



The Bryological Times



Volume 149



SPECIAL ISSUE

Abstracts from the 2019 joint conference between the International Association of Bryologists, the Spanish Bryological Society, and the International Molecular Moss Science Society

In 2019, The International Association of Bryologists celebrated its 50th anniversary and held its biennial conference in Madrid, Spain, together with the Spanish Bryological Society, which was founded 30 years ago, and the International Molecular Moss Science Society (iMOSS). The event (www.bryology2019.com), was hosted by the Royal Botanical Garden, a 260 year old institution in the historic center of Madrid, and organized by an committee led by Dr. Jesús Muñoz. Two hundred and fifteen colleagues from 40 countries attended this historic conference, including nine students who earned travel awards from IAB. Seventy-nine oral presentations and 87 posters, spanning a broad spectrum of topics from floristic inventories to gene function were made over the two and a half days, which each morning or afternoon session launched by inspiring talks by five keynote

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speakers, Drs. Silvia Pressel and Robbert Gradstein invited by IAB, Jill Harrison and Mitsuyasu Hasebe (iMOSS) and Javier Martínez-Abaigar and Rubén G. Mateo (SEB). At the closing ceremony IAB recognized several bryologists for their significant contributions to bryology: Dr. Matt Renner (Spruce award), Dr. Juan Guerra (Hattori Prize), and Dr. Juan Larrain (Grolle award) (for more info visit: <http://bryology.org/iab-awards-2019/>).

Stanley Greene research awards were earned by two young researchers, Eugene Lorence R. Logatoc (University of the Philippines, Los Baños) and Brian Espinoza-Prieto (Universidad Nacional Mayor de San Marcos, Peru). The conference was preceded by a two-day training workshop of the IUCN Bryophyte Specialist Group (BSG) on IUCN red-listing methodology. This workshop was

organized by the Steering Committee of the IUCN SSC Bryophyte Specialist Group (Drs. Irene Bisang & Jacques van Rooy, Co-chairs BSG; Ariel Bergamini, Red List Authority BSG), and Dr. Matt von Konrat (IAB Council), and sponsored by the Mohamed bin Zayed Species Conservation Fund, IUCN-Centre for Mediterranean Cooperation Málaga, Spain, IUCN Global Species Programme Red List Unit Cambridge, UK, Royal Botanic Garden (CSIC), Madrid, Spain and IAB. Organizers also proposed two field trips to explore the regional bryoflora: a one day excursion led by Francisco Lara, Juanjo Calleja, Maren Flagmeier and Isabel Draper (Universidad Autónoma de Madrid) to the Mediterranean mountain area of La Pedriza, close to Manzanares el Real, and a three day post-conference excursion led by Modesto Luceño, to Sierra de Gredos, an area known

for its biodiverse mesotrophic mires. We, the presidents of IAB, iMOSS and SEB wholeheartedly thank the Royal Botanical Garden for hosting this joint event, and Dr. Muñoz and his organizing and scientific committees for coordinating this tremendously successful meeting, as reflected by the diversity and quality of the abstracts compiled and indexed here.

Bernard Goffinet (IAB), Stefan Rensing (iMOSS) & Patxi Heras (SEB).

Editors: Matt von Konrat, Bernard Goffinet, Yarency Rodriquez, Beth McDonald, Caroline Zapata, Mendkhuu Enkhbayer, Elena Arnett, Jessica Harris and Jo Martinec



Oral abstracts

OR-01

Johannes Hedwig and the founding of modern bryology

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Johannes Hedwig (1730-1799), one of the founding fathers of modern bryology, was a pioneer of his time. He maintained an impeccably organized herbarium, described 82 mosses that were new to science and greatly increased the number of moss genera in use at the time, effectively beginning the process of scientific recognition of moss diversity. Above and beyond these taxonomic contributions, however, he revolutionized the bryological thinking of his era, detailing different morphological structures in mosses, as observed under the microscope. He later used features to group and classify them (presence/absence of an operculum or a

peristome, peristomes with one or two rows of teeth), introducing a substantial number of concepts or terms into the bryological lexicon along the way that we still use today (antheridia, sporangium, spore). A practicing medical doctor for many years in Chemnitz, Hedwig studied and collected plants, including bryophytes, in his free time. After receiving a microscope from J.D. Schreber sometime around 1760 he became interested in the features and functioning of structures in smaller and smaller organisms. Realizing that microscope-based observations revealed natural variations and traits of scientific importance, around 1770 he learnt to draw and began to illustrate his findings. His original illustrations accompany his works and they are a great testament to both his observational and illustration skills. He was interested in the natural history of mosses (*Fundamentum historiae naturalis muscorum frondosorum*) and also studied the reproduction and reproductive organs of cryptogams more generally (*Theoria generationis et fructificationis plantarum cryptogamicarum*). He went on to produce a four volume series containing detailed descriptions

and illustrations of the mosses known to him (*Descriptio et adumbration microscopico-analytica muscorum frondosorum*) before embarking on what would become his posthumous magnum opus *Species muscorum frondosorum*, a work that was finished by his student C.F. Schwägrichen for publication in 1801. Hedwig's body of work has had a long lasting influence on our particular branch of science, not only as his 1801 work is the designated starting point of the nomenclature of mosses (expecting the Sphagnaceae), but also due to the perspicacity of his observations of morphological features in the mosses.

OR-02

Kurt Goebel, George and Andreas Schimper: their eclectic contributions to bryophyte biology

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Most of the founding fathers of bryology are remembered for what might best be described as floristic works viz. species descriptions and illustrations and floras that we all rely on and indeed take for granted today. Kurt Goebel (1855-1932), George Schimper (1804-1878) and his son Andreas' (1856-1901), most important contributions to bryophyte biology are somewhat different and have important implications today far beyond that envisioned when the original studies were carried out. Perusal of the beautiful illustrations in the 6 volumes of B.S. & G., for which George Schimper is best known as the 'S', reveal the only illustrations of the paraphyses in a multitude of taxa and dextral coiling of peristomes across mosses whereas the setae switch from sinistral at the base to dextral immediately below the capsules. His uncannily accurate description of stem ontogeny in *Sphagnum* is a supreme model for plant anatomists whose reinvestigation in recent years led to the discovery that *Sphagnum* stems contain food-conducting cells with organelles aligned along longitudinal arrays of endoplasmic microtubules like those in peristomate mosses. His son Andreas gave the first descriptions of plastids, and then went on to explain the

interconversion of the different types and showed their transmission through germ cells (the eggs of hornworts). In 1883, he postulated the endosymbiotic origin of chloroplasts, long before this notion gained general credence in the 1960s. Goebel was a student of Hofmeister who must certainly have influenced his lifelong interests in morphology comparative functional anatomy, and the developmental physiology of plants particularly in phylogenetic contexts. Perhaps one of the greatest services to non-German speaking botanists was the translation of his book 'Organography of Plants' by Balfour in 1905. In this book we find a compilation of just about everything known at that time about how plants work with significant amounts of coming from his own research which included a meticulous description of the fungal endophyte in *Treubia*. Ultrastructural re-examination this association followed by experimental and molecular studies have now led to the establishment of mucoromycote fungi as probably the earliest symbionts at the dawn of land plant evolution.

OR-03

The contribution of Richard Spruce to the hepaticology and tropical bryology

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Spruce was interested in botany since his childhood. He was a paragon of Victorian age scientists, having multiple talents, becoming familiar not only with vascular and cryptogamic botany, but also with tropical crops (like quinine and the rubber plant), ethnography, linguistics, geography and geology, and being an amateur musician. He was contemporary of Humboldt, Martius, Darwin and Wallace. His first major bryological work was *The Musci and Hepaticae of the Pyrenees* (1850), including a new genus (*Southbya*). Encouraged by Hooker and Bentham, he went to Brazil, Peru and Ecuador, to collect plants for Kew Garden. His expedition, through the tributaries of Amazon River and the Andes to the Pacific coasts, lasted for 15 years (1849-1864) and resulted in an enormous number of bryophytes, more than 7000 vascular plant species, seedlings and seeds of rubber and quinin trees and a lot of economic, ethnographic,

geologic and linguistic observations, but cost him his health and fortune. His magnum opus, after publishing the *Palmae Amazonicae* (1869), was *Hepaticae Amazonicae et Andinae* (1884-85), in which he described near 400 species and 4 genera new to science. The greatest taxonomic significance of this work was the subdivision of genus *Frullania* in up to 6 still valid subgenera and the division of the giga-genus *Lejeunea* into 39 subgenera. The majority of these gained generic rank and form today the basis of the classification of the Lejeuneaceae. His strenuous efforts to make valuable plant collections under difficult conditions and many adventures were documented in his diary and letters, edited after his death by his friend, Alfred Russell Wallace. His liverwort specimens, processed by himself, are deposited in Manchester herbarium (MA), his moss collection, identified by Mitten, in the New York Botanical Garden herbarium (NY), while his vascular plant collections are in Kew Garden herbarium (K) with duplicates in numerous other herbaria.

OR-04

Victor Ferdinand Brotherus' contribution to world diversity of mosses

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Finnish bryologist V. F. Brotherus (1849–1929) became internationally known after his thesis for Ph.D. “*Études sur la distribution des mousses au Caucase*” (1884) and his “*Enumeratio muscorum Caucasi*” (1892) were published. He began to get letters from botanists and expeditions asking him to identify their collections. Brotherus became soon known of his ability to identify the specimens from exotic areas such as Japan, the Philippines, Australia, and Argentine and publish the material quickly. His fame was later confirmed when Adolf Engler (1844–1930) asked him to write the major part of “*Musci*” for “*Die natürlichen Pflanzenfamilien*” (1901–1909). The classification system in the 1st edition was oldfashioned, and A. Engler requested Brotherus to adopt M. Fleischer’s (1900–1922) phylogenetic system for the 2nd edition (1924, 1925). At the same time with the 2nd edition, he wrote the flora “*Die Laubmoose Fennoscandias*”

(1923) and studied the material from China collected by H. Handel-Mazzetti (1882–1940). These were published in “*Musci*” in Handel-Mazzetti’s series “*Symbolae sinicae*” (1929). Altogether Brotherus published 176 articles or books, and described c. 80 genera and c. 1800 species of mosses. His collection of letters, preserved in the library of the University of Helsinki, contains 4751 letters from 504 different persons.

OR-05

The dawn of bryology in North America: a tale of a cursed flora

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The *Manual of the Mosses of North America*, written by Léo Lesquereux and Thomas Potts James in 1884, was the first attempt to complete a comprehensive moss flora of the United States and a key milestone in the botany of the country. The history of this work, however, involves a long process that spans almost four decades and that was compromised by the different life circumstances of everyone involved. Perhaps the most eloquent anecdote that illustrates the long development of this book is the one recovered by Elizabeth Britton in a note written in 1924 and found in a specimen of NY: she was told that the *Manual* was published “by a man who knew nothing of mosses, for a blind man, and a dead man”. Using this quote as a prompt we explore biographic and epistolary sources to understand the history of the development of this flora starting when it was first commissioned to William Sullivant by Asa Gray. The members of the “Sullivant circle”, and in particular the partnership between the latter and Lesquereux, are behind the first golden period of the study of bryophytes in the United States.

OR-06

International collaboration among bryologists: past, present, future

Robbert Gradstein

International collaboration among bryologists, commonplace today, has a long history that spans almost two hundred years. The article on the moss genus *Spiridens* by Christian G. D. Nees von Esenbeck from Bonn and Carl G.C. Reinwardt from Leiden may be considered the first international bryological publication. The first major international undertakings, with participation of bryologists from different nations, were *Bryologia Europaea* (1836-1851) spearheaded by Wilhelm Philipp Schimper in Strasbourg and *Synopsis Hepaticarum* (1844-1847) initiated by Christian G. D. Nees von Esenbeck. These works are the culminations of the "Golden Period" of bryophyte morphology and taxonomy around the mid-19th century. In the first half of the 20th century international collaboration was promoted by Frans Verdoorn in Utrecht through *Annales Bryologici* (1927-1939), the first bryological journal with an international editorial board, and the multi-authored *Manual of Bryology* (1932) with contributions from six nations. In 1966, at the Pacific Science Congress in Hawaii, William C. Steere (USA) together with Stanley W. Greene (UK) and Zennoske Iwatsuki (Japan) took the initiative towards the establishment of an International Association of Bryologists, founded three years later in Seattle. Several multinational endeavors were successfully promoted by the organization, which this year celebrates its golden jubilee. Today, technological advances have enabled a multitude of international projects, resulting in major advances in the field. Nevertheless, fruitful international collaboration remains a challenge that requires active communication, creativity, friendship, flexibility and enthusiasm.

OR-07

Genetic and morphological differentiation in the genus *Conocephalum* (Hepatics).

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The genus *Conocephalum* Hill is a sole member of the Conocephalaceae (Marchantiidae). It includes three species, i.e., pan boreal *C. salebrosum*, European *C. conicum* (L.) Dumort. and East Asia endemic *C. japonicum* (Thunb.) Grolle. A number of studies using allozymes and DNA sequences (*rbcL*, *psbA*), revealed unexpected complex structure and nowadays it is widely accepted that there are probably three additional species in *C. conicum* complex (A, F, J) and three in *C. japonicum* (JN, JS and CS). Though they are highly differentiated and thus should be treated as different species, only the *C. conicum* "S" has been described as separate species, *C. salebrosum*. Inter-relationship among these cryptic species especially for A, F, and J, is left ambiguous because of limited sampling. We used *rbcL+rps4* sequences to study distinctiveness of each cryptic species and their exact inter-relationship. Samples used in this study were from the long-cultivated strains maintained in Poland as well as newly gathered ones mainly from Japan and Taiwan. As a result, presence of total six species in *C. conicum* and three in *C. japonicum* were confirmed. Among them, there is one additional species previously recognized as *C. conicum* R (Miwa et al. 2009) or *C. conicum* Type III (Toyota 1994, Kim et al. 2001); it is analyzed as being sister to the rest of five species. It has unique metabolic and morphological features, such as presence of trans-methyl cinnamate in natural conditions and absence of mucilage cavity in the central part of thallus. Based on DNA haplotypes, we examined morphological features and distributional patterns of the three cryptic species (*C. conicum* F, J, R) and *C. salebrosum* distributed in the Japanese Archipelago. Each species shows separate distributional pattern well coincided to climate and soil pattern.

OR-08

UV tolerance in a Mojave Desert biocrust moss

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Terrestrial mosses dehydrate and go quiescent between precipitation events. Although many mosses are found in cool, low light environments, a number are abundant in drylands. We investigated the effects of ultraviolet (UV) radiation on the desert moss *Syntrichia caninervis*. This species is highly desiccation tolerant; it can lose almost all of its cellular water and recover after rehydration. In nature, desert mosses not only have to withstand the damage of desiccation itself but must also be able to recover from any damage incurred while dry, or have adequate mechanisms for injury prevention. They have no ability for active repair when quiescent and face risk of damage to sensitive molecules, including DNA, which absorbs UV wavelengths. We used chlorophyll fluorescence and transcriptomics in field and laboratory experiments to better understand the dimensions of UV tolerance in *S. caninervis*. 40 naturally occurring patches of *S. caninervis* were covered with UV-filtering (>80% reduction) or UV-transmitting (>80% transmission) windows. After one year, chlorophyll fluorescence was used to compare photosynthetic performance of the UV-reduced and control mosses after collection and during an 8-day simulated winter recovery in the laboratory. Next, a growth chamber experiment was performed to test the combined effects of UV radiation and desiccation and to identify candidate genes for UV tolerance. We find that, interestingly, UV-reduced mosses have poorer maximum photosynthetic efficiency (F_v/F_m) and this difference persists over 8 days in recovery. Additionally, we find differential abundance of photosynthesis-related transcripts in response to UV treatment, controlling for desiccation effects. These field and laboratory experiments uncover detailed information about this plant's response to UV and desiccation, improving our understanding of the combined effects of UV and desiccation stress on this desert moss species.

OR-09

From the South to the North – The evolutionary history of the simple thalloid liverwort *Metzgeria* (Metzgeriaceae, Jungermanniopsida)

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Most studies that deal with the evolution of epiphytic liverworts focused on leafy liverworts. Here we employ the study system *Metzgeria* to investigate the historical biogeography of the only epiphytic thalloid liverwort genus. *Metzgeria* has a worldwide distribution with hotspots of diversity in the southern hemisphere, particularly the Neotropics and Australasia. Currently there are around 100 species accepted of which we could include about 40%, covering its full geographic range. We used Maximum likelihood and Bayesian analyses on a chloroplast dataset (trnL-trnF, rps4, rpl16) to infer the phylogeny of *Metzgeria*. Divergence times were estimated with a Bayesian relaxed clock approach and the fossil *Metzgeriothallus sharonae* (Late Middle Devonian, 387-382 Ma). Ancestral areas were estimated in BioGeoBEARS. *Metzgeria* likely originated in the Permian and its crown group diversification took place in the Cretaceous, followed by Cenozoic radiations. The evolutionary history of *Metzgeria* was shaped by ancient Gondwana vicariance and subsequent dispersal events to the Northern hemisphere.

OR-10

Functional traits related to growth and decomposition in *Sphagnum*

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Net primary productivity of northern peatlands is relatively low, but in combination with slow

decomposition it has led to extensive postglacial storage of carbon in peat. Peatmosses (*Sphagnum*) are ecosystem engineers that largely govern carbon sequestration in these ecosystems. My thesis concerned functional traits in *Sphagnum* species, and I will present the parts of this work addressing three questions: (I) Are growth, photosynthesis and decomposition, and the trade-offs between these traits related to habitat or phylogeny? (II) What are the determinants of decomposition and are there trade-offs between metabolites that affect decomposition? (III) How do macro-climate and local environment determine growth in *Sphagnum* across the Holarctic? We found support for a trade-off between growth and decay resistance, but innate qualities translated differently to field responses in different species. There were no trade-offs between production of different decay-affecting metabolites (soluble phenolics, lignin-like phenolics and the cell-wall carbohydrate sphagnum), instead, the species with lower decomposition had more of all these. We found that metabolite production was constrained by phylogeny, but the effects of the metabolites on decay were modified by nutrient availability in the habitat. Precipitation, temperature and vascular plant cover were the best predictors of the growth of two species (with different functional traits) across the Holarctic. In a changing climate, *S. fuscum* will retain its carbon uptake, while *S. magellanicum* will decrease its carbon uptake if a warmer climate coincides with less precipitation. My work has advanced the emerging field of trait ecology in *Sphagnum* revealing an ever more complex picture of *Sphagnum* ecology. Also, the data offer opportunities for improvements of peatland ecosystem models. Functional trait-relationships are necessary for understanding the long-term dynamics of peatland communities; in a changing world such relationships will affect carbon sequestration and management of carbon stocks.

OR-11

The rare male enigma in bryophytes – what do geographic scales, environment and life histories tell

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The female bias in adult sex ratios in unisexual bryophytes that are reproductive remains intriguing. In most cases, it is unresolved whether it is due to more female than male genotypes (genotypic) or higher proportions of sex expressing females (phenotypic). Previous sex ratio studies have mainly dealt with species in dry habitats, or with species of disturbed habitats that grow fast and freely reproduce sexually in cultivation. Here, we investigate intraspecific sex ratio variation and its drivers in the *Syntrichia ruralis*-complex and in long-lived pleurocarpous mosses. We focus particularly on northern European populations of three mosses that occasional to rarely reproduce sexually and occur in different wetland habitats (*Drepanocladus turgescens*, *D. trifarius*, *D. lycopodioides*). In these, we identified sex based on sexual structures, when present, or used specifically designed molecular markers, when sex structures were absent, and calculated phenotypic and genotypic sex ratios. In all studied species, reproductive females outnumbered reproductive males, sex expression levels and phenotypic sex ratios varied among regions, and they were partly related to sporophyte occurrences. Phenotypic and genotypic sex ratios of the *Drepanocladus* species were all female-skewed in the Scandinavian populations, and overall, there was no difference between the sexes in the proportions of sex expression. In *D. turgescens*, females were relatively more often sex expressing than males on the Baltic islands, but not on the Mainland. The genotypic sexes of *D. trifarius* were randomly distributed with respect to each other and to environmental conditions, suggesting absence of sexual niche partitioning at a Central Swedish site where the moss remains largely non-reproductive. In *D. lycopodioides* finally, wetness was negatively related to overall sex-expression and to genotypic sex ratio, i.e. relatively more genotypic females than males occurred in wetter places. This could be due to higher resource demands of females for sporophyte production, or higher male sensitivity to wet environments. Bryophyte sex response to

environmental factors seems complex. We hypothesize that it depends on the species' life history traits, including the level of sexual reproduction, general habitat, and their interactions, and it may thus vary among geographic regions and scales.

OR-12

Intraspecific variation in heavy metal tolerance in two terrestrial moss species

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Heavy metal (HM) toxicity constitutes a strong selective pressure that has led to ecotypic differentiation of many flowering plants in very short time frames. In bryophytes, there is still contrasting evidence about the relative contribution of population differentiation and phenotypic plasticity to adaptation to HM pollution, and limited information about the molecular pathways involved. In this study, we explored the molecular mechanisms underlying intraspecific variation in HM accumulation and tolerance in the Cu moss *Scopelophila cataractae*, and the cosmopolitan moss *Ceratodon purpureus*, two terrestrial moss species with contrasting affinity to HM. We sampled four populations of *S. cataractae* from different contamination levels within a former Cu mine, one population of *C. purpureus* in an urban area, and studied male and female plants of *C. purpureus* that were already growing in axenic lab conditions. We cultured all populations under control and Cu enriched conditions. To understand the response to this pollutant we measured Cu accumulation and plant performance (growth and oxidative damage), and used RNA sequencing to detect expression

changes associated with HM exposure. Both species showed population-specific responses for tolerance, but Cu accumulation was similar in all populations within each species. *S. cataractae* isolates from the most polluted location in the mine were significantly more tolerant than the others. For *C. purpureus*, the field-collected population grew better than the lab-maintained population after Cu treatment. Gene expression profiles in control and Cu-treated plants revealed differential expression patterns in response to Cu in the two species. Furthermore, in *C. purpureus*, Cu-treated females had more differentially expressed transcripts (n=549) than Cu-treated males (n=4), when compared to control plants. These results provide evidence of significant population differentiation for HM tolerance at a very small spatial scale in *S. cataractae*, and of sex-specific molecular responses to Cu in *C. purpureus*.

OR-13

Bryophytes underground: diaspore banks in coastal dune systems

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Hidden below ground, bryophyte diaspore banks remain very poorly understood and are usually ignored when undertaking conservation management activities. The purpose of this study is to investigate, for the first time, the occurrence and composition of diaspore banks in coastal dune systems. From eight sites in Wales (UK), 485 soil samples were collected from up to 30 cm depth and subject to germination trials in a growth chamber. Species that germinated were identified by morphological characters, supported by DNA barcoding. Bryophytes germinated from 291 samples (60%), mostly at shallow depth (<10 cm), represented by 35 species (7 liverworts and 28 mosses). Analysis of ecological attributes shows species in diaspore

banks are significantly smaller in size, shorter lived and produce asexual propagules more frequently than species present aboveground. Of particular note, *Amblyodon dealbatus*, Red Listed in Wales, germinated from the diaspore bank of four sites, including a dune system where it was last seen in 1964 and considered extinct. The study highlights the fact that bryophyte diaspore banks comprise an important conservation resource that deserves careful consideration when planning management activities.

OR-14

Polyphyly of a common biocrust liverwort: *Riccia inflexa*.

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The genus *Riccia* is one of two genera which belong to the complex thalloid liverwort family Ricciaceae. *Riccia* is the most species rich with around 53 species described for Australia and approximately 200 species worldwide. They are most diverse in Mediterranean-type environments and are the most common liverwort species found in biological soil crusts. Polyphyly within a widespread and common southern Australian species of *Riccia* prompted a more detailed examination of this group which was usually placed under the species name *Riccia limbata* but more recently transferred to *Riccia inflexa*. In order to test this further, we sequenced collections identified as *R. inflexa* or *R. limbata* across a broad geographical range to determine relationships within the group. We also carefully re-examined the morphology of the group to uncover any overlooked vegetative and in particular spore characters that would support the phylogenetic relationships inferred from molecular data.

OR-15

Predicting bryophyte species diversity in Canadian boreal forests using remote sensing data

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Bryophytes account for a significant fraction of biodiversity in boreal forests and play a crucial role in the functioning of these ecosystems. However, distribution and diversity patterns of bryophytes are poorly documented to date in Canadian boreal forests, hindering conservation tasks in the face of the high industrial activity in the region. The objective of this study was to develop predictive models and cartography of the total bryophyte richness as well as of the richness at the guild level (mosses, liverworts and sphagnum; four models in total) using remote sensing data. Our ultimate goal is to provide an ecological planning tool that allows identifying sites with a high ecological value to exclude them from the industrial development. The study area is located in western Quebec within the region Eeyou Istchee James Bay. A bryophyte presence/absence database from 326 plots was used to develop the response variable for each model, while Landsat spectral bands and indices, ALOS PALSAR data, and bioclimatic, topographic and soil-related variables were used as predictors. 70% of the data was used for model calibration and the remaining 30% for validation. Models and associated cartography were developed using the Random Forest algorithm in R. Resulting models explained 41.6 to 52% and 37.6 to 47.7% of the variation in the richness in the training and test datasets, respectively. Although in general spectral and bioclimatic variables appeared as the most important predictors of the richness of the different modeled groups, the best predictors as well as their relative importance varied among groups, which highlights the importance of working at the guild level to better identify the environmental parameters that determine the richness patterns of these species in relation to their ecological preferences and tolerances. While more accurate and reliable predictive models could be developed in the future using high-resolution data, the results of this study underline the potential of remote sensing in the field of predictive modeling of bryophyte biodiversity and lay the basis for eventual inclusion of

bryophytes, until now overlooked, in ecological planning.

OR-16

Divergence and hybridization in the *Marchantia polymorpha* complex

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The potential role of hybridization and introgression in evolution has gained increased interest in recent years but more examples are needed to generalize its importance, especially concerning organisms with a dominant haploid generation, such as bryophytes. We analyzed genomes of three subspecies of the liverwort *Marchantia polymorpha*. We used available genomic data for subsp. *ruderalis* and carried out whole-genome (PacBio) sequencing for each one individual of subsp. *montivagans* and subsp. *polymorpha* as well as Illumina resequencing of additional genomes for all three subspecies. The three genomes were compared against *M. paleacea* as outgroup. Our analyses revealed separation of the three taxa, but all three possible topologies were richly represented across the genomes, and the underlying divergence order less obvious. This uncertainty could be the result of divergence of the three subspecies close in time, or that introgression has been frequent since divergence. In particular, we found that pseudo-chromosome 2 in subsp. *montivagans* was much more diverged than other parts of the genomes. This could either be explained by specific capture of chromosome 2 from an unknown related species through hybridization or by conservation of chromosome 2 despite intermittent or ongoing introgression, affecting more permeable parts of the genomes. A higher degree of chromosomal rearrangements on pseudo-chromosome 2

support the second hypothesis. Indications of recent hybridization were found in two populations. Species tree analyses recovered an overall topology where *M. polymorpha montivagans* diverged first and *M. polymorpha ruderalis* and *M. polymorpha polymorpha* appeared as sister species and each subspecies was associated with its own chloroplast and mitochondrial haplotype group. Our data suggest introgression but refute a previous hypothesis that subsp. *ruderalis* is a new stabilized hybrid between the other two subspecies.

OR-17

Where, when and what will be the effect of climate change on the distribution of *Anthoceros caucasicus* Steph.?

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The effect of climate change on the species distribution will cause alterations of different sizes and magnitudes depending on the geographical zones and the characteristics of the species. The differentiated effect may be even greater when analyzing species that, although having a wide distribution, present great contrasts in the density of their populations. In this case, we analyze the changes in quantity and quality of the habitat of *Anthoceros caucasicus* Steph. throughout its distribution using ecological niche models. The aim is to evaluate current conditions and how may change in the near future. We used the Maxent algorithm and five global circulation models under three scenarios proposed by the IPCC. We evaluated decade to decade between 2020 and 2080 for the temporal space projection. Results obtained show a considerable increase in the quality of the habitat in Macaronesia as in the regions of the Atlantic cornice (mainly at Macaronesia bioregion, mainland Portugal and

Ireland), the Balkan region, Tunisia and the east coast of the Mediterranean are also shown as areas where the species can reach its habitat in the immediate future. The current Caucasian and Italian population will be negatively affected due to a decrease of habitat availability and habitat quality. *Anthoceros caucasicus* distribution is not compromised in general terms, although large variations are expected on a local scale that could jeopardize the genetic flow (if it still exists) between the east and west Mediterranean populations.

OR-18

A new insight into the genus *Pulviger* (Orthotrichaceae) in North America

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Pulviger lyellii (Hook. & Taylor) Plášek, Sawicki & Ochrya (≡ *Orthotrichum lyellii* Hook. & Taylor) is considered a moss morphologically variable to some extent, especially in North America, and currently includes several synonyms. In this study, we have analyzed its morphological and genetic variation within an integrative taxonomy framework. We have combined morphological and biogeographical pieces of evidence with a phylogenetic reconstruction based on five molecular markers from both the nuclear (ITS2 and one unpublished region) and the chloroplast (trnG, trnLF and rps4 loci) genomes. The detailed study of a considerable number of specimens (over 100 samples in the case of the morphological analyses) reveals solid and constant morphological differences, which are strongly supported by the genetic variability. We conclude that the current concept of *Pulviger lyellii*

comprises no less than four distinct entities at species level. Thus, our results notably increase the recognized diversity in the genus *Pulviger* Plášek, Sawicki & Ochrya, and refute its so far consideration as a monospecific character. The four species include *Pulviger lyellii* s.s., plus three other taxa formerly described but are at present treated as synonyms of *P. lyellii*. Based both on our morphological and genetic results, we propose the reinstatement of these three taxa at the level of species, and we provide the main morphological traits to distinguish them.

OR-19

Recent revisions disclosed a greater difference between eastern and western species in Eurasia

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The recent revisions of moss taxa of the Moss Flora of Russia with integrative taxonomy approach found a number of similar phytogeographical patterns. European species traditionally assumed as circum-Holarctic or at least Eurasian in distribution appeared to be confined to Europe, having eastern boundary of distribution within the European Russia. Examples are provided by *Rhynchostegium riparioides*, *Polytrichum formosum*, *Schistidium apocarpum*, *Lewinskya speciosa*, *Ulota crispa*, *Hedwigia ciliata*, *Plagiothecium laetum*. Eastern vicariants may be well segregated geographically (*Polytrichum formosum* / *P. densifolium*, *Hedwigia ciliata* / *H. mollis*, *Rhynchostegium riparioides* / *R. aquaticum* s.l.) or have a considerable overlap, e.g. *Lewinskya speciosa* / *L. elegans*. Interestingly haplotypes of *Neckera pennata* complex often have coincident geographical limits: amphiatlantic, two amphipacific, circumboreal, South Chinese and two montane; among them only saxicolous *N. oligocarpa* has stable morphological differences and presumably may represent suite of cryptic or semi-cryptic species. Highly supported infraspecific groupings corresponding to geographical patterns were found in course of our molecular phylogenetic studies also in

widespread species of *Anomodon*, Rhabdoweisiaceae, *Amphidium*. Thus, the overall diversity of mosses within the circumboreal region turns to be much higher than it was thought before. Among found bryogeographical boundaries the western administrative border of the former USSR and boundary of the permafrost territory in continental climate of Asia seems more prominent than thought earlier. The work was supported by RSF 18-14-00121.

OR-20

On mosses and springs: environmental, spatial and phylogenetic patterns of aquatic and semi-aquatic mosses

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Mosses are amongst the simplest and oldest plants on Earth. Despite their small size, they played a remarkable role shaping our planet. Still in our era, they are one of the largest groups of land plants and can be found almost everywhere in the world, and they continue to condition the structure and function of ecosystems. Their simplicity and particular physiology make bryophytes interesting subjects of study in ecology, especially because the lack of cuticles makes them extremely sensitive to environmental changes. Nonetheless, the proportion of ecological studies focused on bryophytes is clearly insufficient despite the fact that knowing bryophytes better could provide important insights about unresolved questions of physiology and the ancient evolution of plants.

We have investigated aquatic and semi-aquatic (hygrophytic) mosses growing in semi-natural Mediterranean springs. These springs pour water continuously throughout the year, which makes them behave like small islands, or refugia, where water is available, surrounded by completely different habitats where water is scarce. Here, we analysed water chemical composition and moss communities of 303 semi-natural springs around NE Iberian Peninsula and investigated the relationship between 12 moss functional traits and the environment. Our results indicated phylogenetic conservation of several moss functional traits, and that, most likely, water conductivity acted like an environmental filter. Moss size and spore size were also related to water properties and climate. Hence, our results indicate that moss assemblages in semi-natural springs can be determined by water chemistry, highlighting the role of elements in shaping moss distribution.

OR-21

Northern and mountain bryodiversity must be better understood when the climate gets warmer

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The effects of the gradually warmer climate on organisms and their diversity will be especially strong in mountains and, in the Northern Hemisphere, towards the north. We are likely losing intraspecific genetic diversity faster than diversity related to rare species. From a biodiversity conservation point of view, it is therefore crucial to know more about the frequency of northern and mountain genetic variants in widespread bryophyte species. This investigation examines diversity patterns and the occurrence and distribution of northern and mountain genetic variants in ten widespread mosses in Sweden, a country that extends from the nemoral to northern portion of the northern boreal zone and includes 12.5% alpine and subalpine areas. Between 50-110 specimens were sampled per species, from herbarium S or collected in the field, with the densest sampling in the north. For each species, (2-)3(-4) molecular markers were used to explore haplotype diversity

and patterns of genetic relationships, based on NeighborNet split networks and Jackknife analysis. Eight of the ten species include lineages or groups of haplotypes that occur exclusively in the north or in the mountains. However, also in the two species lacking such lineages or groups, the genetic composition differs (population pairwise Φ_{PT} , or corrected average number of pairwise nucleotide differences) between the north or the mountains on the one hand, and the south or the lowlands on the other. In some of the studied species, the genetic variation is correlated with morphology, which could indicate so-far unrecognized species, whereas in other species no morphological differentiation exists. The geographical distributions of northern or mountain genetic variants coincide with those regions of northern Sweden that will be most strongly affected by the expected future warming; examples of potential climate effects among the studied species are provided. The results of this study show that we will likely lose significant portions of our intraspecific biodiversity in the north, even if the species themselves, as currently circumscribed, will probably survive ‘without problems’.

