plasma mass spectrometry (ICP-MS). We observed that they emit blue fluorescence under UV irradiation, which is suggested to originate from one or two lichen substances in them. Moreover, we found that the fluorescence intensity of the lichen is negatively correlated with Cu concentration, indicating that Cu pollution could be monitored using the fluorescence of *S. sorediiferum*. These results provide a better understanding of the relationship between metals and the fluorescence of metal-hyperaccumulator lichens.

The conservation status of six Bogotá wetlands, using lichens as bioindicators

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The conservation status of six Bogotá wetlands was analyzed by studying lichens as bioindicators of ecosystem health, using the IAP method. Additionally, an inventory of the species in the wetlands was made, then a cluster analysis and management was performed using the system of NMS in order to establish possible relationships between the distribution of communities and the degree of conservation and environmental health of wetlands. As a result, the Bogotá wetlands are in a normal state of preservation, being Córdoba the best preserved wetland with the highest level of lichen communities diversity and abundance, followed by Conejera, Juan Amarillo, Santa María del Lago and Capellanía. The most deteriorated was La Vaca. 57 species of lichens and 32 morphospecies were found in the wetlands, with 18 new records for Colombia, 26 for Cundinamarca and 42 for Bogotá. With this study, *Candelaria concolor*, *Xanthoria parietina*, *Physcia undulata*, *Ramalina celastri* and *Dirinaria appplanata* were established as toxitolerant species and *Heterodermia tremulans*, *Physcia* sp1, *Heterodermia leucomela* and *Amandinea submontana* as sensibility indicators. As conclusion, there are similarities between the lichen communities of different wetlands, which are not dependent on the supporting phophytes but their establishment, and maintenance is due to environmental conditions.

Effects of diesel particulate matter on lichen photosynthesis

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Lichen vegetation reacts very sensitively to a variety of air pollutants including nitrogen compounds and traffic exhaust in general. This makes lichens reliable monitoring organisms for atmospheric pollution. One major source of these atmospheric compounds amongst a wider pollution inventory is diesel exhaust - a mixture of gases and particulate matter. The present study evaluates the impact of diesel exhaust on the viability of four differently sensitive lichen species under controlled environmental conditions. By incubation in a closed stainless steel chamber we could exclude influences from other pollutants than diesel exhaust providing explicit data about the effects of diesel exhaust on lichens. The investigations revealed effects on the photosynthetic capacity and hence the lichen vitality. The conclusions of this study are 1) the particulate matter within the diesel exhaust has strong effects on the lichen vitality in short term, whereas the gaseous phase rich in hydrogen carbons and nitrogen compounds have not, and 2) lichens are regenerating to some extent during incubation-free periods. To our knowledge this is the first study evaluating the impact of diesel exhaust on lichens under laboratory conditions separate from other interfering pollutants.

Lichen colonization in Persepolis – UNESCO World Heritage site

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Persepolis was founded by Darius I in 518 B.C., where it was the capital of the Achaemenid Empire. It was constructed on an immense half-artificial, half-natural terrace, located on the south slope of Rahmat mountain, in the plain of Marvdasht, Fars province. The historical importance and high artistic quality of the monumental ruins make it a unique archaeological site in the world. The purpose of our study was to investigate the lichen diversity in the Persepolis monumental ruins. The lichen colonization of the area was observed by reference to 27 locations in according to Herzfeld's sitemap published in 1932. The 100 species encountered form different locations at the terrace. The majority of the species could be accommodated within the nitrophilous lichen groups. The species component of Persepolis belongs to following the genera *Caloplaca* s. lat. (15 taxa), *Acarospora* (12 taxa), *Circinaria* (8 taxa), *Rinodina* (6), *Lecanora* (5 taxa), *Verrucaria* (5 taxa), *Pyrenodesmia* (4 taxa), *Collema* (3 taxa), *Anaptychia* (2 taxa), *Candelariella* (2 taxa), *Lobothallia* (2 taxa), *Placidium* (2 taxa), *Sarcogyne* (2 taxa), *Staurothele* (2 taxa), *Peltula* (1 taxon), *Peccania* (1 taxon), *Psora* (1 taxon) and 29 other taxa. An illustrated and annotated list, with ecological and distributional remarks was provided

The role of terricolous lichens as rangeland health indicators in Kiyamaki wildlife refuge rangelands, NW Iran

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Changing land use has a major impact on terricolous lichens diversity in the rangelands. Terricolous lichens are an intimate association of biological soil crusts, they are important in soil stabilization and soil fertility. Despite their importance there have been few efforts to examine their potential to be bio-indicators in the rangelands health assessment. Range managers have traditionally focused attention on vascular plants diversity as the key criteria of rangeland health. However, recent studies attempts to identify patterns or trends of terricolous lichens functional groups along land use gradient, ranging from healthy rangelands to agricultural or bare landscape. The aim of our study is showing terricolous lichens as rangeland health indicators in Kiamaki wildlife refuge rangelands East Azerbaijan province. In this study, we evaluated the patterns of lichen functional traits such as growth form, reproductive strategy, and photobiont type as potential indicators for rangeland health monitoring. The result shows that, continuity of biological soil crusts, terricolous lichen diversity value, reproductive strategy, photobiont type as well as thallus pigment types could be a potential indicators in the rangeland health monitoring program.

10 years of lichen monitoring in Labe Sandstones, Czech Republic

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The principal goal was to establish sites for long term monitoring of epiphytic lichens in the area of Labe Sandstones in Northern Bohemia. Sampling is pursued every three years from 2005 on ca 90 wayside trees, especially on common ashes (*Fraxinus excelsior*). Species richness on tree trunks up to 2 m from the ground and LDVs are taken from a single tree. Epiphytic lichen flora has changed during the years – toxitolerant acidophytes are replaced by more neutrophytic (sometimes nitrophytic) species, and, with exception of 2011 measurements, lichen flora increases. There are several influences of environmental variables to the dataset – age of trees, position (intra/extravilan), etc. Among others, a gradual influence of local air pollution sources following overall background air improvements during past two decades could be seen. Unfortunately the onward invasion of the ash dieback fungus *Hymenoscyphus fraxineus* causes several problems with the phorophyte dataset.

