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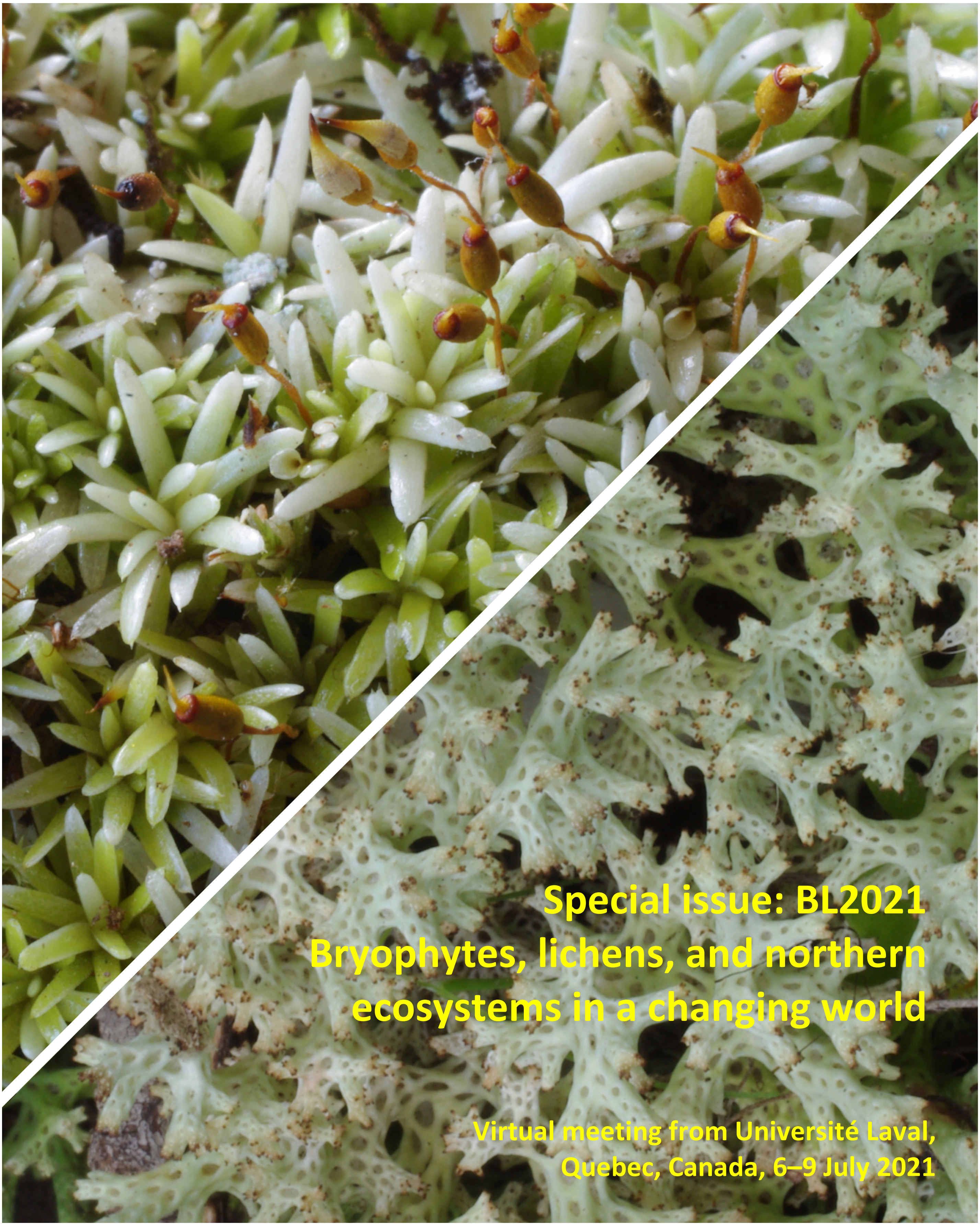

Special issue: BL2021
Bryophytes, lichens, and northern ecosystems in a changing world

Virtual meeting from Université Laval,
Quebec, Canada, 6–9 July 2021

The International Association of Bryologists (IAB), American Bryological and Lichenological Society (ABLS), Canadian Botanical Association (CBA-ABC) and Société québécoise de bryologie (SQB) are organizing the online conference 'Bryophytes, lichens, and northern ecosystems in a changing world' (BL2021), which is hosted by the Université Laval, Québec, Canada, between July 6 and 9, 2021. The scientific program committee (Nicole Fenton and Julia Bechteler [co-chairs] and Mélanie Jean and Amelia Merced) composed an exciting four-day conference, comprising four plenary speakers, 119 oral and 42 poster presentations by plant and lichen biologists and ecologists from 31 countries.

Talks are distributed across ten symposia focused on major advances along specific research axes, such as *Sphagnum* or hornwort biology, bryophyte phylogenomics, bryophytes and climate change, ecosystem restoration, or sex determination, and general sessions centered on broader topics, such as lichen biology, bryophyte ecology or plant anatomy. We are looking forward to an enriching four days that joins together colleagues across different fields from parts of the globe to exchange their contributions to advance our understanding of plants, lichenized fungi, and northern ecosystem biology.