OR-22

Predicting bryophytes’ vulnerability to climate change: combination of niche and spatial metrics matter!

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Range contractions have been predicted for numerous European bryophyte species, as well as range expansions for others at their northern limits. It has been hypothesized that species with different distributions in environmental niche and geographical space may respond differently to

changes in climate. The aim of this study is to assess how niche and spatial metrics are related to bryophytes’ vulnerability to climate change. We used a dataset on mountain saxicolous bryophyte species in Iberian Peninsula that are likely to be most vulnerable to the impacts of climate change. The current and future distribution for 39 bryophyte species were predicted by species distribution models using climatic and topographic variables known to have an important role in limiting such plants. Niche metrics, specifically niche breadth, niche position and niche overlap, were calculated using a new tool based on multidimensional kernel density estimation procedure. The same and corresponding metrics that were used to characterize the environmental space were calculated for the geographic space. Future projections for the year 2050 were derived using two different Global Climate Models recommended for Europe and Mediterranean climates. Species range changes, specifically range contraction, were then related to niche and spatial metrics using linear regressions. Correlation results between species range contractions and niche and spatial metrics revealed that bryophyte species with higher marginality, narrow niche breadth and restricted range are more likely to experience range contractions. Taking in account different climate change scenarios in 2050, the best models explaining bryophytes’ range contractions included the single effect and combination of niche metrics (breadth and position) and also the combination of range size and niche metrics (breadth and position). Our results suggest that the combination of niche and spatial metrics may improve predictions about bryophytes’ vulnerability in the context of global changes.

OR-23

Dissecting the genetic basis of seasonal reproduction in a basal land plant, the moss *Physcomitrella patens*

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Many plants make use of environmental cues, such as daylength and temperature, to synchronize reproductive development with favorable climatic conditions, thereby increasing their reproductive success. Although the genetic mechanisms that regulate reproductive development in response to seasonal cues are largely conserved across flowering plants, it is not known whether this conservation extends beyond angiosperms to other land plant lineages. We are using the model moss *Physcomitrella patens* to probe the evolutionary origin of seasonal regulation in land plants, with the long-term goal of determining whether a core mechanism evolved in the common ancestor of all land plants, or if convergent mechanisms arose separately in distinct land plant lineages. We are coupling transcriptomic and genomic analyses of a set of *P. patens* ecotypes that vary in reproductive timing in response to seasonal cues with traditional mutagenesis screens to identify and characterize the genetic networks that underpin seasonal regulation of sexual reproduction in this basal land plant. Using a combination of cross-population genome-wide measures of selection and differential co-expression network analysis comparing ecotypes across daylength and temperature conditions, we have narrowed in on candidate genes homologous to upstream components of angiosperm temperature and daylength induced flowering time pathways. We have generated CRISPR-Cas9 mutants in four gene families and are currently evaluating their phenotypes. In parallel, we designed a mutagenesis screen, which has yielded heritable mutants with striking differences in the timing of onset of reproductive development in response to seasonal cues.

OR-24

A new bryophyte Red List and Checklist for Europe

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A new European Red List for bryophytes is being published. This is a collaborative project between the European Committee for the Conservation of Bryophytes (ECCB), the Species Survival Commission (SSC) Bryophyte Specialist Group and the International Union for the Conservation of Nature (IUCN), with support from the EC LIFE fund. To accomplish this task – the assessment of 1,817 species occurring in Europe – more than 100 bryologists have been working on this list over the last 3 years. The system used for species assessment follows the IUCN methodology but critical terms (e.g. generation length) had to be interpreted to become applicable for bryophytes. 22.5% of the European bryophyte flora is threatened (VU, EN, or CR), although only 6 species are considered Extinct (EX) or Regionally Extinct (RE). Mountainous regions, especially the Alps, are particularly rich in threatened species; hyperoceanic areas are particularly rich in endemic and near-endemic species. Major threats to European bryophytes include natural system modifications, including forestry and agricultural intensification, and climate change. Concurrently, a new European bryophyte Checklist is being prepared. This will include a published checklist and also a spreadsheet showing the distribution of species by country throughout Europe. It is intended that both projects will contribute to future research into bryophytes in Europe, and particularly provide a tool for their conservation.

OR-25

The Pyrenean bryoflora: erasing national borders in the FLORAPYR Atlas

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In southwestern Europe, the Pyrenean range extends 440 km from West to East, 30 – 150 km from North to South, in latitude 42 – 43.3° N. Its highest point is Aneto summit (3.404 m), but it contains more than a hundred peaks over 3.000 m, and therefore stands out from the other mountain ranges in Southern Europe, excepting the Alps. Its 44.000 km² extend over three countries (France, Spain and Andorra); constituting the limit between two large bioclimatic regions, the temperate and the mediterranean. A first global bibliographic checklist in 2013 compiled data from more than 700 publications spanning over 230 years, so gathering the contribution of over 250 authors, and yielded 1.069 taxa, 60% from 1.780 estimated for Europe, 73% of the bryophytes reported for metropolitan France and 89% of those reported for peninsular Spain. The online resource *Atlas of the Flora of the Pyrenees* was developed for vascular plants in the POCTEFA 2007-13 OPCC project (Interreg European Union). The new POCTEFA 2014-20, FLORAPYR Project now includes the bryophytes in this Atlas; compiling bibliographic, herbarium and observational data from six institutions and main collaborators, and drafting a factsheet for each taxon which includes a distribution map, a biological file with different sections, and images. The updated (but still evolving) list now includes 1069 taxa at species level, amounting to 1121 taxa at infraspecific level. These species are distributed in 4 anthocerotales, 266 liverworts and 799 mosses. The strong dissymmetry north-south is barely reflected in global species figures, but distribution types for the different elements (arctic-alpine, atlantic or mediterranean) are becoming evident. The Pyrenees are shown to be an area of extraordinary bryological richness. This cross-border collaborative effort being made will in future provide a solid basis for conservation action on a total Pyrenean scale.

OR-26

One Mountain, Two Slopes – Heterogeneity of epiphytic bryophytes communities on Mt. Gede

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Variations among bryophyte communities along elevational gradients in the tropics have been reported in several studies. However, not much information is available on the epiphytic bryophyte species richness pattern, composition, and zonation in South-East Asia. This study aims to compare the bryophyte species richness pattern, composition, and zonation between two slope aspects of Mt. Gede, West Java, Indonesia. One elevational gradient transect was established on the drier North-North-East (Cibodas) slope and another one on the wetter South-South-West (Selabintana). Both transects range from 1500 to 2700 m asl., and epiphytic bryophytes were sampled at 200 m intervals. Our study finds that the Cibodas transect is richer (160 species; 71 mosses and 89 liverworts) than the Selabintana transect (149 species; 57 mosses and 92 liverworts), probably due to topographic variations. Species richness pattern on both slopes showed quadratic responses for mosses and cubic responses for liverworts. Lejeuneaceae, Lepidoziaceae, and Plagiochilaceae were the most common families on both transects. Statistical analyses on species composition showed five significantly different zones – Submontane, Lower Montane, Transition, Upper Montane, Subalpine – on each slope aspect, with wider Lower Montane zone on Selabintana and Subalpine zone on Cibodas. A distinct transition zone was present between Lower and Upper Montane zone on both slope aspects, which was not reported in previous bryophyte studies. Every zone has its own indicator species, except for Upper Montane zone on Selabintana. No indicator species were shared among zones of Cibodas and Selabintana, except for *Syrrhopodon tristichus* at Lower Montane zone. The present study contributes to a better understanding of bryophytes communities in tropical mountainous areas.

OR-27

Genetic diversity in bryophyte population with facultative nannandry

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Male dwarfism is uniquely found in unisexual mosses. It is a strategy that brings males and females close together, thereby facilitating sexual reproduction. Hence, dwarf males could significantly contribute to the gene pool transmitted to the next generation through the sporophytes. However, a dwarf male breeding system can also lead to complete homozygotization after only a few generations if repeated mother-son fertilization occurs. In the widespread moss species *Dicranum scoparium* Hedw., the female gametophore is always normal-sized, whereas males are facultatively nannandrous. This means that male individuals can either be normal-sized and free-living (“NMs”) or dwarfed and attached to females (“DMs”). We analysed the spatial distribution of female and male haplotypes to assess the influence of this mixed breeding system on genetic variability, population structure and clonality. We used 119 SNPs to genotype plant material from 11 sites in seven localities in southern Sweden. A total of 403 individuals were analysed (211 females, 135 DMs and 57 NMs). DMs and NMs were encountered in all localities but one for NMs. If NMs were much less frequent than DMs, the exact female:male ratio is difficult to assess. Nevertheless, our overall ramet- and genet-level data suggest a rough female:NM estimate of 4:1 respectively 3.5:1, which is comparable to what was found in other species such as in *Mnium hornum*, *Bryum argenteum*. AMOVAs (analysis of molecular variance) indicated a low differentiation at site and locality levels while most of the variance was found between cushions for females and NMs and within cushions for DMs. Haplotypes were sometimes shared among individuals of the same sex, suggesting clonal propagation. Dwarf males had mostly one haplotype per individual and were genetically more diverse than the two other groups. We also found two haplotypes that were shared between females and DMs and one haplotype that was shared between a DM and a

NM. The results suggest effective and frequent gene flow between populations, even over long distances, via male spore dispersal. Demes are often genetically diverse, but we also see indications of inbreeding, probably caused by repeated mother-son fertilizations.

OR-28

The acrocarp moss *Atrichum undulatum* tolerates pollution of copper and zinc depending on environmental conditions

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Mosses are frequently used to monitor atmospheric metal contamination but few studies focus on the mechanisms of metal adsorption under controlled conditions. Here, we studied the accumulation of the heavy metals copper and zinc in the acrocarp moss *Atrichum undulatum*, which has been frequently used in biomonitoring. An *in vitro* culture of *A. undulatum* was established and the same line, size and equally old remets were exposed to six different treatments representing various metal exposure times and washing scenarios as rain simulation. The metal treatments were done in two concentrations of copper and zinc salts (Cu-acetate, CuSO₄, ZnSO₄ and ZnCl₂, respectively). Energy-Dispersive X-ray microanalysis (EDX) was employed to detect bound heavy metals on the moss plantlets. Element distribution in stems and leaves was measured separately. The results clearly showed that *A. undulatum* is tolerant to contaminations with zinc and copper, and that zinc is less toxic and less bound to the plant than copper. An aqueous solution of metal salts facilitated an adsorption of both elements in the moss tissue as compared to solid medium. Furthermore, *A. undulatum* tolerated pollutions of zinc and copper in a distinctive extent; our data point towards a zinc tolerant species whereas copper is rather

harmful. Interestingly, a strong positive correlation between the accumulation of copper/zinc and iron, and a strong negative correlation between copper/zinc and magnesium, respectively, was documented.

OR-29

Elucidating subcosmopolitan disjunctions: ancient origin, migrations via Bering land bridge and the Miocene diversification of a species-rich liverwort genus *Lejeunea*

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[†]deceased. This work is dedicated to the memory of the late Jochen Heinrichs who contributed greatly in the field of systematics and evolution of leafy liverworts.

An interesting distribution pattern of most liverworts shows that they are of ancient Cretaceous origin and their diversification started in the Cenozoic. For example, in the most species-rich family of liverworts, Lejeuneaceae, divergence-times estimation indicates a rapid establishment of the major lineages in the Cretaceous followed by steady diversification through the Cenozoic. Here we aimed at investigating the historical biogeography of the subcosmopolitan genus *Lejeunea* (Lejeuneaceae) based on phylogenetic analyses and to explore how the genus achieved its subcosmopolitan distribution. Relying on a taxon sampling that covers approximately the full geographical distribution, we used macroevolutionary analyses

to estimate the ancestral areas of origin and assess whether palaeoenvironmental changes and sexual system influenced the species diversification of *Lejeunea*. Maximum likelihood and Bayesian inference were used for phylogenetic analyses using sequences of two chloroplast regions and one nuclear region. Divergence times were estimated using a Bayesian molecular relaxed-clock constrained with fossil calibrations. Diversification rate analyses were carried out under time-dependent, environmental-dependent, and trait-dependent models. Ancestral areas were reconstructed with likelihood-based methods using the Dispersal-Extinction-Cladogenesis model. *Lejeunea* diverged from its sister group at the Paleocene-Eocene boundary (56.7 Ma, 95% credibility interval: 46.3-63.8) and the initial diversification of the crown group occurred in the early to middle Eocene (47.5 Ma, 95% credibility interval: 37.6-54.7). *Lejeunea* is most likely to have originated in the Neotropics, however, the “out of North America” hypothesis cannot be ruled out. The evolutionary history of *Lejeunea* shows several biogeographic scenarios in shaping the global distribution of the genus. The unusual northern routes of colonization through the Bering land bridge may have facilitated the dispersal from North America to Continental Asia at least twice during the Oligocene and late Miocene. The Miocene was an important period for *Lejeunea* when they diversified globally. Monoicy is associated with higher diversification rates in *Lejeunea* lineages while past temperature did not influence the diversification of *Lejeunea*. Moreover, the results point to the constant accumulation of diversity through time in *Lejeunea*, in line with the previous evidence in Lejeuneaceae, which underwent a steady diversification through the Cenozoic.

OR-30

Study of cryptic peptides biological activity in plants

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Despite the lack of an adaptive immune system, plants have a complex innate immune system that has developed during the process of co-evolution of plants and microorganisms. Cell wall receptors, such as receptor-like kinases, recognize conservative molecular patterns of pathogens (PAMPs) as well as host damage associated molecular patterns (DAMPs). PAMPs and DAMPs are often peptides - fragments of functional or non-functional precursor proteins. Recent studies have shown that plant endogenous peptides, such as PEP, are able to activate the expression of defense genes, thereby regulating the immune response of plants. The role of cryptic peptides encoded in the functional protein sequences of both plants and pathogens has been little studied. Such peptides can have both signaling and antimicrobial activities. For the discovery of new functional cryptic peptides, the intracellular and secreted peptide pools of a model plant, moss *Physcomitrella patens*, were analyzed during the treatment with stress hormones salicylic acid (SA) and methyl jasmonate (MeJA). An analysis of the mass spectrometry data revealed a number of peptides unique to the treated samples, among which potential candidates for bioactive peptides were identified. We have shown that treatment with hormones led to an increase in the antimicrobial activity of the extracellular peptide, and an addition cocktail of protease inhibitors, on the contrary, reduced it, which may indicate the role of proteases in the formation of the bioactive peptide pool. Using bioinformatics methods, we predicted proteases that respond to stressful conditions. In addition, we have shown the effect of SA treatment on the proteasomal activity inside the cells, which is obviously involved in the change in peptide pools. We also synthesized eight peptides with predicted antimicrobial activity. We showed that a peptide INIINAPLQGFKIA derived from predicted protein precursor inhibited bacterial growth in 16

µg/ml concentration and influenced the transcription of defense genes.

OR-31

Which climatic and environmental factors determine liverwort diversity patterns in tropical montane forests?

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Global biodiversity is not equally distributed. Typically, species richness declines with increasing latitude from the equator towards the poles. Also on regional and local scales, the distribution of biodiversity is heterogenous: along elevational gradients, many organisms, including early diverging land plants, show a hump-shaped pattern, peaking at middle elevations. The knowledge about the mechanisms and processes determining this pattern have not yet been fully elucidated. The aim of this study was to examine the species richness distribution patterns and the underlying causes of liverworts along an altitudinal gradient in the tropics. We surveyed the species richness of epiphytic and non-epiphytic liverworts in 24 plots in mountain forests at 680-3200 m above sea level in Uganda. A total of 120 liverwort species and subspecies from 18 families were identified. Generalized linear models (glm) were calculated to assess the impact of climatic and environmental factors on species diversity. Our results provide evidence for different altitudinal maxima of species richness in epiphytes (1800 m) and non-epiphytes (2200 m). The predicted species richness also shows a hump-shaped pattern when contrasted against mean annual temperature, and against annual precipitation peaking at around 17 °C, and 1450 mm, respectively. Our data also suggest that species diversity in liverworts increases with increasing precipitation in the dry season, and

decrease in diversity with increasing habitat homogeneity. Epiphytic and non-epiphytic species seem to have different preferences regarding precipitation, temperature and cloud cover.

OR-32

The development of spatial structure in epiphyll communities in a tropical lowland rainforest

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Liverworts are among the most common epiphylls on leaves in tropical rainforests. Due to their fast life cycle and the great replication of well-delineated communities, epiphyllous liverworts, together with algae, fungi, and lichens, represent a promising model to test ecological theories about biodiversity maintenance and community development. The aim of this study is to understand how neighbor interactions shape epiphyllous liverwort communities and how these interactions differ between closed-forest and gaps. To this end, we characterized the spatial structure of epiphyll communities on ten leaves each in gaps and closed-forest over time, resampling at four-time intervals (at 0, 6, 9 and 12 months). For analysis, epiphylls were divided into four functional groups: liverworts, algae, fungi and lichens. We analyzed the spatial and temporal structure of epiphyll communities using point-pattern analysis, assuming that spatial aggregation indicates positive interactions and segregation indicates negative interactions, while random patterns indicate chance processes being dominant. We found that with time, more leaves started to show aggregated rather than random patterns in liverwort distribution.

Spatial associations between liverworts and other epiphylls were mostly positive or random on young leaves, but became negative on some of the aging leaves. The more random patterns on young leaves probably indicate that the pattern is determined mostly by chance arrival of propagules. On older leaves, aggregation may indicate local dispersal or facilitation. Inter-

specific negative associations on aging leaves may point at competition for space between these functional groups. Epiphyll communities were shown to be highly dynamic, with spatial patterns and interactions changing during community development, from random to interactive.

OR-33

Adaptation of regulatory mechanisms of photosynthesis upon land colonization

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Life on earth depends on photosynthetic organisms capable of exploiting sunlight to fuel synthesis of ATP and reducing power. Natural environmental conditions are highly variable and photosynthetic electron transport requires continuous modulation to maintain the balance between light availability and metabolic demands. Photosynthetic organisms evolved multiple mechanisms to modulate the flow of excitation energy and electrons according to metabolic constraints and environmental cues. Even if photosynthesis is finely regulated in all organisms, the molecular mechanisms are generally not conserved and different phylogenetic groups show significant differences. In the past few years we investigated how mechanisms for regulation of photosynthetic electron transport adapted during land colonization, using the moss *Physcomitrella patens* as a model. As example, we showed that Flavodiiron proteins (FLVs) have a major role in *P. patens* response to light fluctuations but FLV-encoding sequences were nevertheless lost during evolution by Angiosperms, suggesting that their activity become superfluous or even detrimental for photosynthetic efficiency in those species. By generating *P. patens* KO plants depleted in regulatory electron transport mechanisms, we also demonstrated that different mechanisms for electron transport regulation have strong functional overlap and, when one is depleted, the others can compensate for the activity. When multiple mechanisms are simultaneously inactivated, however, plants showed major

reduction in growth, demonstrating that photosynthesis cannot work efficiently without regulation.

OR-34

Climate change effects on the carbon balance of tropical lowland bryophytes

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Different effects of climate change have already been recorded and the future might be too hot for some organisms, especially in the tropics. Bryophytes in tropical lowlands have low abundance even under current conditions and may suffer if their climate warms further. Possible reasons for negative warming effects are increased rates of night respiration that are hard to compensate by short photosynthetic activity (due to faster drying) and/or low photosynthetic rates (due to low light in the forest understorey). We therefore study how carbon balances of tropical bryophytes may change with changes in climate by modelling long-term carbon balances based on microclimatic conditions. As a study case we use selected understory epiphytic bryophytes from the tropical lowlands of Costa Rica, for which we also simulated climate change in open-top chambers in an *in situ* experiment. Photosynthetic responses to different light, temperature, CO₂ concentration and water content were measured using an infra-red gas analyser. These response curves were used to parameterise the carbon module of our model. The hydration module (calculating water content depending on temperature and relative humidity) is based on empirical measurements of bryophyte drying speeds. With this model we simulated warming effects on photosynthetic rates and/or on drying. Even with a moderate increase of temperature of 3K, modelled carbon balances show significant decreases, although these depend on weather conditions. Increasing

atmospheric CO₂ partly compensated for this negative effect in the model, but in the *in situ* experiment increased CO₂ did not increase the performance of the bryophytes, which suffered from warming. By combining modelling with experimental results, we will present possible future carbon balances of tropical lowland bryophytes. With further development of the model, it could also be used to predict biogeographical distributions of bryophytes.

OR-35

Biocontrol Potential of Himalayan Bryophytes against different microorganisms

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Most of the natural plants products that are in use worldwide are obtained from angiosperms. Lower group of plants like bryophytes are relatively unexplored and underutilized worldwide. In the present study the acetone and ethanol/methanol (80%) extracts of nine bryophyte species (liverworts and mosses) collected from different altitudes of Kumaon, Himalaya (INDIA) were investigated for their antimicrobial potential against different bacteria and fungi using disc diffusion assay. The minimum inhibitory concentration (MIC) and minimum bactericidal or fungicidal concentration (MBC/MFC) was observed employing micro broth dilution methods. Lowest MIC and MBC/MFC (0.97 to 125 µg/mL) was found in methanolic extract of *Conocephalum conicum* (liverwort) against bacteria (*Salmonella enterica*, *Erwinia chrysanthemi*, *Pseudomonas aeruginosa*) and fungi (*Colletotrichum falcatum*, *Aspergillus* sp., *Fusarium oxysporum* f. sp. *lycopersici*). Further, *in vivo* study through green house experiments confirmed the potential of *C. conicum* as an efficient biofungicide to control fusarium wilt disease in tomato. Scanning electron microscopic studies also helped in confirmation of biocontrol potential of *C. conicum* to control *Aspergillus* sp. Biochemical profiling of the methanolic extract

of *C. conicum* was done through antioxidant (phenol, flavonoids) and GC-MS analysis. Out of 18 different organic extracts, methanol extract of *C. conicum* was found most potent showed highest antioxidant activity ($90.17 \pm 1.63\%$). In GC-MS analysis, riccardin C, a biomarker compound along with sesquiterpenoids (citronellol, trans-Squalene, geranylgeraniol, lactone G), phytol and steroids were detected in *C. conicum*. Future optimization of these bioactive compounds may emphasize upon their potential role in its application in the development of novel antimicrobial agents.

OR-36

Exploration of the Southeast European bryophyte flora with a special attention to the species of conservation interest

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In the last 20 years, the Bryological Collection of the Hungarian Natural History Museum (HNHM) has dealt intensively with the Balkan Peninsula, from where there is still relatively few data compared to other parts of Europe. Several joint field trips with SE European bryologists were organized. Special attention was paid to the investigation of the habitats of rare, threatened species. As a result more than 18.000 specimens have been deposited in the HNHM and 87 papers have been published. Voucher specimens of 619 species can also be found in HNHM, which were reported for the first time from the various countries of Balkan.

From conservation point of view wetlands are the most important habitat types in SE Europe, threatened mainly due to climate warming. Their extension is decreasing, and they are continuously losing the sensitive bryophytes of their species pool. Although the suitable bogs are small and sporadic in the Balkans, they still maintain several populations of wetland species of European conservation interest, such as *Campyliadelphus elodes*, *Drepanocladus polygamus*, *Hamatocaulis vernicosus*, *Scorpidium scorpioides*, *Tomentypnum nitens*. The alpine grasslands are also threatened due to climate warming. The Balkan high mountain

areas still preserve very diverse bryoflora. Especially areas with acidic bedrock in high elevations have special conservation interest, because they are rare and scattered in the predominantly calcareous Balkan area. The bryophyte flora of acidic soil and siliceous outcrops contains many calcifuge species regarded as rare in this region and red-listed in many SE European countries, e.g. arctic, alpine leafy liverworts such as *Marsupella sphacelata*, *Scapania praetervisa*, *Solenostoma confertissimum* or saxicolous species like the members of Grimmiaceae family (*Grimmia caespiticia*, *G. reflexidens*, *Schistidium papillosum*). In shaded limestone rocky habitats, the bryophyte assemblages also contain several species of European conservation interest, e.g. *Anomodon rostratus*, *Mannia triandra*, *Myurella sibirica*, *Taxiphyllum densifolium*. On decaying wood in old forests, we can also find some boreal species rare in Europe, like *Buxbaumia viridis*, *Lophozia ascendens*, *L. guttulata*.

OR-37

Towards a unified bryophyte names index and bryophyte checklist: a community-focused bryophyte resource

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Our aim is to merge the three bryophyte names indexing initiatives, Index Muscorum, Index Hepaticarum and the Early Land Plants Today project, and use our combined resources to produce and maintain a single, centralized reference database for all bryophyte names: a unified *Bryophyte Names Index*. This single index will serve as a community-managed reference for bryophyte taxonomy, nomenclature and systematics, as well as being a focal point for bryologists to contribute new names, make corrections to existing entries, and resolve outstanding nomenclatural issues. Such a unified index will also serve as a platform to organize data regarding references (Recent Bryological Literature), typifications, and other

nomenclatural acts. We anticipate that this platform will also be used to fulfill the pending requirements for the registration of new bryophyte names. Our goal is to engage the bryological community at large (via the IAPT Bryophyte Nomenclature Committee and the International Association of Bryologists) in a bottom-up community approach to the maintenance of bryophyte name data, with all its associated metadata, in this centralized resource. In an increasingly digitally connected world pooling our resources and expertise into one community-based tool will allow us to share tasks, advance together, and work towards the production of a global bryophyte consensus checklist. A unified approach will also ensure that this taxonomic backbone of accepted names, synonyms and consensus classification will become the nomenclatural reference used by global initiatives such as the World Flora Online, Catalogue of Life Plus, and the Global Biodiversity Information Facility. The flow of digital data regarding bryophytes will be greatly enhanced if our efforts succeed.

OR-38

Moss species on the move in East Antarctic terrestrial communities

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Antarctica has experienced major changes in temperature, wind speed and stratospheric ozone levels over the last 50 years. Whilst West Antarctica and the peninsula showed rapid warming and associated ecosystem change, East Antarctica appeared to be little impacted by climate warming, thus biological changes were predicted to be relatively slow. Detecting the biological effects of Antarctic climate change has also been hindered by the paucity of long-term data sets, particularly for organisms that have

been exposed to these changes throughout their lives. We monitored vegetation communities in the Windmill Islands, East Antarctica from 2000 to 2014 and found significant changes in moss species composition. In addition, we have shown that radiocarbon signals preserved along shoots of the dominant Antarctic moss flora can be used to determine accurate growth rates over a period of several decades, allowing us to explore the influence of environmental variables on growth. Carbon stable isotopic measurements suggest that the observed effects of climate variation on growth are mediated through changes in water availability and most likely linked to the more positive phase of the Southern Annular Mode and changing westerly wind patterns. For cold remote locations like Antarctica, where climate records are limited and of relatively short duration, this illustrates that mosses can act as microclimate proxies and have the potential to increase our knowledge of coastal Antarctic climate change.

OR-39

Elevational patterns of bryophyte and lichen biomass and species richness on different substrates in the tropical montane forest of Baru volcano, Panama

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A distinctive condition of tropical montane cloud forest is the abundant presence of bryophytes and lichens on all available substrates, from the forest floor to the canopy. These cryptogams have important ecological functions, but they are threatened by climatic change. Current elevational patterns may indicate climate dependencies of these organisms, but these patterns have been described for only few tropical mountains so far. Most of those studies were focused on epiphytes and none have previously addressed substrate-specific patterns. We therefore analyzed patterns in the abundance and diversity of bryophytes in an elevational gradient on the western slope of Baru Volcano, Panama, explicitly taking into account different substrates. The bryophyte and lichen layer was collected from 600-cm² plots on six substrate types with

four replications at eight elevations along a gradient from 1900 to 3300 m a.s.l. We determined the thickness, water-holding capacity, biomass, and bryophyte richness patterns of all samples. At lower elevations, substrates had a similar biomass and water-holding capacity per area, but with increasing elevation, terricolous substrates showed the strongest increase (highest values at 3100 m). With the data currently obtained (considering the diversity of only bryophytes), this increase in biomass was not accompanied by an increase in species richness at the plot level (alpha diversity). Instead, species richness decreased with elevation in all substrates and the highest richness at high elevation was found in epiphytes rather than terrestrial species. Biomass and diversity were not correlated, and variation in both variables along elevation was substrate dependent. Local species richness is highest at the lower, warmer elevations (which, importantly, are middle elevations on the scale of the whole mountain), in all substrates except soil. Warming might thus lead to higher local species richness at the higher elevations, but it would probably reduce richness at the lower elevations (1900 and below, outside the range studied here) as the warm tropical lowlands are known for holding fewer species. In any case, overall diversity would probably not increase, as there is a strong turnover of species along elevation and cold- and moisture-adapted species might be lost under warmer drier conditions.

OR-40

Morphological diversity in the peristome of the Neotropical moss *Octoblepharum albidum* Hedw. (Bryophyta, Octoblepharaceae)

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Octoblepharum Hedw. is a widely distributed tropical and subtropical moss genus. Hedwig, in his *Species Muscorum Frondosorum* erected the genus in 1801. The genus was described as having a simple peristome, of eight teeth, a sporangium without apophysis and male and female gametocoea (*flos masculus femineo*) in the same plant (Hedwig, 1801). The name derives

from the Greek words *okto* (οκτώ) meaning eight and *blepharis* (βλεφαρις) (an eyelash) based on the eight-peristome teeth of the Type species *O. albidum* collected by Swartz in Jamaica. Today, 19 species are recognized worldwide (Salazar Allen & Chantanaorrapint 2018). Geographically, the most widely distributed species is *O. albidum* Hedw. It occurs in the tropics, subtropics and temperate zones. The gametophyte is characterized by loose turfs or cushions, leaves erect to patent to curved-spreading, strap-shaped apiculate and with a hyaline lamina of elongated hexagonal finely pitted leucocysts. Unlike the nearly uniform gametophyte morphology, the sporophyte, displays a wide range of variation in peristome morphology. Three main types of peristome are distinguished. The first type is represented by the peristome of the Type specimen with eight solid teeth composed of two outer rows of cells with faint wall striations and obtuse apex. Variations from this type include additional rows of cells, mainly towards base of teeth, pronounced vertical cell wall striations, foveolae, few apertures and obtuse to acute apices. The second type consists of teeth with wide basal apertures separating the two outer rows of cells, mostly acute apices and cell walls with vertical striations. The third type has smooth, paired short teeth with obtuse apices. These three types of peristomes and their variations occur throughout the Neotropics. A hypothesis on the evolution of these peristome types is presented.

OR-41

Changes in the nomenclature of liverworts and hornworts 2013-2019. What has happened since the World Check List was finished?

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In 2016, the World Check List of Horn- and Liverworts was published. It was built on an 8-year long work involving 40 co-authors and some additional contributors. The cut-off for accepting any further nomenclatural or taxonomic changes was set to 1 July 2015. Thus, the checklist is a snapshot of the knowledge that day! The ELPT

project is continuously registering changes and is feeding Catalogue of Life with the latest updates once a year (including distribution but not yet synonymy). In this presentation we will outline the changes happened from the publication of the WCL until today, to give an idea of how much the taxonomic work is changing our view on the group.

OR-42

More, new, and better understood bryophyte taxa in the Netherlands based on integrative taxonomy

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The bryophyte flora of the Netherlands has been extensively studied and is considered well known. However, problems with morphological species delimitations still hamper the recognition of several taxa, especially in taxonomically difficult genera and species complexes. To test whether the current number of 600 species correctly represents the bryophyte diversity of the Netherlands, Naturalis and the Dutch Bryological and Lichenological Society (BLWG) carried out an integrative project combining DNA barcoding and analysis of morphological (and ecological) characters. *TrnL-F* and ITS sequences were generated from almost all bryophyte taxa currently occurring in the Netherlands. Based on the comparison of genetically distinct groups with morphologically defined species and morphometric analyses in difficult taxa, we conclude that the bryophyte diversity in the Netherlands has been underestimated by at least 10% when based on morphology alone. At least 21 species and subspecies were newly discovered for the country (including three species new to science), the previously uncertain presence of another 45 taxa was confirmed, and few previously recognized species were excluded from the Dutch bryoflora. Species delimitations in difficult genera such as *Bryum*, *Drepanocladus*, *Fissidens*, *Schistidium*, *Trichostomum*, *Ulot*, *Warnstorfia*, and *Weissia* could be clarified. Morphological characters and

ecological preferences were assessed in terms of their suitability to be used for field identification and in revised identification keys. The results are expected to facilitate the identification and use of bryophytes in biodiversity assessments and environmental monitoring in Western Europe.

OR-43

Disentangling the hidden diversity within the widespread moss *Lewinskya affinis* (Orthotrichaceae).