Lichens and climate change in Southern Baikal Region

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Lichens are responding to local and global climate change. Effects so far are most pronounced in temperate and Arctic regions (Aptroot 2009). Our studies focused on lichen-rich *Abies sibirica* forests at Baikalskiy Reserve (Southern Baikal, Russia). Between 1992 and 2015, 400 m² of steady-state plots were investigated at 5 altitudinal levels (670-1300 m). Over some 20 years, many sample plots experienced dramatic changes in the structure of the pine-fir forest. Significantly, increases in the number of dying and dead trees were noted among the forest stands. Quantitative surveys were carried out and epiphytic lichen groups described colonising *Abies sibirica* trunks in 1992 (Urbanavichene, 2001). A detailed analysis was carried out of the changes in epiphytic lichen composition since 1992 within the investigation plots. Data for different years were compared and analyzed in relation to air temperature and precipitation. Results suggest that the lichens are not resistant to climate change (warming and changes in rain regimes). Warming and aridity have a significant impact on the dark coniferous forest community. These factors lead to changes in the dominance, average projective coverage and composition of epiphytic lichens species on the sample plots in Baikalskiy Reserve.

Diversity of epiphytic lichens as a tool for evaluating the role of green spaces in improving air quality

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Management actions to improve air quality in urban areas are essential to minimize citizen's exposure to pollution. Understanding the role of green spaces in increasing air quality is crucial for the establishment of informed management policies. Since lichens are well established air quality biomonitors in urban areas, we used them to quantify the air purifying role of green spaces, with high spatial resolution data. This study aimed at building a model to predict green spaces contribution to improve air quality in urban areas using lichen diversity data. Forty-two green spaces were randomly selected and stratified by size (area), location and urban density. Epiphytic lichen diversity was sampled following the standard European method in the four suitable trees closest to the centroid of the green spaces. Vegetation density and other environmental variables were also evaluated. Most lichen metrics were very significantly related to air quality, which was then modeled considering background pollution, vegetation density and green spaces size. The model showed that high gains to air quality can be attained by creating green spaces of small areas in the most polluted sites of the city. This model can now be used as a tool for informed urban management and supported decision-making.

Biogeographical origin of the foliicolous lichen biota from humid forest enclaves in northeast Brazil

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Foliicolous lichens have a wide distribution in humid tropical forests. The Atlantic Forest, one of the most biodiverse forests worldwide, also comprises a biogeographic unit known as Brejos de Altitude (BA), isolated sub-montane fragments of humid forests inserted in the semiarid Caatinga vegetation. The aim of this work was to elucidate the biogeographic origin of foliicolous lichens in five Brejos de Altitude by comparing the composition of the foliicolous lichen biota of five BA with the lichens of 21 areas in the Neotropics. 158 species were identified from five BA. The majority have a wide distribution in tropical America, and only ten species, recognized as undescribed species, have the potential to be endemic. The results show that Brejos, Atlantic forest and Eastern Amazonia present a biogeographically closely related lichen biota, while the lichen biota of Western Amazonia is more similar to that of the Andes and the lowland and mountainous forests in Central America. No indicator species of the BA vegetation was identified. The major biogeographic differences between the regions should be related to the Pleistocene period, when diverse climatic and geological changes occurred affecting the isolation of the Brejos de Altitude and the temporary fragmentation of the Amazonian regions.

From 14 to 760: Assembling the lichen biota of a Brazilian state from scratch

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Brazil is considered the most megadiverse country in the world. In terms of lichen diversity, a checklist is being compiled containing no less than 4,000 species. At least 25 % of these have been added in recent years, mostly resulting from numerous inventories undertaken in North and Northeast Brazil, such as the ongoing work in the state of Sergipe. Sergipe is the smallest state in Brazil, with 21,910 km², which is about 15 times smaller than Finland. It is also the state with the highest rate of deforestation for the Atlantic Forest and the semiarid Caatinga biomes. Until the year 2000, only 14 lichen species had been reported for Sergipe. The present work documents our ongoing efforts towards assembling the lichen biota of Sergipe, as a signature of yet unrecognized lichen diversity in Brazil. As a result, the number of reported taxa increased dramatically by a factor of 50 over the past 15 years, with a total of 760 species now known, including corticolous, foliicolous, saxicolous, and terricolous lichens, from a diverse range of vegetation types. Among these, 10 species and one genus have been described as new to science so far.

Underestimated biodiversity in the tropical family Pyrenulaceae

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The Brazilian tropical forests are quite unique in its species richness and composition of some lichenized fungal families. Many species are restricted to undisturbed forest, especially pyrenocarpous lichens, which has a higher biodiversity in different types of vegetation in Brazil. The majority of the lichen species are corticolous crusts and there is a divergent species composition when the successional stages are analyzed. As part of a study about Pyrenulaceae (lichenized Ascomycota) in the Neotropics, six new *Pyrenula* species were found as new to science by the first author during several recent field trips in different biomes, such as Atlantic Forest (including Restinga and Brejo de Altitude) and in the Amazon Forest. The new species are named as *Pyrenula aurantiothallina*, *P. coccinea*, *P. diamantinensis*, *P. lilacina*, *P. pallida*, and *P. violaceastroidea*. It is important to note that about 50 new Pyrenulaceae species were described as new to science in the last five years. With this discovery rate, the conservation of Brazilian forests becomes extremely important, revealing a still underestimated biodiversity.

Molecular systematics of *Sporacestra* and relatives

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Sporacestra A. Massal. (1860) is a small corticolous lichen genus in the family Ramalinaceae, found in tropical/subtropical moist forests and rainforests. Tropical members of the Ramalinaceae is generally poorly known, *Sporacestra* in particular. Preliminary molecular phylogenetic investigations show that the genera *Bacidia*, *Bacidiopsis*, and *Sporacestra*, as well as a few species of *Phyllopsora* (not the type) form a supported clade, hereafter called the *Sporacestra – Bacidia – Bacidiopsis* -clade. This MSc thesis will address taxonomic challenges linked to this clade. For example, the type species of *Sporacestra* seems to be congeneric to *Phyllopsora pertexta*, rendering the name *Sporacestra* the correct name to use. Moreover, a number of specimens collected through the years may belong in the *Sporacestra–Bacidia–Bacidiopsis* – clade. These will be included, as well as material collected during fieldwork in Brazil in 2015, in an integrative taxonomic framework. Methods to be used include comparative DNA sequence analysis, morphological investigations and TLC. The expected outcome from this study of the *Sporacestra – Bacidia – Bacidiopsis* -clade include: (1) description of one or more new species, (2) resolution of one or more species-complexes, (3) reports on species new to various regions, (4) and a key for one or more of the genera in question.