The organizing committee is thankful to the Université Laval for its critical support enabling this international event.

The organizing committee

Juan Carlos Villarreal[1] and Bernard Goffinet[2] [co-chairs], Matt von Konrat[3] [treasurer], Marc Favreau[4], Nicole Fenton[5] and Scott Schuette[6]

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OP 2	Bisang. What we want to know about bryophyte life history traits and how they relate to bryophyte sex ratios, dispersal ecology and extinction risks.	214-QFN3-114	15
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OP 5	Medina. Beyond the sphinxes: current (and renewed) challenges in bryophyte systematics and evolution.	214-NDZN-124	18
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OP 7	Flores et al. Arboreal gastropod grazing in macro-lichen communities of western Newfoundland.	214-NjBR-124	20
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OP 13	Bippus. The fossil record of haplolepideous mosses and its potential for time-calibrating phylogenies.	214-L87Q-134	26
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OP 17	Escolástico-Ortiz et al. Elucidating the phylogeographic history and post-glacial demographic signatures of the moss *Racomitrium lanuginosum* Brid.	214-DwKv-114	30
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OP 19	Higgins. Liverwort oil bodies: often overlooked beautiful and distinct cell features.	214-8KsE-104	32
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Abstracts of oral presentations

Where do they live? Discerning the unknown distributions of bryophytes

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The number of bryologists per km^2 varies widely across the planet. Consequently, while some parts of the globe have a very detailed knowledge of the distribution of bryophyte species, other areas are still discovering new species. When detailed spatialized knowledge of species distributions is lacking or impossible, species distribution models are an essential tool to determine the distribution of species. However, species distribution models rely on detailed knowledge of habitat requirements, and interactions between micro and macro factors that determine habitat suitability for an individual species. In the absence of this information, the potential distribution of many species becomes simply ‘eastern boreal North America’.

Drawing on a variety of approaches, we are (1) increasing the documentation of species distributions, (2) describing landscape and cross scale factors influencing bryophyte habitat occupation, and (3) developing novel remote sensing tools to map distributions of bryophyte species in eastern boreal North America. The results of these research projects will help determine the actual distribution of bryophyte species, essential for their eventual conservation, and will suggest methods that could be applied to other regions of the globe where there are gaps in our knowledge of bryophyte distributions.

What we want to know about bryophyte life history traits and how they relate to bryophyte sex ratios, dispersal ecology and extinction risks

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Out of the 50 questions that eventually qualified as the ‘fundamental research questions in bryology’ from more than 220 suggestions, almost 30% (14) sort under the wide general topic ‘GT2 Bryophyte Ecology, Physiology and Reproductive Biology’. In my presentation I will focus on the first subsection and outline how an improved understanding of bryophyte life history traits is essential for the advance of many other fundamental future topics identified in this project. Briefly, Life History Theory seeks to explain how natural selection shapes organisms to achieve survival and reproductive success. Bryophyte life histories are tightly linked to the bryophyte life cycle; the latter is unparalleled among land plants and has a major bearing on nearly every aspect of bryophyte biology.

Among such unique characteristics, I will highlight the roughly similar frequencies of hermaphroditic and dioicous mating systems expressed in the gametophyte, and the high proportions of non-reproductive individuals and populations in many, especially dioicous, species. It is therefore critical to distinguish between genotypic and phenotypic (functional; realised) sex. I will present examples of genotypic and phenotypic sex ratio variation along environmental factors, and of possible phylogenetic constraints on sex ratios. I will also illustrate relationships between life history traits and dispersal capacity.

Finally, I will present an approach to disentangle species’ life histories traits, habitat specificity and environmental factors that affect rarity and vulnerability of European bryophytes. Studying species and organisms with widely varying life histories, beyond the common model species, will contribute evidence to general life history and ecological theory.

Bryophyte conservation in a biodiversity crisis

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According to the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services IPBES, corresponding with the UN Intergovernmental Panel on Climate Change, IPCC, we risk losing one million or c. 12% of our world's species. Like climate change, the loss is gradual and if we do not act the loss is inevitable. After a general introduction to the theme, I will address in some detail four of the 14 identified fundamental questions in bryology that concern bryophyte conservation and management.

How will global climate change affect extinction risk of bryophyte species and, consequently, their ability to adapt to changing environmental conditions? What are the key drivers of decline in bryophyte species and intraspecific diversity, at both the global and regional level? What are the highest priority areas for the conservation of bryophytes in the face of land-use change, habitat destruction and climate change? Where are the global hotspots of rare or threatened bryophyte species and how do these relate to hotspots of species and intraspecific diversity?

These questions are currently addressed by descriptive or statistical comparisons, red-listing, spatial analyses, monitoring, and modelling approaches. Considering the current rapid biodiversity loss, we need ways of pin-pointing the most efficient conservation measures. Important issues include: Which species are most important to conserve? How should genetic diversity be considered? Can diversity at one level be forecast by diversity at another level? And which factors are most important to explain the observed (and predict the future) bryophyte diversity loss?