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The high capacity for long distance dispersal and relative low diversification rates of bryophytes arise as one of the mechanistic hypotheses to explain the strikingly lower number of species, in particular of endemics, and the larger distribution ranges in comparison with angiosperms. We test here these assumptions using as a model *Lewinskya affinis* ($\equiv$ *Orthotrichum affine*), a moss species widely distributed across the western Palearctic, eastern Africa and the western Nearctic. Within an integrative taxonomy framework, we generated competing taxonomic hypotheses derived from separate and combined analyses of multilocus sequence data, morphological characters, and geographical distributions. The taxonomical hypotheses were then validated under a Bayes factor molecular delimitation approach. Our results suggest that *Lewinskya affinis*, as currently conceived, comprises no less than seven distinct sibling species, including *L. affinis* s.str., *L. fastigiata*

and *L. leptocarpa*, three species so far considered synonyms, plus four new species. We provide morphological traits for the identification of the seven species, as well as their known distribution ranges. Noteworthy, none of the species exhibits a trans-oceanic range, which suggest, on one hand, that the broad distributions typically exhibited by moss species could largely result from taxonomic shortcomings, and, on the other hand, that there is a tendency for a within-continent diversification rather than recurrent dispersal following speciation.

OR-44

Mosses as Bioindicators of Metal Contamination in Karst Bauxite, northern Guizhou, China

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Bauxite mining on karst provokes numerous ecological and environmental problems, including metal pollution, water and soil erosion and the destruction of vegetation. Among them, the most important environmental problem consists in soil metal pollution. Mosses are often used as bioindicators to assess levels of metal contamination in soil. Supported by the National Natural Science Foundation of China (NSFC No.31760050 and No.31360043), three bryological surveys were conducted in karst bauxite, northern Guizhou, China. The objective of this study was to determine whether mosses could be used as bioindicators of metal contamination in abandoned karst bauxite mine. Mosses were collected from an abandoned karst bauxite mine at Shangdong, Xiuwen County, northern Guizhou Province, China. Three dominant mosses were collected and identified as *Barbula rigidula* (BR), *Semibarbula orientalis* (SO) and *Barbula vinealis* (BV). The concentrations of Al, Fe, Cu and Zn were analyzed by inductively coupled plasma mass spectrometry (ICP-MS). Levels of four metal

elements (Al, Fe, Cu and Zn) were determined in the three moss species, where concentrations of Al, Fe, Cu and Zn, respectively, resulted to be 2,491-95,580 mg/kg, 3,635-65,870 mg/kg, 72.7-148.2 mg/kg and 7.4-387.1 mg/kg. The results showed that the metal content determined in mosses was relatively high, and easily exceeded the background value for Guizhou Province, particularly in the moss BR. The metal contents also differed in the three mosses: BR > SO > BV. Data also suggested that BR colonies were able to tolerate and accumulate high levels of metal elements, which evidences their suitability to be used as a bioindicator of soil metal contamination provoked by mining activities.

OR-45

Molecular basis of convergent evolution: parallel reduction of the sporophyte phase in mosses

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The phenomenon of convergent evolution, the repeated evolution of traits in independent lineages, provides ideal replicates to test for constraints on the trajectory of evolutionary processes. We aim at investigating the molecular mechanisms of convergent evolution by studying the evolutionary-developmental mechanisms underlying the repeated evolution of reduced sporophyte phenotypes in the moss family Funariaceae. Recent research on the phylogeny of the family has shown that a highly reduced sporophyte phenotype has evolved multiple times independently. This repeated morphological reduction, the simple structure of the sporophyte phase, and the amenability for reverse genetic work makes the Funariaceae family an ideal model system to study convergent evolution in a set of closely related taxa. We have chosen two

species that represent the end-points of sporophyte complexity within the family. *Funaria hygrometrica* has an elongated seta and specialized structures for controlled spore release, while *Physcomitrella patens* exhibits a reduced sporophyte phenotype, characterized by a short seta and a simple spherical capsule. The molecular mechanisms connected to the evolution of convergent phenotypes are diverse. To get an overview of the transcriptional landscape of sporophyte development, we extracted and sequenced RNA from four developmental stages of sporophytes from both species. The prediction of orthologous genes allowed us to directly compare expression patterns of conserved genes between the two model organisms. We identified known regulators of sporophyte development, as well as a set of genes involved in phytohormone synthesis, signalling, and other cellular processes that are differentially expressed between the two species. We could also determine that a large fraction of genes specifically expressed during sporophyte development have no orthologous relationships. Furthermore, we used co-expression network analysis to identify new regulatory connections potentially contributing to the evolution of divergent sporophyte phenotypes. Taken together, our analyses suggest that both, rewiring of existing regulatory networks and the addition of non-conserved genes to regulatory cascades, have contributed to the evolution of a reduced sporophyte phenotype in Funariaceae.

OR-46

Testing the evolutionary history of *Ceratodon purpureus*, the sister species *C. amazonum*, and the recombinant *C. ×conicus*

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The difference in time scale between the evolution or reproductive isolation and changing ecological circumstances means that current

species ranges are likely to be imperfect proxies for distributions at the time of speciation. Statistical analysis of current genetic structure and diversity in populations of related species can identify historical processes of vicariance, history of dispersion, and episodes of expansion and contraction of population sizes, and provide insights into the speciation process. Evaluating the demographic history of speciation requires a quantity of genetic data which has been generated for relatively few bryophyte species. We employed coalescent analyses of nucleotide polymorphism data to reconstruct the demographic and evolutionary history of the cosmopolitan moss *C. purpureus*, the recently discovered sister species *C. amazonum*, and the recombinant *C. ×conicus*. For these aims, population genetic summary statistics were calculated, demographic parameters (divergence time, effective population sizes and migration rates) were estimated and evolutionary scenarios were simulated. Moreover, we calculated if hybridization between parental taxa occurred in one or several events. We found evidence for asymmetric gene flow between *C. purpureus* and *C. amazonum*, favoring introgression from the common, cosmopolitan species into the rare southern European species. We estimated the effective population size of *C. amazonum* to be smaller than *C. purpureus*. These observations suggest that if the event that produced these two daughter species involved a population bottleneck, the effective population size of *C. amazonum* has recovered relatively quickly, potentially as a consequence of recurrent gene flow from *C. purpureus*. Finally, we find clear evidence that *C. ×conicus* was formed by multiple hybridization events between *C. purpureus* and *C. amazonum*, further supporting the role of gene flow in the speciation process in bryophytes.

OR-47

Light and phyto-hormone interplay in development of *Physcomitrella patens*

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Plant growth and development is controlled by a crosstalk among different internal factors and environmental cues. Light is one of the major environmental signal regulating plant development. Phytohormones, on the other hand, modulate different internal responses of plants. How light and hormone together regulate the plant responses is a focused area of research. Majority of work in this concern has been carried out mainly in higher plants such as *Arabidopsis thaliana*. In *Arabidopsis* phytochromes and cryptochromes have been shown to inhibit response of plant hormones such as auxin. But how the light-hormone crosstalk modulates the development in lower plants like mosses is not well understood. In this study, we investigated the light and hormone interaction in moss *Physcomitrella patens* using different mutants. We have evaluated the response of WT, phytochrome (*phy1*, *phy3*) and *fhy1* mutants of *Physcomitrella* under different light conditions in presence or absence of auxin and cytokinin. The plants were cultured under long day (LD) condition (16 hour light/8 hour dark) in all the light conditions used. We made the following observations: 1) Under far-red (FR) light LD cycle caulonema differentiation was promoted in WT plants. Furthermore, caulonema induction was independent of exogenous auxin under FR light, 2) Cytokinin mediated bud formation was inhibited under FR light, 3) Cytokinin mediated bud formation under red light was enhanced by glucose in *Physcomitrella*, 4) *phy1*, *phy3* and *fhy1* mutants displayed differential sensitivity to auxin and cytokinin in terms of chloronema-caulonema transition and bud induction. Results suggested that the functions of phytochromes are redundant and FHY1 may play a major role in protonema differentiation and bud induction in *Physcomitrella*.

OR-48

Gene transfer across species boundaries in bryophytes: evidence from major life cycle stages in *Homalothecium lutescens* and *H. sericeum*

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The mosses *Homalothecium lutescens* and *H. sericeum* are genetically, morphologically and ecologically differentiated, but mixed populations sometimes occur. We determined genotypes using SNP markers to estimate the degree of genetic mixing in 449 moss samples collected from seven sympatric and five allopatric populations on Öland, south Sweden. The samples represented three generations: haploid maternal gametophytes, diploid sporophytes, and haploid sporelings. Admixture analyses identified a majority of pure *H. lutescens* and *H. sericeum* samples, but 76 samples were identified as mildly admixed (17%) and 17 samples (3.8%) as strongly admixed. Admixed samples were represented in all three generations in several populations. Hybridization and introgression were bidirectional. Our results demonstrate that admixed genomes are transferred between the generations, so that the populations behave as true hybrid zones. Earlier studies of sympatric bryophyte populations with admixed individuals have not been able to show that admixed alleles are transferred beyond the first generation. The presence of true hybrid zones has strong evolutionary implications because genetic material transferred across species boundaries can be directly exposed to selection in the long-lived haploid generation of the bryophyte life cycle, and contribute to local adaptation, longtime survival and speciation.

OR-49

Population genomics of a Southern Appalachian bryophyte with extreme sex allopatry

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The southern Appalachian Mountains (SAM) is one of the most biodiversity-rich areas within North America and has been considered a refugium for many disjunct plant species. Extreme examples of disjunct bryophyte taxa include the liverwort *Acrobolbus ciliatus*, known only as males in Japan and females in the SAM. Extreme sex allopatry may have profound implications on the genetic diversity of the species and potentially leading to local extinction. Our study focuses on a SAM hornwort, *Nothoceros aenigmaticus* (R. M. Schust.) J. C. Villarreal & K. D. McFarland. This hornwort was described from North Carolina and it's widespread in the SAM, growing on rocks near streams in six watersheds of the Tennessee River. The species reproduces clonally; males and females occur in different watersheds, ca. 30 miles apart. *Nothoceros aenigmaticus* has been recently found in Mexico, where it reproduces sexually. Here we test whether there is a genomic imprint from such extreme case of sex allopatry or whether the genomic diversity is partitioned by watersheds. We have answered these questions using nuclear and organellar microsatellites from 250 individuals from six watersheds (7 populations) in the SAM and two populations from Mexico (23 individuals). We, then, selected 86 individuals from seven populations and used genotyping by sequencing to obtain over 600 bi-allelic markers. The phylogenetic analysis forms four clusters: Mexico (as the outgroup), male plants (Little Pigeon and Pigeon river watersheds) and two cluster of female plants: 1) Little Tennessee and Hiwassee River and 2) Ocoee and Coosa River. All cluster have high population differentiation (F_{st} values of 0.9). In addition, our individual assignment analyses and PCAs corresponded to the phylogenetic results grouping the SAM samples in three clades and recovered that males and female plants have high population differentiation (F_{st} values over 0.6 using microsatellites and biallelic markers). Our

results point to an extreme sex biased ratio confirmed by genomic data and, at least three potential dispersal events into the SAM in the Pleistocene. SAM *Nothoceros aenigmaticus* seems to be in a dead-end situation only surviving through clonal reproduction.

OR-50

Comparative genomic analysis and genetic variation within the leafy liverwort genus *Scapania*

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The genus *Scapania* comprises a group of leafy liverworts distributed throughout many bryophytic assemblages. While many *Scapania* species grow widely, some are assessed as endangered and appear to be specialists with distinct niche environments. Several are found only in alpine forest communities, inhabiting decaying logs in streams, typical of an environment that is threatened by both logging activity and changes to watercourses. Another species, *S. nimbosea*, has an unusual Oceanic-Montane distribution across Ireland, Scotland, Norway, China and Nepal. Since gemmae and sexual reproduction are absent the species is hypothesized to be primarily dispersed by fragmentation. In Norway *S. nimbosea* occupies an area of only 13 x 20 km, at altitudes between 300-980 m, and is frequently found with another more abundant asexual species, *S. ornithopodioides*. This makes *S. nimbosea* susceptible to local extinction through climate change or perhaps interspecific competition. Genomics is being increasingly used to infer demography and the evolutionary history of a species. Ascertaining levels of genetic variation can also contribute towards an effective conservation management

plan. Besides, very little is known about the genomic organization and sexual determination in leafy liverworts. To generate new knowledge about the genus *Scapania* we sequenced the genomes of the sexual species *S. nemorea* (both male and female isolates), *S. undulata* (a single isolate), and several asexual *S. ornithopodioides* and *S. nimbosea* isolates. Illumina paired-end (2x 300 bp) and Oxford Nanopore long reads were used to create genomic references. Initially organellar genomes were assembled, annotated and genetic variation was discovered. This revealed that variation is indeed present even for *S. nimbosea* and *S. ornithopodioides* at Norwegian sites. Next we focussed on creating a high quality nuclear reference genome for *S. nemorea* using the SPAdes assembler (v3.13). Qualities of each assembly and isolate were assessed with QUAST and BUSCO. While one assembly spans 202.6 Mb (10930 scaffolds; N50 of 66 Kb), other isolates of *S. nemorea* show larger assembled genome sizes and different Kmer distributions, consistent with the expected alternative sexual chromosome complement. We further analyse genomic synteny and diversity, but emphasize that difficulties in extracting DNA from herbarium specimens really hamper analysis.

OR-51

A cost reduced variant of epi-GBS for studying DNA methylation in non-model organisms

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Contemporary understanding of epigenetics encompasses the study of changes in gene function that are heritable and do not entail a change in DNA sequence. Although these changes comprise histone variants, posttranslational modifications of amino acids on the amino-terminal tail of histones, and covalent

modifications of DNA bases, most research on epigenetics focuses on DNA methylation. One elegant way to study differences in DNA methylation between samples is based on bisulfite sequencing. This technique takes advantage of the fact that sodium bisulfite causes the deamination of cytosines, unless they are protected by methylation. This results in a uracil residue, which is later converted into thymine by a PCR reaction using a compatible polymerase. With the introduction of Next Generation Sequencing (NGS) platforms, scientists became aware of the possibility of obtaining the methylation pattern of all cytosines of a given genome. While whole genome bisulfite sequencing has many advantages when studying model organisms with a known genome sequence, it cannot be applied to non-model organisms, because of the absence of a reference genome. Reference-free reduced representation bisulfite sequencing makes it possible to study the DNA methylation of thousands of markers of a high number of individuals in natural populations of non-model organisms with NGS techniques. In this work, we present a modification of the epi genotyping by sequencing (epi-GBS) protocol that requires the use of only one hemimethylated common adapter, which is combined with unmethylated barcoded adapters. Unlike other comparable methods like epi-GBS and BsRADseq, which require the use of a higher number of methylated DNA oligos with a significant cost, in our protocol, the unmethylated cytosines of one chain of the barcoded adapter are replaced by methylated cytosines using nick translation with methylated cytosines in dNTP solution. The basic version of our technique uses only one restriction enzyme, and as a result, genomic fragments are integrated into two orientations with respect to the adapter sequences. Comparing the sequences of two chain orientations makes it possible to reconstruct the original sequence before bisulfite treatment with the help of standard software and newly developed software written in C.

OR-52

Speciation with gene flow in peatmosses - using whole genome sequencing to explore gene flow within and among species

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The contribution of gene flow to speciation is controversial since it has been reported as both a constraining and a promoting factor depending on the groups of organisms investigated. Recent studies indicate that gene flow is a potentially important factor for speciation in plants. Peatmosses (*Sphagnum* spp.) are a species-rich plant genus with high ecological and morphological plasticity, especially in the Northern Hemisphere. Peatmosses are a phylogenetically old group, but most extant species originated through a recent radiation, and hybridization among taxa is common. Most peatmosses are haploid and have small genome sizes, which makes them an excellent model for studying speciation-with-gene-flow on the genomic level. In this study, we use whole-genome resequencing to quantify genetic distance within and between several peatmosses as a proxy for gene flow and to explore phylogenetic relationships between species. We produced low depth (2-12×) whole-genome shotgun resequencing data for 99 individuals from 12 haploid peatmoss species sampled in several localities in Norway and Austria. A draft genome of *Sphagnum magellanicum* was used as a mapping reference. Overall, Nei's mean genetic distance based on 22000 unlinked SNPs was low (0.029 ± 0.037 , mean $\pm$ SD) within species and high (0.33 ± 0.07) between species. This observation was further supported by phylogenetic analysis using nuclear and plastid genomes resolving almost all species as well-supported monophyletic clade. Phylogenies based on nuclear and plastid genomes were congruent with each other and with previously published phylogeny of the genus. One of the species, *S. lindbergii*, was placed within subgenus *Cuspidata* and as a sister clade to subgenus *Acutifolia* in phylogenies based on nuclear and plastid genomes, respectively. This indicates potential homoploid hybrid origin of this species.

All species were phylogenetically highly distinct, but no clear geographical structure was observed within species. Together with the genetic distance estimates, this pattern might indicate that level of intraspecific gene flow in haploid peatmoss species is high, whereas interspecific gene flow is detected, but more restricted. Work in progress aims to quantify the levels of gene flow and to explore how differences in gene flow are associated with life-history traits, relatedness and populations genetic parameters of the studied species.

OR-53

The gene regulatory map of *Physcomitrella patens* life cycle reveals key components of the developmental transitions modulated by membrane-anchored calpain DEFECTIVE KERNEL

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Recent work in land plants supports an intriguing evolutionary phenomenon where conserved developmental regulators are co-opted to control diverse morphogenetic programs. The membrane-anchored calpain DEFECTIVE KERNEL 1 (DEK1) has been implicated in positional signalling required for cell fate control during embryogenesis, shoot meristem formation and endosperm development in seed plants. In the moss *P. patens*, DEK1 is essential for oriented cell divisions that lead to the transition from filamentous growth to organized three-dimensional growth, but also effects other phases of the life cycle. During its life cycle, *P. patens* undergoes additional developmental switches that lead to the formation of new cell types and major body plan reorganizations. So far, only few

associated regulators have been identified. In order to elucidate the complex effect of *DEK1* on the *P. patens* transcriptome, we first constructed a global regulatory network (GRN) using Gene Network Inference with Ensemble of trees (GENIE3) based on 299 *P. patens* atlas transcriptome libraries representing most *P. patens* tissues, seventy four libraries from five different *DEK1* genotypes (WT, *dek1* deletion mutant, mutants carrying internal *DEK1* domain deletions and *DEK1* over-expressing line) harvested at five time points and a set of 1700 regulators. Partitioning of the generated GRN resolved eleven subnetworks representing distinct phases of the *P. patens* life cycle. Here, we describe the effect of *DEK1* on transcripts involved in *P. patens* gametophyte development, including the chloronema-to-caulonema transition, bud initiation and gametophore development together with recent genetic analysis that provide additional clues to the *DEK1* function in plant morphogenesis. This project is supported by the Slovak Research and Development Agency grant APVV-17-0570.

OR-54

Chromosomal-scale assembly of the *M. polymorpha* genome reveals similarities and differences to *P. patens* and *A. thaliana* genomes with respect to DNA-methylation and recombination rate

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Marchantia polymorpha has recently become a prime model for cellular, evo-devo, synthetic biological, and evolutionary investigations. We present a chromosomal-scale assembly of the *M.*

polymorpha genome making comparative genome structure analysis and classical genetic mapping approaches feasible. We anchored 88% of the *M. polymorpha* draft genome to a high-density linkage map resulting in eight pseudomolecules. We found that the overall genome structure of *M. polymorpha* is in some respects different from that of the model moss *Physcomitrella patens*. Specifically, recombination rates are greatest in the middle of the chromosome arms like in most vascular plant genomes, which is in contrast to *P. patens* where recombination rates are evenly distributed along the chromosomes. Nevertheless, some other properties of the genome are shared with *P. patens*. As in *P. patens*, DNA methylation in *M. polymorpha* is spread evenly along the chromosomes, which is in stark contrast to *Arabidopsis thaliana*, where DNA methylation is strongly enriched at the centromeres. Nevertheless, DNA methylation and recombination rate are anticorrelated in all three species. Taken together, the chromosomal-scale genome assembly we present opens new avenues for *M. polymorpha* research by linking the physical and genetic maps, making novel genomic and genetic analyses, including map-based cloning, feasible.

OR-55

PEATmoss (Physcomitrella Expression Atlas Tool): a unified gene expression atlas and gene model lookup database for *Physcomitrella patens*

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Physcomitrella patens resources are of great importance for comparative genomics and evo-devo approaches. However, publicly available expression data from *P. patens* were so far produced in three different technologies, Combimatrix and Nimblegen expression microarrays and RNA-seq, using gene annotation versions 1.2, 1.6 and 3.3, respectively. Three tools host some of these data, Genevestigator, the *P. patens* eFP Browser and Phytozome. However, these tools are limited to data from one single gene version or technology, few data sets and few visualization methods. Genevestigator, in the non-commercial version, is limited to few visualization plots for one single query gene from v1.2. The eFP Browser is limited to query one single gene in only one data set from gene v1.6. Phytozome contains RNA-seq expression data for the current gene annotation v3.3, but the only visualization method is an HTML table with gene expression values for only one gene. Here, we present PEATmoss (<https://peatmoss.online.uni-marburg.de>), a new expression atlas for *P. patens* integrating gene expression data from all the mentioned platforms and tools. It contains 109 experiments classified in 9 data sets, of which 35 are new experiments not available in any other tool. PEATmoss is very interactive and provides visualization methods such as a 3D expression cube, expression data in cartoons, bar plots, hierarchical clustering heatmap, scatterplot and tabular data downloading. The expression cube shows gene expression for the query gene and co-expressed genes, a custom list of genes or the output from BLAST, allowing multiple gene comparison. Additionally, a lookup database was developed and integrated to automatically convert between gene versions to facilitate querying expression data from any gene and data set. Furthermore, the lookup database contains tools for bulk gene conversion and sequence downloading, and provides cross link annotations for *P. patens* genes to NCBI, Phytozome, Ensembl Plants, TAIR, PLAZA, CoGe, TAPscan and genome browsers.

OR-56

Evolutionarily distinct pathways are present to regulate chloroplast proliferation in the moss, *Physcomitrella patens*

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OR-57

Investigating Myosin XI function in *Physcomitrella patens* tip growth by conditional mutagenesis

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Physcomitrella patens is an ideal model system to study tip growth, which depends on the actin cytoskeleton and cell wall secretion. Myosin XI plays an essential role in tip growth: plants where myosin XI genes have been silenced exhibit an altered morphology composed of round cells. To further characterize the role of myosin XI in tip growth, we developed mutant plants in which myosin XI protein is temperature sensitive (TS) at 32°C. At 32°C, cells undergo morphological changes within 3 hr: the zone behind the tip swells, and the tip narrows. The swelling morphology of the TS plants at 32°C is different from the swelling induced by latrunculin B-treatment. The morphology differences were quantified by measuring the curvature of the tip, showing a significant change between conditions. These values are being used as input to constrain a mathematical model of tip growth. In addition, in TS plants exposed to 32°C for 24 hr, a

significant number of caulonema cells die, compared to the TS at 20°C or the WT at 32°C. Surprisingly, we found that F-actin depolymerization reduces the number of dying cells. These results suggest myosin XI directs exocytosis to the cell apex determining the polarized morphology of the cell, and it is important for caulonema survival. Furthermore, in cells deprived of functional myosin XI for 1 hr, the vacuole morphology appears altered--vacuole tubules fuse together, suggesting myosin XI is involved in vacuole homeostasis. We also used the myosin XI TS line to study the interplay between myosin XI and F-actin. Following treatment of cells with low concentration of latrunculin B, myosin XI and vesicles generate F-actin, producing motile clusters that resemble actin comet tail based motility. We used the formation of these clusters to study if myosin XI is essential for their formation. Experiments with the myosin XI TS cells expressing the vesicle marker VAMP72 and the F-actin marker lifeact-mEGFP show that the clusters do not form in myosin XI TS at the restrictive temperature. Our results suggest myosin XI is essential for cell polarization and survival, vacuole homeostasis and for the formation of F-actin-vesicles clusters.

OR-58

Strigolactones signalling repression in land plants: Is SMXL function conserved between vascular plants and the moss *Physcomitrella patens*?

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Strigolactones (SL) are the newest discovered plant hormones, which play major roles in several developmental processes in vascular plants. Notably, they repress the outgrowth of axillary

buds, acting as a component of the well-known apical dominance machinery, together with auxins and cytokinines. Recent phylogenetic studies suggest that while the SL biosynthesis pathway seems to be broadly conserved across land plants, the signalling pathway as it has been partly uncovered in vascular plants appears to be a much more recent innovation. The molecular function of the SL signalling pathway's repressors, the SMXL proteins, remains especially mysterious even in vascular plants. In the lab, we are investigating the evolution of SL signalling using three diverse plant species: *Pisum sativum*, *Arabidopsis thaliana* and the moss *Physcomitrella patens*. To uncover whether the function of SMXLs as repressors of SL signalling has been conserved across land plants' evolution, we have devised genetical and biochemical approaches to study the four SMXL homologs of the moss *Physcomitrella patens* (*P. patens*). Several combinations of *Ppsmxl* loss-of-function mutations have been obtained via CRISPR-Cas9 mediated mutagenesis to investigate the role of these genes in *P. patens*' development and sensitivity to SL. Previous characterization of the SL biosynthesis mutant *Ppccd8* has shown that SL repress filaments' expansion in moss, making it an easy phenotype to test SL response. Characterization of a first generation of *Ppsmxl* mutants has suggested that the four genes were split between two functional clades, with only one involved in SL signalling. Additional genetic analyses using the *Ppsmxl* mutations will be carried on, such as complementation studies in the *Ppccd8* SL biosynthesis mutant. Moreover, generation of transgenic lines expressing either transcriptional or translational fusions of *PpSMXL* sequences enables us to determine where and when the PpSMXLs are expressed and whether their localization/stability is affected by SL. Biochemistry experiments such as Y2H, biFC and GFP-trapping have also been initiated in order to uncover the protein interaction network of PpSMXLs to further corroborate results from the mutants.

OR-59

Single nucleotide polymorphism charting of *Physcomitrella patens* accessions

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Physcomitrella patens was collected by H.L.K. Whitehouse in Gransden Wood (Huntingdonshire, UK) 1962 (Ashton and Cove 1977) and distributed across the globe starting 1974. Hence, it has been distributed in laboratories for half a decade. Today, more than 13 different pedigrees derived from Gransden are known. Additionally, accessions from other sites were collected during the last decades.

In this study we present single nucleotide polymorphism (SNP) analyses based on RNA-seq data of four different accessions (probably ecotypes) and 13 different Gransden pedigrees. SNPs were overlaid with meta data and known phenotypic variations. Defining SNPs were identified that can be used to determine the different accessions. Interestingly, independent mutations apparently came to be in the different Gransden pedigrees.

OR-60

A cis-acting bidirectional transcription switch regulates sexual dimorphism in *Marchantia*

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Plant life cycles alternate between haploid gametophytes and diploid sporophytes. Regulatory factors determining male and female sexual morphologies have been identified for sporophytic reproductive organs, such as stamens and pistils of flowering plants. In contrast, those regulating sex-specific traits in the haploid gametophytes that produce male and female gametes and hence are central to plant sexual reproduction are poorly understood. To reveal mechanisms of sexual differentiation in gametophyte, we used *Marchantia polymorpha* (*Marchantia*), a dioicous liverwort, as a model. We focused on a gene encoding MYB type transcription factor named *FEMALE GAMETOPHYTE MYB* (*MpFGMYB*). Using expression analyses, molecular genetics and microscopic observation, we revealed function of *MpFGMYB* in sexual differentiation of *Marchantia*. Our expression analyses indicated specific expression of *MpFGMYB* in developing archegoniophores. Surprisingly, genetic females of *Mpfgmyb* developed antheridiophores instead of archegoniophores. These mutants even differentiated sperm. These sex conversion phenotypes were rescued by a transgenic copy of *MpFGMYB*, confirming a causal relationship between these phenotypes and *MpFGMYB* function. Altogether, our result clearly indicated that *MpFGMYB* is required for female sexual differentiation in *Marchantia*. Since *MpFGMYB* is an autosomal gene, its expression must be suppressed in males. We found that this suppression is achieved by antisense long non-coding RNA of *MpFGMYB*, named *SUPPRESSOR OF FEMINIZATION (SUF)*. Genetic males of *suf* mutants exhibited male-to-female sex conversion phenotype accompanied by ectopic expression of *MpFGMYB*. Additional *Mpfgmyb* mutation suppressed this phenotype. Altogether these results clearly demonstrated that bidirectional transcription of *MpFGMYB* acts as a toggle between female and male sexual differentiation in *Marchantia* gametophytes. *Arabidopsis thaliana* *MpFGMYB* orthologues are known to promote development of embryo sacs, highly reduced female gametophytes. Thus, members of *FGMYB* subfamily transcription factors regulate female gametophyte development across land plants.

OR-61

Evolution of MurE functions from moss plastid division to angiosperm chloroplast development

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Bacterial peptidoglycan (PG) is a continuous covalent macromolecule comprised of a sugar-amino acid polymer. We have documented that the moss *Physcomitrella patens* contains a set of genes capable of generating PG (*Mur* genes) and that knocking out these genes causes defects in chloroplast division. Recently, we were able to visualize PG in moss under epifluorescence microscopy with a novel metabolic cell wall-labeling method of D-amino acid using click chemistry (Hirano et al. 2016). Most *Mur* genes have been lost from the genomes of chlorophyte algae and angiosperms, suggesting that no plastid PG systems work in these species. By contrast, *MurE* genes, encoding an enzyme that catalyzes the formation of UDP-*N*-acetylmuramic acid (UDP-MurNAc) tripeptide in PG biosynthesis, are generally found in green plants, including green algae and seed plants. In contrast to the huge chloroplast phenotype in the *MurE* knockout lines of *P. patens* (Machida et al. 2006), T-DNA- tagged lines of *AtMurE* (*atmurE* mutants) displayed a white-seedling phenotype, suggesting the *AtMurE* is related to chloroplast development in *A. thaliana* (Garcia et al. 2008). Moreover, *AtMurE* could not rescue the macrochloroplast phenotype caused by *PpMurE* mutation in *P. patens*, showing that *AtMurE* is functionally divergent from the bacterial and moss *MurE* proteins (Garcia et al. 2008). In the sequenced gymnosperm genomes, we could identify 10 homologs of bacterial *Mur* genes, including *MurE*, suggesting the retention of the plastid PG system in gymnosperms (Lin et al. 2017). Cross-species complementation assay with *MurE* mutants of *A. thaliana* and *P. patens*

showed that the expression of *MurE* cDNA from the larch, *Larix gmelinii* completely rescued the albefaction defects in *A. thaliana* but did not rescue the macrochloroplast phenotype in *P. patens* (Lin et al. 2017). Recently, we found that one gymnosperm *MurE* gene could complement both phenotypes of *P. patens* and *A. thaliana* *MurE* knockout plants. This may connect the functions between PG biosynthesis in moss and chloroplast development in angiosperms.

OR-62

Network of Epigenetic Regulators in *Physcomitrella patens*

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Epigenetic mechanisms are regulatory processes in which DNA/histone modifications such as methylation, acetylation or phosphorylation including nucleosome repositioning lead to heritable changes in gene expression without altering the underlying nucleotide sequences in the genome. These mechanisms play crucial roles in priming plants to tolerate recurring and chronic biotic and abiotic stresses. However, there are many lacunae in our understanding of these mechanisms in stress management in flowering plants. We choose the early land plant *Physcomitrella patens* to understand the evolution of network of epigenetic regulators and to gain insight into how these regulators are wired and connected because around 500 million years ago in an attempt to colonize land and complete their life cycles on harsh terrestrial habitats these plants developed elaborate stress signaling pathways and robust stress tolerance machineries. Hence, using gene knockout strategies and different protein-protein interaction techniques we deciphered a well-connected network linking chromatin remodeling proteins such as the SWI/SNF-related ATP-dependent DNA helicases, chromatin modifying proteins such as the cytosine DNA methyltransferases and the polycomb repressive complex proteins that together function to maintain DNA methylation and genome integrity in *P. patens* genome. Based

on our results we propose that activities of epigenetic regulatory proteins remained functionally relevant in early land plants where they possibly contributed in fine tuning developmental programs and in regulating physiological processes, including stress management, that eventually contributed in sustaining existence of these plants on terrestrial habitats.

OR-63

A knockout of *PpMED18* enhances salt tolerance in the moss *Physcomitrella patens* **Chandra Shekar Kenchappa**, Mikael Ulfstedt, Guo-Zhen Hu, Hans Ronne

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During stress conditions all organisms are capable of adapting to the environment by modifying gene expression through signaling pathways. The RNA polymerase II Mediator complex consists of 25-30 subunits which are evolutionarily conserved across the kingdoms and plays a vital role as a switchboard that integrates signals from different pathways to regulate gene expression. The Mediator complex consists of the Head, Middle, Tail and Cdk modules (1). We are studying the role of Mediator during abiotic stresses. We are working with the model organism *Physcomitrella patens*, which separated from flowering plants around 450 million years ago. *PpMED18* is a single copy gene encoding a non-essential subunit in the Mediator head module. In flowering plants, *MED18* is important for organ development (2). To study the role of *MED18* in moss, we generated independent *med18* knockout lines by using the CRISPR/CAS9 genome editing method. We found that the *med18* knockout lines are phenotypically smaller in size and show a somewhat higher tolerance to salt stress than the wild type. These observations are consistent with a model where Mediator integrates the responses to different signaling pathways and balances these responses against other physiological needs such as growth (3).

OR-64

The monthly transcriptome dynamics of Antarctic moss, *Sanionia uncinata* (Hedw.) Loeske, throughout the year in natural environments, reveals seasonal adaptation of extremophile plants

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Most organisms on Earth have evolved and adapted to the seasonally changing environment. The maritime Antarctic is covered with snow and ice for most of the year, but during the austral summer season, snow melts and a variety of vegetation is revealed. During this three-month period, terrestrial plants actively perform cellular activities under the prolonged daytimes. But even this short summer, the sub-zero temperatures, dryness, continuous strong light and UV radiation are very extreme conditions for plant growth, and after these summers are over, the snow starts to pile up and the plants stop growing and enter dormancy in a long and dark winter. Here, in this study, we investigated the annual transcriptome response of extremophile plants in a natural environment. During the 2015-2016 winter/summer station study, we had sampled *Sanionia uncinata*, one of the dominant bryophyte species of the maritime Antarctic, naturally habituated in the King George Island (62°14' S; 58°44' W), on a monthly basis, and conducted transcriptome analysis. As a result, we could identify groups of genes that fluctuate with rhythmicity according to the seasonal changes. The weighted co-expressed gene network analysis enabled to construct a correlation network on climate-gene expression and to identify the groups of genes responding to changing climatic factors in a natural environment.