The lichen family Trypetheliaceae (Dothideomycetes, Ascomycota) in Bolivia

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The Amazon Basin, the humid Andes and the semi-arid region of the Gran Chaco in Bolivia belong to the world's most species-rich areas. Various plant communities developed there, such as lowland Amazon forest, Moxos savannah, Yungas and Tucumano-Boliviano forests, Chaqueño forest, and Chiquitano forest, offer a wide range of potential habitats for lichens of the family Trypetheliaceae. We have extensively studied Trypetheliaceae in Bolivia and as a result a total of 75 species are currently known from the country, of which 37 have been reported for the first time. A surprisingly high number of 24 species was new to science. Bolivia harbours about 20% of world diversity of Trypetheliaceae recognized so far. The presence of such a high number of new species could suggest that Bolivia is one of the centers of speciation of the family, at least of the genera *Astrothelium* and *Bathelium*.

High diversity of lichenicolous fungi in the tropical Andes of Bolivia

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The tropical Andes are one of the richest centers of biodiversity on the Earth due to numerous vegetation types at the altitude between 500 and 5000 m. Lichenicolous fungi, that form obligate associations with lichens, are essential components of these ecosystem as well. However, there were no detailed studies conducted on this group in Bolivia, a country considered to be the most diverse in terms of ecosystems in South America. Our survey revealed that the Bolivian Andes harbour a high diversity of lichenicolous fungi, which are especially common in cloud forests. We have identified 135 genera with about 600 species, including a significant number of new taxa. This represents around one third of the worldwide diversity of these fungi. They have been recorded on 93 host genera, however, more than half of species have been found only on 10 lichen genera: *Hypotrachyna* (43 species), *Heterodermia* (42), *Sticta* (38), *Usnea* (36), *Lobariella* (30), *Parmotrema* (29), *Leptogium* (24), *Lecanora* (23), *Punctelia* (17) and *Cora* (15). This is the highest number of lichenicolous fungi reported from one mountain range, what makes the tropical Andes a unique diversity center of this organisms worldwide.

Lime on the coconut! *Cocos nucifera*: an important host for pantropical lichens

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Coconut, *Cocos nucifera*, a ubiquitous symbol of the tropical beach idyll, can be an excellent host for epiphytic lichens. Coconut plantations were established, e.g. on Palmyra Island, near Hawaii, early in the last century. Yet clearances are now underway, e.g. on British Indian Ocean Territory (BIOT), even though coconuts provide food security, shelter, they survive typhoons and they are host to a wide range of local flora and fauna. How lichen species assemblages on *Cocos nucifera* differ from the native Pacific-Indian Ocean zone to the Atlantic zone is as yet unclear. Barclay (1992) has shown that lichens on coconuts in coastal locations of Belize differ from those inland. *Cocos nucifera* bark was sampled from Niue Island, French Polynesia and Saint Lucia. Ascomatal characters were observed under a Nikon Eclipse 80i microscope. So far we have noted 70 species with few differences between the regions supporting a strong overall pan-tropical biogeographic pattern. Lichen lists collated from our own and online herbaria show small variations between Atlantic and Pacific coconut-hosted lichen species compositions. It is clear that some lichen species are at risk at a local level from the environmental impact of *Cocos nucifera* clearance.

Symbiont diversity of *Coccocarpia* in New-Caledonia and Kenya

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We studied symbiont diversity in the lichen genus *Coccocarpia* (Coccocarpiaceae, Peltigerales) collected from New Caledonia and Taita Hills in Kenya. The ITS (internal transcribed spacer) gene was sequenced to determine fungal species identities and to study phylogenetic relations. Cyanobionts were identified on the basis of tRNA^{Leu}(UAA) intron sequences and haplotypic networks were constructed to illustrate sequence differences between different cyanobacterial genotypes. The results reveal that all *Coccocarpia* thalli have *Rhizonema* cyanobionts and that many species house their own unique cyanobiont genotypes. New Caledonia and Kenya do not appear to have any symbiont genotypes in common.

Cyanolichen guilds in montane cloud forests of East Africa

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Most lichen-forming fungi are highly specific in their choice of symbiotic cyanobacterial strains. The availability of compatible strains can limit the establishment success of the spores, and it has been suggested that local assemblages of lichen species utilizing the same cyanobiont strain could improve their mutual success by sharing compatible cyanobionts. We studied fungal-cyanobacterial association patterns in approximately 450 cyanolichen specimens including representatives from over ten peltigeralean genera forming symbiosis with two nostoclean cyanobacterial genera, *Nostoc* and *Rhizonema*. The material is collected from the montane cloud forests of Taita Hills, Kenya, which are part of a well-known biodiversity hotspot. The results reveal the vast diversity of lichen forming fungi and associated cyanobionts, and demonstrate widespread sharing of symbiotic cyanobacteria across different fungal species, genera and families. The patterns of symbiont sharing are diverse but nonrandom. A majority of the studied lichen-forming fungi participate in photobiont-mediated guilds, involving complex interaction networks centered on shared cyanobiont genotypes. The superficially invisible guild structure has important implications for lichen community ecology and offers valuable insights into symbiotic processes that may steer the evolution of lichens.

Hidden diversity of sterile crustose lichens in the Neotropical forests of Bolivia, a hotspot of biodiversity

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Lichens, especially sterile crustose species, are a group of organisms, which in many cases can be easily overlooked as their diversity is not always accessible to naked eyes. As sterile lichens lost the ability to reproduce their systematic position is obscure and the identification of species is often difficult or even impossible. The main aim of the project is to explore the hidden diversity of usually or commonly sterile crustose lichen species in Bolivia as the model for the Neotropics. At present morphological and chemical analyses of specimens are conducted. So far 21 non-leprarioid and 22 leprarioid species have been identified, many being new to Bolivia. Also at least 8 undescribed species (5 belonging to the genus *Herpothallon*) have been found. Many of those species are particularly common in cloud forests (Tucumano-Boliviano forest, Yungas forest), but the species do not show clear preference for the habitat. In the next step ITS nu-rDNA barcodes will be developed to allow rapid determination of morphologically completely or nearly identical species. Also their phylogenetic position will be specified. Research is funded by National Science Centre (no DEC-2015/17/B/NZ8/02441).