OP4

Bryophyte biotic interactions and productivity with a focus on mycorrhizal-like associations

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Bryophytes are key components of several biomes worldwide, where they contribute significantly to biomass and productivity and are thought to exert a major influence on ecosystem processes, including water, carbon and nitrogen cycles. Appreciation of the roles of bryophytes and their interacting microbiomes in ecosystem functioning has increased dramatically in the last few decades; however fundamental questions still remain as to the mechanisms involved and on how diverse microbes and types of interaction influence bryophyte development, community composition and functional significance across ecosystem types. Here we will discuss latest advances in understanding and future major challenges in the broad context of bryophyte biotic interactions and productivity focusing particularly on mycorrhizal-like associations.

While it has been known for a very long time that the rhizoids and/or thalli of liverworts and hornworts are colonised by filamentous fungi with characteristic morphologies, only in the last decade has the mycorrhizal-like nature of these associations in liverworts and the diversity of fungal symbionts involved been demonstrated through extensive global sampling combined with cytological, physiological and molecular investigations. This diversity includes endogonaceous members of the fungal sub-phylum Mucoromycotina, alongside Glomeromycotina arbuscular mycorrhizal fungi and members of the Dikarya. Mucoromycotina symbionts form distinct partnerships with an apparently prominent role in liverwort nitrogen nutrition and, given their distribution in the liverwort phylogenetic tree, most likely represent the ancestral type. Whether the Glomeromycotina and Mucoromycotina endophytes of hornworts also exchange resources with their hosts and possibly interact with their hosts' ubiquitous cyanobacterial symbionts remains to be determined.

OP5

Beyond the sphinxes: current (and renewed) challenges in bryophyte systematics and evolution

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In recent years we have witnessed a substantial step forward in our understanding of bryophyte evolution and systematics, facilitated by the advances of molecular phylogenetics. This responds to the interest of bryophyte specialists, but also to the growing attention received by non-vascular systems: bryophytes provide contrast to better known models and help us determine the universality or distinctiveness of plant evolutionary mechanisms. However, some fundamental questions, from the most ancient branches of the bryophyte tree of life to the ongoing microevolutionary processes, are yet to be answered. This presentation focuses on a few of these stimulating themes to demonstrate that even what seemed well-settled principles are now being questioned and re-examined with new evidence. This is the case, for example, of the early branching pattern of the three bryophyte lineages, a long-standing matter with deep implications in our understanding of plant evolution. Some other seemingly basic aspects of this tree are poorly understood: bryophytes have the potential to undergo rapid diversifications, and we now have evidence of many examples of such events in their history. However, it is still not clear which phenomena, both intrinsic or extrinsic, have triggered said radiations, nor the role that extinction played shaping them. Finally, as we learn more about bryophyte speciation and microevolution, we need to reflect on how to integrate this knowledge in new species descriptions to effectively advance towards the completion of the global bryophyte assessment.

Investigating the relationship between tree ecophysiology and hosted communities of epiphytic bryophytes and lichens

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Epiphytic bryophytes and lichens are abundant on a variety of tree species in different biomes. Trees within a single forest stand can exhibit contrasting states of health as a function of their physiological performance that may influence the epiphytic community. For example, a healthy tree may have a well- formed full crown structure while unhealthy tree crowns may be more eroded. Consequently, different physiological states of trees may support different communities. At a larger scale, this variation in tree health and subsequent variation in hosted communities may contribute to biodiversity and ecological processes, such as nutrient accumulation and carbon cycling, in unique ways. However, to date these links remain speculative. This study seeks to disentangle the relationship between tree ecophysiology and epiphytic communities at the local level.

The ecophysiology of 20 black spruce (*Picea mariana*) from a northern Quebec boreal forest was characterized through measurements of age, diameter at breast height, basal area increment, stem water potential, maximum photosynthetic capacity, foliage density, and live crown ratio. Each tree was surveyed at the branch and trunk level for epiphytic species richness and coverage. Principal component analysis and linear regressions revealed that older, larger trees possessed poorer foliage and decreased in epiphyte coverage at the trunk level, likely due to the development of unsuitable habitat conditions along the trunk with age. Preliminary results suggest opposite trends at the branch level. The links between tree physiology and epiphyte community composition and abundance could lead to predictive landscape level models for conservation planning.

Arboreal gastropod grazing in macro-lichen communities of Western Newfoundland

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Gastropod grazing has recently emerged as a potential threat to the continued existence of some species of epiphytic macro-lichens in eastern North America. The island of Newfoundland represents a strong hold for many species of rare or endangered lichen species.

This study examines how gastropod species currently alter lichen communities in western Newfoundland by investigating three questions: (1) Has lichen grazing by arboreal gastropods occurred in western Newfoundland? (2) What is the abundance and richness of arboreal gastropods present in the study area? (3) Does damage by grazing to lichen thalli vary in relation to tree level environmental factors (e.g., lichen diversity, DBH)?

We used field lichen grazing surveys and lichen abundance and diversity surveys to describe the current state of the lichens in the study area. We used nocturnal timed gastropod searches and arboreal pit-fall traps to describe the abundance and richness of arboreal gastropods.