OR-65

***De novo* genome assembly of *Sanionia uncinata* (Amblystegiaceae: Hypnales), a pleurocarpous moss dominant in Antarctica**

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Mosses in Antarctica grow mostly in coastal areas and are expected to have developed various unique physiological/molecular mechanisms to survive in extreme environments. *Sanionia uncinata* (Hedw.) Loeske (Amblystegiaceae: Hypnales) is a dominant moss species in the maritime Antarctic and considered as a good target to investigate genes associated with abiotic stress tolerance of mosses. It has several distinct characteristics when compared to *Physcomitrella patens*, the first model moss species. First, *S. uncinata* is a pleurocarpous moss. Second, it belongs to the order Hypnales which contains the largest number of species in the moss phylogeny. Third, it is an alpine species that lives in cold regions unlike *P. patens* mostly found in temperate regions. Here, we report the draft genome sequence of an Antarctic *S. uncinata*, obtained using third-generation PacBio sequencing technology. About 1 million reads were attained from four Sequel sequencing runs and merged together into a single dataset of 21 Gb. The *de novo* assembly produced 673 contigs comprised of 621 Mb with an N50 contig length of 2.2 Mb and the longest contig length of 10.3 Mb, and a total of 28,651 coding genes were inferred. When the completeness of the genome was assessed by BUSCO analysis with the Eukaryota odb9, *S. uncinata* draft genome showed 91.1% complete, 0.3% fragmented, and 8.6% missing BUSCO. Our dataset can be used as a comparative genome for evolution and speciation studies for bryophytes, as well as for the analysis of molecular adaptation of plants to harsh environment.

OR-66

Phylogenomic analyses of ancient sex chromosomes in *Ceratodon purpureus* highlight the dynamism of sexual systems in bryophytes

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Sex chromosomes have evolved several times across the tree of life, yet the evolutionary processes shaping their gene content remain enigmatic. Sex-chromosomes are well-documented in bryophytes, providing an untapped resource for exploring factors shaping the evolution of sex-chromosome gene content and chromosomal architecture. Sex in dioecious bryophytes is determined by a UV sex chromosomal system. In this system, each sex has a non-recombining chromosome (U for females and V for males). The U and V pair at meiosis in the monomorphic diploid sporophyte and segregate to the haploid male and female gametophytes. Because the sex chromosomes are transcriptionally active in the haploid stage, and therefore subject to purifying selection, we expect many orthologous genes will be retained between the U and V chromosomes. Here we use a combination of Illumina, PacBio, and Hi-C sequence data to generate chromosome-scale assemblies of the 360 megabase (Mb) genomes of a male and a female isolate of the moss *Ceratodon purpureus*. We used genes annotated on the ~100Mb U and V sex chromosomes of *C. purpureus* and existing transcriptome data of other moss species to study the evolution of gene content and chromosome architecture of moss sex chromosomes. These analyses demonstrate that the moss sex chromosomes evolved in the ancestor of nearly all mosses (~300mya) or even may predate the origins of the bryophytes, contradicting earlier results based on ancestral reconstructions of the bryophyte sexual system. Interestingly, the sex chromosomes contain several conserved transcription factor families, with important roles in sexual differentiation across the green plants. In spite of this conservation, the phylogenomic analyses also show that both the U and V have continued to acquire genes over time, and that the genetics of sexual dimorphism are highly dynamic.

OR-67

Expanded delimitation of *Physcomitrium* (Funariaceae) based on targeted sequencing of nuclear exons and their flanking regions

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The architecture of the sporophyte and its spore dispersal mechanisms are a key feature in the evolution and systematics of mosses. Since the selection pressure related to these mechanisms is assumed to be critical in the phylogenetic history of these plants, the loss of sporophytic complexity constitutes a relevant topic of study in moss evolution. The Funariaceae is an optimal commonplace to study sporophyte evolution since this family exhibits variable sporophyte complexities, spanning from long, exerted, operculate capsules with two rings of well-developed teeth, to capsules immersed and completely cleistocarpous. Recent independent studies have confirmed that the family underwent a rapid diversification, but the relationships of taxa with reduced sporophytes and the major genera *Entosthodon* and *Physcomitrium* remained ambiguous. We inferred the relationships of a selection of 70 Funariaceae accessions, including five taxa with highly reduced sporophytes, using 648 nuclear loci (exons complemented by their flanking regions), based on inferences from concatenated data and concordance analysis of single gene trees. *Physcomitrellopsis* is resolved as nested within one clade of *Entosthodon*. *Physcomitrella* s. lat., is resolved as a polyphyletic assemblage and, along with its putative relative *Aphanorrhegma*, nested within *Physcomitrium*. We propose a new monophyletic delineation of *Physcomitrium*, which accommodates species of *Physcomitrella*

and *Aphanorrhegma*. The monophyly of *Physcomitrium* s. lat. is supported by a small plurality of exons, but a majority of trees inferred from exons and their adjacent non-coding regions.

OR-68

High efficient and precise base editing in *Physcomitrella patens* genome using modified CRISPR/Cas9 systems

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The moss *Physcomitrella patens* is now a well established model organism for studying conserved signalling pathways and developmental processes during plant evolution. Its short life cycle, ease of cultivation, and high rate of gene targeting have made it an ideal system for genetic analysis. However, the fact that this moss is haploid and the difficulty of isolating hypomorphic mutants can limit gene function analysis. We have already demonstrated the potential of the CRISPR-Cas9 system for targeted gene knock-out in this plant. Here we developed in *P. patens* an efficient method for targeted base editing, a form of genome editing that enables direct, irreversible conversion of one base pair to another at a target genomic locus without requiring double-stranded DNA breaks (DSBs). For this purpose, we used two different base-editing constructs. The first one consists in a nickase CRISPR/Cas9 (nCas9) fused to Petromyza marinus cytidine deaminase (PmCDA1) and can lead to C→T, C→A, C→G substitutions. The second one consists in a nickase CRISPR/Cas9 (nCas9) fused to an engineered *Escherichia coli* transfer RNA adenosine deaminase (ecTadA) that can operate on DNA and lead to A→G substitutions. As a proof of concept we designed Single-guide RNAs (sgRNAs) to target an endogenous reporter gene, PpAPT, whose inactivation confers resistance to 2-fluoroadenine. Transformation of moss protoplasts with these sgRNAs and the base-editing constructs triggered mutagenesis at the PpAPT locus in about 1.8% of the regenerated

plants (64% of the transfected plants). In addition, we could show in this study that the base-editing system is very efficient for multiplex base editing as we were able to modify bases in four regions of the same gene simultaneously. In one experiment we could obtain 31 variants of the APT protein that gave us original information on important amino acids/peptides for this enzyme, showing the potential of these newly developed CRISPR-Cas base editors for gene function analysis in *P. patens*.

OR-69

A Trans-kingdom Myosin XI interaction with a RabE GTPase is essential for polarized growth

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The fundamental eukaryotic process of intracellular trafficking requires the interconnected activity of molecular motors trafficking vesicular cargo within a dynamic cytoskeletal network. However, in plants, few mechanistic details are known about how molecular motors associate with their secretory cargo to support the ubiquitous processes of polarized growth and cell division. A yeast two-hybrid screen of a *Physcomitrella patens* library identified a RabE GTPase as an interactor of myosin XI and subsequently demonstrated all five RabE members interact with myosin XI. Consistent with a role in polarized transport, we observed RabE at the growing cell apex and at the expanding cell plate during cell division. An *in vivo* cross-correlation analysis of fluorescently tagged RabE and myosin XI revealed that both species are spatiotemporally coupled, demonstrating their simultaneous involvement in polarized growth. To determine if myosin XI and RabE are directly coupled, we first computationally predicted myosin XI:RabE interface through a homology modeling-directed

approach. We identified a structurally conserved residue on myosin XI, V1422, that when mutated abolished RabE binding in the yeast two-hybrid system and resulted in unpolarized plants instead of the characteristic network of filamentous cells when regenerated from single cells. Directed yeast two-hybrid using the cargo-binding domain of myosin XI-K from *Arabidopsis thaliana* demonstrated a direct interaction with RabE from *P. patens*. Furthermore, chimeric myosin XIs comprised of cargo-binding domains from *A. thaliana* successfully rescued growth in a silenced myosin XI moss background. Together, this work demonstrates the requirement of a direct myosin XI:RabE interaction for polarized growth in plants.

OR-70

The first high-quality reference genome for hornworts (Anthoceros) reveals drastically different genome structure from those of mosses and liverworts.

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The monophyletic group of hornworts is believed to represent the immediate sister group of all vascular land plants. However, this traditional view is still debated and cannot be satisfactorily resolved owing to the lack of detailed knowledge on the general biology and genomic features of hornworts. Until now, advancement in this field was primarily hindered by the lack of genomic resources for a hornwort model species.

Here we provide a high-quality genome draft of the model hornwort, *Anthoceros agrestis*, and some of its relatives. With the aid of Chicago and Hi-C libraries we assembled the *A. agrestis* genome into 5-6 chromosomes spanning a total length of ca. 120 Mb. The *A. agrestis* genome drastically differ from the published bryophyte genomes (moss and liverwort) and exhibit a number of unique features. The *A. agrestis*

genome is small and strongly streamlined. In particular, we show that it has few recent paralogs, exhibits no signs of whole-genome duplication and has a moderate repeat content (ca. 30%). Despite of its small size, the genome is densely packed with genes (28 000 genes) of which 30% seems to be unique to hornworts showing no homology to genes of land plant and green algal genomes. We further show that the genome contains over 3000 PPR genes (pentatricopeptide repeat) known to be involved in organellar RNA editing that is pervasive in chloroplast-derived transcripts of *A. agrestis*. Finally, we present a preliminary gene expression atlas which shed light on the regulation of morphological and developmental traits that are either shared with other embryophytes or unique to hornworts. Overall, our analysis suggests that the hornwort genome is radically different from that of other land plants. Its unique and shared features within land plants provides better understanding on the evolutionary genomic events accompanied the origin and evolution of land plants.

OR-71

The genome of the moss *Funaria hygrometrica* provides insights into chromosomal-scale genome evolution in Funariid mosses.

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Thanks to its attractive phylogenetic position and molecular genetic attributes the model moss *Physcomitrella patens* has become a powerful tool for developmental and molecular genetic research during the last decade. Although many of the advantageous properties of the bryophyte system have been used in studies on development and cellular function, several peculiar characteristics have not received much attention so far. In particular, evolutionary genomics and comparative developmental genomics of mosses are still in their infancy and are waiting to be exploited. Here we report the genome of *Funaria*

hygrometrica, a relative of the model moss *P. patens*. *Funaria* and *Physcomitrella* represent end points of morphological and developmental complexities (complex and reduced sporophyte morphology in *Funaria* and *Physcomitrella*, respectively) within the group of Funariid mosses thus providing an ideal model system for comparative studies. Using a polished PacBio assembly and additional Chicago and HiC libraries we present our genome assembly consisting of 26 chromosomes with a total length of ~320 Mb. We show that many features of the *F. hygrometrica* genome are shared with those of *P. patens* but some striking differences exist with strong phenotypic consequences. The two genomes have largely co-linear chromosomes, share 20 000 orthologous genes and two whole-genome duplications. Despite these similarities, the *Funaria* genome is approx. 160 Mb smaller which is associated with the preferential loss of repetitive DNA. It also contains more than 8000 *Funaria*-specific genes preferentially expressed in the complex sporophyte phase. We also show that the *Funaria* karyotype consisting of 26 chromosomes can be easily derived from the 27 chromosomes of *P. patens* via two chromosome fusions and one fission. Overall, our data provides insights into how loss of repetitive DNA, chromosome fusions/fissions and gene losses/gains have contributed to the evolutionary and morphological divergence of the *P. patens* and *F. hygrometrica* genomes.

OR-72

The monophyly of Bryophytes is supported by nuclear and plastidial protein phylogenies

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Determining the phylogenetic relationships among the first land plant lineages is essential for an understanding of the evolution of terrestrial ecosystems. The predominant point of view has been that bryophytes were the first to colonise land and that tracheophytes descend from an ancestral bryophyte. This hypothesis is supported by molecular evidence, including organellar and nuclear protein-coding genes. However, analyses

of the amino acid translation of these same data show an alternative pattern whereby mosses and liverworts form a group that often includes hornworts. We show that the signal supporting the hypothesis of a bryophyte ancestor of land plants is mostly driven by substitutional saturation at synonymous sites in nucleotide data, and that non-synonymous sites and amino acid nuclear data converge on the same supported result, namely, that bryophytes form a monophyletic group. These results indicate that conventional stationary substitution models are inadequate for analyses of molecular data that is highly saturated and affected by composition bias. Analyses of codon-degenerate and amino acid-translated nuclear and chloroplast data, under composition tree-heterogeneous models, strongly support the monophyly of bryophytes, and imply that an ancestral land plant lineage diverged rapidly into bryophytes and tracheophytes. This relationship suggests that the bryophyte life-cycle, characterised by a dominant gametophyte that nurtures an unbranched sporophyte, is not ancestral to all land plants, and that stomata are a symplesiomorphy among all land plants.

OR-73

Geometric cues forecast the switch from 2D-to-3D growth in *Physcomitrella patens*

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Asymmetric cell divisions, in which a daughter cell acquires a new identity, are crucial for plant growth and development throughout evolution. The successful colonization of land by the basal plant *Physcomitrella patens* was achieved by a critical switch in its growth pattern, facilitated by an asymmetric division that initiates a bud from a filamentous cell with gametophore identity.

Insights into the underlying mechanisms coordinating this switch are still unknown. By 2D-, 3D-imaging and image segmentation, we identified and quantified two geometric cues, the width of the initial cell and the angle of the transition division plane, which sufficiently distinguished a gametophore initial cell from a branch initial cell. These identified cues were further confirmed in bud-enriched and bud-deficient mutants, respectively. The identification of a fluorescent marker allowed us to successfully predict the gametophore initial cell with more than 90% accuracy. This high prediction accuracy confirms our hypothesis that before the asymmetric cell division, parental cells of the gametophore initials already possess different cellular properties compared to branch initials. Our results indicate that the cell fate decision of the daughter cell is determined in the parental cell, prior to the completion of the cell division.

OR-74

Genetic pathways controlling meristematic activity and differentiation in hornwort-sporophytes

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A major change that accompanied the evolution of embryophyte land plants from a haplontic ancestor was the elaboration of the sporophyte and parallel reduction of the gametophyte phase. Flowering plants have established complex branched sporophytes, which grow through the continuous activity of a multicellular meristem located at the tip of the shoot. Genetic developmental pathways controlling the activity of this shoot apical meristem have been extensively studied in flowering plants, most notably of *A. thaliana* and *Z. maize*. In contrast, bryophytes, the most basal group of extant land plants, have subordinate, unbranched, monosporangiate and upright sporophytes that remain attached to the gametophyte generation. Bryophyte-sporophytes exhibit multicellular meristems that contribute to sporophyte growth,

referred to as intercalary meristem in mosses and basal meristem in hornworts. Yet, regulatory mechanisms controlling the activity of these bryophyte-meristems are not known. Comparison of regulatory gene networks controlling sporophyte development in bryophytes and vascular plants will help resolving the evolutionary-developmental trajectory between bryophyte-sporophytes and the more complex sporophytes of vascular plants. Therefore, our main goal is to provide a detailed account on the regulatory mechanism governing sporophyte development in bryophytes. To this end, we established transcriptomic profiles for five different sporophyte tissues of the hornwort *Anthoceros agrestis*, using laser-assisted microdissection coupled with RNA-sequencing. Analysis of differential gene expression across these five tissues allows us to establish a hypothetical model of regulatory mechanisms involved in governing sporophyte development in hornworts. Additional comparison of this transcript dataset with data available for the *P. patens* gametophytic apical cell and sporophyte, as well as the SAM of *Z. maize*, enables us to refine hypotheses regarding the evolutionary relationship of multicellular meristems of land plants. Future work will focus on describing fine-scale spatial expression of proposed candidate genes and testing their functional role using reverse genetic approaches.

OR-75

DNA double strand break (DSB) repair in protonema tissue of the moss *Physcomitrella patens*

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Protonema of the moss *Physcomitrella patens* is a unique tissue, which with regard of cultivation conditions enables to study tissue either with majority of cells in chloronema arrested at G2/M stage or that of caulonema arrested at G1/S stage. The objective of this study was to study differences in response of these tissues to DSBs induced by bleomycin. Subculturing of protonema generates fragments of 3-7 cell of

which up to 50% are apical, whereas 7 days after subculture, fragments extend, often branch, and only fraction of cells is apical. By weighting explants, primary caulonema and chloronema showed to be more resistant to 1 hour bleomycin treatment than 7 day grown tissue and, as estimated by comet assay, also more efficiently repair DSBs. Same differences between primary and 7 day tissue are also among lines mutated in *SOL*, *NSE1* and *NSE4*. *SOL* is a homologue of *Arabidopsis* *SOG1* transcription factor that controls response to gamma irradiation. Its mutation allows the cell-cycle progression manifested as a phenotype resistant to bleomycin and efficient DSB repair when compared to wt. Contrary to *SOL*, *NSE1* and *NSE4* are essential kleisin genes of SMC5/6 complex, which in circular form stabilizes DSB during repair. The viable CRISPR/dCas9 *nse1* and *nse4* lines show very similar phenotype with *sol* line. We conclude that in primary tissue the rate of DSB repair is extremely efficient regardless of *SOL* or *NSE1*, 4 mutations, whereas much slower in older tissue, suggesting that repair is not so urgent for cell survival as in dividing cells. When replication is not a primary need for cell survival, more elaborate mechanisms of repair start to be involved and lead to ambiguous repair kinetics. Supported by the Ministry of Education, Youth and Sports of the Czech Republic (LTC17047/2017).

OR-76

Effect of air pollution on species composition of communities of epiphytic bryophytes with respect to bark chemistry

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Epiphytic bryophytes are susceptible to air pollution. Disappearance of sensitive species from highly polluted areas and their return after decrease of pollution load was recorded during the second half of the 20th century in Europe as

well as in recently polluted industrial areas. However, effect of air pollution on epiphytic communities composition and the associated role of host tree bark chemistry has not been sufficiently explored. The main aim of our study was to assess the effect of air pollution on the structure of epiphytic bryophyte communities hosted by tree species with different bark pH. Due to higher buffering capacity of basic substrates, we expected smaller difference between communities on host trees with higher bark pH in areas with distinct pollution loads. Epiphytic bryophytes were studied on 50 study sites with similar climatic conditions but contrasting levels of air pollution (based on model data of SO₂ and NO_x loads) in Central Europe. All species of bryophytes and their abundances were recorded on the five trunks of oaks (*Quercus robur* or *Q. petraea*, lower bark pH expected) and five ashes (*Fraxinus excelsior*, higher pH expected) from the ground to 2 m height at each study site. Additionally, four phytosociological relevés 25×25 cm were recorded on all trees. As a proxy for the current pollution load at each site, thallus N concentration was measured in *Hypnum cupressiforme* or *H. andoi*. We recorded 89 species of bryophytes in total. Epiphytic communities are more species-rich in areas with low levels of air pollution both on oaks and ashes. Air pollution was found to be a significant environmental variable explaining part of variability among studied communities. Bark pH and N concentration in *Hypnum* thalli corresponded to model data of SO₂ and NO_x loads. Bark pH range was shorter on ashes, acidifying impact of pollution was buffered partially. Species composition of communities on ashes differed only under the highest SO₂ load, on the contrary, oak communities were affected by high level of any pollutants as the bark become more acidified. Air pollution thus determines the structure of epiphytic bryophytes communities.

OR-77

The ratio between bryophyte functional groups impacts vascular plants in rich fens

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Fens have well-developed bryophyte layer covering most of the ground. Non-sphagnaceous bryophytes, especially the group of so-called brown mosses, prevail over sphagna under alkaline conditions. In sub-alkaline conditions, rich fens allow the co-occurrence of these both functional groups, but sphagna are competitively superior over non-sphagnaceous bryophytes and seedlings of vascular plants, and they are currently expanding in some regions. We test whether the ratio between the two major bryophyte functional groups (*bryo-ratio*) accounts for species composition of fen-specialized vascular plants. We analyzed two datasets of the vegetation-plot records by Canonical Correspondence Analysis with variation partitioning (community-level analysis) and Structural Equation Modelling (species-level analysis). At the community level, the *bryo-ratio* accounted significantly for species composition of fen-specialized vascular plants. At the species level, most of the species affected significantly by the *bryo-ratio* preferred the fens rich in non-sphagnaceous bryophytes. They were largely those with a low capability of vegetative reproduction. Species preferring brown moss patches include mostly rare and endangered species with a great need for generative reproduction (e.g., *Primula farinosa*, *Triglochin palustris*, *Pedicularis palustris*, *Saxifraga hirculus*). We demonstrate the important role of the bryophyte layer in the structuring of vascular plant communities in fens and highlight urgent conservation needs for brown moss patches.

OR-78

Do we know all types of the arthrodontous moss peristome?

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Molecular phylogenetic studies of mosses revealed two terminal clades, the subclasses Bryidae and Dicranidae, largest in number of species, and the grade leading to them from primarily eperistomate and nematodontous groups through Buxbaumiidae, Diphysciidae and Funariidae. Buxbaumiidae and Diphysciidae have highly specialised peristomes, not splitting into definite number of separated elements. The three subclasses, Funariidae, Bryidae and Dicranidae are characterized by three main peristome types: diplolepidous opposite, haplolepidous, and diplolepidous alternate respectively, and this correlation is a fundamental fact of the backbone moss system. The recent anatomical studies of the peristome development, however, challenge some its aspects: (1) origin of the *Diphyscium* peristome type from the *Buxbaumia*-type; instead *Buxbaumia* is likely a derivative from *Diphyscium*-like ancestor; (2) the occurrence of diplolepidous peristomes in some groups of Dicranidae (which are commonly called just "haplolepidous"); (3) The opposite position of elements of endostome and exostome may repeatedly appear as a kind of peristome reduction, thus Funariidae may be assumed not as one of three basic peristome types, but a side lineage, representing several variants of strongly modified peristome types.

OR-79

Are all paraphyllia the same?

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Paraphyllia and pseudoparaphyllia are two terms which are important in pleurocarpous mosses systematics, yet their misapplication continues. Paraphyllia are treated as adventive structures (appendages) of stem epidermis, in contrast to foliose or filamentose structures around branch primordia commonly referred to the pseudoparaphyllia. One of the reasons for that misapplication is the neglected fact that proximal branch leaves are often not only incised, but sometimes subdivided up to the base, and moreover, their parts might occur spaced from each other to a certain distance, looking as independent subfilamentose structures, which we called compound leaves. Especially puzzling are cases, when compound proximal branch leaves appear around undeveloped branch primordia. These leaves apparently belong to "virtual branch" as they have clear phyllotaxis, as e.g. *Leskea* and *Cratoneuron*. The branch apical cells in this case appear to be hidden almost totally under the stem epidermis. Such filamentose parts of compound branch leaves we suggest to call *Leskea*-type paraphyllia. There are at least two cases where paraphyllia have likely a different type. In genera with papillose stem, e.g. *Pelekium*, there are transitions from unicellular to multicellular raisings on each cell of the stem surface, pointing thus the homology with papillae, comprising *Pelekium*-type paraphyllia. The third, *Climacium*-type paraphyllia is observed in *Climacium* and *Pleuroziopsis*. In this case paraphyllia occur in longitudinal rows along the stem, without any connection to primordial, and possess many characters of rhizoids. New observations in anatomy allow circumscribe *Leskea*-type of paraphyllia in details, revealing facilitation its development by exogenous ABA application.

Poster abstracts

PO-01

AMBRA1 controls plant development and senescence in *Physcomitrella patens*.

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Autophagy is a universal mechanism that in plants control development, resistance to stresses and starvation. The role of autophagy is possible thanks to the programmed degradation of cell material that is delivered to the vacuole where hydrolases and proteases are localized. So far, many autophagy-related proteins (ATGs) have been identified. Some of them are universal, some are either specific to animals, plants or yeast. ATG protein complexes govern autophagosome initiation, nucleation, expansion, and maturation. In particular, the regulation of nucleation by the ATG6 (Beclin-1 in mammals) complex has not been well defined in plants.

Here we described the study of the Activating Molecule in Beclin 1-Regulated Autophagy (AMBRA1) protein, recently identified in mice and then characterized in our department in zebrafish and in the non-vertebrate chordate *Botryllus schlosseri*. In animals AMBRA1 is a positive regulator of autophagy that binds Beclin-1 upon autophagic stimuli. AMBRA1 is a large intrinsically disordered protein, able to bind other regulatory partners involved in cell processes such as autophagy, apoptosis, cell proliferation, development and cancer.

AMBRA1 sequence was found in plant genomes and we are studying its function in *Physcomitrella patens* where two lowly expressed genes are present, *AMBRA1a* and *AMBRA1b*. We have isolated single *ambra1a*, *ambra1b* and double *ambra1a/b* knock-out (KO) plants. The protonema of *ambra1a/b* KO showed growth defects as compared to WT, while *ambra1a* KO and *ambra1b* KO showed either no impairment or a slightly reduced growth respectively. *ambra1a/b* KO is characterized by a high frequency of aberrant branching pattern and a high percentage of senescent protonema cells both on minimum medium or on medium supplemented with glucose and ammonium tartrate. Moreover *ambra1a/b* KO showed unexpected vertical growth when cultivated in the light while it is unable of gravitropic growth when left in the dark for two weeks. Plants treated by protease inhibitors such as E-64d showed that the accumulation of degradation intermediates is

not reduced in the absence of AMBRA1, meaning that potentially autophagy is still possible. AMBRA1 appears to be an important regulator of plant development, further studies will help to better understand the molecular function of AMBRA1 in plants.

PO-02

Plitvice Lakes – the largest area with tufa forming bryophyte vegetation in Europe

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Plitvice Lakes are situated in Dinaric region of Croatia characterized by different karst formations. One of them is the system of 16 larger and several smaller cascading lakes, stretched 8 km in length and interconnected by numerous waterfalls of different size, height and water velocity. They are formed through the biodynamic process of growing tufa barriers in water oversaturated with calcium carbonate, pH value higher than 8 and low concentration of dissolved organic matter. All these tufa barriers are overgrown by rich vegetation dominated by bryophytes. This vegetation was studied using phytosociological methods followed by measurements of environmental parameters and analysis of ecological indicator values. In total 44 bryophyte species were recorded of which 26 are constantly present in 90 vegetation relevés. The main characteristics of vegetation are prominent dominance of bryophytes over vascular plants and very constant species composition with a low number of species present with high abundances. Four main species are *Palustriella commutata*, *Eucladium verticillatum*, *Hymenostylium recurvirostrum* and *Pellia endiviifolia*. Nevertheless, three main types of bryophyte vegetation are differentiated – species poor vegetation of non-shaded waterfalls mostly with

high water velocity, the vegetation of shaded waterfalls with weaker water flow, and species rich vegetation of moist rocks outside direct or constant influence of running water. All of these vegetation types belong to the moss rich vegetation of carbonate springs of montane and subalpine belts of Europe belonging to the alliance *Cratoneurion commutati*. However, due to the complex system of lakes and waterfalls, very large surfaces covered by this vegetation, species richness and their high abundances, Plitvice Lakes represent one of the most important diversity and distribution centres in Europe regarding the tufa forming bryophyte vegetation and is of the highest conservation value.

PO-03

Antifungal effects of some mosses of Iran on the phytopathogenic fungus “*Fusarium solani*”

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Mosses have proved to have anti-cancer, anti-microbial and anti-fungal properties due to their specific chemical compounds. In this study, the antifungal effects of methanolic, ethanolic, acetonic and aqueous extracts from some mosses collected from different regions of Khuzestan province, Iran, were tested on growth of *Fusarium solani*, one of the most important pathogens of agricultural crops, especially wheat and compared to the commercial fungicide Benomyl. For this purpose, moss samples were

transferred to the lab and washed with sterile water and dried in shadow. Then the dried mosses were pulverized and extracted by ethanol, methanol, acetone and distilled water. The antifungal activity was tested by disc diffusion method. Plates of Potato Dextrose Agar (PDA) were inoculated with 6 mm diameter pieces of 7 days old fungal culture margin. Fungal pieces were placed in the middle of PDA medium. The filter paper discs (6 diameter) impregnated with different extracts and Benomyl were placed at a certain distance from the edge of fungus grown and kept in the incubator for 48 hours at 25 ° C. The diameter of the inhibition zone was measured using a millimeter ruler. In order to investigate the effect of moss extracts in vivo, wheat seeds of Chamran cultivar were implanted into moss extract and planted in pots containing 1: 10 mixture of soil and soil contaminated with fungi. Considering that the fungus species *F. solani* causes crown and root rot of wheat, after 35 days the root and crown of wheat plants were examined based on Wallwork scale (Wallwork et al. 2004). The experiment was conducted as a completely randomized design with three replications. The results show that ethanolic and methanolic extracts produced similar inhibitory effects as Benomyl fungicide, and aqueous extracts had limited effects. Statistical analysis using SAS 9.2 showed the significant variances between the effects of ethanolic extract and other extracts. In vivo observations also indicate that ethanolic extracts can prevent the growth of *F. solani* and in some cases, have similar effects as Benomyl.

PO-04

The bryophyte research programme at the Royal Botanic Garden Edinburgh (RBGE)

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Bryophyte research at RBGE focuses on a range of activities integrating international taxonomic

and phylogenetic research with the work of national conservation agencies and the long-established recording programmes of specialist societies to better understand the origins, diversity, distribution and future needs of the globally important Scottish bryophyte flora. British bryophytes are the best recorded in the world, while Scotland harbours much of Europe's remaining bryophyte-rich temperate rainforest and oceanic montane heath, host to many species with highly restricted and disjunct global distributions. RBGE further houses one of Europe's largest bryophyte herbaria (E) with over 500,000 specimens, including much recent, well-curated material and around 4,000 types.

Activities span core phylogenetic research on select groups (Polytrichaceae, thalloid liverworts, austral pleurocarps), large-scale molecular sequencing initiatives targeted at the British flora, and a number of smaller, self-contained projects addressing species-level problems in collaboration with international specialists and UK field bryologists. Our outreach work includes teaching bryophyte identification, contributing to "bioblitz" events, collaborating with visual artists and hosting regular visitors including secondary school and undergraduate students, while we are actively developing our collection of living bryophytes alongside our Horticulture Division. Our ongoing liverwort DNA barcoding project includes multiple accessions of most British and Irish liverworts, providing a reference library for identification. Tangential to this are projects focusing on select taxa including *Aneura*, *Moerckia* and *Scapania*. Recent phylogenetic research highlights include an investigation of relationships between British species of the enigmatic, primarily austral genus *Orthodontium*, in which the native *O. gracile* is shown to belong to a distinct Holarctic and Asian clade that diverged from the rest of the genus early in the Cenozoic. This species has its last European outpost in Britain and appears to be threatened by the introduced *O. lineare*.

A major new project examining the global relationships of Scotland's oceanic liverwort heath community is now underway, aiming to explain the startling disjunctions displayed by many of the species by studying trans-continental phylogenetic structure, functional traits and dispersal capabilities.

Ongoing PhD projects include studies of *Polytrichum* sect. *Polytrichum* (Isuru Kariyawasam; University of Edinburgh), *Andreaea* and *Herbertus* (David Bell; University of British Columbia).

PO-05

Recommendations for the use of critical terms when applying IUCN red-listing criteria to bryophytes

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The IUCN Red List of threatened species (<http://www.iucnredlist.org/>) is widely recognised as an objective system to assess the extinction risk of animals, plants and fungi and as an authoritative tool to catalyse conservation actions. The IUCN criteria developed for estimating the extinction risk of species are most readily applied to large organisms with clearly identifiable sexually reproducing individuals, while they may be difficult to employ to bryophytes and other clonal and colonial organisms. Here, we present refined, pragmatic definitions for three key terms that are critical when using the IUCN red-listing methodology, notably 'mature individuals', 'generation length' and 'severe fragmentation'. These definitions facilitate the application of the IUCN Red List criteria for bryophytes. They have been successfully applied in the recent Red List

assessment of all 1816 bryophyte species of Europe (Hodgetts et al., *in prep.*). The definitions provide an effective way of using the IUCN Red List criteria for bryophytes and may have a wider application to other clonal organisms.

PO-06

Monitoring moss growth and physiological status using a low-cost image analysis system

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The last few decades there has been an increasing interest in using mosses as model organisms for ecological studies. This has brought a need for precise and easy-to-use methods to measure plant productivity and health. We present a non-destructive, cost- and time-efficient protocol for monitoring moss growth and physiological activity. The approach is based on the analysis of visible (VIS) and near infrared (NIR) moss pictures taken with low-cost drone cameras. Applying remote sensing and image analysis techniques we calculated a set of 19 spectral indices usually implemented in teledetection and 13 image segmenting methods. We used the ImageJ software and a modified version of the R package *crustCover* that we developed for these image analyses. Then we evaluate which index-segmentation combination provides higher precision and accuracy for moss area estimation. Finally, we estimate the moss physiological status using the segmented images and the most meaningful indices. To calibrate the protocol, we have used five pictures per moss species, and six common soil moss species (*Dicranum scoparium*, *Hypnum cupressiforme*, *Homalothecium aureum*, *Ptychostomum capillare*, *Tortella squarrosa* and *Syntrichia ruralis*), which were cultured for six months in 2018 in three field localities along an altitudinal gradient in central

Spain. The most informative indices to estimate moss area and physiological status were NDVI, MSAVI, EVI and Saturation. We found differences in the efficiency between methods to estimate moss areas automatically, depending on the relationship between moss and background area in the pictures. This fact calls for a careful use of automatic segmentation, highlighting the importance of manually adjusting the index thresholds on our subject of study. The future implementation of neural networks and deep learning on methods based on spectral indices provides a wide perspective for automated data collection in the field or in the laboratory.