Bioactivity of axenic cultures of mycobionts from the tropical lichen family Trypetheliaceae in Thailand

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Lichens are a source of potentially bioactive secondary substances. Their secondary metabolites are mainly produced by the fungal partner and are specific and different from other organisms. Axenic cultures of lichen-forming fungi have only received limited attention and this is especially the case with tropical species. Trypetheliaceae is a pyrenocarpous crustose lichen belonging to the Trypetheliales, which are a strictly tropical lichen family. Eight genera have been found in Thailand (*Astrothelium*, *Bathelium*, *Campylothelium*, *Marcelaria*, *Laurera*, *Polymeridium*, *Pseudopyrenula* and *Trypethelium*). Mycobionts of representative species of each genus were isolated by the ascospore discharge technique and cultivated on MYA medium. The mycobiont colonies were extracted by methanol and concentrated by a rotary evaporator. Crude extracts were investigated for antioxidant and antimicrobial activity by the bio-autography method. The crude extracts of genera *Marcelaria*, *Laurera* and *Trypethelium* inhibited *Candida albicans*; *Staphylococcus aureus* was inhibited by crude extracts of genera *Astrothelium*, *Campylothelium*, *Marcelaria*, *Laurera*, *Polymeridium*, *Pseudopyrenula* and *Trypethelium* respectively. None of the extracts were effective when tested against Gram-negative bacteria. Five genera of *Astrothelium*, *Bathelium*, *Marcelaria*, *Laurera* and *Trypethelium* exhibited antioxidant activity using 2, 2-diphenyl-1-picrylhydrazyl radical (DPPH) solution.

A preliminary study on photobiont algae isolated from tropical lichens in Thailand

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Photobionts are photosynthetic partners and produce primary metabolites in lichen symbiosis. Tropical photobionts have been poorly studied due to high contamination rate from the lichen thallus based on typical isolation methods and low growth rate. The protocol for photobiont isolation from tropical samples was modified from the lichen tissue culture technique. Four lichen species of *Dirinaria* sp., *Parmotrema tinctorum*, *P. presorideosum* and *Ramalina* sp. were used for photobiont isolation. Lichen thallus fragments were cleaned under running tap water and between 80 solution, and then the fragments were crushed in a mortar and filtrated through stainless steel sieves. After filtration serial dilution was using to select the photobiont cells and reduce the contamination. Dilutions of photobiont cells were cultivated in Bold's Basal medium (BBM) in 96 well plates and incubated at 27–32 °C, 30 µM. m⁻¹.s⁻¹ dark/light (12/12 h). Examination for contamination by microorganisms was observed every day. Four green-algal photobionts were successfully isolated and cultivated and their properties were observed using morphological characters and a molecular study based on ribosomal DNA to confirm the species. The photobionts of tropical lichens should be studied in more detail in the future for diversity, phylogeny and species specification within lichens.

Tropical Thelotremoid Graphidaceae lichens: remarkable species diversity from Thailand

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Thelotremoid lichen was belong to family Graphidaceae, with two tribe; Ocellularieae and Thelotremateae. This is project was studies on species diversity in Thailand were found 87 species and 16 genera such as *Astrochapsa* (4), *Chapsa* (5), *Chroodiscus* (6), *Compositrema* (1), *Cruentotrema* (2), *Glaucotrema* (2), *Leucodecton* (3), *Melanotrema* (2), *Myriotrema* (3), *Nitidochapsa* (2), *Ocellularia* (42), *Pseudochapsa* (2), *Pseudotopeliopsis* (1), *Rhabdodiscus crassus* (3), *Stegobolus* (1), *Thelotrema* (8). Twelve new species from Thailand were reported; *Glaucotrema thailandica*, *Leucodecton confusum*, *Ocellularia cerebriformis*, *O. klinhomii*, *O. kohangangensis*, *O. phatamensis*, *O. pseudopapillata*, *O. pseudokrathingensis*, *O. rotundofumosa*, *O. salazinica*, *O. siamensis*, *O. subdolichotata* and 13 species were found in the first time. The highest species diversity belong to genus *Ocellularia* and most of all Thelotremoid lichen species presented in tropical rainforest.

Composition of lichens from two contrasting ecosystems from Puebla, Mexico: mountain cloud forest and desert

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The state of Puebla in Mexico features various types of ecosystems, ranging from oak-pine forest to tropical rain forest, to dry shrub and desert. Many studies have been performed assessing the diversity of animals and plants in this region, such as amphibians, fishes, mammals, angiosperms, gymnosperms, pteridophytes and fungi. However, little is known about the lichen biota. The objective of this study was to inventory the lichens in a mountain cloud forest of Cuetzalán and in the desert of Tehuacán-Cuicatlán Valley. Sampling was opportunistic and non-quantitative, on all available substrates. We found a total of 111 species, 84 in the mountain cloud forest (belonging to nine families and 32 genera) and 62 (15 families and 24 genera) in the desert. Notwithstanding the differences between these two ecosystems, the most diverse family in both was Parmeliaceae, whereas foliose lichens generally dominated over crustose and fruticose one, and the most commonly colonized substrate was bark. Only four species were shared between the two sites: *Candelaria concolor*, *Lecanora leprosa*, *Parmotrema austrosinense*, and *P. tinctorum*.

Habitat acquisition of tropical lichens in Dong Phayayen – Khao Yai forest complex: Natural World Heritage site, Thailand

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The Dong Phayayen – Khao Yai forest complex is a natural World Heritage site in Thailand. It is home to various kinds of tropical forest habitats, ranging from wet humid tropic to xeric warm conditions, where a high diversity of wildlife is known. More than 500 taxa of lichens are recognized in this site. Lichens are sensitive to environmental change, which could provide precautionary measures for conservation of area under pressures from anthropogenic encroachment and climate change. This study assessed lichen communities across different environmental gradients, among forest structures, ages, tree heights and bark textures. Foliose lichens with phycobionts, Parmeliaceae and Physciaceae, favours open conditions, such as deciduous forest, secondary forest and canopy in tropical rain forest. The crustose groups colonized wide ranges of habitats, of which the thelotremoid-Graphidaceae, Poriaceae and Pyrenulaceae prefer the shady and humid conditions of evergreen forest, old growth forest and tree base. Whilst, the lirellate-Graphidaceae seems highly abundant in more open and dry forests. Therefore, the complex systems existing in the different forests are essential for conservation of genetic diversity of lichens, which provide novel natural products, as well as other ecosystem services that need further intensive study.