Preliminary results show 68% of lichen thalli had severe or extreme grazing. Gastropod sampling methods collected 275 gastropod specimens including 234 slugs and 41 snails. Regardless of sampling method, slugs outnumbered snails in the observed arboreal gastropod community. Grazing damage was significantly higher for trees with lower lichen species diversity and those where lichens were found on the tree bole. *Lobaria pulmonaria* (L.) Hoffm. was the most severely grazed of all lichen species surveyed.

Overall, lichen communities in western Newfoundland were severely impacted by widespread gastropod grazing, but further research is required to understand the relationship of lichen species diversity and grazing severity.

Calicioid fungi and lichens from an unprotected intact forest ecosystem in Québec

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Calicioid lichens and fungi form a diverse polyphyletic group whose species richness is often associated with old-growth forests and ecological continuity. One of the last intact forest landscapes south of the 50th parallel in Québec includes the *Ya'nienhonhndeh* territory, which has been the focus of a protected area project directed by the Huron-Wendat First Nation for more than ten years. To contribute to the characterization of its conservation value, we report the calicioids from the area. We identified 34 species in eight genera from 187 samples collected in old growth stands of balsam fir, black spruce, and yellow birch. Our four most remarkable discoveries are *Chaenotheca nitidula* Tibell (n = 11), *Chaenothecopsis australis* Tibell (n = 1), and *C. tsugae* Rikkinen (n = 2), which are reported for the first time from the province, as well as *Sclerophora coniophaea* (Norman) Mattsson & Middelb. (n = 18), which is rare in North America and was previously reported only once in Québec. As a result of this inventory, the *Ya'nienhonhndeh* is now the second richest area known for calicioids in Québec, after Parc national de la Gaspésie. We conclude that it is an ancient forest ecosystem whose conservation value is high based on its unique biodiversity, and that it warrants protection.

Les lichens et les champignons calicioïdes constituent un groupe polyphylétique diversifié dont la richesse spécifique est souvent associée aux forêts anciennes et à la continuité écologique. Le territoire du *Ya'nienhonhndeh* fait partie de l'un des derniers fragments de paysage forestier intact au sud du 50e parallèle au Québec et fait l'objet, depuis plus de dix ans, d'un projet d'aire protégée dirigé par le Conseil de la Nation Huronne-Wendat. Afin de contribuer à la caractérisation de la valeur de conservation de ce territoire, nous documentons les calicioïdes s'y trouvant. Nous avons identifié 34 espèces appartenant à huit genres à partir de 187 échantillons collectés dans des sapinières à bouleau blanc, des pessières noires et des bétulaies jaunes anciennes. Nos quatre découvertes les plus remarquables sont *Chaenotheca nitidula* (n = 11), *Chaenothecopsis australis* (n = 1) et *C. tsugae* (n = 2), qui sont nouvelles pour le Québec, ainsi que *Sclerophora coniophaea* (n = 18), qui est rare en Amérique du Nord et qui n'avait été rapportée qu'une seule fois auparavant dans la province. À la suite de cet inventaire, le *Ya'nienhonhndeh* devient, après le Parc national de la Gaspésie, le deuxième territoire connu au Québec répertoriant la plus grande richesse de lichens et de champignons calicioïdes. Nous concluons qu'il s'agit d'un écosystème forestier ancien dont la valeur de conservation pour la biodiversité est unique et incontestable.

OP9

Microbial community associated to lichens in a post-fire succession

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Lichens are symbiotic organisms between fungi (one–several species), green algae and/or cyanobacteria and numerous bacteria. While the interactions between the photobiont and fungus have been intensively studied, the characterization of microorganisms and its role in the symbiosis is still in its infancy. In this project we aim to assess the abundance and diversity of the whole microbial community associated to two reindeer lichen species, *Cladonia mitis* and *C. stellaris*, and to compare the changes of those microorganisms in a post-fire succession.

To achieve these goals, DNA and RNA from lichen samples were extracted. We carried out library preparation and sequencing on an Illumina MiSeq platform. We binned the assembled contigs to group and assign them to individual genomes, such as fungi, algae, bacteria, or viruses. Microbial composition analyses were performed using both, R and MetaVir2 softwares.

Our preliminary results show that c. 190 potential RNA viruses are found in both lichen species, whereas the number of potential DNA viruses varied between them. Around 300 potential DNA viruses are associated to *C. mitis*, by contrast less than 10 are found in *C. stellaris*. The abundance of bacteria associated to reindeer lichens follows the opposite pattern. Samples of *C. stellaris* harbor 10 times more bacteria taxa than *C. mitis*. Regarding the microbial composition along a post-fire succession, we expected to find that, in the first stages of the postfire succession, abundance and diversity of microorganisms will increase but, decrease over time once the environmental conditions are stable.

OP10

Ecosystem scale evidence for the contribution of vanadium-based nitrogenase to biological nitrogen fixation

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Biological nitrogen fixation (BNF) is catalyzed by the enzyme nitrogenase, for which three isoforms have been described; the molybdenum nitrogenase and two alternative nitrogenases, the vanadium and iron-only nitrogenases. The low availability of Mo on land has been shown to limit BNF in many ecosystems. Alternative nitrogenases have been suggested as viable alternatives to cope with Mo limitation of BNF, however, field data supporting this long-standing hypothesis have been lacking.