PO-07

Elucidating the role of eIF5A in growth and stress response in *Physcomitrella patens*

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The control of protein translation is a central aspect of adaptive responses to environmental stress in plants, as well as in development. Translation initiation is a highly regulated and rate-limiting step of protein synthesis that requires more than 12 eukaryotic initiation factors (eIFs). In this study, we have used RNA-seq to identify genes involved in translational regulation of gene expression during high temperature stress in *Physcomitrella patens*. A gene encoding a eIF5A protein homolog (*PpeIF5A*) was shown to be highly induced in response to high temperature. *PpeIF5A* encodes a 17.5 kDa deduced protein, with a theoretical pI of 5.60 and a predicted signal peptide. In planta transient expression of *PpeIF*-GFP fusion protein indicated that *PpeIF5A* localized in the nucleus of plant cells under non stress conditions. Expression profiling of this gene showed that, in addition to heat stress, *PpeIF5A* was upregulated in response to dehydration, abscisic acid and salicylic acid treatments. 5A translation initiation

factors have been suggested to play an important role in the selective translation of proteins that, due to their biochemical nature, are difficult to be translated. Among the possible target genes, whose expression are expected to depend on eIF5A, are those that encode proteins rich in PPP (Pro-Pro-Pro) and/or PPG (Pro-Pro-Gly) sequences. A search in *P. patens* genome revealed the presence of a number of putative target genes. The expression profile of those genes was analyzed in RNA-seq transcriptomic data, in response to heat and salicylic acid treatment. The aim of this work is to characterize the function of PpeIF5A and to identify the proteins involved in stress responses that require the activity of this factor for proper translation.

PO-08

Population genetic diversity, genetic structure and phylogeography of *Riella helicophylla* (Riellaceae)

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Riella helicophylla (Bory & Mont.) Mont. (Riellaceae, Sphaerocarpaceae) is an aquatic, liverwort of brackish, temporary Mediterranean lagoons. It is a dioicous, ephemeral species, with highly fluctuant populations, which relies on spores for population regeneration after summer droughts. Nonetheless, it can also spread vegetatively during the growing season due to propaguliferous scales. It has a widespread fragmented distribution in Mediterranean countries and mainland Spain is where the largest number of populations have been reported. The species is considered threatened and included in Red Lists of the corresponding countries and in the Annex II of the European Union Directive. The species is being studied both morphologically and molecularly as earlier studies have shown it consists of at least two taxa. Here we present the results of a population genetic study aimed at describing the genetic diversity and population structure within and

among populations and phylogeographical patterns of this liverwort. For this purpose 756 individuals from 26 populations of the most widespread taxon of the *R. helicophylla* complex, covering the whole Spanish range and of some of the western Mediterranean countries have been genotyped at 9 nuclear microsatellite loci specifically designed for the species. From this analysis, 90 alleles were detected showing moderate to high levels of genetic diversity (overall genetic diversity among individuals across populations ranging from 0.148 to 0.532). Distance based clustering and Bayesian analysis of population structure showed a strong genetic association of populations within areas. However, geographical areas with longer fluctuations on habitat suitability or more prone to shorter flooding times, showed higher among population genetic structure within geographical areas. This may be related to temporal variation of population development thereby affecting population connectivity through migratory routes of aquatic birds.

PO-09

Mosses of Central Florida: Current progress in their documentation and in development of new identification tools

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Central Florida is a region with a distinctive floristic composition, where the mosses from temperate North America and the neotropics are interfused. Presently we review the recent status of the documentation of the mosses of Florida and progress in the development of modern interactive identification tools for Central Florida. The primary database is in the Atlas of Florida Plants, based on the species listed in the Flora of North America (FNA) as occurring in Florida, with county distributions of moss species collected from the database of the Consortium of North America Bryophyte Herbaria (CNABH). Development of new identification tools include species portraits on the Botany professor blogsite and a new interactive key to the mosses of Central

Florida. Data reveal that Seminole County is the most heavily collected county with 132 species out of 264 listed in the FNA. Analysis of species abundance shows the three most common species found in Central Florida are *Isopterygium tenerum*, *Leucobryum albidum*, and *Octoblepharum albidum*. To date, 55 mosses have been incorporated into the key and 53 moss portraits have been posted. This project is still in progress. The publication of innovative identification tools is intended to increase curiosity and encourage others to study the mosses of this region.

PO-10

The effect of lead pollution on chlorophyll fluorescence in two moss species

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Heavy metals may produce structural and reproductive alterations in mosses. Their biomonitoring potential depends on the relationship of the extent of these effects and the pollutant level in the environment. In order to develop a non-invasive, easy measurement of these alterations on mosses, we present here an analysis of chlorophyll fluorescence, to test the effect of experimentally supplied lead on two moss species, *Homalothecium aureum* and *Tortula muralis*, with contrasted growth forms and ecological requirements. We applied three doses of Pb(NO₃)₂ and a control with water on greenhouse cultures of each species (6 replicae per experiment). The doses were sprayed twice every week during two months. We analysed chlorophyll fluorescence using two techniques: 1) fluorescence imaging using a CCD camera, and 2) spectroscopic analysis of the emission spectrum. The chlorophyll fluorescence was excited by using a low-power laser beam (405 nm, 10 mW), and detected in the red region of the spectrum (600-700 nm) by placing several filters. Both techniques provide us information about the

chlorophyll content, which is affected by the lead pollution. Initially *H. aureum* presents a higher chlorophyll content, and apparently adjusts better to culture conditions before lead spraying. After the lead supply experiment, the specimens of both species survive, although visually *H. aureum* showed more conspicuous damages (yellowing), whereas *T. muralis* presented little apparent alterations, and was able to produce new sporophytes. The fluorescence results point at a reduction of fluorescence in *H. aureum* in higher lead doses, more remarkable than in *T. muralis*. We interpret that *T. muralis* is more naturally resistant, and that *H. aureum* shows a greater extent of adaptation of its photosystems to pollution stress. These techniques allows a non-invasive, periodical monitoring of the effects of pollutants on mosses, showing pollutant effects on chlorophyll and possible coping mechanisms of pollution-stressed plants.

PO-11

Dust in the wind... How to improve air quality monitoring using terrestrial mosses

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Terrestrial mosses have been used for more than 40 years to monitor trace elements in atmospheric deposition because of their high cation exchange capacity and suitable morphology for fixing and accumulating particulate and gaseous pollutants. The most common type of active biomonitoring using moss transplants is the “moss bag technique”, which consists of the exposure of moss samples held within mesh bags and the subsequent analysis of contaminant concentrations in their tissues. Standardized protocols have unfortunately still not been developed and research has mainly focused on evaluating methodological variables such as the selection of species and the shape and size of the moss bag. However, it has been suggested that the orientation of the bags relative to a pollution source may greatly influence the efficiency of interception and capture of atmospheric

contaminants by moss. Thus, the objective of this study was to investigate whether the optimal orientation of flat moss bags containing the moss *Sphagnum palustre* improves the retention of Al, As, Cd, Cr, Cu, Fe, Hg, Ni, Pb, V and Zn. Three replicate moss bags were exposed in each of eight industrial sites (in the surroundings of two ferrous-smelters, a ceramics factory, a paper and wood factory with cogeneration production, and a coal-fired power plant) in two different ways: attached to weathervanes (bags in devices rotating downwind) and attached to static poles (static bags). The results demonstrate that in the most polluted sites, the metal uptake capacity (for As, Cu, Fe, Pb and V) in the moss bags attached to the weathervanes was higher than in the moss bags attached to the static poles, so the moss bags attached to the weathervanes were more effective for detecting pollution than the others. Data suggest that the orientation of the bags with respect to the source of contamination should be considered and that further research is required to standardize the methods used in the moss bag technique.

PO-12

The importance of ash stands for the diversity and conservation of epiphytes in broad-leaved forests of Latvia.

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In recent years, a rapid destruction of the European ash *Fraxinus excelsior* caused by the ascomycete *Hymenoscyphus fraxineus* has been observed throughout Europe. Latvia, located in northern part of Europe in the boreo-nemoral vegetation zone, has been exposed to ash dieback as well, which has resulted in decreasing habitats for many epiphytic bryophyte species. The objective of this study was to determine the diversity of epiphytes in broad-leaved forests, highlighting the flora of bryophytes in *Fraxinus excelsior* forests. The data were collected during

previous four summer seasons (from 2015 till 2018). Epiphytic bryophytes were examined in 62 forest stands throughout the territory of Latvia. The stands were classified into five groups according to dominant tree species. The results of this study indicate that ash stands were hosting the highest species richness. Overall, 82 bryophyte species were recorded on 848 tree trunks, including 14 especially protected species for Latvia. Among these, 70 species were found in ash stands, of which 13 epiphytes were recorded only in plots of *Fraxinus excelsior* forests. The number of species per plot were significantly higher in ash stands (24 species/plot) compared to lime (15), oak (14), hornbeam (14) and elm (10) stands. Ash stands were characterized also by the highest abundance of protected species (in total, 12 species). The composition of epiphytes does not differ significantly between different forest stands. However, 23 epiphyte species showed their preference to ash forests, including two protected species – *Homalia trichomanoides*, *Anomodon longifolius* and one rare species in Latvia – *Frullania fragilifolia*. According to the results, the lime and oak stands had the highest proportion of epiphyte species that were also recorded in ash stands. In conclusion, it could be assumed that ash stands in Latvia represent high conservation value for epiphytes. The recommendations for forestry politics to preserve old oak stands in Latvia might compensate decreasing ash substrate in future perspective.

PO-13

Spatial analysis of qualitative pollution data in moss samples at a regional scale

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Terrestrial mosses have been used as air pollution biomonitors for more than 40 years, but despite this, and due to certain technical limitations, moss biomonitoring has hardly had any impact or has influenced decision-making regarding environmental pollution. One of the causes of this is the scarce bibliography or theoretical knowledge about the process of accumulation of pollutants by the mosses and the real relationship between atmospheric deposition and the concentrations of pollutants found in moss tissues, which makes it difficult to interpret the results. Even so, most of the studies carried out in this field carry out a quantitative analysis of the concentrations, which clearly seems to be contraindicated. The objective of the present study is the analysis of the spatial structure of various pollutants in Galicia (NW Spain) through a new statistical procedure. This procedure is presented as a new possibility for the qualitative treatment of quantitative data on the concentration of pollutants in terrestrial mosses. This analysis proposes a new allocation rule for the categorisation of quantitative data into the dichotomous variable of "polluted" and "uncontaminated" levels. This rule is based on the hypothesis that the concentration of heavy metals in the moss, in the absence of pollution, follows, like the nutrients, a normal distribution. In this study we categorized moss samples collected in the 150 points of Galicia sampled in spring and autumn of different years. Once the data had been categorised, the spatial analysis was carried out, calculating the indicator semivariograms and obtaining the predictions by means of indicator krigging. The results showed the existence of dependence and spatial structure for some metals such as Hg, where significant differences in pollution can be observed between different points of the study area, which is in line with the results observed in the bibliography. Based on this, we can conclude that this seems to be a suitable procedure for the qualitative treatment of the data, although this procedure could not in itself determine whether a point is contaminated or not, but rather determine whether it is contaminated with respect to the background contamination level.

PO-14

Bryophyte Phylogeny Poster (BPP)

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The educational Bryophyte Phylogeny Poster (BPP) provides a graphic overview of the relationships among Bryophytes s.l. (liverworts, mosses, hornworts) with divisions, major subclasses, orders, and families along with relevant apomorphic and plesiomorphic traits. This depiction of our current understanding of phylogenetic relationships is an ideal tool designed for teaching, studying, and research.

The original poster is available for free downloading from PeerJ Preprints at <https://peerj.com/preprints/27571/> in its most recent updated version. The BPP so far has been translated into 16 languages (English, German, Spanish, Portuguese, French, Chinese, Japanese, Mongolian, Thai, Indonesian, Russian, Ukrainian, Polish, Swedish, Finnish, and Lithuanian). All versions are freely available to the international community via ResearchGate and via the FU Berlin online webpages. Regular updates of the posters will be made as new research and data are published.

PO-15

Towards a database of the Romanian bryophyte vegetation. Status and perspectives.

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A vegetation database represents a valuable resource for the continuous adjustment of the syntaxonomical system, as well as inestimable

information about species coenology, synecology and syndynamics, particularly for species of conservative interest. Our aim is: 1. to compile all phytosociological data from Romania into a database which will be related to other existing inventories, e.g. Romanian Grassland Database (RGD), integrated into the Global Index of Vegetation-Plot Databases (GIVD); 2. to review the coenotaxonomic knowledge on bryophyte communities according to the new European syntaxonomical framework (Mucina et al., 2016); 3. to identify the bryophyte communities hosting bryophytes of conservative interest.

The first step was to assemble all epiphytic relevés from the literature and to add them to our own data. The nomenclature follows Grolle & Long (2000) for liverworts and Hill et al. (2006) for mosses. Syntaxonomical classification is a minute and complex process: in a first phase, updates (added as new columns) were made according to Marstaller, 1992.

The epiphytic database comprises 620 relevés: 574 are from the literature (16 papers and two PhD theses) and 46 relevés are unpublished. Surveys were conducted on 31 tree species (with a diameter between 15-180 cm); most of the relevés were sampled on beech, pedunculate and sessile oak, and only 4.03% were sampled on coniferous bark. Concerning the vegetation classes, corticolous moss communities are best represented by *Neckeretea complanatae* Marst. 1986 and *Frullanio - Leucodontetea sciurioidis* Mohan 1978 em. Marst. 1985, and on acid or old bark, by *Cladonio - Lepidozietea reptantis* Jez. et Vondr. 1962 em. Marst. 1993. Ten species are of conservative interest: *Dicranum viride* (HD/BC/EN), *Lescuraea mutabilis*, *Metzgeria violacea*, *Neckera pennata*, *N. pumila* and *Zygodon viridissimus* are vulnerable, *Habdrodon perpusillus*, *Hypnum jutlandicum*, *Leptodon smithii* and *Pseudoleskea saviana* are critically endangered. Data gaps are inherent to such a large study (e.g. elevation, aspect, host species, sample area, tree diameter, GPS coordinates or location). Some relevés were not assigned to any association. We plan to analyze and improve the syntaxonomical knowledge about epiphyte communities from Romania and then to extend the available data about bryophyte communities.

PO-16

Competition and facilitation in the early development of three common Iberian mosses

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Although biotic interactions affecting the spore germination may play a major role in the establishment of a moss community, they are rarely documented and their extent is not well known. In order to analyze the effects of shoots and spores of mosses on germination and early protonematal development, we have modified the sandwich technique, a widely used *in vitro* assay that was designed to assess allelopathic effects in vascular plants, and adjusted it for living bryophyte material. We have performed intra- and interspecific assays with three common mosses in central Spain: *Hypnum cupressiforme* Hedw., *Tortula muralis* Hedw. and *Dicranum scoparium* Hedw., using both spores and disinfected vegetative apical shoots to test their effects on spore germination and growth. We have obtained different patterns of response for each species. The protonemata of *H. cupressiforme* are inhibited only by its own spores and by shoots of *D. scoparium* (both co-habiting in their natural environment), but not by *T. muralis* (a non-coexistent species). In turn, *T. muralis* is inhibited by both the spores and shoots of *H. cupressiforme*, and by the presence of shoots of *D. scoparium*. Strikingly, the sporeling development of *D. scoparium*, although quite limited in control experiments, is enhanced, not inhibited, by the presence of spores or shoots of any of the three species (most especially, by shoots of *H. cupressiforme*). We have found that the effect of shoot leachate is similar to shoots themselves, suggesting that the facilitation or inhibitory effects may depend either on a stable, water-carried factor, or on the development of shoot epiphytic communities of micro-organisms that interact with spore germination and growth. Our results in these three species point at several interesting implications: 1) a pre-colonization

requirement for the spores of *D. scoparium*, combined with an inhibitory strategy of their shoots over the establishment of new mosses; 2) the occurrence of spore-spore intraspecific competition in *H. cupressiforme*, but not between adults and spores; and 3) the sensitivity of *Tortula muralis* even to naturally non-coexistent species. These interactions, usually neglected in bryophytes, may play a crucial role in their distribution and dynamics.

PO-17

Sporophyte and spore characters in three genera of difficult morphological characterisation within the family Brachytheciaceae

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The traditional genus *Brachythecium*, the most important taxonomic group in the family Brachytheciaceae, was split on molecular grounds into three monophyletic genera: *Brachythecium* s. str., *Brachytheciastrum* and *Sciuro-hypnum*. Morphological characters, usually more centred on the gametophyte, yield little support for this phylogenetic classification. However, the sporophyte and the spores of this group remain poorly addressed. Here we present an anatomical and ultrastructural study on the sporophyte and spores in this group in order to find some sound characters allowing morphological support for the molecular classification. We have studied either freshly collected samples or herbarium specimens of 20 Palaeartic species of *Brachythecium* s.l., and of 4 additional external species (two in Brachytheciaceae, and two in other families of O. Hypnales). We have observed them using both light and electron microscopy: scanning electron microscopy for spore ornamentation and peristomes, and transmission electron microscopy for the spore inner structure. Our

results provide novel descriptions for the sporophyte and spore ultrastructure for the species studied. Besides, we could identify the most valuable sources of morphological characters supporting the molecular circumscription of the group, namely the anatomy of the seta and the sporoderm inner structure. In *Brachytheciastrum* the inner cortical cells in the seta are distinctively small, in *Brachytheciastrum* s. str. the cell walls of this layer are thinner, and in *Sciuro-hypnum* most of the internal seta structure corresponds to a thick-walled cortex. In turn, the spore in *Brachytheciastrum* has an isopolar, thin sporoderm; whereas in *Brachythecium* the intine is thicker, with marked polarity, and in *Sciuro-hypnum* it is even thicker and highly heteropolar.

PO-18

Green workshops – a focus on biodiversity using bryophytes for urban children

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One of the missions of the Conservatory and Botanical Garden of Geneva (CJBG) is to transmit our knowledge on plant biodiversity, and the importance of biodiversity for our planet, to the public. As an institution that holds rich bryophyte collections (Hedwig-Schwägrichen, Stephani) we have been seeking ways to inform on biodiversity using bryophytes through our Green Workshops programme. The Green Workshops are open to children from Geneva from 9-12 years old and represent a rich collaboration between the scientists and education staff of the CJBG with members of the University of the Third Age (U3A) of Geneva. The aim of our newly developed workshop was to introduce children to bryophytes – an often integral part of the flora of cities – and to scientific enquiry in the field of biodiversity. We also wanted to demonstrate some of the science done on bryophytes at our institution. To bring bryophytes to life in a playful way for urban children, an activity based on the search for a ‘lost’ moss professor was created. The children needed to find Professor “Mousse-tach” using her notebook on bryophytes and by finding clues

or answering questions to fill in parts of the notebook that were blank. In groups, the children visited different ‘exploration stations’ that were run by the workshop team. Each station specialist demonstrated something about bryophytes (What is a bryophyte? What are their main features? Where do they grow? How do they survive?). The notebook itself, created in-house and distributed to each child, contains historical drawings, brief explanations about bryophytes and spaces for them to add pictures or specimens of bryophytes. When the children had found the lost professor, they had to search for some common species within the botanical garden grounds with her using their hand-lenses. To see bryophytes close-up and to get a taste for the scientific study of bryophytes, the children then went into the laboratory and observed bryophytes using stereoscopes working through a key to determine six different species. Once they had identified their material, they added it to the notebook to make a mini-herbarium that they could take home.

PO-19

Investigating the Biosynthesis and Function of Complex Sphingolipids in *Physcomitrella patens*

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Sphingolipids are essential and characteristic membrane components of eukaryotic cells. In addition, sphingolipids are signalling molecules. They contribute to membrane integrity, are required for normal growth and development, and mediate plant-pathogen interactions. There are two broad classes of complex sphingolipids found in plant cells, glucosylceramides (GlcCers) and glycosyl inositolphosphorylceramides (GIPCs), which both consist of a hydrophobic ceramide backbone and a polar sugar head group.

Both GlcCers and GIPCs have proven difficult to study due to the technical challenges of extracting amphipathic lipids, and genetic challenges posed by the fact that GlcCer- and GIPC-deficient mutants are either lethal or have severely impaired development. The model bryophyte *Physcomitrella patens* is an appealing system for the study of sphingolipid metabolism, as mutant phenotypes may be easier to interpret within its relatively minimalist developmental program compared to the conventional angiosperm model *Arabidopsis thaliana*. Further, a model bryophyte presents an opportunity to study the most ancestral functions of complex sphingolipids in land plants. We have profiled the sphingolipid composition of *Physcomitrella patens* by ultra-performance liquid chromatography coupled to mass spectrometry (UPLC-MS/MS). Unlike other plant species in which GIPCs are highly abundant, *Physcomitrella patens* accumulates a high level of GlcCers, while GIPCs are barely detectable. We identified candidate genes associated with both GlcCer and GIPC biosynthesis in the *Physcomitrella patens* genome based on homology to *Arabidopsis thaliana*. We are confirming these annotations with biochemical assays, and by generating and characterizing loss-of-function mutants. We generated a *ceramide glucosyl transferase* (*cgt*) mutant by homologous recombination; this mutant lacks GlcCers entirely, and accumulates ceramides. The mutant has abnormal growth, and appears unable to produce caulonema in a dark-growth experiment. Single and higher-order *inositol phosphorylceramide synthase* (*ipcs*) mutants are being generated using CRISPR/Cas9. This work sheds light on the evolution of the metabolism of an enigmatic class of lipids, and contributes to our understanding of their cellular and developmental functions.

PO-20

Of turf, trees and air quality: does roadside moss trap more particulate matter than leaves?

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Plants in urban areas interact with air quality in numerous ways. Firstly, pollutants from industry, vehicular and residential sources can be detrimental to plant growth. Secondly, plants sometimes contribute to poor air quality, for instance by emitting allergens such as pollen, or by trapping pollutants in street canyons and thirdly, with appropriate placement some species improve air quality through phytoremediation. A common urban pollutant is particulate matter (PM - small particles of solid or liquid). While this is of concern to human health, less well known is its effect on vegetation and while moss is commonly studied as a biomonitor, there is little research on how it is affected by urbanisation. Our objective was to measure PM entrapment by roadside moss turfs and compare it to leaves of a common Australian tree species, *Pittosporum undulatum* on an urban gradient. We also wished to compare stress levels on this gradient using chlorophyll fluorescence (F_v/F_m). We sampled nine sites in the coastal city of Wollongong, NSW, three in each of three levels of urbanisation: low, medium, and high according to road type (freeway, suburban road, quiet peri-urban road). At one site of each urban class we measured PM_{2.5} over a two-week period using a mobile monitor. PM of three size fractions was isolated by filtration and washing with both water and chloroform. Site averages for moss turfs were much higher than leaves: between 5.60 and 33.00 mg per g dry weight for total PM (moss) compared to between 2.15 and 10.24 mg per g dry weight (tree). Moss appears to be more sensitive to increasing urbanisation in terms of photosynthetic stress, with moss F_v/F_m declining by a site average of 40% from low to high urban “class” (0.76 to 0.45). We also found increased wax deposition in moss with urbanisation, raising the hypothesis that it is a defence mechanism in these environments. Our study highlights the stressors potentially limiting moss persistence in cities and quantifies moss turf ability to trap PM.

This trait could be exploited in applications relating to urban greening or air quality and should be further explored.

PO-21

Bryophytes of Myanmar. Inventory, characteristics and affinities.

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Indochina is bryologically one of the least known regions in Asia. Especially the flora of Myanmar (Burma) is still insufficiently known. It lies between latitudes 9° and 29°N, and longitudes 92° and 102°E, situating in the monsoon region of Asia. It also extends from the mangrove forests and coral reefs of the Andaman Islands in the south to the snow-capped peaks of Mt. Kakaboradzi (5881 m) in the north. The situation in the surrounding area suggests that there is incredible floral diversity in Myanmar. The National Museum of Nature and Science, Japan, together with the Forest Research Institute, Myanmar, embarked the international joint inventory research project to collect the materials for a “Flora of Myanmar” under the MoU since 2016. This study aims to present a preliminary report of the results of our field surveys, intending to highlight the characteristics and affinities of the bryophytes of Myanmar. Field surveys were conducted on Tanintharyi Nature Reserve (elevation lower than 250 m) of southern part in January, 2017, and on the montane area of Chin State (elevation 1200-2600 m) of western part in November, 2017. A total of ca. 550 bryophyte specimens were collected in both field surveys. The bryophytes recognized in Tanintharyi Nature Reserve mainly consist of the species of Calymperaceae, Fissidentaceae, Sematophyllaceae, Lejeuneaceae, etc., which are similar to those of lowlands of subtropical or tropical regions of Asia. On the other hand, the bryophytes recognized in montane area of Chin State are mainly composed of the species of Brachytheciaceae, Dicranaceae, Hylocomiaceae,

Meteoriaceae, Neckeraceae, Thuidiaceae, Lepidoziaceae, Plagiochilaceae, etc., which are similar to those of the forests of temperate regions of Asia.

PO-22

Knock-down of essential subunits of SCM5/6 complex in *Physcomitrella patens*

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SMC5/6 complex participates in many vital cell processes including DNA repair and most of its eight subunits are essential. In haploid *Physcomitrella patens* mutations of essential genes leading to loss-of-function are lethal and their study requires rather attenuation of transcription or expression that allows partial viability of mutant than hard knock-out. We used two different techniques - RNA interference (RNAi) and CRISPR/dCas9 interference (CRISPRi) - to knock-down essential genes of SMC5/6 complex for generation of lines manifesting deficiency of protein of interest, but still viable. RNAi was performed by transformation of plasmid expressing short hairpin RNA (shRNA) targeted to SMC6 mRNA and produced stably transformed lines with decreased levels of SMC6 transcript and strong phenotype. Nevertheless, the RNAi effect disappeared after 3-4 cycles of subcultivation of primary transformants. The loss of SMC6 gene silencing was most probably caused by methylation and subsequent transcriptional inactivation of shRNA construct. To gain lines with stably silenced subunits of SMC5/6 complex, plasmid expressing catalytically dead Cas9 (dCas9) and gRNA targeted near to START codon of NSE1 or NSE4 was introduced into protoplasts of *Physcomitrella*. Recovered CRISPR/dCas9 lines were screened by qRT-PCR for transcript levels of NSE1 or NSE4 and the lines with decreased level of NSE1, NSE4 mRNA were tested for their sensitivity/resistance to acute DNA damage induced by radiomimetic drug bleomycin. Although only mild reduction (20-30%) of NSE1 and NSE4 mRNA levels was detected the CRISPRi lines manifested clear

resistance to acute DNA damage. The decreased mRNA level and resistant phenotype has been maintained even during consequential cycles of subculturing. Our data show that, unlike RNAi, CRISPRi allows long-term effective repression of essential genes in *Physcomitrella*.

PO-23

Evolutionary conserved epigenetic silencer Polycomb repressive complex 2 in the bryophyte *Physcomitrella patens*

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Polycomb Repressive Complex 2 (PRC2) is a protein complex composed of proteins that belong to the family of Polycomb group (PcG). Together with the Trithorax group (TrxG), PcG complexes regulate development and differentiation in all eukaryotic organisms. PRC2 was firstly described in *Drosophila melanogaster* and later on recognized as an evolutionarily conserved stabiliser of gene suppression. Here, we examine PRC2 subunits FERTILIZATION INDEPENDENT ENDOPLAST (FIE) and CURLY LEAF (CLF) in *Physcomitrella patens* to determine their effect on phototrophic development. *P. patens* PRC2 mutants ($\Delta PpCLF$ and $\Delta PpFIE$) generated in our laboratory were analysed by RT-qPCR which showed a successful deletion of *PpCLF* and *PpFIE* gene correspondingly. Western Blot assay was further conducted to confirm the loss of post-transcriptional modifications which are installed by PRC2. A phenotypic analysis was performed to describe the defects in the mutants. To limit the developmental contribution of PRC2 absence to the analysed phenotypes, we focused especially on protonemal stage. PRC2 dysfunction in *P. patens* under long term cultivation in the presence

of glucose results in morphologically different phenotype. Together with increased light intensity it promotes a formation of structures described as sporophyte-like bodies. Further RT-qPCR analysis of candidate genes whose dysregulation may be connected to the observed light and metabolism-related phenotypes provides first insights into the role of PRC2 in the moss photoautotrophic growth and development.

PO-24

Interspecific variation in the fitness of six Iberian soil mosses assessed through biomass production and colonization success

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Vegetative dispersal is key for understanding the distribution of species with vegetative reproduction. However, the mechanisms behind it are often poorly understood. In moss species in which all species are potentially capable of propagating from fragments the role of mechanical fragmentation is crucial. We examined the colonization success of different fragment sizes and types in six Iberian soil mosses (*Hypnum cupressiforme*, *Dicranum scoparium*, *Ptychostomum capillare*, *Homalothecium aureum*, *Tortella squarrosa* and *Syntrichia ruralis*). We obtained three classes of shoot fragments through mechanical milling and sieving of dry samples (large, medium and small). Additionally, wet fragments were directly cultured as a fourth distinct class. All fragment classes were examined using light microscopy to assess fragment origin (leave or shoot), presence of meristems and size. After two months in culture, we measured the percentage of colonized surface and biomass (i.e. the viable biomass in relation to sown dry weight). Fragments milled in wet had, in general, lower success in our experiments. For dry fragments the intermediate size shows lower intraspecific variability and a

fair performance (above 25% of colonization), while small fragments present much worst performance. Some species stand out because of their higher variability. Two of the species show larger differences between fragment sizes. *H. cupressiforme* had biomass production rates above 100% in the large fragments, and below 30% for the rest of fragment types, while *P. capillare* presents biomass production above 100% for intermediate and big fragment sizes and below 50% for the rest. These results seem to be related with the presence of a sufficient number of apical meristems in the shoot fragments and the ability of the species to reproduce directly from leaf cells. We also show that intermediate fragment sizes are probably more effective for culture experiments. Regarding natural population establishment success, it is interesting to note that the smallest fragment sizes, that have the higher potential for longer distance dispersal, show the lowest success rates.

PO-25

Drivers of ground bryophytes diversity in temperate beech forests - stand structure vs. soil characteristics

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Bryophyte diversity and distribution is defined by large number of factors which act within time and space scale. Various studies showed the importance of soil characteristics and stand structure on bryophyte diversity and distribution. However, studies which deals with influence of these factors on ground bryophyte flora in temperate beech forests of South-eastern Europe are still lacking. The aim of this study was to determine the influence of soil characteristics and stand structure on bryophyte diversity in broadleaved temperate forests with *Fagus sylvatica* as dominant species. The survey was performed in Fruška gora Mountain (Northern Serbia) on 5 forest sites. Within each site, 5 plots (100x100 m in size) were placed, and Microcoenose sampling method was performed for quantitative sampling of ground bryophytes.

Soil moisture, soil temperature and pH were measured within each site as soil characteristics, as well as herbaceous cover, litter cover, stream distance, number of trees and bushes as characteristics of stand structure. Shannon diversity index and Pielou's evenness index were used as diversity measures. Generalized linear model (GLM) and CCA analysis were performed for testing the influence of individual factors on bryophyte diversity. Variation partitioning analysis was performed for testing influence of stand structure and soil characteristics on bryophyte diversity. Total number of 54 species was found on all 5 sites. GLM analysis showed that all factors, except soil temperature and soil pH, have significant influence on ground bryophyte diversity. CCA analysis showed that largest percent of variability in bryophyte diversity can be explained by litter cover, herbaceous cover, soil moisture, tree number and stream distance, respectively. Variation partitioning analysis showed that stand structure explains 18.7% of total variability in bryophyte diversity, while soil characteristics explains 9.5%. Together, these two factors explain 14.1% of variability. The results of this study showed that stand structure is a more important factor influencing ground bryophytes in comparison to soil characteristics. Determination of the most important factors that influence bryophyte diversity in forest stands is of high importance in forest ecology, especially for establishing adequate methods of management in order to preserve biodiversity.

PO-26

Morphological and phylogenetic notes on *Trachycarpidium* species (Pottiaceae, Bryophyta)

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Pottiaceae is the most generic- and species-rich family in Bryophyta (Mosses), with around 1500 species in ca. 80 genera. The taxonomy of the family has been difficult and controversial due to problems of morphological variability, the unclear significance of several anatomical characters, the reduced size of many species, the obscure leaf areolation, and sterility of many specimens. Although some molecular phylogenetic studies have been conducted to resolve relationships of the family at (supra-) generic level, the status and phylogenetic position of ca. 20 genera are still unrevealed due to the lack of useable specimens for successful DNA extraction and amplification. *Trachycarpidium* Broth. is one of these genera. It comprises five species with tropical distribution. This genus is characterized by immersed, cleistocarpous capsules with mamilliose-bulging exothecial cells. In contrast to its unique sporophytic characters, the gametophytic similarity to *Tortella* (Müll. Hal.) Limpr. or *Weissia* Hedw. was suggested by some authors. However, the generic status of *Trachycarpidium* has been retained due to the lack of decisive evidence, as molecular data were not available then. In the present study, we investigated the anatomical structure of capsules in *Trachycarpidium*. In the context of previous molecular studies, here we also successfully obtained chloroplast DNA sequences from two species of the genus, and inferred their phylogenetic positions within the Pottiaceae. The anatomical comparison of the capsules allowed us recognizing two different thickening types of exothecial cell walls (outer walls): 1) evenly thick, including both sides and tip of its central mammilla; 2) markedly thicker at the mamilla sides and much thinner at its tip. We suggest that thickenings of exothecial walls could be useful as a taxonomic character in this group for species discrimination. However, phylogenetic analyses using concatenated sequences of chloroplast *rbcL* and *rps4* genes showed that *T. brisbanicum* (Müll.Hal.) I.G.Stone and *T. lonchophyllum* (G.Roth) R.H.Zander were nested in the *Weissia* clade, pointing at a polyphyletic origin for capsules with mamilliose-bulging exothecial cells. Our results support the congeneric treatment of *Weissia* and *Trachycarpidium* and also suggest that the

sporophyte morphological diversity is much higher than expected within *Weissia*.