The project Lichens of Peru

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The knowledge of the taxonomy of lichens in Peru is limited, because of paucity of comparison material in national herbaria, difficulties in the access to scientific literature and the lack of specialists in this group. The focus is mainly the taxonomy and the use of lichens as bioindicators of air quality. For this project specimens in the national herbaria USM, HUSA, HUT, CUZ, CPUN, TKA and PGR have been studied and different parts of the country were surveyed; numerous courses in different universities, a symposium and a workshop. At present, there is 872 species; a preliminary key for determining crustose and foliose lichens has been produced and taxonomic studies for *Teloschistes* and *Diploschistes*; distribution maps of 100 genera; in relation as bioindicators of air quality a study of the city of Lima has been done in which the IPA has been calculated and heavy metals quantified in *Roccella gracilis*; in terms of academics two students were advised in their theses and there are four more currently advised. However, it is necessary to increase the collections of national herbaria; having duplicates cited in scientific articles; increase the number of new specialists, so that this country better advances in the field of lichenology.

Corticolous lichens of Chocó biogeographic of Valle del Cauca

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The Chocó is a broad region extending latitudinally from Ecuador to southern Panama, and longitudinally from the Pacific coast to the watershed of the western slope of the Andes. Although it is considered one of the biodiversity hotspots on the planet, hosting high levels of endemism, this region's flora, especially the non-charismatic groups such as lower plants and Lichenized fungi, remains mostly understudied. Thus we aim to evaluate the diversity of corticolous lichens in Chocó region covering Valle del Cauca, Colombia. Lichens were collected in different localities of Valle del Cauca, covering most Life Zones within Chocó region: Chucheros (tropical rainforest), Queremal (wet montane forest), Cerro del Inglés (montane forest). We reviewed 700 specimens belonging to 188 lichen species, 66 genera and 25 families. The genus *Myeloconis* is reported in Colombia for the first time. The dominant growing form was the crustose (531 specimens), followed by foliose (42 specimens), while squamulose and filamentose were less frequent (37 and 33 respectively).

Molecular systematics of *Eschatogonia*

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Eschatogonia Trevis. is a small genus of corticolous lichens in tropical/subtropical moist forests and rainforests. Although the genus was described as early as in 1853, there were very few collections of *Eschatogonia* prior to Timdal's collection trip to Peru in 2006. With additional fieldwork in Brazil (2014 and 2015) and Venezuela (2015), the NHM-lichen group has now collected more than 200 specimens of *Eschatogonia*. This MSc project will report on these findings in a molecular systematic context, building upon a first phylogeny of Southeast Asian *Eschatogonia* and relatives (Bendiksby and Timdal, in revision). Their results suggest that *Eschatogonia* may not be monophyletic as currently circumscribed, and that there are several new species to be described and species-complexes to resolve. This MSc project will focus New World *Eschatogonia*, with the aim to report on new findings of *Eschatogonia* and to answer questions regarding taxonomic affiliation and taxon delimitation. Moreover, we want to test whether molecular divergence and/or geographic distance correlate with morphological/chemical divergence in *Eschatogonia*. Methods to be used include comparative DNA sequence analysis, morphological investigations, and thin-layer chromatography.

Alto Patache, a biodiversity hotspot for Chilean Roccellaceae in the Atacama Desert

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The family Roccellaceae is a diverse group of lichenized fungi including crustose to fruticose species. They are characterized by their trentepohlioid photobiont, apotheciate to nearly lirellated ascomata normally with a carbonized proper margin, fissitunicate asci and an amyloid or hemiamyloid hamathecium. The family is cosmopolitan in the tropics and semi-arid subtropics. In Chile the family has traditionally been considered to have approximately 50 taxa, including some members recently transferred to the Opegraphaceae, and mostly distributed in coastal areas of northern and central Chile. While studying lichen communities in an isolated fog-induced oasis in the Coastal Cordillera of northern Chile, we came across a highly diverse community of Roccellaceae s.l. After analyzing the samples we came with an estimate of ca. 20 species, from at least 11 genera in the family, constituting 40% of the reported species in the family for the entire country. These results indicate Alto Patache is a biodiversity hotspot for the family, highlighting the need of further studies on this family in Chile and in other areas of the Pacific coast of Southern South America.

Morphological and molecular studies on the genus *Caloplaca* s. lat. (lichenized Ascomycota, Teloschistaceae) from Bolivia

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Our understanding of the diversity of *Caloplaca* s. lat. in South America remains poor. Surprisingly, only c. 140 species of *Caloplaca*, the most species-rich genus within the family Teloschistaceae, have been recorded in the whole area to this date. In this study, we improve our knowledge of this genus in Bolivia, a country with a wide range of suitable habitats for *Caloplaca* and for which only six species are currently known. The purpose of the study was to examine the species diversity in Bolivia using classic taxonomic tools and genetic variation, and placing the collected species within a broad phylogenetic context at family level. Samples were collected by the first author and A. Flakus, and complemented by material from several herbaria. Three rDNA regions were sequenced (nITS, nLSU and mtSSU) and embedded in publicly available datasets to perform the phylogenetic analyses. Almost 50 species were recognized in the examined material; most of them are new records for the country and some of them are new to the South America or even Southern Hemisphere. The final aim of this project is to present a comprehensive revision of the genus in Bolivia with keys to species identification.

In vitro antiproliferative activity of *Porina internigrans* and *P. mastoidea* (Porinaceae, Ostropales) crude extracts against human cancer cells

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Porina spp. consists of forty-one species in Thailand. *Porina internigrans* and *P. mastoidea* commonly colonize moist evergreen forest, dry evergreen forest and plantation. The aim of this study was to investigate in vitro antiproliferative activity of crude extract of the two lichens by using different solvents with increasing polarity. The lichens underwent extraction with chloroform and methanol using the maceration process. The cytotoxic activities of the four lichen extracts were evaluated in vitro using three human cancer cells – KB (human epidermoid carcinoma), HepG₂ (human hepatocellular carcinoma) and HeLa (human cervical carcinoma) – and sample of non-cancerous cells, Vero (African green monkey kidney cells). The inhibition of cell proliferation by the crude extracts were determined by MTT colorimetric assay and active standard value at IC₅₀ 30 µg/ml. The crude chloroform extracts of the two lichens had activity against KB, HepG₂ and HeLa at the IC₅₀ values of 0.3–40, 0.2–37.5 and 0.3–60 µg/ml, respectively. The methanolic extract of *P. internigrans* had weaker activity than that of *P. mastoidea*. However, it exhibited lower toxicity with normal cells than other crude extracts, except the crude chloroform extract of *P. mastoidea*. Purification and identification of the bioactive components from these lichens are under investigation.