Here, we elucidated the contribution of the vanadium nitrogenase to BNF by cyanolichens across a 600 km latitudinal transect in eastern Canadian boreal forests. We report a widespread activity of the vanadium nitrogenase which contributed between 15 to 50% of total BNF rates on all sites. Vanadium nitrogenase contribution to BNF was more robust in the northern part of the transect and at the end of the growing season. By including the contribution of the vanadium nitrogenase to BNF, estimates of new N input by cyanolichens increase by up to 30%, a significant change in these low N input ecosystems. Finally, we found that Mo availability was the primary driver for the contribution of the vanadium nitrogenase to BNF with a Mo threshold of ~ 250 $\mathrm{ng.g_{lichen}^{-1}}$ for the onset of vanadium based BNF.

This study provides evidence, at an ecosystem scale, that vanadium-based nitrogenase greatly contributes to BNF when Mo availability is limited. Given widespread findings of Mo limitation of BNF in terrestrial ecosystems, additional consideration of vanadium-based BNF is required in experimental and modeling studies of terrestrial biogeochemistry.

OP11

Toward the transportome of the lichen *Peltigera britannica*

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Background: Unlike most other members of the predominantly cyanobacterial lichen genus *Peltigera*, the lichen *Peltigera britannica* is tripartite, having a green alga (*Coccomyxa* sp.) as its primary photobiont and a cyanobacterium (*Nostoc* sp.) as a secondary photobiont housed in specialized structures called cephalodia in which atmospheric nitrogen is fixed. In tripartite lichen associations, nutrient exchange occurs both between the alga and the fungus and between the cyanobacterial partner and the fungus at separate interfaces. Accomplishing these nutrient exchanges requires an efflux step and an import step across the symbiotic interface, each needing a different transporter.

Objective: To define the 'transportome' of a tripartite lichen by identifying in *P. britannica* thalli the transporters hypothesized to mediate the flux of carbon and nitrogen between symbionts.

Methods: Genome and transcriptome data were employed to identify in *P. britannica* thalli the transporters mediating the exchange of sugar and sugar alcohols, ammonium, nitrate, amino acids, and other substrates. A subset of these transporters was cloned and expressed in heterologous systems, including yeast and *Xenopus* oocytes, for characterization.

Results: Multiple members of each transporter type were identified in the genomes of each of the symbionts. Two putative polyol transporters were identified in the genome of the lichenizing fungus. When expressed in *Xenopus* oocytes, neither was functional, necessitating additional assays.

Conclusions: Both yeast and *Xenopus* oocytes can be useful for heterologous expression of genes from lichen symbionts. Additional yeast mutants engineered to metabolize specialized substrates such as polyols are required.

OP12

The backbone of bryoinformatics: compiling, maintaining, and disseminating a critical taxonomic resource

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In order to precisely identify and communicate information about a plant species, biodiversity researchers must use its scientific name. However, determining the correct application of a scientific name is often a complex process that involves not only the name itself, but also how it relates to the many thousands of other published names. Two massive bibliographic works form the foundation of our current knowledge regarding the nomenclature of bryophytes, namely *Index Muscorum* and *Index Hepaticarum*. In more recent years these data have been updated, digitized and spread across the internet, but all of these copies are slowly becoming more and more outdated. It has become clear that a new initiative is needed, one that not only keeps the data current but also makes it more accessible to researchers who require it. Our experience as editors of bryophyte nomenclatural data in Tropicos has shown us that there is demand for a complete list of accepted names (with synonymy) that is well curated and updated regularly.

To this end, we have built a website that summarizes the nomenclatural and bibliographic data in Tropicos and presents them as comprehensive list of accepted bryophyte taxa. We would like this site to serve as the focal point for a renewed effort to maintain these data as an authoritative community resource. We feel that this list ought to reflect as much as possible the consensus opinion of experts that are most familiar with the taxa in question and encourage them to get involved in the process.

OP13

The fossil record of haplolepideous mosses and its potential for time-calibrating phylogenies

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Background: The moss fossil record is notoriously limited, with most fossils known from relatively recent Cenozoic deposits. Pre-Cenozoic moss fossils primarily consist of coalified compressions, which typically do not preserve anatomical details that are required for identification at even broad taxonomic levels. However, recent advances in bryophyte paleontology have significantly expanded the number of moss fossils that can be assigned to extant families.

Objectives: The objectives of the present study are to: (1) conduct a comprehensive review the fossil record of haplolepideous mosses (Subclass Dicranidae) in order to identify fossils that may be used to time-calibrate phylogenies, and (2) to present a summary of these results for phylogeneticists.

Methods: A database of haplolepideous moss fossils was compiled from a comprehensive literature survey. Using this database, fossils assignable to clades within Subclass Dicranidae were identified.

Results: The oldest haplolepideous mosses are gametophytes from the Early Cretaceous of Canada that can be assigned to the families Leucobryaceae and Grimmiaceae. Fossils assignable to extant genera in the families Dicranaceae and Rhabdoweisiaceae are found by the Late Cretaceous. The Eocene Baltic and Rovno ambers preserve additional diversity, including six extant genera assignable to four families (Leucobryaceae, Grimmiaceae, Rhabdoweisiaceae, Rhachitheciaceae) as well as the oldest reports of extant species of Dicranidae. Five extant genera assignable to five families (Calymperaceae, Leucobryaceae, Octoblepharaceae, Pottiaceae, Rhachitheciaceae) are also known from Miocene Dominican Amber.