PO-27

Towards a new IUCN based Red List of bryophytes for Switzerland

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At the Swiss Data and Information Centre for bryophytes work on a new Red List is underway. Although the data basis is extensive (> 300'000 data sets) various challenges have to be faced: heterogeneity of data, taxonomic changes, interpretation of IUCN criteria as well as an appropriate assessment of global and regional threats such as climate change and landscape changes. Specific field surveys (e.g. searching for rare species) and herbarium revisions are carried out to close data gaps. Furthermore, with the intention to provide an improved data basis for future red lists, a permanent plot survey is set up to monitor selected priority species and habitats. The new Red List is to be published in 2020.

PO-28

Specificity of Caucasian liverwort flora: phytogeographical peculiarities and hidden diversity

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We have analyzed the liverwort flora of Caucasus based on data obtained during the study of liverworts diversity in this mountains for ca. 15 years. Ca 4000 specimens from almost sea level up to 3000 m alt. were gathered mainly in Russian part of the Caucasus and about 2000 of them were identified. Labels data are available in Cryptogamic Russian Information System (<http://kpabg.ru/cris/?q=node/16>). Some of the

specimens were studied recently using molecular phylogenetic approach. Many new species for the Caucasus and some new ones for science were revealed. At present ca. 200 species are recorded for the Russian part of the Caucasus. The core of the flora are widespread Holarctic liverworts including boreal and arctic-montane species restricted mostly to the middle and upper belts of the Caucasus that were classified by A.Takhtadjan (1978) as the Caucasian Province of Circumboreal Region. The arctic-montane species are restricted to upper belts of Caucasus and probably are remnants of arctic-terrestrial flora. A number of predominantly Mediterranean species are in Caucasus near the eastern and northern limits of their distribution and occur mostly in presumably not glaciated Euxine Province. Several mostly Asian species are in the Caucasus on their western limit. The long isolation of the Caucasus vegetation is reflected in its richness in endemic flora of vascular plants whereas among hepatics for a long time only *Solenostoma caucasicum* (Váňa) Konstant. was known as endemic of the Caucasus. Using integrative approach, we found that some species are represented in the Caucasus by distinct genetic units. Some of them were described as new for science, e.g. *Jubula hutchinsiae* (Hook.) Dumort. subsp. *caucasica* Konstant. & Vilnet., *Jungermannia calcicola* Konstant. et Vilnet. We found as well that Caucasian population of *Liochlaena subulata* (A.Evans) Schljakov is molecularly distinct from that in Europe and Siberia. One more *Jungermannia* species presumably new for science and phylogenetically allied to *J. atrovirens*, was discovered by us in Euxine Province of the Caucasus and will be described in nearest time. We believe that based on integrative approach careful study of recent Caucasian liverworts collections will show relatively high level of hidden endemism of the Caucasian liverwort flora.

PO-29

A multi-scale approach to drought in *Sphagnum*, the cellular basis of an ecosystem engineer

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As a key component of most peat-forming ecosystems, *Sphagnum* is of major importance for the ecosystem services it provides. Due to the increase of global temperature and extreme weather events, in combination with anthropogenic alteration of the ecosystem, the peatlands are increasingly exposed to oxygen and as the length of dry periods increases, the peat deteriorates and releases large amounts of greenhouse gases. Therefore, understanding the adaptations that these mosses have for avoiding or coping with desiccation is essential for the preservation of functioning peatland ecosystems. By combining approaches at the ecological, photo-physiological and genetic levels, the present research aims to elucidate the basic processes that are involved in desiccation tolerance in *Sphagnum*, such as the typical distinction that is made between hollow and hummock occupying species and their varying degrees of desiccation tolerance. Through the measurement and imaging of photo-physiological variables in different ecological settings such as stem density and subjection to periodic drought. Initial results regarding the effect of colony density on photo-physiological parameters suggest that at higher stem density, *S. fallax* can tolerate longer periods of drought and maintains photosynthetic activity in the lower parts of the plant. Future aspects of this project will replicate these experiments on different species of *Sphagnum*, and also investigate possible within-species variation as a result of ecological niche differences. In parallel, we aim to look at the expression levels of desiccation-related genes and how their expression changes in different tissues, sections of the plant and throughout time during the drought and recovery period. Taken together our results will provide a better understanding of the genetic and physiological basis of desiccation tolerance in *Sphagnum* and will help inform peatland recovery projects.

PO-30

Unique epigenetic features of ribosomal RNA genes (rDNA) in early diverging plants (bryophytes)

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Introduction: In plants, the multicopy genes encoding ribosomal RNA (rDNA) typically exhibit heterochromatic features and high level of DNA methylation. Here, we explored rDNA methylation in Bryophyta (15 species) and Marchantiophyta (4 species) using methylation-sensitive Southern blot hybridization in all species. We also carried out whole genomic bisulfite sequencing in *Polytrichum formosum* and *Dicranum scoparium* and used available model plant methylomes in *Physcomitrella patens* and *Marchantia polymorpha* to determine rDNA unit-wide methylation patterns. Chromatin structure was analyzed using *in situ* hybridization and immunoprecipitation assays.

Results: In contrast to seed plants, bryophytes rDNAs were efficiently digested with methylation-sensitive enzymes indicating no or low levels of CG and CHG methylation in these loci. The rDNA methylome analyses revealed variation between species ranging from negligible (<3%, *P. formosum*, *P. patens*) to moderate (7 and 17% in *M. polymorpha* and *D. scoparium*, respectively) methylation levels. There were no differences between coding and non-coding parts of rDNA units and between gametophyte and sporophyte tissues. However, major satellite repeat and transposable elements were heavily methylated in *P. formosum* and *D. scoparium*. In *P. formosum* rDNA, the euchromatic H3K4m3 and heterochromatic H3K9m2 histone marks were nearly balanced contrasting the angiosperms data where H3K9m2 typically dominates rDNA chromatin. In moss interphase nuclei, rDNA was localized at the nucleolar periphery and its condensation level was high.

Conclusions: Unlike seed plants, the rRNA genes seem to escape global methylation

machinery in bryophytes. Distinct epigenetic features may be related to rDNA expression and the physiology of these early diverging plants which exist in haploid state for most of their life cycles.

PO-31

Peptides encoded by long non-coding RNAs influence proteome in the moss *Physcomitrella patens*

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The biological functions of peptides encoded by small Open Reading Frames (sORFs) are generally unknown. However, based on few studied peptides, we can suggest that they can regulate the diverse range of cellular processes in plants, such as cell proliferation (ROT4), nodulation and sugar metabolism (ENOD40), pollen grains germination (Zm908), programmed cell death (KOD) and root growth (PLS).

Using mass spectrometry analysis, we identified nine translatable sORFs located on long non-coding RNAs in the moss *Physcomitrella patens*. To study an impact of sORF-encoded peptides (SEPs) on plant growth and development, four of these SEPs (PSEP1, PSEP3, PSEP18 and PSEP25), ranged from 40 to 61 aa, were chosen for knockout by CRISPR-Cas9 method and overexpression in *P. patens*. Phenotypic analysis of mutant lines has shown that the knockout of all SEPs led to significant reduce in growth rate of moss protonemata. However, the number of leafy shoots was increased in PSEP25 knockout lines.

To evaluate the changes at the protein level, we performed quantitative proteomic analysis with iTRAQ labels. Proteomic analysis of SEPs knockout lines revealed the different number of differentially expressed proteins (DEPs).

Proteomic changes in PSEP1 and PSEP3 (142 differentially expressed proteins in both knockout lines) are more extensive than in PSEP18 and PSEP25 (8 and 14 differentially expressed proteins respectively) knockout lines. According to GO enrichment analysis both PSEP1 and PSEP3 knockout lines have shown a similar down-regulation of proteins participated in basic metabolic processes. Also, knockout of PSEP1 led to down-regulation of proteins participated in translation, whereas PSEP3 knockout led to changes in photosynthesis and photorespiration processes. Both PSEP18 and PSEP25 knockout induce changes in content only of a small number of individual proteins. Taken together, morphological and proteomic analysis of SEPs knockout lines have shown that peptides PSEP1, 3, 18 and 25 can regulate growth and development of moss plants. Thus, peptides encoded by long non-coding RNAs play an important role in plants.

PO-32

Towards a clarification of the *Aloina catillum* (Müll. Hal.) Broth. (Pottiaceae) complex

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Aloina Kindb. (Pottiaceae) is a rather widespread genus found on most continents, which comprises 12 species. This genus has been infrequently collected in South America where only five species are recognized. One of these species, *Aloina catillum* (Müll. Hal.) Broth. is endemic of the Tropical Andes. It is mainly characterized by suborbicular leaves with apex broadly cucullate, hyaline marginal cells at the leaf base, costa with 2-3 stereids layers, red seta, ovoid-cylindrical and dark red coloured capsules, peristome strongly twisted, with basal membrane differentiated and operculum conical. However, these characters can overlap with those of *A. rigida* (Hedw.) Limpr. and especially *A. brevirostris* (Hook. & Grev.) Kindb. In this study we aim to evaluate the phylogenetic relationships and to critically examine boundaries between these three species that are easily confused with each other based on

their similar morphologies. To this purpose a morphological study and a molecular analysis using the rDNA ITS 1-2 region in several specimens of South American species of *Aloina* was carried out. In addition, other species of the genus such as *A. brevirostris*, *A. bifrons* (De Not.) Delgad., *A. aloides* (W.D.J. Koch ex Schultz) Kindb. and *A. ambigua* (Bruch & Schimp.) Limpr. from other locations worldwide were included. Our phylogenetic results indicate that *A. catillum* specimens constitute several groups nested in the clade of the genus suggesting different species, while the morphological analysis does not show a clear variation among these entities. The controversial data obtained show the necessity to study more samples and the use of other molecular markers in order to clarify the possibility of the existence of cryptic species.

PO-33

Interaction between three Mediterranean mosses: influence of competition and abiotic factors in biogeographical distribution.

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The distribution and dynamics of plant communities depend on abiotic factors and biotic interactions. Aiming at assessing the role of these factors on the presence, coexistence and distribution of moss species, here we present a study assessing the effect of interspecific competition along an altitudinal gradient (500 m-1500 m). We have tested three species, *Homalothecium aureum*, *Hypnum cupressiforme* and *Tortella squarrosa*, all very common in central Spain. We have used two experimental approaches, one based on natural conditions and the other on artificial outdoors settings. In each, we established three different altitudinal bands. In the natural habitats, we have registered the abundance and coexistence through systematic samplings favouring plots where coexistence occurs. In the outdoor cultures we have

established artificial moss communities using individual shoots to obtain homogeneous tufts, both monospecific and mixed (using all three species, or in pairs), grew them settings, and assessed their interactions through differences in the moss area coverage, dry weight and shoot length for each species. In their natural environment, we have not observed all three species coexisting. *H. aureum* is present along the whole altitudinal gradient. *T. squarrosa* predominates in the lowest and medium altitudinal band, and *H. cupressiforme* is dominant in the highest localities. However, when coexisting with the other species, *H. aureum* seems to perform better. In outdoor cultures, all three species grow better in the plot at lowest altitude. Mixed communities of two species and, to a lesser extent, the monospecific ones, show the largest increase of area coverage. Both *T. squarrosa* and *H. cupressiforme* are able to survive outside their natural altitudinal range. Mixed communities of all three species seem to perform worse, as they only show a coverage increase in the lowest altitude. *H. cupressiforme* presents the highest growth, although *H. aureum* is visually the healthiest. We conclude that climatic variables matter but interspecific interactions affect greatly the performance of individual species, highlighting the importance of considering them in ecology studies.

PO-34

Dynamics of development and change of biodiversity in natural forests

Mikulášková E., Běťák J., Halda J., Procházka J. *Výzkumný ústav Silva Taroucy pro krajinu a okrasné zahradnictví, v.v.i., Odbor ekologie lesa, Lidická 25/27, CZ-602 00 Brno* (evamikul@gmail.com)

Natural forests have been transformed during centuries into a forest-free area or cultural forests with different degree of conservation in Central Europe. If we want to support a primaeval character of cultural forests by management, we need to understand the processes and dynamics in the natural forests. We investigate species diversity of epiphytic and epixylic bryophytes in several types of primaeval forests. Based on long-term dendrometric measurements, species composition is possible to link to clearly identified objects (live and dead trees, stumps,

rotting logs at all stages of decomposition). It provides information about distribution and ecology of species and real-time community development, it allows to study interspecific and ecological relationships across groups of organisms and to study communities bounded to less common tree species (fir, elm, oak).

We collect species data on permanent circular plots of 500 m². In 2018, research was focused on two forest reserves: Stožec (Šumava NP) and Rejvíz (Jeseníky PLA). The Stožec research area includes mixed debris forests with large amounts of old tree stands and abundant decaying wood, including logs with a large diameter. The vegetation in the Rejvíz research area includes pine and spruce peat forests with a low amount of decaying wood. Over 400 objects were examined in both reservations. 113 species of epiphytic and epixylic bryophytes including wood specialists were recorded in the Stožec reserve, of which 14 species are included in one of the categories of the red list of bryophytes of the Czech Republic (Kucera et al. 2012). 59 species of bryophytes were recorded in the Rejvíz research area, of which 6 species are included in the red list of the Czech Republic. The presence of rare species on the site, including the highly endangered ones, confirms that existing management is appropriate for the study group. The non-intervention mode, along with leaving dead wood on the site, provides the necessary substrate for species typical of natural forests.

PO-35

Can the content of bryophyte ultraviolet-absorbing compounds be estimated by non-destructive methods? A case study in the Colombian Andes

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Bryophytes inhabiting high mountains like the Andes are exposed to harsh environmental conditions, such as high levels of ultraviolet (UV) radiation. The bryophyte UV protection capacity

is usually evaluated by quantifying their amount of phenolic UV-absorbing compounds (PUVAC) by spectrophotometry or HPLC. Unfortunately, these methods are destructive and not applicable under field conditions. However, Dualex® (Force-A) is a portable instrument allowing the non-destructive estimation of PUVAC in plants, although it has rarely been tested (if ever) on bryophytes. In this study, we measured the bulk level of PUVAC in 56 samples of 28 bryophyte species (18 mosses, 9 liverworts and 1 hornwort) by both destructive (methanolic extracts and then spectrophotometry) methods in the laboratory and non-destructive (Dualex®) methods in the field. Our aim was to evaluate the potential use of Dualex® to assess the UV protection capacity of bryophytes under field conditions. The experiment took place in the Colombian Andes in July 2018 and bryophytes were collected in an elevation range of 700-3500 m under different sun exposures, from full sun to deep shade. For the spectrophotometrical measurements, we differentiated the PUVAC present in vacuolar soluble forms (S-PUVAC) from those present in cell wall-bound insoluble forms (I-PUVAC), because each type of compounds may represent a different modality of UV protection. We also calculated the total PUVAC (T-PUVAC) as the sum of S-PUVAC and I-PUVAC. Regarding Dualex® measurements, we obtained both the flavonol index (Flav) and the anthocyanin index (Anth), given that flavonols and anthocyanins belong to different PUVAC families. Mosses showed higher contents of I-PUVAC and T-PUVAC than liverworts, whereas liverworts showed higher contents of S-PUVAC than mosses, as occurred in temperate bryophytes. The only hornwort collected showed higher contents of T-PUVAC and S-PUVAC than mosses and liverworts, respectively, and similar I-PUVAC contents to liverworts. Flav (but not Anth) reproduced the same results of T-PUVAC for mosses and liverworts. In addition, Flav was strongly and positively correlated with I-PUVAC, in both mosses and liverworts, but no correlation was found between Flav and S-PUVAC. Thus, Dualex® have certain limitations to be used in the non-destructive evaluation of UV protection in bryophytes.

PO-36

The Moss Flora of Nuluhon Trusmadi Forest Reserve in Sabah, Malaysian Borneo.

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Nuluhon Trusmadi Forest Reserve (NTFR) is located in the central part of Sabah, Malaysian Borneo, and covers an area of 74,736 ha. NTFR is gazetted as Protection Forest Class I, where timber-harvesting activities are not permitted since 2010. The main aim of this research is to carry out a comprehensive study on the moss flora of NTFR, to collect, identify, prepare descriptions, construct keys to species, and to assess the general phytogeographical affinities of mosses from NTFR. Specimens of mosses were randomly collected in all existing trails and excursions in accessible areas of the reserve. Herbarium specimens from SAN and BORH are also included in this study. In total, 903 moss specimens were collected from the reserve and were examined. From this collection, 232 species, 18 varieties and five subspecies belonging to 95 genera and 34 families of mosses have been identified. This number represents 33.2% of the 767 reported mosses from Borneo and 39.4% of the 647 mosses in Sabah. Sematophyllaceae appeared to be the most dominant family in NTFR, with 23 species and seven varieties, followed by Calymperaceae with 27 species, and Pylaisiadelphaceae with 19 species and two varieties. Out of these, 16 taxa are newly reported for Sabah including 11 taxa new to Borneo. The moss flora of NTFR has a close affinity to Crocker Range Park (CRP), whereby 165 (55.6%) taxa of mosses in 81 (76.8%) genera and 30 (83.3%) families are common in both areas. NTFR also recorded four endemic species to Borneo, adding value to this forest reserve. In conclusion, NTFR has a relatively rich moss flora in terms of number of taxa, which is greater than Mount Tambuyukon but lower than Crocker Range Park in Sabah. There are moss entities in NTFR that are not

found elsewhere in Borneo, including Mount Kinabalu, adding to the importance of protecting this area. As the current study only covered the accessible routes in this forest reserve, it should be further explored bryologically in the future, which will definitely increase the number of mosses presented here.

PO-37

Methods to transform the new model species for hornworts, *Anthoceros agrestis*

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Recently, a new bryophyte model species has received increased attention – the hornwort. Analyzing the hornwort genome will help to resolve fundamental questions of plant evolution and developmental biology, in general, and unique aspects of hornwort biology, in particular. However, having a fully sequenced genome does not fulfill all requirements of a well-established model organism. Here we report our progress concerning culturing, genetic transformation and laser capture microscopy assisted small-scale gene expression profiling (LCM RNA-seq) of the model organism *Anthoceros agrestis* achieved over the last year. In particular, we will elaborate on the tractability of the system for experimental research by first introducing main features of its nuclear genome and present our results on the protoplastation, transient transformation, and regeneration of hornwort tissues. Finally, we will show some of our first results on the stable genetic transformation of the species. Altogether, these achievements show that *Anthoceros agrestis* is becoming, step by step, a better-studied model organism for developmental, molecular, genomic, and genetic studies.

PO-38

Revisiting the Mediterranean *Bartramia rosamrosiae* with phylogenetic, morphological and ecological tools

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Species delimitation in mosses is not a trivial task in many cases. Their often rather small size and limited amount of prominent diagnostic structures make it hard to pinpoint critical identification criteria between closely related species. This is also true for the section *Strictidium* of the acrocarpous moss family Bartramiaceae and its prominent widespread “Mediterranean” species *Bartramia stricta* and relatives. Based on detailed molecular and morphological analyses, Damayanti et al. (2012) recently showed that *B. stricta* from South America is indeed a different species compared to the Mediterranean *B. stricta* from Europe and California. As the Bridel type refers the South American species Damayanti et al. (2012) segregated the “Mediterranean” species from *B. stricta* as a new species *B. rosamrosiae*. But in 2014 Müller claimed that this species was already validly described as *B. aprica* from the Sudan and thus rendering *B. rosamrosiae* as an illegitimate name. Since no samples from the Sudan were incorporated in the former study by Damayanti et al. (2012) and the type pictures provided by Müllers (2014) are somehow of intermediate morphology we conducted a more detailed study on *B. aprica*. Here we show that *B. rosamrosiae* is a different species from *B. aprica*, by providing molecular as well as morphological and ecological evidence. The molecular analyses clearly show a significantly supported sister group relationship of *B. aprica* and *B. rosamrosiae*, each being monophyletic. Furthermore, the morphological analysis shows that *B. rosamrosiae* has an overall higher plant length and smaller stem diameter as well as a slimmer central cylinder diameter, in comparison to *B. aprica*. In addition, climate niche modelling shows that *B. aprica* prefers much more arid and desert like habitats, while *B. rosamrosiae*

occupies area with Mediterranean climate. Our results show, that species delimitation in mosses should sometimes be done with more care, a sensible combination of tools and looking at a representative set of vouchers.

PO-39

Liverwort richness and range size distribution along elevational gradient in Serbia

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Biogeographical variation in species richness is important for our understanding and conservation of biological diversity. While there are insights of the tracheophyte's distribution along the elevational gradient in the Central Balkan, there are no similar studies on bryophytes in this region up to date. The aim of our research is to investigate how liverwort species richness varies along the elevational gradient in Serbia, and to evaluate if the range size of the species differs with elevation in the studied area. The study was conducted along a 2155 m altitudinal gradient in Serbia, a country in South-Eastern Europe. Digitized distribution data compiled from the literature and herbarium collections were used for the analysis. The presence of the species was interpolated between the minimum and maximum recorded elevations, and assessment of species richness for 100 m elevation bands is given. Elevational range size and the range midpoint is calculated for each taxon recorded. For species recorded at only one site, the adjusted range size of 100m was used. Species were considered wide-ranging in cases where their ranges cover at least half of the domain (range size ≥ 1077 m) and narrow-ranging if their ranges cover less than half the domain (range size < 1077). A humped relationship between species richness and elevation was observed, with maximum richness recorded at middle elevations, in 1100-1200 and 1200-1300m bands. According

to the size of the occupied domain, the majority of the liverwort species in Serbia (56.5%) are narrow-ranged. Moreover, narrow-ranged liverworts tend to be more common towards the lower and higher elevations, whereas wide-ranging species occupy middle elevations. Only five wide-ranging species were found to extend their elevational ranges from the lowlands to the highest peaks. Our study provides the very first insights in liverwort's distribution and richness along elevation in Serbia. However, additional field data and more detailed research on influencing factors would lead to a better understanding of the distribution patterns of this plant group in Serbia.

PO-40

Is drought stress driving the morphological variation of *Hypnum cupressiforme* HEDW. (Hypnaceae)?

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Being poikilohydric plants, mosses depend on external capillary water to regulate their metabolic activities. The dependence on atmospheric conditions such as relative air humidity and air temperature led to the development of various adaptations to enable the survival of drought periods of different lengths. Drought stress is a real issue regarding the growth form and life form of, especially epiphytic, bryophytes. We hypothesize that drought stress is a driving factor for morphological variations in *Hypnum cupressiforme*.

The objective of this study is to investigate the morphological variation of *H. cupressiforme* within a tree and to check for a correlation to microclimatic conditions. Moss samples were taken at the 20th of October 2018 in two oak trees at the Hardtwald, Tübingen, Germany. The in total 39 samples are patches of about 10 x 10 cm and were collected from different positions within the tree from the stem basis to the treetop, including various inner and outer canopy positions. Every sample was first examined for species composition with the result of a definite dominance of *H. cupressiforme*. Thereby, distinct morphologies of this species have been observed

depending on its origin. Climate data was collected over a two-month period from 21st of October to 17th of December 2018. Ten temperature/humidity (°C/%) data loggers were placed at several positions where moss samples have been taken within one of the two oak trees. For statistical analyses mean daily minimum relative humidity, mean daily maximum temperature and mean daily maximum VPD, as well as the number of days in which RH was below 85% have been calculated. To test for a correlation between morphology and microclimate point-biserial analyses have been performed. The results show a correlation between the morphology and the mean daily minimum air humidity, as well as the mean daily maximum VPD, whereas temperature has no effect.

PO-40

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PO-42

The rare and scattered moss *Acaulon piligerum* (Pottiaceae) new to the Iberian Peninsula with comparison to other Southern Hemisphere species of subgenus *Alaticosta*

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Phascum bulbosum Voit. var. *piligerum* De Not. was described in 1938 from a sample collected in Cagliari (Sardinia) and five decades later transferred to *Acaulon* (*A. piligerum* (De Not.) Limpr.). After a revision of the type material, Sérgio in 1992 was the first to notice the presence of short lamellar outgrows on the ventral part of the nerve. This unique trait among Holarctic species served to assign it to subgenus *Alaticosta* I.G. Stone, together with the Australian *Acaulon chrysacanthum* I.G. Stone and the Australian-South African *A. leucochaete* I.G. Stone. The two southern hemisphere species have not been to date critically compared to *A. piligerum*, because

very few collections have been made since its description, and some were misidentifications for the widespread *A. triquetrum* (Spruce) Müll.Hall. In March 2017, during field work in temporary lagoon areas of Castilla la Mancha (Central Spain), samples of a moss which keyed to *Acaulon piligerum* were collected. The Spanish samples were studied and described in detail using optical and scanning electron microscopy techniques and compared to representative Australian specimens of subgenus *Alaticosta*.

Acaulon piligerum is a small, yellowish-brown, bulbiform plant, of 2.5-2.8 mm high that grows in compact turfs. Leaves are concave with nerve excurrent in a flexuose hyaline arista of 286-551 µm long; cells on ventral side of costa smooth, inflated, with up to 2 chlorophyllose lamellae of up to 6 cells high that extend to the tip from the upper half of leaves. It is distinguished from *A. chrysacanthum* by its white flexuose arista of perichaetial leaves (straight, golden reddish in *A. chrysacanthum*). It is more similar to *A. leucochaete* with slight differences on leaf margin denticulation and papillosity of terminal cells of lamellae (both smooth in *A. piligerum*). Molecular data would be necessary to confirm the identity of these taxa. In its current circumscription *A. piligerum* has a scattered Mediterranean distribution including isolated localities in Sardinia, Crete, Lacroma Island and the new Spanish population reported here. As for its conservation status, according to these data it is proposed as Endangered (EN) B2a + biii.

PO-43

Climatic differences in the geographic range of moss sister taxa at both sides of the Atlantic.

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Bryophyte disjunctions between the New World and the Old World are common and often entail morphological variations that are structured in space. These geographically structured differences lead to controversies regarding the taxonomic status of the populations at both sides of the Atlantic. Those disjunctions have often been evaluated through genetic and/or morphological analyses, however, the ecological differences among disjunct mosses have rarely been assessed quantitatively, despite their potential importance for speciation processes. We evaluate the similarities on the climatic responses between two pairs of terricolous mosses under controversial taxonomic status: *Homalothecium aureum* and the synonymized *H. pinnatifidum*; and *Pleurochaete squarrosa* (= *Tortella squarrosa*) and the American *P. luteola*, so far considered synonymous of the former. We first modelled their responses to large-scale environmental gradients using publicly available data of their global distributions. Then, we evaluate the reliability of the modelling approach based on climatic information and Ecological Niche Factor Analysis (ENFA). Finally, we assess the similarities in their responses using niche overlap analysis. The results indicate that both moss taxa pairs show climatic differentiation. The *Homalothecium* pair shows similar responses to climate in both regions, but the American populations use a subset of the climatic domain occupied by the European populations. This contrasts with the *Pleurochaete* pair, which presents partially different distributions in some climatic gradients. Although the two taxa of this latter pair mainly respond to the mean temperature in the dry season, the European populations of *P. squarrosa* grow in areas that are colder during the wettest season, while the American ones (*P. luteola*) thrive in areas that are progressively warmer in this period. This suggests that these two taxa have clearly different (macro)climatic requirements, that do not depend on the different types of climate available in each continent. This supports the idea that they may be not the same species having different ecological requirements.

PO-44

Not as straightforward as expected: Disentangling the genetic structure of *Funaria hygrometrica* along a climatic gradient within Spain using genotyping-by-sequencing (GBS)

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There are a number of reasons that support why bryophytes are ideal models for studies in molecular ecology and evolution. Among others, the specific mechanisms influencing their diversification and the haploid nature of the dominant phase of their life cycle greatly facilitates genetic analyses, and their small size allows us to cultivate them in reduced spaces. Some of the model bryophyte species in molecular biology have a worldwide distribution, with intercontinental dispersal events having been inferred to be more frequent than previously thought. Under these circumstances, the question arises whether these ubiquitous species exhibit genetic variants that are locally adapted to certain types of habitats, or whether there is a “generalist genotype” which supports very different climatic conditions. In the present study, a total of 183 specimens of the cosmopolitan moss *Funaria hygrometrica* were sampled from 80 locations spread over several biogeographical areas of Spain influenced by different climates, ranging from the Mediterranean climate in the south (The Sierra Nevada Mountains and Murcia province) to the Atlantic Ocean influenced climate in the north (Asturias and Leon provinces). The Sierra Nevada Mountains present a high altitudinal range from 0 to 3500 m. For molecular analysis all the specimens were grown *in vitro* under axenic conditions from individual spores. Genotyping-by-sequencing (GBS) technique was employed to obtain two multiplexed DNA

libraries and identify single-nucleotide polymorphisms (SNPs). Based on the GBS data, F_{ST} values between populations were low with the exception of the high altitude populations from Sierra Nevada Mountains, which were clearly differentiated from all other populations, even the neighbouring Sierra Nevada lowland populations. These results were confirmed by additional analyses, including genetic distance, PCA and Structure-like approaches. Our data seem to exclude geographic distance as a relevant mechanism to explain the observed differences between the highland and lowland populations of *F. hygrometrica* within Sierra Nevada. Further analyses are needed in order to support the hypothesis that climatic factors are responsible for the observed distribution pattern of genetic variants or whether other factors (e.g. historical migrations, human influence) might be the main drivers.

PO-45

Ten years of bryological research in Croatia - Where we were, where we are, where we are going

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Despite the fact that Croatia is bryologically one of the most explored countries of former Yugoslavia and Southeastern Europe, the data are to a large extent spatially and temporally biased. Beginning in the first decades of the 19th century, the research had the highest peak at the end of the 19th and at the beginning of the 20th century, intensified again in the 1950s and 1960s, followed by the almost complete absence of any bryological work until 2009. Thenceforward, during the last 10 years, mainly owing to cooperation between the Hungarian Natural History Museum and the University of Zagreb (Croatia), 58 new taxa were discovered as new for Croatia. Apart from this, in order to summarise all historical literature and herbarium data, a

publically available database with nearly 31.000 geocoded spatio-temporal entries has been established. Concluding, at the current state of knowledge, Croatian bryoflora includes 789 taxa - 606 mosses, 178 liverworts and five hornworts. Future studies should be focused on (1) Croatian regions with lack of bryological data, (2) many taxa with single and very old records and (3) threatened species and species of conservation value.

PO-46

Species richness and communities of bryophytes in heath forest, Khao Ngon Nak Mountain, Krabi Province, southern Thailand

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Previous studies have shown that the heath forests are unique habitats and harbor an interesting bryophyte flora. Unfortunately, most of them have been disturbed by human activities, the undisturbed forests only persist as separated fragments. Consequently, the aim of this study was to determine the species richness and communities of corticolous and terrestrial bryophytes in the heath forest located at the summit of Khao Ngon Nak Mountain, Krabi Province, southern Thailand. The collection and investigation of bryophytes were carried out during February-April 2019. The corticolous bryophytes were taken from 40 selected tree trunks at 0.8 to 1.5 m height above the ground whereas the terrestrial bryophytes were collected from 40 quadrats of 2.5 square meters. The species richness, cover and life form of bryophytes were recorded during this study. In total, 43 species distributed in 27 genera and six families of bryophytes were found, which include 26 species of liverworts and 17 species of mosses. Among these, the most common families of liverworts and mosses were Lejeuneaceae and Calymperaceae, respectively. In addition, *Acromastigum echinatum* (Gottsche) A. Evans and *Pycnolejeunea cavistipula* (steph.) Mizut are

reported as new species records for Thailand. According to the microhabitats, there were 37 corticolous species and 15 terrestrial species. Based on Two-way cluster analysis, four communities of corticolous bryophytes and six communities of terricolous bryophytes could be recognized. The most common life form of corticolous bryophytes was mats whereas turfs corresponded to most of the terricolous bryophytes.

PO-47

Observations of anisomorphic spores in Portuguese populations of *Homalothecium sericeum* (Hedw.) Schimp. s.s. and *H. meridionale* (M. Fleissch. & Warnst.) Hedenäs (Brachytheciaceae)

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Despite the normal homospority in bryophytes, two ranges of spore sizes (anisosporous) have been reported mostly in dioicous species (Korpelainen, 1998; Glime & Bisang, 2017) and *Homalothecium* Schimp. is a dioicous genus. Evidences have been described that in some bryophytes male and female spores are unequally sized, and that smaller spores will produce male plants (Ramsay, 1979). On other hand, some publications referred the presence of dwarf males in *Homalothecium* Schimp. (Sérgio *et al.*, 2003; Rosengren & Cronberg, 2014).

In this work, the anisosporic condition was analysed in individual capsules of selected samples of *Homalothecium sericeum* (Hedw.) Schimp. s.s. and *H. meridionale* (M. Fleissch. & Warnst.) Hedenäs, and the observed values of spore size present a distinct bimodal distribution in both species. Some spores were photographed under scanning electron microscopy to reveal the anisospory of these *Homalothecium* species using herbarium samples. In conclusion, this study shows that we are facing a typical phenomenon

of anisospory, and we can suspect that the occurrence of anisospory is linked to the presence of dwarf males in *Homalothecium sericeum* s.l.