Phylogenetic position, metabolic profile, and antibacterial extracts of the Antarctic lichen *Himantormia lugubris*

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Lichen forming fungi produce a tremendous diversity of metabolites, with at least 1050 metabolites described so far. To elucidate the properties of some of these in more detail, we obtained the metabolomic profile of the Antarctic endemic *Himantormia lugubris*. The phylogenetic position based on a six-gene phylogeny (ITS, nuLSU, mtSSU, RPB1, Mcm7 and Tsr1) shares a sister relationship with *Coelopogon* and *Menegazzia*. Metabolic profiles were determined by non-targeted 1H-NMR and GC-MS analysis of a methanolic extract. 5,7-Dihydroxy-6-methyl-phthalide was identified as a key marker compound. Specimens growing on either rock or mosses did not differ in their main secondary metabolites. Antibacterial activity of the extracts was screened against multidrug-resistant bacterial strains isolated from clinical specimens in Chilean hospitals. Most of the bacterial strains – methicillin-resistant *Staphylococcus aureus* (MRSA), vancomycin-resistant enterococci (VRE), *Escherichia coli* and *Acinetobacter baumannii* – were inhibited in their growth or killed at concentrations >100 g/mL. *Klebsiella pneumonia*, however, were killed only by concentrations >250 g/mL.

Yellow species of genus *Rhizocarpon* and their secondary metabolites in the Czech Republic

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As part of a herbarium revision of yellow *Rhizocarpon* species group, we examined also secondary metabolites in lichen thalli. 14 *Rhizocarpon* species was identified by presence of specific lichen acids determined by TLC. *Rhizocarpon geographicum* group has shown high intraspecific variability of secondary metabolites and also frequent morphological transformation. Three species *Rhizocarpon ferax*, *R. riparium* and *R. sorediosum* have been discovered for the first time in the Czech Republic. It seems that current investigation of chemical and morphological characters could show interesting results if compared with molecular phylogenetic.

From lichen chemistry to lichen herbaria: the lichen research group in Rennes

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Since the early 2000, a phytochemist group in the University of Rennes1 is focusing its research on secondary lichen metabolites to be valued, mainly for pharmaceutical properties. The work is carried on with full respect of lichen preservation and collaboration with lichenologists is a key point to go on. The team is composed of chemists (phytochemists, analytical, organic and medicinal chemists). Two unique lichen herbaria (H des Abbayes and L JC Massé) which are preserved as associated facilities to the lab are also kept and valued with their attached library. Some results on lichen chemistry will be presented along with perspectives for the development of new analytical tools. Mass spectroscopy and other analytical methods, particularly suitable to obtain accurate data will be discussed. Results obtained with minute amounts of lichen material allow to include some historical herbarium specimens and generate informative data through histolocalization of lichen metabolites. As the lab activities are expanding through the study and cultivation of the bacteria associated to the lichen thallus, along with international networks, interdisciplinary approaches appear to be a challenge and a real opportunity.

Antifungal activities of crude extracts of *Parmotrema* against some plant pathogenic fungi

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The three dominant species of Parmelioid lichens were collected at Phu Luang Wildlife Sanctuary and identified as *Parmotrema gardneri*, *P. maclayanum* and *P. tinctorum*. They were air-dried for 24 hrs., and then macerated and extracted in either dichloromethane or ethyl acetate for 48 hrs. The dried crude extracts were suspended in dimethyl sulphoxide and tested for antifungal activity against the mycelial growth of seven plant pathogenic fungi including *Botrytis cinerea*, *Colletotrichum gloeosporioides*, *Curvularia lunata*, *Fusarium moniliforme*, *Phytophthora palmivora*, *Pythium aphanidermatum* and *Sclerotium rolfsii*. The dichloromethane crude extract of *Parmotrema maclayanum* possessed the greatest bioactivity of all of the lichen extracts tested. At 500 ppm it produced effective inhibition to the mycelial growth of *Botrytis cinerea*, *Phytophthora palmivora* and *Pythium aphanidermatum* at 94, 87 and 94%, respectively, whereas it inhibited 70, 78% mycelial growth of *Colletotrichum gloeosporioides* (70%) and *Curvularia lunata* (78%). The dichloromethane and ethyl acetate extracts of the other lichens also were effective against the test fungi but not to the same extent. This work points out the prospects of finding interesting novel sources of bioactive compounds from the world's lichens.

Aspects of biodiversity and chemical diversity studied in Hungarian lichen herbaria

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Due to HPTLC studies the knowledge of lichen substances in Hungarian samples has developed a lot since 1998. The distribution patterns of secondary metabolites within lichen thalli are often taxon specific, and therefore have been widely used in lichen taxonomy and systematics since they represent cryptic chemical diversity additional to morphological-anatomical biodiversity. *Cetrelia* and *Xanthoparmelia* species were studied in details. A total of 430 specimens of historical and recent collections (6 Hungarian herbaria) were studied mostly from Central Europe, the Balkan and Eastern Asia. Vegetative propagules (soredia, isidia), pseudocyphellae, rhizines, features of lower surface are the main morphological characters analysed against alectoronic acid, anziaic acid, α -collatolic acid, imbricarinic acid, 4-demethyl imbricarinic acid, microphyllinic acid, 4-O-demethylmicrophyllinic acid, olivetoric acid, 4-O-methylolivetoric acid, perlatolic acid, physodic acid, 4-O-methylphysodic acid (*Cetrelia*), fumarprotocetraric acid, norstictic acid, salazinic acid, stictic acid (*Xanthoparmelia*). Cortical pigments, atranorin in *Cetrelia*, usnic acid in *Xanthoparmelia* are usually present, but some specimens are lacking these substances. Comparing the distribution of species before and after the taxonomic revision based both on morphology and lichen secondary chemistry, several striking examples are presented for demonstrating the importance of lichen substances in identification. Our work was supported by the Hungarian Scientific Research Fund (OTKA K81232).