Conclusion: Paleontological data document the diversification of Dicranidae since the Early Cretaceous, and provide minimum-age constraints for extant families, genera, and species of haplolepideous mosses.

OP14

Recent advances in Dicranidae phylogenetics

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The increasing availability of phylogenetic methods has been a fundamental contribution to the study of the haplolepideous mosses, the second largest moss lineage with 4000 species and a range of gametophytic and sporophytic traits. Our goal with this work was to summarize the latest studies and our own results, and thus set the stage for new research. Our analyses were based on mitochondrial and chloroplast markers of specimens representing 37 of the 38 haplolepideous moss families.

Phylogenetic reconstructions have shown that the Dicranidae tree comprises a basal grade of early diverging lineages, the proto- haplolepideous mosses, and a derived clade, the core haplolepideous mosses. Their relationships are not in line with the traditional ordinal classification and historically recognized main haplolepideous peristome types. Many lineages were newly recognized, especially within the proto-haplolepideous grade. Part of this newly recognized phylogenetic diversity was identified within weakly morphologically circumscribed taxa shown to be highly polyphyletic, e.g. Ditrichaceae s.l. and *Dicranella* s.l. In some cases, the morphology of overlooked gametophytic characters, e.g. rhizoidal tubers, appears to be informative of the relationships, however some lineages still lack known diagnostic morphological characters. In other cases, remarkable morphological patterns were confirmed not to correspond to monophyletic groups, e.g., the leucobryoid leaf.

Changes to the classification are required in all taxonomic levels to better describe the new findings on the evolutionary relationships, some of which were already formally proposed. Additionally, phylogenetic analyses also indicate many more haplolepideous moss taxa which demand further studies.

OP15

Peristome anatomy and ontogeny studies advance the understanding of evolution within the haplolepideous mosses

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The structural complexity of the peristome makes it a powerful feature for unraveling evolutionary events across mosses. In the monophyletic Dicranidae, peristome architecture has been found to hold informative signals across the group, with 13 species from the Dicranales, Grimmiales and Pottiales having been examined so far. The newly developed Technovit 7100® protocol for microtome sectioning of the sporophyte allows for a thorough histological investigation of the peristome, in its entirety and at different stages of development, using 3 µm stained sections. Anatomical features observed in longitudinal serially sectioned slices of the peristome and morphological features of the external surfaces of the structure observed using SEM techniques are combined for a global comparison of peristomes in this group of mosses. The observations of peristome features in 13 species from 8 families in the Dicranales, Grimmiales and Pottiales will be presented and discussed, in a phylogenetic context.

La complexité structurelle du péristome en fait un caractère efficient pour démêler les événement évolutifs chez les mousses. Après examen de 13 espèces de Dicranales, Grimmiales et Pottiales, l'architecture du péristome a révélé d'importants signaux informatifs au sein des Dicranidae monophylétiques. Le protocole Technovit 7100® récemment développé pour la coupe au microtome du sporophyte, permet une étude histologique approfondie du péristome dans son intégralité et tout au long de son développement, avec des coupes colorées de 3µm d'épaisseur. Les caractères anatomiques observés en coupes longitudinales sériées du péristome, et les données morphologiques de la surface de la structure observées en microscopie électronique à balayage, sont combinés pour une comparaison globale des péristomes dans ce groupe de mousses. Les observations des caractéristiques du péristome chez 13 espèces appartenant à 8 familles de Dicranales, Grimmiales et Pottiales seront présentées et interprétées dans un contexte phylogénétique.

Dicranidae in North Asia: cryptic species, clear species and higher level lineages unknown so far

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Recent integrative taxonomic revision of the Rhabdoweisiaceae (Fedosov et al., 2021), although mainly dealing with the circumscriptions of the genera, suggested the need of attention to the species-level taxonomy. Early diverged lineages like *Rhabdoweisia* and *Dicranoweisia* demonstrate high support for geographically isolated infraspecific groupings, so far believed to represent the same species. Although rather sparse, our sampling managed to revealed the presence of cryptic (or semicryptic) species in *Amphidium*, *Arctoa*, *Cynodontium*, *Symblepharis*, etc. and confirmed a wide Asian distribution of the species, recently estimated by Hedenäs. High morphological and molecular variability revealed within *Blindia acuta* and several species of *Ditrichum* might reflect the need for circumstantial species-level taxonomic studies.

Along with diversity, uncovered by phylogenetic studies, several bright records sound solely due to their remarkable morphology. In particular, a complete description of sporophytes of ‘*Dicranella’* cf. *staphyllina* will appear soon based on extensive specimens collected in Subarctic Siberia, the area where occurrence of this species can hardly be expected. Several previously unknown lineages of Aongstroemiaceae, Ceratodontaceae and Ditrichaceae s.l. also wait to be addressed. Recent study of *Dicranum* in north Asia resulted in descriptions of several species as new for science, but several questions remain pending and should be solved in the near future in the course of the Moss flora of Russia project. Our work was supported by RSF grant # 18-14-00121.