PO-48

Developmental stage determines the accumulation pattern of UV-absorbing compounds in the model liverwort *Marchantia polymorpha* subsp. *ruderalis* under controlled conditions

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The liverwort *Marchantia polymorpha* subsp. *ruderalis* is emerging as a new model plant, but relatively little is known on basic aspects of its physiology and responses to environmental factors (particularly, UV radiation). Thus, our aim was to study the influence of the developmental stage on the accumulation patterns of phenolic UV-absorbing compounds (UVACs) in samples exposed and non-exposed to UV radiation. Samples of three different developmental stages (gemmae, one-month-aged thalli and two-month-aged thalli) were exposed to only PAR (P regime) and to a combination of PAR + UV-A + UV-B radiation (PAB regime) for 38 days, using moderate realistic UV doses. At the end of this period, the bulk level of methanol-soluble UVACs and the contents of six soluble individual UVACs (derivatives of apigenin and luteolin) were measured.

Both the radiation regime and the developmental stage strongly influenced UVACs accumulation pattern, and the responses to UV radiation were different in the diverse developmental stages. Plants exposed to UV from juvenile stages (gemmae or 1-month age thallus) were the most UV-responsive and showed a strong increase in every UVAC measured, being the increase stronger in the most juvenile stage. However, when samples were exposed to UV from 2-month age thalli, only apigenin derivatives increased and more modestly. In fact, the phenolic profile

of these plants was not very different from the profile of the plants non-exposed to UV. Thus, as age increased, the responses to UV were weaker, probably due to senescence and a consequent decrease in metabolic responsiveness. Nevertheless, the thalli became progressively tougher due to continuously decreasing water content, representing a possible structural protection against excess UV. On the other hand, 1-month age thalli exposed to UV radiation showed a transitory conversion of apigenin mono-glucuronide into apigenin di-glucuronide. In plants non-exposed to UV, temporal variations of UVACs were much less marked and compound dependent. A PCA ordination of the different samples summarized the findings described above.

The pattern described should be taken into account in experiments in which accumulation of UV-inducible compounds is expected, in order to select the adequate thalli age and better interpret the results obtained.

PO-49

The moss flora of Borneo: Progress and challenges

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This paper presents the progress and challenges of completing the moss flora of an island as large as Borneo, which is politically divided by three countries, namely Malaysia (Sabah and Sarawak states), Indonesia (Kalimantan province) and Brunei. The previous catalogue of mosses from Borneo was published in 2006 which reported 721 taxa distributed in 185 genera and 50 families. Since then, 16 new localities in Sabah and one in Sarawak were studied by the author, including moss floras of large protected areas such as the Crocker Range Park, Imbak Canyon Conservation Area, Nuluwon Trusmadi Forest Reserve and Maliau Basin Conservation Areas. There were a couple of surveys in Brunei and Sarawak by other Malaysian bryologists but none in Kalimantan, which accounts for two-thirds of the island's territory. Kalimantan was not explored by Malaysian bryologists due to accessibility, more costly and research permit

requirement. The current number of mosses reported for Borneo is 766, an increase of 47 taxa since 2006. The highest number of species is from Sabah, followed by Sarawak and East Kalimantan. Sabah had the highest additions of new records, followed by Brunei and Sarawak, with 71, 68 and 34 taxa, respectively. The lowest was Kalimantan with only three additions. Efforts need to be given to Kalimantan though the “Heart of Borneo” initiative, a transboundary effort agreed by the three countries to enable conservation and sustainable development. The Bornean moss flora is far from being completely surveyed. More students also need to be trained to carry out bryological work in less explored areas in Borneo.

PO-50

A Calcium-Dependent Protein Kinase Gene *RcCDPK* from *Racomitrium canescens* enhanced plant drought and salt tolerance

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Drought has already been a globally severe issue, crop decrease caused by drought led to great loss every year. For enhancing drought-resistance of plants, finding out functional drought-resistance related genes from plants with drought-tolerance is an effective and important way. *Racomitrium canescens* is a moss with great drought-tolerance and rehydration ability, a calcium-dependent protein kinase gene named *RcCDPK* from *R. canescens* was found in response to dehydration and rehydration treatments in mRNA expression level, and was selected for functional analysis in this study. Firstly, the expression of *RcCDPK* was furtherly determined by qPCR in *R. canescens* under different desiccation and rehydration treatments, the expression of *RcCDPK* was dramatically increased after desiccation treatment for 20 min then decreased, and also changed differently in rehydration treatments, suggesting the potential of *RcCDPK*

participating drought resistance responses of *R. canescens*. For further functional verification, *RcCDPK* overexpression transgenic *Arabidopsis thaliana* strains were constructed for researches. T₃ generation *RcCDPK* overexpression transgenic plants showed better phenotypes under 150 mmol/L NaCl, 6% and 8% treatments. The *RcCDPK* overexpression transgenic *Arabidopsis* performed longer root length, more rosetted leaves and bigger rosette leaf size, more and longer lateral roots existed under stress treatments compared with wild type *Arabidopsis*. This study demonstrated overexpression of *RcCDPK* will increase drought and salt stress tolerance of *Arabidopsis thaliana*, inferring the genes from *R. canescens* can be used to improve properties of other plants and more stress resistance related genes from *R. canescens* may be valuable to be explored.

PO-51

Genetic and morphological variation in the circumpolar distribution range of *Sphagnum warnstorffii*

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The Quaternary climatic oscillations caused pronounced changes in the distribution of the genetic variation among populations as well as phenotypic diversification worldwide. We studied how important are these processes in plants with high gene flow potential - peat mosses (*Sphagnum* sp. div.). High level of phenotypic plasticity is common for peat mosses and it should be caused by both local habitat conditions and early cladogenesis.

Sphagnum warnstorffii is a dioicous species that occurs in intermediate and rich fens and calcareous moss tundra. Phenotypic variation has been observed among plants from the arctic zone. The previous studies show signals of genetic

adaptation to microhabitat calcium and magnesium levels, however, study area was limited to the Central Europe. In this study, we aimed to explore the genetic structure of *S. warnstorffii* throughout its wide distribution. We want to investigate whether morphological divergence in arctic and boreal (boreo-nemoral) plants has a genetic basis, whether diversifying evolution has taken place and to what extent this might have resulted from vicariance events during the Quaternary period.

We used single nucleotide polymorphism genotyping to investigate the patterns of genetic diversity in 112 plants (105 localities) sampled throughout the species distribution range and explored correlation with phenotypic variation. Genetic cluster analysis identified two main genetic lineages with an average *F* of 0.21 between them, and patterns of genetic structuring are highly correlated with morphological differentiation. The first cluster is restricted to the Arctic region, whereas the second has a wider distribution range covering the Arctic, boreal and boreo-nemoral regions of Eurasia and North America. The first cluster is morphologically stable also in areas where both clusters co-occur. However genetic differentiation between clusters are not high that's why we conclude that, for the time being, there is no clear evidence that the two *S. warnstorffii* morphs represent separate species. Based on approximate Bayesian computation simulations, we find that the two lineages probably diverged from each other before the Last Glacial Maximum. It seems likely that the first cluster has survived the glacial cycles in the northernmost areas, in 'in situ' refugia and/or in unglaciated regions of Beringia.

PO-52

A revision of family Bryaceae sensu lato (Musci) in China*

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This paper focuses on the research classification of Bryaceae (s. l.) in China. Morphological characters of more than 4000 specimens of the

Bryaceae (s. l.) and its related groups in China were analyzed. Combining morphological and molecular data in the analyses showed that: (1) Not only were the *Mielichhoferia* group and the family Bryaceae in the different clade in the molecular tree, but also morphological features, such as the leaf shape, the leaf cells of the two groups were different. *Mielichhoferia* group should be separated from the Bryaceae. And then, no morphological synapomorphy can be detected for *Mielichhoferia* group and the family Mniaceae, although they were in the same clade in the molecular tree. So we adopted views that the Mielichhoferiaceae was circumscribed as a single family. There were five genera, *Mielichhoferia*, *Pohlia*, *Pseudopohlia*, *Epipterygium* and *Synthetodontium*, in the Mielichhoferiaceae in China, total 36 species and 2 varieties. (2) The genera *Orthodontium* and *Leptobryum* were respectively transferred from Bryaceae (l. s.) to family Orthodontiaceae and Meesiaceae. (3) Members of re-circumscribe Bryaceae include 5 genera, *Anomobryum*, *Brachymerium*, *Bryum*, *Plagiobryum* and *Rhodobryum* in China, total 77 species and 2 varieties. Some intraspecific changes or interspecific changes have been made for Bryaceae (l. s.) also. *Synthetodontium kunlunense* J.C. Zhao et Y.Y. Liu and *Haplodontium zangii* X.R. Wang & J.C. Zhao were named as new species. Three new combinations, *Synthetodontium gossypinum* (X.J. Li & M. Zang) J.C. Zhao & Y.L. Niu, *Haplodontium himalayana* (Mitt.) X.R. Wang & J.C. Zhao and *H. sinensis* (Dixon) X.R. Wang & J.C. Zhao were proposed. *Bryum blandum* ssp *handelii* (Broth.) Ochi was treated as *B. handelii* Broth. *B. petelotii* Thér. & Henr. and *B. yunnanense* Broth. were treated as independent species. Six species of Bryaceae (l.s.) were reported for the first time from China, e.g., *Bryum amblyodon* Müll. Hal., *B. weigeltii* Spreng, *B. moravicum* Podp., *Pohlia andrewsii* A.J. Shaw, *P. andalusica* (Höhn.) Broth. *P. marchica* Osterw. and *Anomobryum concinnum* (Spruce) Lindb. were resurrected for species. *Pohlia minor* Schleicher ex Scheaegr. was reduced as *P. elongata* var. *greenii* (Brid.) Shaw. Three propaguliferous species, *Pohlia flexuosa* Harv., *P. leucostoma* M. Fleisch., and *P. prolifera* (Lindb. ex Breidl.) Lindb. ex Arn. were correctly identified in China.

PO-53

Flora of bryophytes and their ecological distribution in karst Tiankeng, Southern China

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Karst Tiankengs (limestone sinkholes or collapse dolines) are special landforms with unique bryophyte flora. Some huge and interesting Tiankengs were found in recent three decades from China, such as Xiaozhai Tiankeng (the depth 662m, length 625m, width 535m,) and Haolong Tiankeng (the depth 520m, length 809m, width 426m,). This work aims to carry out some preliminary study on flora of bryophytes and their ecological distribution from karst tiankengs. From July 2017 to March 2019, supported by the National Natural Science Foundation of China (NSFC. No.31760050, No.31760043, No.31360043 and No. 31360035), many surveys were conducted in southern China, about 2640 samples and specimens were collected from 18 karst Tiankengs.

As main results, 236 species distributed in 78 genera and 24 families were found in Karst Tiankeng areas in Guizhou, Chongqing and Guangxi province, China. The phytogeographical elements of the bryoflora include: Tropical Asian (18.64%), Tropic Asian to Tropic African (2.12%), Pantropical (3.39 %), North Temperate (20.34%), East Asian (20.33%), East Asian and North America disjuncted (4.24%), Old World Temperate (2.12%), Temperate Asian elements (3.38%), Endemics to China (12.71%) and Cosmopolitans (13.56%). Ten types of bryophyte life-forms were found distribution in Karst Tiankengs. Among them, Tall turfs, Mats, Wefs and Dendroids were dominant, which suggested that the whole sinkhole is dark, damp and shadow. The vertical distribution of bryophytes caused by gradient effect of the light, humidity and temperature, and the diversity of bryophyte

communities was the result of the combinations of three environmental factors and human activity. The rich bryophyte flora indicates that Karst Tiankeng is a natural refuge for bryophyte conservation in the vast karst area from southern China.

PO-54

Diversity of moss peristomes and their distribution in karst fengcongs (Cone Karst) in Guizhou Plateau, China

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Peristome is an important structure for mosses, but related research on this issue is very weak in karst plateau from both China and abroad.

From October 2017 to January 2019, supported by the National Natural Science Foundation of China (NSFC. (No.31760043, No.31760050), we carried out bryological surveys in the three typical karst fengcongs (Cone Karst) of Guizhou, China, in the course of which about 860 samples were collected. A hundred-eight taxa of mosses were identified from these samples.

Among them, 42 taxa were studied focusing on the diversity of moss peristome structure by means of Optical microscope and Electron Microscope, and the SDR, Sorenson similarity index and RDA were used for analysis of the ecological distribution and the effect of environmental factors. As main result, two moss groups of peristome morphology were found: one group is an Arthrodontae peristome with 38 taxa, the other group is a Nematodontae peristome with only 4 taxa. Among the Arthrodontae mosses, there were 16 taxa belonging to Acrocarpi-haplolepideae, 10 species in Acrocarpi-diplolepideae and 12 taxa in Pleurocarpi-diplolepideae, respectively. The results showed that: the Pleurocarpi-diplolepideae group was mainly distributed at the bottom of the karst fengcong, while the Acrocarpi-haplolepideae mosses dominated the middle and top of the fengcong. The RDA analysis showed that the

distribution of the Acrocarpi-haplolepidaceae mosses was mainly influenced by the light intensity and the environmental temperature; the distribution of the Peurocarpi-diplolepidaceae mosses was mainly influenced by the relative humidity; and the distribution of the Acrocarpi-diplolepidaceae mosses was mainly affected by the altitude. From the top to the bottom of the karst fengcong, the distribution of the Arthrodonatae mosses also changed regularly with the gradient decreasing of the relative humidity. The results provide some interesting data to study the diversity of moss peristomes and conservation mosses in karst mountain areas in southwest China

PO-56

Diversity, distribution and socio-cultural importance of bryophytes in the Sudano-Guinean and Sudanian areas in Benin

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Benin exhibits very few bryological studies. These were conducted by foreign authors in a part of the country, leading to a great inadequacy and insufficient knowledge of the bryophyte flora of Benin. Our work was carried out in the Sudano-Guinean and Sudanian areas of Benin. We then sought to: (1) Inventory and set the distribution of bryophyte species; (2) Determine the ecological and anthropogenic factors explaining their distribution; (3) Document traditional knowledge related to bryophytes and determine the socio-cultural and ecological factors influencing this traditional knowledge. Bryophyte distribution models were examined in three microhabitats in closed (forest) and open (savannah) environments. The uniform nature of the environments provided an excellent system for studying the relationship between environments and species, diversity and distribution, while avoiding confusing the multiple effects of substrate and vegetation heterogeneity. The

bryophytes were studied using 50 X 50 m blocks on the ground, on the hills and in the waterfalls. A semi-structure interview survey of traditional therapists was conducted to collect local names, uses, treated conditions, preparation methods and different forms of use of bryophytes. In our study, the diversity of bryophytes increases with the closed environment. The species richness is very high; sixty bryophyte species have been identified. Diversity was also controlled by ecological conditions of the microhabitats (humidity, shade). Tillage and soil moisture seem to exert a strong selection on species capable of living in a given environment. These factors are therefore relevant to explain the distribution of specific diversity as well as the dynamics of bryophyte population in Benin. The results reveal that the diversity of Benin bryophytes is partly favoured by the richness in mineral substrate (limestone). Twenty-five species have been related to the treatment of forty-two diseases. They are involved in the preparation of sixty recipes. Decoction and maceration are the most frequent methods of preparation. Educational level, ethnicity and ecological zone determine ethnobotanical knowledge. Mineral environments and the rest of Benin tropical forests should be preserved for their high bryophyte diversity.

PO-57

A contribution to the knowledge of the bryophytes of the Cape Verde Islands, with an emphasis on Santo Antão and São Vicente

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During 2016 Santo Antão and São Vicente in the Cape Verde archipelago were visited and surveyed for bryophytes. Five species are

reported new to Cape Verde, *Cheilolejeunea rigidula* (Nees ex Mont.) R.M.Schust., *Riccia trabutiana* Steph., *Lindbergia patentifolia* Dixon, *Lewinskya acuminata* (H.Philib.) F.Lara, Garilleti & Goffinet and *Timmiella cameruniae* Broth. The presence of *Porella canariensis* (F.Weber) Underw in the archipelago is also confirmed. Additionally, *Frullania spongiosa* Steph., *Bryum dichotomum* Hedw., *Cryptolepton longisetus* (Mont.) Enroth and *Didymodon hastatus* (Mitt.) R.H.Zander are reported for the first time from Santo Antão island. *Cheilolejeunea rigidula*, *Lindbergia patentifolia* and *Timmiella cameruniae* are new to Macaronesia.

PO-58

Which bryophytes are preferred by bryophagous insects?

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Bryophytes provide an ideal environment for great diversity of arthropods and also a food source for remarkable guild of invertebrate bryophages. Since proper and unbiased estimates of bryophages density cannot be made by any standard sampling method (including sieving) but only by thorough examination of bryophyte cushions, the host preferences of bryophages have been almost exclusively concluded from observations of individuals on particular host mosses. We focused on the largest group of insect bryophages – Byrrhidae (Coleoptera) to find their preferences for bryophytes. We sampled 416 quadrates (0.25 m² each quadrate) of 48 species of bryophytes across 26 localities and we examined them thoroughly for presence of bryophagous and bryobiontic invertebrates. Additionally, we kept and repeatedly checked the samples to raise insect juvenile stages. We analysed data using generalized linear mixed models and multi-level pattern analysis to find: a) differences in beetle density in different moss taxa, b) the associations between particular byrrhid species and bryophytes. The density of Byrrhidae differs strongly among moss species and this pattern could be simplified on moss

orders. Filtering only mosses with sampled area > 2.5 m², the greatest densities of beetles we found on *Pohlia nutans*, *Polytrichum piliferum*, *Dicranella heteromalla*, *Barbula unguiculata*, *Bryum argenteum*, *Brachythecium rutabulum* or *Ceratodon purpureus*, whereas very low or zero densities were on *Hypnum cupressiforme*, *Dicranodontium denudatum*, *Thuidium tamariscinum*, *Syntrichia ruralis* or *Didymodon rigidulus*. We did not find significant differences between host preferences for observed byrrhid species. Our results bring first insights in host preferences of bryophages based on intensive quantitative sampling.

PO-59

The phenotypic plasticity of *Philonotis hastata* (Duby) Wijk & Margad.

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Bryophytes are undergoing many morphological variations, physiological adaptations and various reproductive strategies since they colonized terrestrial habitats. *Philonotis* Brid. (Bartramiaceae) has a high level of identification difficulty because of the existing intergradation between its species. This study aimed to assess the phenotypic plasticity of *P. hastata* (Duby) Wijk & Margad. under different strength of Murashige and Skoog “MS” nutrient medium. Approximately 40 characters of protonema and gametophyte stages were recorded. The shape of gametophytes were more or less similar in half strength MS and full strength MS to typical form of *P. hastata* in natural habitats. While in zero strength MS medium caused phenotypic changes of the gametophyte of *P. hastata*. It had triangular leaf lamina with excurrent costa and slightly revolute margin, and it lost the ability to form detachable branches. These overall characters are typical of either *P. falcata* (Hook.) Mitt., *P. marchica* (Hedw.) Brid. or *P. rigida* Brid.. The phenotypic plasticity of *P. hastata* opens a new dimension towards the study of the speciation in *Philonotis*.

PO-60

Distribution pattern of epiphytic mosses from Orthotrichaceae family in western provinces of China

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Species distribution modeling (SDM) is very widespread method how to find out species distribution pattern of species. Despite the frequent used of this method there are still few studies how to evaluate the potential current distribution structures and spread of epiphytic mosses from Orthotrichaceae family. The main aim of this research is to find out which kind of environmental conditions and how way they can influence the distribution structure of selected species from Orthotrichaceae family in western provinces (Sichuan, Yunnan, Xizang, Gansu, Xinjiang a Qinghai) of China. For our purpose, we have chosen the following five epiphytic mosses for SDM: *Lewinskya hookeri*, *Nyholmiella obtusifolia*, *Orthotrichum alpestre*, *O. pamiricum*, and *O. scanicum*. Named species are rare and endangered in the world scale. The obtained results can contribute to the conservation and get better understanding to ecological requirements of target species. As the basic data for the evaluating of species distribution pattern of selected epiphytic mosses, we used data from Chinese herbarium collections and field survey. A total of 203 samples (presence-only data) were analysed. The obtained data were evaluated by using Maxent software, R and Qgis for data preparation and individual environmental layers. Maxent from input data - GPS coordinates and environmental variables which we used (17 bioclimatic layers WorldClim, layer 0.5 km MODIS-based Global Land Cover

Climatology, Vegetation layer (Percent Tree Cover) and slope) generates a model that predicts the most appropriate locations for the occurrence of the monitored moss species. Respectively, the model identifies regions with environmental factors that will allow the species to maintain a viable population. The final models have showed that the distribution of selected mosses is most affected by the environmental layer called LandCover. LandCover is physical material on the surface of the earth like grass, asphalt, trees, bare ground, water, etc. The model also confirmed that temperature and precipitation play an important role in the distribution of studied epiphytic mosses.

PO-61

Singularity and distribution of epiphytic bryophyte communities in the NW Iberian Peninsula

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Bryophytes and vascular plants differ in many biological traits, but at the same time they occupy the same landscape and thus are subject to the influence of similar large-scale factors, such as environmental change. We search out the similarities in diversity patterns between vascular plants and bryophytes. To do so, we analyse the changes in community composition of the epiphytic bryophyte communities in the NW

quadrant of the Iberian Peninsula, and compare them to the bioregions based on vascular plants. We used network modularity analysis to identify chorotypes (groups of species with overlapping range), finding four distinctive modules. Chorotype 1 was located mostly in the extreme northwestern area under Atlantic climate, and was the most singular, made out of exclusive species that were very frequent within this module but very rare outside (*Hypnum andoi*, *Ulota crispula* and *U. bruchii*). Chorotype 2 mostly occurred in Mediterranean mountain areas, and it was characterized by species that were more frequent inside the module but could also be found in other areas (i.e. *Lewinskya acuminata*, *Lewinskya affinis*, *Hypnum cupressiforme* and *Homalothecium sericeum*). Chorotype 3 was mainly distributed in Mediterranean plains and basins and was characterized for having species that were frequent within the module and more or less rare outside, such as *Fabronia pussilla* or *Zygodon catarinói*. Chorotype 4, showed no clear geographic pattern and was characterized by a handful of facultative epiphytes that may be indicating anthropic influence. These modules reflect the relatively steep transition between the Atlantic and Mediterranean regions, as well as the gradual replacements between different climatic zones within the Mediterranean. Interestingly, our results have important similarities with Bolós' (1985) phytogeographic division for vascular plants. Although the precise limits of the regions are difficult to establish, the consistency in their definition across biotic groups suggests that the factors that differentiate the Atlantic and Mediterranean floras have similar effects on vascular plants and bryophytes.

PO-62

Taxonomic studies on type material of the family Trichocoleaceae from Central and South America with two new combinations of the genus *Leiomitra*

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The family Trichocoleaceae is one of the major components of the leafy liverworts, and over 70

species have been described in the three genera (*Eotrichocolea* R.M.Schust., *Leiomitra* Lindb., *Trichocolea* Dumort.). In the series of our taxonomic studies of the family, the generic concept for each genus was outlined and worldwide keys to the species of the genus *Trichocolea*, including eleven species, and *Eotrichocolea*, including two species were given. However, for the genus *Leiomitra* taxonomic studies were limited to Southeast Asian species. *Leiomitra*, which includes about fifteen species, is distributed mainly from tropical and subtropical areas of Central and South America. *Leiomitra* is distinguished from the other genera of the family by such characters as succubous leaf insertion, sublongitudinally inserted leaves, anisophyllous leaves and underleaves, and presence of a well-developed calyptra and perianth. In Central and South America, the taxonomy of the Trichocoleaceae has not been revised since Hatcher (1957) and Fulford (1963) and both authors recognized twelve species. Among these species, several remain morphologically ill-defined or otherwise little-known. The taxonomic position of some of these species also remains tentative and needs critical taxonomic reassessment, since no reproductive organs or annex structures are known. In the present study, three poorly known species: *Trichocolea brevifissa* Steph., *T. sprucei* Steph., *T. floccosa* Herzog & Hatcher with similar morphological characters, and one common species widely distributed over Central and South America, *Leiomitra flaccida* Spruce, are reevaluated based mainly on their type specimens. On the basis of the presence of perianths *T. brevifissa* and *T. sprucei* are newly included in the genus *Leiomitra*: *L. brevifissa* (Steph.) T.Katag. and *L. sprucei* (Steph.) T.Katag. *T. floccosa* from Costa Rica is newly synonymized with *L. sprucei*. The worldwide key to the species of *Leiomitra* is given for the first time.

PO-63

Bioactivity and phytochemical characterization of *Anoetangium thomsonii* Mitt. for the antimicrobial potential

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The use of antibiotics is one of the most common means of treatment of diseases. However, prolonged use of drugs slowly develops resistance in microbial pathogens. The use of higher plants in the medicine reported from time immemorial but the lower group of plants like bryophytes is less explored. In the present study, the antimicrobial potential of ethanol and acetone extracts of *Anoectangium thomsonii* Mitt. (Moss) were studied against different microorganisms like *Staphylococcus aureus*, *Erwinia chrysanthemi*, *Bacillus cereus*, *Salmonella enterica*, *Eshcherichia coli* and *Aspergillus parasiticus*. Disc diffusion assay was done for the screening of the potent extracts and concentration dependent (100 -1000 µg/mL) growth inhibition was observed for all the organic extracts of Bryophytes. The minimum inhibitory concentration (MIC) and minimum bactericidal or fungicidal (MBC/MFC) was observed in employing micro dilution methods which ranged from 0.97 to 125 µg/mL against different microbes. Among studied microorganism, *S. enterica* was found the most sensitive with lowest MIC (0.97 µg/mL). The highest zone of inhibition (ZI=31±0.57 mm) was shown by ethanol extract of *A. thomsonii* (Dwarahat) with MIC=0.97 µg/mL and MBC=1.95 µg/mL. The GC-MS data obtained in ethanol extract of *A. thomsonii* showed a high percentage of sesquiterpenes, steroids, fatty acids, and alcohol derivatives attributing to its antibacterial potential.

The present study establishes the antibiotic potential of *A. thomsonii* against *S. enterica*. Ethanol extract of *A. thomsonii* possess significant potential to inhibit the growth of *S. enterica* due to presence of large number of unique chemical compounds. It will eventually help in reassuring the validation of *A. thomsonii* an ethnomedicinally important Bryophyte as a potent cure for *S. enterica* infections.

PO-64

Unravelling the genetic basis of the hornwort-cyanobacteria symbiosis

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Plant-microbial associations are becoming increasingly recognized as major drivers of plant evolution and ecosystem dynamics. One of the most significant events in earth's history, the colonization of the terrestrial environment by the green lineage, is also postulated to have only been possible by the association with fungal and putatively with cyanobacterial partners. While functional significance of the association with fungal partners is actively investigated, plant-cyanobacterial associations of early land plants are poorly understood. Our project is meant to fill this gap and investigates the molecular and genomic bases of the plant-cyanobacterial association in the extant representatives of the earliest land plants, the hornworts.

To begin to understand the molecular bases of the plant-cyanobacteria association in details we are investigating (1) gene expression changes (RNA-seq) using a time series analysis both for the plant and the cyanobacterial partner. (2) We analyze this data using custom network analysis to identify conserved and divergent regulatory networks involved with the establishment of the association in the hornwort and in other land plants. (3) To better characterize the genes necessary for symbiosis establishment and maintenance we are currently conducting a forward genetic experiment. (4) Finally, using results of the previous analyses we will identify candidate genes and begin to verify their putative function using reverse genetics.

Our phylogenetic analysis suggests that members of the common symbiosis pathway are present in the hornwort genome. Nevertheless, a first pass analysis of gene expression dynamic during symbiosis establishment suggests that most genes

of the common symbiosis pathway are not differentially expressed. This either means that communication in the hornwort-cyanobacteria symbiosis does not involve the common symbiosis pathway or genes are post transcriptionally regulated. We are currently conducting experiments to clarify this.

This study will provide fundamental information on the regulatory networks governing the plant-cyanobacteria association in basal groups of land plants. Moreover, it will provide information on the conservation of gene regulatory networks involved with plant-microbial interactions in general over many million years of plant evolution. Our poster will provide information on the current state of the project.

PO-65

Bryophyte acclimation to sun conditions is influenced by both photosynthetic and ultraviolet radiations

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We studied the acclimation of bryophytes to sun and shade under ambient conditions, measuring variables usually influenced by photosynthetically active (PAR) and ultraviolet (UV) radiations. Our aim was to elucidate to what extent the responses to changing radiation were influenced by PAR and UV wavelengths. For this aim, we used three taxonomically and structurally different species: the thalloid liverwort *Marchantia polymorpha* subsp. *polymorpha*, the leafy liverwort *Jungermannia exsertifolia* subsp. *cordifolia* and the moss *Fontinalis antipyretica*. In the field, liverworts were more radiation-responsive than the moss, and the thalloid liverwort was more responsive than the leafy liverwort. Sun plants of *Marchantia polymorpha* showed, in comparison to shade plants, higher sclerophylly, lower Chl *a+b* contents, higher Chl *a/b* ratios, higher (antheraxanthin + zeaxanthin) / (violaxanthin + antheraxanthin + zeaxanthin) ratios (xanthophyll index), lower F_v/F_m values, higher contents of methanol-soluble vacuolar UV-absorbing compounds (soluble UVACs),

higher values of the ratio between the contents of methanol-insoluble cell wall-bound UVACs (insoluble UVACs) and soluble UVACs, higher contents of soluble luteolin and apigenin derivatives and riccionidin A, and higher contents of insoluble *p*-coumaric and ferulic acids. Overall, these responses reduced light absorption, alleviated overexcitation, increased photoprotection through non-photochemical energy dissipation, increased UV protection through UV screening and antioxidant capacity, and denoted photoinhibition. *Jungermannia exsertifolia* showed moderate differences between sun and shade plants, while responses of *F. antipyretica* were rather diffuse. The increase in the xanthophyll index was the most consistent response to sun conditions, occurring in the three species studied. The responses of soluble UVACs were generally more clear than those of insoluble UVACs, probably because insoluble UVACs are relatively immobilized in the cell wall. These modalities of radiation acclimation were reliably summarized by Principal Components Analysis. Using the most radiation-responsive species in the field (*M. polymorpha*), we found, under close-to-ambient greenhouse conditions, that sclerophylly and Chl *a+b* content were only influenced by PAR, F_v/F_m and luteolin and apigenin derivatives were only determined by UV, and xanthophyll index was influenced by both radiation types. Thus, responses of bryophytes to radiation can be better interpreted considering the influence of both PAR and UV radiation.

PO-66

Type III Phosphatidylinositol 4-kinase genes in *Physcomitrella patens*: CRISPR/Cas9 mutagenesis uncovers both novel and conserved functions in development

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Phosphoinositides (PIs) are key signaling lipids involved in many fundamental cellular processes. In *Arabidopsis*, the PI, phosphatidylinositol 4-phosphate (PtdIns4P), is involved in polarized growth of root hairs and pollen tubes, chloroplast movements and division, modulation of stomatal opening/closing and salicylic acid-dependent immunity. In contrast, there is limited work on the role of PtdIns4P in bryophytes. To dissect the function of PtdIns4P in *Physcomitrella patens*, we are using CRISPR/Cas9 mutagenesis to knockout the Type III Phosphatidylinositol 4-kinases (PI4Ks) that produce PtdIns4P – PpPI4K1, PpPI4K2, PpPI4K1 and PpPI4K2. Multiplex CRISPR/Cas9 editing of the PpPI4K1 and PpPI4K2 genes yielded only single null mutants, suggesting that *pi4k1/pi4k2* double mutants are lethal. Polarized cell growth was unaffected in *pi4k1* and *pi4k2* mutants; neither the size and solidity of colonies regenerated from protoplasts, nor the size of plants grown from protonemal cell fragments, were significantly different from wild-type. However, the number of leafy gametophores produced by *pi4k1* was 50% of that observed on *pi4k2* or wild-type plants. Furthermore, the *pi4k1* gametophores were abnormal in morphology with irregularly shaped phyllids, composed of disorganized, misshaped cells. As PI4K1 is involved in the regulation of chloroplast division in *Arabidopsis* and in rhizoid development in *Marchantia*, these results point to a novel role for *Physcomitrella* PI4K1 in 3-dimensional growth and phyllid development. CRISPR/Cas9 mutagenesis of the PpPI4K1 and PpPI4K2 genes resulted in both single and double null mutants. Mutant *pi4k1*, *pi4k2* and *pi4k1/pi4k2* plants, regenerated from protoplasts, were not significantly different in size from wild-type after one-week on PPNH₄ medium. However, after 2.5 weeks, the size of *pi4k1/pi4k2* plants was <40% that of wild-type or single mutants, suggesting an effect on polar growth of caulonemata. Growth of *pi4k1/pi4k2*, compared to wild-type, was also reduced in plants grown on PpNO₃ or in the dark, both conditions that elicit polar growth of caulonemata. These results suggest that PpPI4K1 and PpPI4K2 play overlapping roles in polar cell growth, similar to the role of these genes in flowering plants.