The influence of melanins on iron accumulation in parmelioid lichens

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The external surfaces of parmelioid lichens, particularly the lower cortex, are frequently dark pigmented by melanins, which can bind metal ions and carry out photo-protective and antioxidant functions. In this study the content of iron (Fe) in 10 lichens with different degree of melanisation were evaluated by means of micro-XRF and ICP-AES. For each lichen 3 groups of 3 lobes were analyzed. Micro-XRF analyses were conducted on the upper (U) and the lower (L) cortex and also on the medulla (M) for 6 selected species. ICP-AES analyses were conducted on the lobes with the lower cortex intact (U+L) or mechanically removed (M). Sequential elutions (SE) were carried out on the heavily melanised *Melanelixia subaurifera* and the poorly melanised *Punctelia subrudecta* to verify whether Fe was effectively bound to melanins. The highest Fe content was observed in the lower cortex but SE data also indicate that the majority of Fe is included in the residual fraction and is not bound to melanins. Furthermore, the extracellular fraction of Fe was similar in both species suggesting that melanins are not a pivotal factor in the total Fe accumulation, although they might play a role in the sequestration of Fe ions.

Can parietin transfer energy radiatively to photosynthetic pigments?

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The main role of lichen secondary compounds is the protection against biotic and abiotic stresses. Among the latter, induction by/protection from UVA and UVB has been demonstrated for many species. These compounds frequently are deposited as crystals outside the fungal hyphae and some of them emit visible fluorescence when excited by UV. We wondered whether the conversion of UV into visible fluorescence might be photosynthetically used by the photobiont, thereby converting UV into useful energy. To address this question, thalli of *Xanthoria parietina* were used as model system. In this species the anthraquinone parietin accumulates in the outer upper cortex, conferring the species its characteristic yellow-orange colouration. In ethanol, parietin absorbed strongly in the blue and UVB and emitted fluorescence in the range 480–540 nm. In intact thalli, it was determined by confocal microscopy that fluorescence emission spectra shifted 90 nm towards longer wavelengths. Then, to study energy transfer from parietin, the response to UV of untreated thalli was compared with that of parietin-free thalli (pretreated with acetone for its removal). The effects of radiative transfer between parietin and photosynthetic pigments after excitation with UVA or UVB and their implications for photoprotection and photosynthetic performance of photobiont are discussed.

Secondary metabolites from lichen and lichen-forming fungi of *Marcelaria cumingii*

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Marcelaria cumingii, a crustose lichen from tropical region in Thailand, led to lichen culture with the ascospore discharge technique. Parietin, emodin, and lichexanthone which produced from lichen whereas (–)-5'-hydroxytryptelone, (–)-tryptelone methyl ether, (–)-8-methoxytryptelone methyl ether, (–)-4'-hydroxy-8-methoxytryptelone methyl ether and (–)-tryptelone were isolated from lichen-forming fungi. These secondary metabolites were purified by chromatographic methods, analyzed with HPLC and elucidated their structures by spectroscopic techniques on the basis of 1D, 2D NMR and HRMS. The absolute configurations were characterized by optical rotation and circular dichroism.

Gene expression analysis of polyketide synthases in mycobiont culture of *Usnea rubrotincta*

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Lichen substances have been used as medicines, dyes and perfumes since ancient times all over the world. However, it is difficult for stable mass production of useful lichen substances by mycobiont culture. To clarify the biosynthetic pathway of depsidones of *Usnea rubrotincta* for heterologous production, we investigated the relationship between secondary metabolism and gene expression of the six polyketide synthase (PKS) genes, which had been selected by RNA-seq analysis. Mycobiont cultures were transferred from liquid to solid media to induce salazinic acid and norstictic acid, that are depsidones in *U. rubrotincta*. Metabolites and mRNA were extracted and subjected to HPLC analysis and real-time RT-PCR, respectively. The production of salazinic acid and norstictic acid was induced and peaked at 4 weeks after transfer. Among six genes, PKS5 transcript level was only found to increase markedly and reach a maximum level at 4 weeks. The expression pattern was similar to the production of depsidones. Thus, PKS5 may play an important role in the biosynthesis of depsidones in mycobiont culture of *U. rubrotincta*.

Types in melanic pigments in non-Peltigeralean and nitrogen-fixing Peltigeralean lichens

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Melanins are a diverse group of dark pigments found in most organisms, including many lichens. As UV light induces melanin synthesis in some species, cortical melanins may have an important role in photoprotection. In free-living Ascomycetes, melanins are synthesized by the enzymatic polymerization of N-containing or N-free polyphenols. "DOPA" melanins are synthesized by the tyrosinase-catalyzed polymerization of 3, 4-dihydroxyphenylalanine, producing melanin containing c. 10 % N. By contrast, "DHN" melanins are synthesized by polyketide synthases and other enzymes that polymerize 1, 8-dihydroxynaphthalene, producing melanin containing c. 1 % N. In our earlier work we showed that, Peltigeralean lichens display high tyrosinase activities, while tyrosinase activity is often absent in non-Peltigeralean species. Furthermore, Peltigeralean lichens often contain N-fixing cyanobacterial photobionts, while non-Peltigeralean have chlorophycean photobionts. It was then hypothesized that tyrosinase-producing lichens are most likely to produce DOPA melanins, while tyrosinase-limited lichens are more likely to be of the DHN type. To test our hypothesis, we developed protocols for extracting and precipitating melanins from a variety of lichens. Nitrogen determinations of these melanins were consistent with our hypothesis that Peltigeralean and non-Peltigeralean species produce DOPA and DHN melanins respectively. The biosynthesis and roles of melanins in lichen biology are discussed.

New species of *Lecanora* s.lat. in Northern Europe

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The genus *Lecanora* s.lat. in the Nordic countries comprises at least 132 species. It includes many difficult groups, among them the *L. dispersa* group that was recently segregated as the genus *Myriolecis* Clem. Other taxonomically difficult groups include the *L. subfusca* group, and the *L. polytropha* group. Several new species are being proposed as new to science in these groups and new relationships between and within groups or segregated genera are presented. For example, the normally sorediate *L. impudens* is shown to have an unknown completely esorediate but fertile counterpart that is impossible to separate morphology from *L. allophana*. However, as with the sorediate morph there is a slight chemical difference between the species. A similar case is found within *L. chloroleprosa*, a species described as sorediate, rarely with apothecia. It is actually rather often occurring with only apothecia and no soralia. The species *Myriolecis albescens* and *M. salina* are both shown to consist of two sister species, that seems to be unknown to science.