OP17

Elucidating the phylogeographic history and post-glacial demographic signatures of the moss *Racomitrium lanuginosum* Brid.

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The evolutionary history of plants in the Northern Hemisphere has been greatly influenced by the climatic oscillations of the Quaternary, mainly the Last Glacial Maximum (LGM). The moss *Racomitrium lanuginosum* is widely distributed in this region covering arctic, subarctic, and alpine environments. The study aims are to resolve the phylogeographic structure of this species, evaluate the genetic diversity and infer the impact of the LGM in the species distribution range. First, we used the ITS marker to resolve the deep relationships and estimate the divergence times using maximum likelihood and Bayesian analyses. Then, we applied the genotyping-by-sequencing method to infer the phylogeographic structure and migration events among genetic groups using single nucleotide polymorphisms (SNP). Finally, we obtain species records to conduct species distribution models in the present time, the LGM (22 kya), and the Last Interglacial period (110 kya).

Phylogenetic analyses based on ITS indicate the presence of three well-differentiated clades suggesting cryptic speciation. Molecular dating indicates that *R. lanuginosum* originated during the Pliocene (~5.3 Mya). Genetic structure based on SNP's revealed four groups dispersed across Alaska, Canada, Greenland, and Scandinavia, with active migration between them. Species distribution models indicate a reduction in the distribution area of *R. lanuginosum* during the LGM followed by post-glacial expansion. We hypothesized that one group of Alaskan samples represents refugial populations of the LGM. The phylogeography of *R. lanuginosum* was shaped by incomplete lineage sorting, admixture, and cryptic speciation. These events highlight the complex demographic history that plants experienced in sub-arctic and arctic regions.

OP18

Narrow species concept and the unsupported subgeneric delimitations in the molecular phylogeny of *Lejeunea* (Lejeuneaceae)

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Incongruence of morphospecies concepts and molecular phylogenies is not uncommon in liverworts and has increased significantly over the past decade. Morphological similarity does not necessarily indicate genetic similarity and multiple accessions of morphologically similar species may nest in different main lineages of molecular phylogenies. Morphology alone was shown to be inadequate to classify liverworts of the Lejeuneaceae due to their high level of homoplasy, which has been recognized as a problem in the establishment of natural relationships among their taxa. The subcosmopolitan genus *Lejeunea* includes between 200 to 300 species and is well known for its extensive morphological homoplasy. Molecular data are therefore essential for reconstructing relationships between taxa and establishing robust species hypotheses.

The current subgenera concepts of *Lejeunea* are based on morphology alone and are not supported by molecular phylogenies. We leveraged a recent molecular phylogeny of *Lejeunea* to demonstrate relationships among taxa from the molecular perspective and to reveal discrepancies to the traditional classification based on morphology. Morphological investigation includes 14 gametophytic characters, which were scored for each of the species in the present study. Those characters were selected due to their former use in sectional and subgeneric circumscriptions. Maximum likelihood and Bayesian inference were used for phylogenetic analyses of a dataset composed of two plastid markers and one nuclear marker.

Our investigations point to narrow species concepts and led to a deeper understanding of morphologically vague and controversial species complexes and also identified several new species.

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* This work is dedicated to the memory of the late Jochen Heinrichs, who contributed greatly in the field of the systematics and evolution of leafy liverworts.

Liverwort oil bodies : often overlooked beautiful and distinct cell features

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GeoFlora, Canada

It is well-known that liverwort oil bodies are useful features for identifying specimens -- when examined fresh. These beautiful and distinct features of liverwort cells are also elusive : they disappear a few days after being collected. As such, identification keys tend to treat oil bodies as a last resort, only when they are absolutely necessary. Generally, attempts are made to accommodate the bryologist who pulls out the specimen for identification after a field campaign (days or months or even years after collection). However, much information is lost when oil bodies are not prioritized as a crucial if not primary identification characteristic. For example, *Lophozia silvicola* and *Lophozia ventricosa* have been considered as a single species by some taxonomists.

Many keys rely on length : width ratios that are notoriously difficult to ascertain and can be quite variable within a single shoot. Yet *L. silvicola* has distinct biconcentric oil bodies that are evidently different from the simple oval ones of *L. ventricosa*. This presentation will present the variety of oil bodies found in Quebec liverwort taxa with an emphasis on their distinguishing shapes and sizes for identification.

OP20

Why do bryophyte gametophytes lack stomata?

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Background: Although stomata are the most important structural innovation in the evolution of land plants, their absence from gametophytes, save for Devonian fossils, has long remained mysterious. The recent realisation that moss sporophytes are homeohydric prompts a reappraisal of this enigma.

Objectives: We set out to explore features of gametophytes that might preclude the presence of stomata.

Methods: We used cryo-scanning electron microscopy and hypertonic sucrose to investigate bryophytes under different hydration states.