PO-67

Deciphering the role of FHY1 protein in mediating light-hormone crosstalk in *Physcomitrella patens*

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Phytochromes are proteins that sense red and far-red light (FR) in the environment and modulate internal responses by altering gene expression in plants. In higher plants, such as *Arabidopsis thaliana*, five types of phytochromes (PHYs) are present, which are categorized into type-I, PHYA (for FR) and type-II, PHYB-PHYE (for red light). Type-II phytochromes upon activation by light translocate to nucleus independently, but type-I phytochromes i.e. PHYA requires FHY1 (Far red elongated hypocotyl) protein for its nuclear translocation. This response is conserved in basal land plants such as mosses. *phyA* and *fhy1* mutants of *Arabidopsis* display elongated hypocotyl as compared to wild type (WT) under FR light. However, in mosses such as *Physcomitrella patens*, *fhy1* plants do not display etiolated growth of gametophore. Rather, etiolated growth is observed in WT and *phy1* plants under FR and they show elongated gametophore. This FR light dependent growth pattern in *Physcomitrella* differs from that observed in *Arabidopsis*. Gametophore formation and elongation related responses are primarily controlled by hormones such as auxin and cytokinin in *Physcomitrella*. Light and hormone interaction in regulating development of *Physcomitrella* is poorly understood. In this study, we have investigated whether FHY1 protein plays any role in development of *Physcomitrella* under FR light in response to different phyto-hormones. To find the role of FHY1 in hormone signaling, we have evaluated protonema differentiation and bud induction pattern in WT, *fhy1* and different phytochrome mutants (namely *phy1* and *phy3*) under different light conditions in response to auxin and cytokinin. We observed that; (i) FR light induced caulonema formation irrespective of presence or absence of exogenous auxin in WT plants, (ii) red light promoted bud induction in WT plants in

response to cytokinin in glucose dependent manner, (iii) *fhy1* plants showed defective growth under FR light as well as altered hormone sensitivity to both auxin and cytokinin. While the function of different phytochromes may be redundant for the observed responses, FHY1 appears to play major role in *Physcomitrella* development under FR light.

PO-68

The MADBRYO project, laying the groundwork and some preliminary results
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The MADBRYO project aims to close the gaps in our knowledge of Malagasy bryophytes by gathering the specimens and taxonomic data that are currently scattered across multiple institutions, supplementing them as necessary with targeted collecting efforts, and using them to develop a comprehensive flora for the bryophytes of Madagascar. Together, these efforts will provide a strong foundation for pursuing further scientific research on Malagasy bryophytes and for promoting their conservation.

Many historical specimens of Malagasy bryophytes have been accumulated in herbaria over the years. Together they represent a large and mostly untapped source of vital taxonomic and biogeographic data, but many of them have not been fully curated and are consequently difficult to use. In turn, the inaccessibility of the information they contain hampers scientific research into all aspects of the biology of Malagasy bryophytes.

The project began in September 2017 with the important task of specimen sorting and digitization of collection information at the partner herbaria (MO, PC, TAN). Recently an identification workshop was conducted at the Antananarivo herbarium (TAN), Madagascar in September 2018. This workshop resulted in seven new reports for the Malagasy bryoflora (Candollea, in press). Taxonomic information is also being added to the XPer3 knowledge database system, allowing interactive species

identification as well as flexible storage of taxa and characters as new information is gathered on the flora. We present here our very preliminary results in order to promote dynamic exchanges on Malagasy bryology.

PO-69

The hornworts (Anthocerotophyta) and thalloids liverworts (Marchantiophyta) of Cuba: challenges and perspectives

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The main challenge of the botanists in Cuba is the upgrade of the bryologist studies. Presently work analyses the state of the knowledge of the hornworts and thalloids liverworts (*Marchantiophyta*) in the island, based on the review of National Herbarium (BSC), specialized literature, Databases of National (BSC) and International Herbarium (NY, MGB). The hornworts and thalloids liverworts registered for Cuba are listed. The ecology, geographical distribution and state of conservation of the species are analyzed. About 60 species of hornworts and liverworts are recorded, 5% of the totals are endemic and 10% are threatened. The species registered for the island mostly present a dubious taxonomic status in response to the new World bryophyte Checklist. The hornworts and liverworts thalloids live in Cuban fragile ecosystems. This study sets the basis for the publication of the Checklist of Bryophytes of Cuba, as well as aims to awaken the interest to collaborate in future bryological investigations on the island.

PO-70

Assessing the resistance to lead and accumulation capacity of shoots, spores and adult plants to lead in four common moss species

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Mosses are frequently used as bioindicators because they absorb nutrients (and pollutants) directly from the ambient moisture across their entire surface. However, the effects of pollutants on their growth and development is not fully understood. For instance, we know little about the effective doses in different species, patterns of response or the ability of diverse moss species to exclude pollutants. In this study, we assess the sensitivity to lead and its accumulation on four common species of Iberian mosses with contrasted sensitivity to urban pollution: *Homalothecium aureum*, *Hypnum cupressiforme*, *Ptychostomum capillare* and *Syntrichia ruralis*. We tested four lead nitrate doses (0-10⁻³ M) on *in vitro* cultures of spores, shoot tips and adult stages of all those four species. Both spores and tips were cultivated directly in liquid medium with the corresponding lead dose. In adult stages, mosses were irrigated twice a week for 2 months with the different lead doses. In germination studies, we recorded survival and developmental stage of the spores, for shoot tips we recorded survival and damage rates. Finally, for adult populations we assessed damage using semiquantitative and quantitative measures and analysed its accumulation at the highest lead dose (10⁻³ M) using SEM/EdX.

The four species were more resistant to lead than anticipated. Lethal effects were evident only at the highest dose (10⁻³ M). Furthermore, a low but significant number of shoot tips and protonemata of *H. aureum* survived at the highest dose, and *S. ruralis* was able to produce sporophytes under all the doses. The SEM/EdX analysis showed that the mosses here analysed presented frequent lead aggregates on their surface, but were able to block effectively the entrance of this metal to the tissues. These results point at an exclusion mechanism, which allows them to survive at unexpectedly high lead doses, and that could seriously affect biomonitoring inferences of environmental lead pollution from metal levels found in living moss tissues.

PO-71

Micro-morphology and anatomy of the peristome in the Dicranales: exploring the

use of Technovit 7100 Methacrylate embedding resin for microtome sectioning

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Peristome characteristics in mosses have long been used for classification at the higher taxonomic ranks. The complex architecture of the peristome provides traits that are also of importance at lower taxonomic levels. The micro-morphology and anatomy of peristomes within and across the Dicranales will be explored, with the aim of elucidating evolutionary patterns. Peristome architectural features may provide a new set of characters that can provide insights into the deep-rooted problems of clade resolution and taxonomy in this monophyletic group of plants. The first objective was to elaborate protocols and test techniques that would allow for detailed observations and the comparison of microscopic features within sections of the peristome of *Dicranum scoparium* Hedw. and selected taxa from *Dicranum* Hedw. and the Dicranales. A protocol for sample preparation, widely used in plant tissue observations, was adapted to the study of the peristome. Technovit 7100 is a commercial product based on glycol methacrylate (GMA) resin that is used for embedding specimens before microtome sectioning. For the peristomes, very thin (3 to 10 µm) longitudinal sections of the peristome and peristome insertion region were made revealing the cellular patterns and the intricate architecture of the peristome teeth and peristome-capsule wall region. This embedding and sectioning technique has many advantages in histology as the sample can be easily orientated in the transparent resin before sectioning where it can be serially sliced into thin sections allowing for high resolution imaging. The protocol and images obtained are presented

PO-72

Antioxidant enzymatic analysis on bryophyte *Syntrichia ruralis* [Hedw.] in semi-arid sandy grassland, Hungary

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Bryophytes are poikilohydric and act as an experimental model plants to study the mechanism of desiccation tolerance. However, there has been little is known about biochemical activities in non-vascular cryptogram. The objective of this study was to examine the antioxidant enzymatic activities (CAT, APX, POD) during rehydrated and air-dried states in *S. ruralis* to understand how this plant survives in different seasons.

Moss cushions were collected from semi-arid grasslands near Bócsa-Bugac, Kiskúnság region in Hungary from the two microhabitats based on orientation of the sandy dunes; north-east (NE) and southwest (SW) directions respectively in spring, summer, autumn and winter 2018.

Our results showed the statistical differences in the mean values of CAT, APX and POD antioxidant enzymatic activities ($p \leq 0.05$) between the microhabitats in rehydrated state except CAT and APX values in air-dried state. However, the mean values of CAT, APX and POD were found to be statistically significant within each pair of seasons for both states. In rehydrated state, higher CAT, APX and POD values in summer, autumn and spring respectively whereas in air-dried state only in autumn season.

In conclusion, NE slope showed higher antioxidant enzymatic activities as compare to SW slope in both rehydrated and air-dried states and has different responses in each season. Differences in the antioxidant activities of slopes can refer different adaptation level on desiccation tolerance under even close microhabitats. Depending on the exposure, various recovery level of *S. ruralis* also can be hypothesized after rehydration.

PO-73

***Physcomitrella patens* dehydrin, PpDHNA, acts like “chaperone” by conferring protection against stress effects through protein stability enhancement**

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Drought tolerance was an ancient adaptation that must be considered to have played an essential role in colonization of the terrestrial environment. The most primitive of extant land plants, the bryophytes may provide resources as to how this adaptation was achieved. *Physcomitrella patens*, the model bryophyte, is highly tolerant to dehydration, salinity and other abiotic stress factors, and thus also a model for stress tolerance. Our objective is to better understand drought and salt stress tolerance in *Physcomitrella* so as to generate tools for increasing abiotic stress tolerance in crops. We studied the functional importance of a *Physcomitrella* gene encoding a protein from the dehydrin family, PpDHNA. Knockout mutant of this gene exhibited reduced tolerance to osmotic, salt and sugar stress. We studied the role of ABA in dehydrin protein stability, as we have previously shown that PpDHNA is rapidly degraded upon recovery of stress. Our results suggest a role for ABA in dehydrin protein stability. Furthermore, *ppdhna* knockout mutant is unable to recover from exposure to protein denaturation inducing agent DTT, and in vitro activity of this protein prevents chemical or heat denaturalization of enzymes.

PO-74

A comparative study of corticolous bryophytes on three-needle pine and oak tree in Chiang Dao wildlife sanctuary, Chiang Mai province, Northern Thailand

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Previous studies in pine forest have shown that the most important phorophyte attributes in determining corticolous bryophytes species is bark features. However, no study on this topic has been addressed in this country. Therefore, this study aimed to compare the richness, community and life form of corticolous bryophytes that occur on two majority trees with different bark characteristics at pine-oak forest, Chiang Dao wildlife sanctuary, Chiang Mai province, Thailand. The trees were three-needle pine (*Pinus kesiya* Royle ex Gordon) and oak (Fagaceae). Twenty-four trunks of each phorophyte were selected. Bryophytes were collected from tree trunk at 1-1.5 m height. In addition, bark characteristics of each phorophyte were examined. The results of bark characteristics show that bark pH and bark water-holding capacity of oak were significantly higher than three-needle pine. Nineteen species were recorded on three-needle pine and 35 species were found on oak. *Ochrobryum subulatum* Hampe was found only on three-needle pine, whereas 17 species were found only on oak. Species richness ranged from three to eleven species and four to fourteen species on three-needle pine and oak, respectively. Bryophytes community on three-needle pine was dominated by *Leucobryum aduncum* var. *scalare* (Müll. Hal. ex M. Fleisch.) A. Eddy, but a distinctive species on oak was *Wijkia surcularis* (Mitt.) H.A. Crum. The study of life form showed that cushion was the highest cover on three-needle pine whereas the most widespread life form on oak was weft. Our results found that species richness and cover of life forms appeared to relate to the moisture conditions and acidity of the tree bark. These results helped to explain some differences of corticolous bryophyte species among host trees in pine-oak forest, Thailand.

PO-75

The research progress and prospect of bryophytes in Tibet

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Tibet (E 78°25'-99°06', N 26°50'-36°53') lies on the southwest of the Qinghai-Tibet Plateau. The region covers more than 1.2 million square kilometers and the average altitude is more than 4000 m, has the obvious vertical climate characteristics. In addition, it has low oxygen content, strong solar radiation and low temperature. Rainfall decreases from southeast to north. Its complex landforms, physiognomy, and climate create a special heterogeneous environment for bryophytes.

In the early stage, William Mitten (1859) and Chen Pan-Chieh (1962) formulated the bryophytes in Tibet. From 1952 to 1979, more than 7000 specimens were collected in many scientific investigations in Tibet. After identification and classification, BRYOFLORE OF XIZANG was published in early 1985, laying a foundation for the study of bryophytes in Tibet. In the past decade, Bryologists have done a lot of work in the area and a total of 1,027 species of bryophyte have been recorded, belonging to 307 genera of 90 families 28 genera and 132 species of Pottiaceae were identified here. We have studied the spatial distribution of it. *Didymodon* and *Bryoerythrophyllum* are its dominant genera, the main environmental variables affecting their spatial distribution were temperature and altitude. In the context of climate warming, the two distribution centers will be mainly in semi-arid areas in the future and are about to move to higher altitudes and higher latitudes.

Studies on the morphological traits of bryophytes found that the morphological traits of *Bryum argenteum*, *Didymodon constrictus* and *Didymodon rigidulus* are different in adapting to the high-cold-drought environment in Tibet, revealing that different species have different response strategies to environmental change.

Future research should pay more attention to the physiological traits and biochemical stoichiometry of bryophytes, contact molecules

and microorganism, to explore the adaptation strategies of bryophytes in different environments, and provides scientific basis for ecosystem service function assessment in Tibet and global climate change.

PO-77

Bryophytes of submontane calcareous beech forests on dolomites of Central Slovakia

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In the last century, an intensive phytosociological research on beech forest vegetation has been carried out in Slovakia. However, many regions are still unexplored and, moreover, bryophytes are often omitted in phytosociological relevés. In this paper, we analyzed bryophyte species richness and composition in relation to elevation, xericity, slope, cover of bare rocks, cover of herb, shrub and tree layer, height of tree layer and vegetation unit (association), as well as traits of the recorded bryophytes regarding their ecological and habitat preferences in forest ecosystems dominated by European beech (*Fagus sylvatica*) in the hilly region around Banská Bystrica built by dolomite rocks and covered by rendzina soils. The analysis was based on 67 bryophyte species (59 mosses and 8 liverworts) recorded in 45 phytosociological relevés from 400 m² plots. For the statistical analysis between bryophyte species richness and composition and selected environmental variables Spearman's rank correlation coefficient, ANOVA and CCA were used. Ellenberg's indicator values and BRYOATT database were used to compile trait information. The most frequent species in the relevés was *Tortella tortuosa*, followed by *Hypnum cupressiforme*, *Brachytheciastrum velutinum* and *Ctenidium molluscum*. Average species richness of bryophytes was 8, compared to 39 species of vascular plants in the forest understory. Bryophyte species richness was negatively affected by xericity and positively by cover of rocks on soil surface. Species composition was affected significantly by xericity, cover of bare rocks and cover of tree layer. The majority of the

taxa (88.1%) are adapted to moderately moist soils, and roughly two thirds prefer moderately to strongly basic soils but 14% are acidophilous. Semi-shade species are the most numerous (71.2%) but a significant portion (23.7%) are semi-light or found in full light, whereas 50.9% are indicators of colder climate. Proportionally, species show habitat preference mostly to hard rocks (84.1%), living wood (66.7%) or soil (52.4%). Our results indicate that in the studied area, bryophyte species composition is mostly influenced by moisture availability (conditioned by xericity and cover of tree layer) and the amount of bare rocks greatly contributes to the overall diversity of available substrates and thus to a higher species richness of bryophytes.

PO-78

Effect of peatland degradation on bryophyte species composition in Latvia and Lithuania

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Bryophytes are pioneer species that occupy degraded sites, both after natural disturbances (e.g. fire) and human impact (e.g. logging). Post-harvested peatlands can be inhabited by bryophyte species that are adapted to extreme conditions such as drought, exposure to high sun radiation, wind erosion, etc. Still, bryophyte richness is higher in intact or less affected peatlands – raised bogs, transition mires and fens with different ecological niches. The role of bryophytes, especially *Sphagnum*, in mires involves also peat formation and carbon sequestration. Climate change mitigation by reducing greenhouse gas (GHG) emissions, low groundwater fluctuations are only some functions that are strongly related to processes in intact peatlands. To study bryophyte species composition in peatlands with different management history, data were collected in eight

sites: three peatlands with minor drainage impact in Latvia and five significantly drained, post-harvested peatlands in Lithuania. Vegetation cover (bryophytes, lichens, herbs, shrubs, trees) and physical parameters (degree of site degradation, soil moisture) were recorded in 269 plots in 2017–2018 during the LIFE Peat Restore project (LIFE15 CCM/DE/000138). Additionally, vegetation data together with environmental parameters were used for indirect GHG emission assessment applying the recently developed GEST (*Greenhouse Gas Emission Sites Types*) approach. In all sites, 382 species were recorded, including 85 bryophyte species (10 liverworts and 75 mosses, including 19 *Sphagnum* species). Bryophyte species richness showed moderate positive correlation with total species richness ($r_s=0.53$, $p<0.001$), weak correlation with moisture ($r_s=0.34$, $p<0.001$) and herb cover/species richness ($r_s=0.24$, $p<0.001$; $r_s=0.28$, $p<0.001$, respectively). Bryophyte species richness was best explained by total number of species per plot, bare peat and bryophyte species cover and was site-specific. Species composition significantly differed between degraded and near-natural sites. From all recorded bryophytes, 24 species were related to one of four previously defined degradation classes using indicator-species analysis. *Campylopus introflexus*, *Pleurozium schreberi*, *Pohlia nutans*, *Polytrichum* spp. were indicators of the most degraded sites, while *Cephalozia bicuspidata*, *Dicranum bonjeanii*, *Mylia anomala*, *Sphagnum angustifolium* were found only in sites with minor drainage impact. The results suggest that bryophytes can be used as indicators to assess the degradation of peatlands.

PO-79

***Codonoblepharon forsteri* (Orthotrichaceae) has its most important population in Southwestern Spain**

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Codonoblepharon forsteri (Dicks.) Goffinet is a peculiar moss from the Atlantic area of Europe, North Africa and Macaronesia. Despite its extensive range, it is a rare species in practically all the countries in which it has been found. This seems to be due to the fact that it is a very specialized and highly stenoicous epiphytic moss, with very specific ecological requirements: it invariably lives on large trees, limited to runoff areas of the bark associated with holes, scars, tree forks and other well-lit, humid and nutrient-rich situations (tree stumps, exposed roots, etc.). The rarity of this moss could also be due to demographic reasons, since the species shows very low densities throughout its range.

In the Iberian Peninsula, *Codonoblepharon forsteri* has been reported from scattered localities, mostly in the northern and western areas. Without exception, only one or very few colonized trees are known in each locality. Thus, only 10 colonized trees have been found in all the 9 localities reported for Portugal (Garcia, 2006) and almost all the 16 known Spanish localities showed each only one colonized tree (Heras Pérez *et al.*, 1997).

In the present communication, a large population of *Codonoblepharon forsteri* is reported from Ronda (Andalusia, Southern Spain). We provide data on the size of the population, the distribution of the colonies in the surveyed area, and the environmental characteristics, at different ecological levels (forests, phorophyte and microtope), in which the moss grows. Local practices of forest management that affect and can threaten this extraordinary population are also identified.

PO-80

Moss-water-interactions: Effects of dehydration and hydration on moss surface structures

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Mosses as poikilohydric plants do not actively regulate their water content, which is in equilibrium with environmental humidity. They are able to survive long drought periods by several adaptations, leading to a pronounced desiccation tolerance. Photosynthetic activity, however, requires hydrated tissue. It is long known that available water is taken up via the whole moss surface. On the other hand, mosses need to avoid the formation of a water film covering the assimilating tissue and hampering photosynthesis by acting as a diffusion barrier. Despite the vital importance of efficient water absorption, information on moss surface interactions with water are sparse. In this study, four epiphytic moss species were analysed with respect to surface structure response to the dehydrated and hydrated state. Samples were collected at four sites in the district of Tübingen, Germany, during October and November 2018. Samples were kept dry for at least 30 days. To study hydrated phylloids, samples were submersed in distilled water for 10 min. To conserve cell structures in a dehydrated or hydrated state, dry and hydrated samples were shock-frozen with liquid nitrogen, directly followed by lyophilisation for 24 h. Subsequently, the morphological response towards the different water conditions was analysed using a scanning electron microscope. Dry and turgid state differed in cell width, cell length and surface structure. Also, species reaction on hydration and dehydration was distinct from one another in the way surface structures changed. In a next step, the analysed structures will be further examined with respect to adaptive significance and a possible application potential.

PO-81

Trace elements concentrations in Greece using *Hypnum cupressiforme* Hedw. as biomonitor

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Data of the Greek participation to the *European Surveys of Heavy Metals accumulation in Mosses* are presented in this study (United Nations Economic Commission for Europe International Co-operative Programme on Effects of Air Pollution on Natural Vegetation and Crops). The area selected for study was Northern Greece (Districts of West, Central and East Macedonia and Thrace). The study aimed at mapping of heavy metals and toxic elements accumulation (Al, As, Cr, Fe, Ni, Sb, V, Zn) in the moss *Hypnum cupressiforme* Hedw., reflecting wet and dry atmospheric deposition. Moss samples were obtained from 95 sites situated in Northern Greece, covering ca 42,000 km². Preliminary moss samples preparation, chemical analysis, quality control, etc., followed the ICP Vegetation Monitoring Manual requirements and the procedure was done in Frank Laboratory of Neutron Physics, Joint Institute for Nuclear Research (Dubna, Russian Federation). *Hypnum cupressiforme* samples were analyzed using the Neutron Activation Analysis (NAA) technique and the elements concentrations were determined. The chemical composition database of the moss samples was further used for the application of source apportionment by Positive Matrix Factorization (PMF). In total thirty chemical elements were used for source apportionment (Na, Mg, Al, Si, Cl, K, Ca, Sc, Ti, V, Cr, Mn, Fe, Co, Ni, As, Br, Rb, Sr, Mo, Cd, Sb, Cs, Ba, La, Ce, Tb, Hf, Ta and Th). The big

sampling density provided information about the elemental deposition from the atmosphere to terrestrial systems over the region of Northern Greece. The source apportionment results revealed contribution from five sources: (1) Soil Dust, (2) Aged Sea Salt, (3) Vehicular Traffic, (4) Heavy Oil Combustion and (5) Mining Activities. Soil Dust displayed the highest contribution to the measured metal concentrations among all other sources. Additionally, two areas in Northern Greece, the Megali Panagia area and the Ptolemaida-Amyntaio area were well connected with specific sources; for Megali Panagia there was high contribution of road dust and Mn-rich sources which are related to the nearby existing mining activities, while the Ptolemaida-Amyntaio area was correlated with the heavy oil combustion source related to the lignite power plants located in the wider area.

PO-82

The role of prenyltransferases in the thallus development of *Marchantia polymorpha*

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Protein prenylation is one of the most important post-translational modifications that plays an important role in processing of normal cellular mechanisms, such as signal transduction, polar cell growth, membrane and cell wall modifications. All of these processes are an integral part of the functioning of multicellular organisms. Knockouts in prenyltransferase genes can lead to dramatic changes in plant growth and development, up to the loss of the ability to form normal multicellular tissues. Multicellularity transition is one of the most important events in the evolution of living organisms, but most facts about this event remain to be unknown. Using of plants, especially evolutionally ancient groups like Bryophytes, allows us to find out new regulatory mechanisms involved in development of multicellular organisms.

We investigated the role of farnesyltransferase and geranylgeranyltransferase genes in the *Marchantia polymorpha* multicellular thallus' development. We obtained knockout lines for three genes of prenyltransferases subunits: a gene of the alpha-subunit PLP (Mapoly0093s0047), common for farnesyl- and geranylgeranyltransferase; a gene of farnesyltransferase beta-subunit ERA (Mapoly0123s0027) and a gene of geranylgeranyltransferase I beta-subunit GGB (Mapoly0010s0084). Knockout plants for each gene were generated by CRISPR/Cas9 technology. It was shown that *Marchantia* lines with mutations in the sequence of the alpha subunit gene (*Δplp*) formed callus-like dense tissues that were composed of round-shaped cells of various sizes and easily disintegrated into separated fragments. Although *Δplp* mutants retained the ability to aggregate into tissue, they were not capable for forming a normal thallus that undoubtedly indicates the important role of prenyltransferases in the development of tissues, cell differentiation and the formation of multicellular thallus.

PO-83

Campylopus introflexus colonization in the Atlantic secondary dunes of the Iberian Peninsula

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Campylopus introflexus (Hedw.) Brid. is considered one of the 100 worst alien invasive species in Europe. Thanks to its high ecological tolerance, this moss species has spread throughout all European countries especially in places subject to a high anthropic influence. Despite its high tolerance *C. introflexus* prefers dry, sandy, nutrient-poor sites with little herbaceous vegetation which make the coastal dunes an optimal habitat for the emergence and spread of this invasive species. The presence of bryophytes in dunes is common thanks to their

poikilohidric features where they can play an important role in stabilization of dune surfaces. However, the existence of a threatening species such as *C. introflexus* can endanger the fragile equilibrium of the plant communities in these coastal habitats. This work intends to assess the causes of the presence of *Campylopus introflexus* on secondary dunes in relation with several biotic and abiotic factors including bryophyte and vascular plant communities. For this, we sampled transects parallels to the coastline and identified bryophytes and other vegetation type using the point-intercept method in 15 beaches along a climatic gradient in the western coast of the Iberian Peninsula. The results showed that *C. introflexus* is only present when aridity decreases, and in fact its presence is strongly correlated with precipitation variables. In addition, at intermediate values of aridity, it seems that there is a competition between *Campylopus i.* and the common native moss *Pleurochaete squarrosa* (Brid.) Lindb. Negative correlations were also found between *Campylopus i.* and perennial vegetation cover and diversity, that can be due to anthropic disturbance. These findings suggest that the level of aridity, vegetation cover and diversity and anthropic influence can contribute to the colonization of secondary dunes by the alien invasive moss *Campylopus i.*

PO-84

Impact of transposable elements in the generation of phenotypic variability in *Physcomitrella patens*

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Transposable elements (TEs) comprise 57% of the genome of *Physcomitrella patens* (Lang *et al.* 2018). Using a recently published RNA seq gene atlas of the *P. patens* genome (Perroud *et al.* 2018) we have been able to assemble the complete transcripts of 6 active families of transposable elements, including retrotransposons (LTRs-retrotransposons and LINES) and DNA transposons. These transposable elements show different pattern of

expression in tissues or stress conditions. These results suggest that different TE families are active in *Physcomitrella patens*. We have searched for TE polymorphism in four ecotypes of *Physcomitrella patens* using resequencing data of these ecotypes. The results suggest that these families have been recently active and may be at the origin of some of the phenotypic differences observed in these ecotypes. As a first approach, we are analysing the patterns of expression of genes with a TE polymorphisms in the proximal upstream region of the gene. As an example, we found that the expression of a transcription factor highly expressed during rhizoid development is downregulated in Villersexel as compared to Gransden and that this decrease of expression is potentially due to an LTR-retrotransposon insertion. We have generated a knock out of the corresponding gene by CRISPR/Cas9 in Gransden and show that rhizoids development in this mutant is reminiscent of the one observed in Villersexel, suggesting that the LTR-retrotransposon insertion, and the decrease of expression of this gene, could be at the origin of the differences observed in rhizoid development between Gransden and Villersexel. In order to confirm this hypothesis, we are performing locus replacement between the two varieties in order to check the hypothesis that insertion of the TE is indeed involved in the phenotype observed.

PO-85

New insights in taxonomy and phylogeny of liverworts

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The liverworts, one of three early diverging extant land plant lineages, are represented by over 7000 species in 371 genera. Although much progress in molecular phylogenetics has been made in recent years, the division of liverworts into natural genera has not yet been satisfactorily solved. The phylogenetic relationship of many enigmatic genera is still not clear. The main objective of this study is to resolve the phylogenetic relationship of key groups of liverworts using molecular data including

complete chloroplast genomes and transcriptomes. Our new data support the current higher-order classification of liverworts. The sporophyte of *Mizutania* Furuki et Z.Iwats., an extraordinary genus previously placed in the simple thalloid liverworts, is found for the first time. On the basis of morphological and molecular data, several enigmatic genera such as *Aphanotropis* Herzog, *Calatholejeunea* K.I.Goebel, *Cephalolejeunea* Mizut., *Dactylophorella* R.M.Schust., *Sinomylia* P.C.Wu et al., are reduced to be new synonyms. Two new genera from Oceania and tropical Asia are proposed. The status of several genera of Lejeuneaceae with rampant homoplasy, rapid radiations, and presence of neoteny, e.g. *Tuyamaella* S.Hatt. and *Schusterolejeunea* Grolle, is greatly challenged. A more intensive analysis of chloroplast genomes and transcriptomes from extended samples on a broader scale may provide better phylogenetic resolution.

PO-86

Results of long-term bryophyte monitoring of dry rocky grasslands in Hungary

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The bryophyte vegetation monitoring is an ongoing project started in 2000 in the frame of the Hungarian Biodiversity Monitoring System and includes 50 sampling plots of various habitat types (wetlands, dry grasslands, saline-alkali areas and forests). The size of the permanent plots are 10 m x 10 m and twenty-five 0.25 m² sized quadrats are placed regularly at the corners of a grid of 2 m spacing within the plots. In each quadrat, the presence of bryophyte species is recorded. The recent presentation focuses on the changes in the bryophyte assemblages of dry rocky grasslands. The survey has been carried out in eight permanent plots by biennial sampling, and there are already 8-10 repetitions per plots.

The species richness of dry rocky grasslands is high compared with the bryophyte assemblages of other habitat types surveyed. The species richness was between 11 and 28 in the plots. The species pool of the plots has been continuously increased; the mean species number per plot was 18 in the first year (between 11 and 30) and the mean cumulative species number was 32.5 in the last year (between 21 and 42). The mean number of new species in plots was 3.6 (between 0 and 8). The one-third part of all detected species per plots were present in each surveyed year, almost 60% of species occurred at least half of relevés and 17% of them were detected only once per plot. General structure of the assemblages of different years was analysed by PCoA using plot level frequency data. There were many fluctuations at bryophyte species level, but there were no trends at assembly level. To study the annual dynamics of the species, the relationships between mean annual increment and mean annual turnover were evaluated. Most of the species showed the dynamic expected on the base of their life strategy, but colonist species formed a very heterogeneous group. Surveyed dry grasslands seem to be stable. The differences in species richness and species composition in various years derives from their natural population dynamics.

PO-87

The *Hypnum* organellar genomes – An update

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The low genetic variation within organellar and nuclear markers targeted for species and genus level phylogenies among pleurocarpous mosses leads us to survey whole organellar genomes of seven closely related species. We sought to detect regions with higher variation, which can be used in DNA barcoding approaches and phylogenetic

reconstructions among closely related species. Next-generation sequencing (NGS) data of seven *Hypnum* species (*H. andoi*, *cupressiforme* var. *lacunosum*, *H. jutlandicum*, *H. leptothallum*, *H. subjulaceum*, *H. uncinulatum*) and one species formerly known as *Hypnum* (*Callicladium imponens*) were generated using paired-end shotgun sequencing of genomic DNA on the Illumina HiSeq/MiSeq platforms. Generated reads were paired and mapped against organellar reference genomes available in GenBank using Geneious v8.1.3. Genomic organisation is congruent to published hypnalean/dicranalean plastomes (cp) and chondromes (mt), with the plastomes (~125 kb) being approx. 20 % larger than the chondromes (~104 kb). The overall observed genome wide number of substitutions (cp: 4082; mt 929) is 4—5 times higher compared to the number of microstructural mutations (cp: 516; mt: 119). 23% (cp) to 18% (mt) of the microstructural mutations comprise simple sequence repeats (SSRs). To our surprise, we detected 22 hairpin associated inversions (cp: 14;

mt 8), which represents 2% (cp) and 4% (mt), respectively of the total number of microstructural mutations. Overall mutations (substitutions & indels) are almost four times lower in the chondrome compared to the plastome. E. g. a comparison of the most closely related *H. andoi* and *H. uncinulatum* revealed only 9 genome wide substitutions and 49 indels in the chondrome, whereas 119 and 328 indels were counted in the plastome. p-distances between the seven species reveal that the prominent organellar molecular markers (i. e. *trnL-F*, *rbcL*, *rps4*, *atpB-rbcL*, *nad5*) are in fact less variable than e.g. the *clpP* group II intron or the *rpl32-trnP* spacer, which show a 2—3-fold greater variation. Markers that are currently used in phylogenetics are targeted given the availability of primers and amplification protocols, i.e. tradition. However, a vast array of other organellar regions outperform traditionally used markers, in terms of variability and phylogenetic signal.

Keywords: Oral (OR)/Poster (PO) Presentation Number

2D-to-3D development	OR-73	<i>Anthoceros caucasicus</i>	OR-17
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abiotic stress	OR-63	antifungal effects	PO-03
abscisic acid	OR-56	antimicrobial activity	OR-35
accumulation	OR-28	antioxidant	OR-35
actin cytoskeleton	OR-57	antisense transcription	OR-60
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Africa	PO-57	Arctic	PO-51
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air quality	PO-20	asexual reproduction	OR-49
<i>Aloina</i>	PO-32		PO-24
altitudinal gradient	PO-33	ash stands	PO-12
Ambra1	PO-01	asymmetric cell division	OR-73
anatomy	OR-78	ATG6	PO-01
	PO-71	Atlantic islands	PO-57
anisospory	PO-47	atlas	OR-25
<i>Anoetangium thomsonii</i>	PO-63	atmospheric deposition	PO-81
<i>Anomobryum</i>	PO-52	atmospheric pollution	PO-11
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<i>Anthoceros agrestis</i>	PO-37, PO-64	auxin	OR-47
		Balkan Peninsula	OR-36

Banská Bystrica	PO-77	chloroplast proliferation	OR-56
Bartramiaceae	PO-38	chorotypes	PO-61
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Britton	OR-05	compound leaves	OR-79
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Brunei	PO-49	conservation ecology	OR-77
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bryophagous beetles	PO-58	CRISPR mutagenesis	OR-58
Bryophyta	PO-55	CRISPR/Cas9 mutagenesis	PO-19
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