The habitat traits drive genetic diversity of a widespread epiphytic lichen *Usnea subfloridana* in hemiboreal forests

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Patterns of genetic diversity, an imperfectly studied aspect of biodiversity in lichenized fungi, could be shaped by exogenous factors of habitat. We aimed to study the genetic variation of vegetatively reproducing epiphytic lichen *Usnea subfloridana*. Seven populations from two geographical regions located in 210 km from each other, in Estonia (Northern Europe) were researched. We sampled 319 *Usnea* thalli from *Picea abies*, in forest stands between 84–143 years. Recently developed nine fungus specific microsatellite markers were used to measure the genetic diversity (H) among populations. The GRM analysis with stepwise selection procedure was applied to study the relationship between H and characteristics of forest stands. We also estimated genetic differentiation among populations using AMOVA analysis. Our results revealed low but significant genetic differentiation between regions as well as among the populations. The H of *U. subfloridana* populations was significantly higher in forest stands of south-eastern than of northern region. The H was also positively correlated with forest stand age in both regions. The forest structure (percentage of *Pinus sylvestris* in the first tree layer) also had an effect on the genetic variation of lichen populations. Our results indicated that habitat characteristics influenced the genetic diversity of lichen populations.

Specific dispersal patterns and population structures of saxicolous lichens on the stone cultural heritage

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Functional trait and genetic analyses have suggested relationships between reproductive strategies and specific population structures and dynamics. However, hypotheses on different levels of dispersal limitations have been poorly supported with an aerobiological approach. In this work, we examined lichen colonization on three calcareous balustrades in monumental sites of Turin (NW-Italy), combining analyses of specific population structures and of dispersal patterns of sexual and asexual propagules. In particular, short- and long-distance dispersal effectiveness was investigated in laboratory under controlled conditions of air flow using deposition samplers and a Hirst-volumetric sampler, respectively. Eight species commonly found on the stone Cultural Heritage were considered, representative of epilithic and endolithic, apotheciate, peritheciate and sorediate crustose lichens. Species with larger propagules displayed higher dispersal limitations, reflected by a lower and aggregated occurrence on the monumental surfaces. Whereas, higher dispersal of small meiospores to both short- and long-distances likely favoured the more frequent and disperse occurrence of remnant lichens. Such an information may contribute to improve the Cultural Heritage management supporting the prevention of rapid recolonization processes after restoration works. Species with more or less dispersal limitations represent indeed a different threat for the cleaned monumental surfaces if fertile thalli persist in the nearby areas.

Local genetic differentiation between *Usnea aurantiaco-atra* and *U. antarctica*

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Lichens constitute the principal components of Antarctic terrestrial biota. The most common species in the Maritime Antarctic are *Usnea aurantiaco-atra* and *U. antarctica*. On King George Island (South Shetland Archipelago), the two species occupy the same areas but show different dispersal strategies and morphology; *U. antarctica* produces soredia while *U. aurantiaco-atra* has apothecia and is usually larger. *Usnea antarctica* is reported to have the widest distribution, while *U. aurantiaco-atra* is absent from Continental Antarctic. Previous studies showed that genetic differentiation between the taxa and morphological variation were both structured along a latitudinal gradient. Authors suggested to synonymize the taxa arguing that reproductive mode is not strictly correlated with genetic differences. Indeed, both sexual reproduction strategies are often observed on the same individual. However, the sample size of previous studies was rather small and samples were collected from distant areas. In this work, we studied genetic differentiation at the local scale. We investigated 120 individuals from mixed stands close to the Argentinian research station Carlini on King George Island. We sequenced the ITS (internal transcribed space) and mtSSU (mitochondrial small ribosomal subunit) regions to quantify differentiation between the two morphotypes and study haplotype networks to infer their taxonomic status.

Intraspecific variation of *Polycauliona candelaria* (L.) Frödén, Arup & Söchting (Teloschistaceae)

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Lichens with bipolar distribution constitute about 40% of the known flora in Antarctica. Currently, most of the studies on the evolution of bipolar species of lichens point to a probable Holarctic origin and colonization of the southern regions through dispersion. *Polycauliona candelaria* is a fruticose lichen, with rare apothecia, frequently sorediate, and markedly ornithocoprophilic. The aim of this work was to evaluate the genetic patterns along its wide distribution with DNA sequence data. We requested herbarium material from north and south hemispheres, except Antarctica (sampled by our research group). After DNA extraction, ITS region was amplified and sequenced in a preliminary analysis. Until the moment, 50 sequences were obtained and 17 haplotypes detected: 10 from northern hemisphere specimens and seven from Antarctica. Only one point mutation differentiated northern and southern haplotypes indicating the absence of a marked geographic subdivision of the genetic variation. After this initial screening, more genetic markers and specimens will be added to analyses in order to provide a complete overview of the origin and dispersion routes of this species. CNPq, PROANTAR, FUNDECT

Phylogeographic patterns of *Sphaerophorus globosus* (Hudson) Vainio (Sphaerophoraceae)

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Studies on bipolar lichens have been based on morphological and molecular data to understand its striking geographical distribution. Lichens present exceptional dispersion abilities. Exclusively fungal structures appear to be more effective over long distances. *Sphaerophorus globosus* species complex is composed by *S. globosus* (a supposed bipolar species), *S. tuckermanii*, *S. venerabilis* and *S. fragilis*. In this study, our main objective is to achieve a comprehensive sampling of these taxa to provide a better understanding of its evolutionary patterns. We analyzed freshly collected (Antarctica and Alaska) and herbaria specimens (northern hemisphere) along the known geographic distribution of the complex. Different regions of the nuclear and mitochondrial genomes were tested, amplified and sequenced. Despite the high morphological diversity and phenotypic plasticity presented by the specimens, sequences obtained showed low values of intra and interspecific genetic distances, interspecific haplotype sharing and limited phylogenetic resolution. These patterns are congruent with a recent process of diversification followed by dispersion events, probably from northern to southern hemisphere. We confirmed the existence of a bipolar species of *Sphaerophorus* (whose nomenclatural status is not resolved), and registered the first records of fertile specimens in Antarctica. CNPq, PROANTAR, FUNDECT.