Results: Whereas plasmolysis in hypertonic sucrose is universal in vascular plant and bryophyte sporophytes, the poikilohydric gametophytes of bryophytes undergo cytorrhysis followed by full recovery in water thus mimicking their natural behaviour during desiccation and rehydration. Morphologically we see the repeated evolution in mosses, thalloid and leafy liverworts, hornworts and pteridophyte gametophytes, of unistratose lamellate structures whose very construction precludes stomata as does the absence of gas-filled intercellular spaces. Reversible cytological changes during dehydration, including depolymerisation of the cytoskeleton and rounding of organelles and vacuolar shrinkage are remarkably similar to those in desiccation-tolerant streptophyte algae. In contrast to the inflexible guard cell walls and fixed apertures in bryophyte stomata, extreme gametophytic wall pliability is geared to cytorrhysis.

Conclusions: Future research should focus on differences in cell wall composition associated with plasmolysis versus cytorrhysis. A reappraisal of the possible loss of sporophytic stomata in liverworts including highly structured placentas in basal clades, the presence of a stomatal construction toolkit in the capsule walls of *Haplomitrium* and plasmolysis of liverwort setal cells all hint at a more complex ancestry.

Rotation angle of apical cell division plane controls spiral phyllotaxis in mosses

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Phyllotaxis in vascular plants is produced at a multicellular meristem, whereas bryophyte phyllotaxis emerges from a single apical stem cell (AC) that is embedded in a growing tip of the gametophyte. An AC is asymmetrically divided into itself and a single `merophyte', producing a future leaf and a portion of the stem. Although it has been suggested that the arrangement of merophytes is regulated by a rotation of the division plane of an AC, the quantitative description of the merophyte arrangement and its regulatory mechanism remain unclear.

To clarify them, we examined three moss species, *Tetraphis pellucida, Physcomitrium patens*, and *Niphotrichum japonicum*, which exhibit 1/3, 2/5, and 3/8 spiral phyllotaxis, respectively. We measured the angle between the centroids of adjacent merophytes relative to the AC centroid on cross-transverse sections. At the outer merophytes, this divergence angle converged to nearly 120° in *T. pellucida,* 136° in *N. japonicum*, and 141° in *P. patens*, which was nearly consistent with phyllotaxis, whereas the divergence angle deviated from the converged angle at the inner merophytes near an AC.

A mathematical model, which assumes scaling growth of AC and merophytes and a constant angle of division plane rotation, quantitatively reproduced the sequence of the divergence angles. This model showed that shape and the centroid position of an AC inevitably result in the transient deviation of the divergence angle. As a result, the converged divergence angle was equal to the rotation angle, predicting that the latter is a major regulator of the phyllotaxis diversity in mosses.

Somatic embryogenesis of weevil-resistant phenotypes of Sitka spruce

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A somatic embryogenic system was created using material from the Sitka spruce (*Picea sitchensis*) breeding program for resistance to the white pine weevil (*Pissodes strobi*) of the British Columbia Ministry of Forests, Lands, Natural Resource Operations and Rural Development. Embryogenic lines were derived from controlled crosses of parental genotypes previously ranked for the abundance of three physical traits: sclereid cells, constitutive resin canals and traumatic resin canals. Seeds from open-pollinated and controlled crosses of weevil-resistant and control populations were used to induce somatic embryos.

Of 135 genotypes, 88.1% produced mature embryos. Nearly all genotypes germinated. However, the overall conversion rate of somatic embryos was only 5.5%. We used a cryopreservation method developed in house that did not use dimethyl sulfoxide. Seedlings were acclimated in a greenhouse before planting in soil. Having reached a dozen years of age, the phenotypes of these trees were assessed.

After trees were allowed to grow for a decade, we dissected and sectioned materials and found that we were able to confirm high sclereid abundance, typical of resistant phenotypes, in apical leaders of trees derived from somatic embryos multiplied from seed of resistant breeding stock. The initial investment in highly skilled labour is warranted, if the longer term possibilities of having unlimited material for testing can be exploited.

OP23

Using computational models to investigate vein patterning and programmed cell death in lace plant (*Aponogeton madagascariensis)* leaves

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Programmed cell death (PCD), the genetically encoded destruction of cells, is essential in regulating several activities required to maintain health and function in both plants and animals. The lace plant provides a unique example of developmental PCD, which generates perforations in a regular lattice pattern over the surface of its leaves. These perforations develop in a predictable manner initiating in the center of areoles of young leaves and expanding towards the surrounding vasculature. Treating lace plants with auxin transport inhibitors or antioxidants yields leaves with fewer perforations, indicating their involvement in PCD signaling pathways. The objectives of this research are twofold; create computational models to (1) analyze vein patterning and perforation formation when treated with known regulators, and (2) predict which cells will undergo PCD during early leaf development.

Leaves were harvested from sterile cultures and quantitative data was collected via light microscopy to construct computational models. The number of cell layers from perforation area to veins, area of areoles and number of perforated/nonperforated areoles were collected for model construction. Preliminary data show perforations stop 4–5 cell layers away from veins, establishing a boundary during early leaf development that persists until maturity. To elucidate the role of regulators such as auxin in lace plant PCD, leaves from auxin-inhibitor-treated sterile cultures will be harvested and analyzed to construct models. This research will provide insight on how different regulators of PCD are integrated to precisely coordinate cell death, and has significance to medical research attempting to halt PCD in certain scenarios.

OP24

Reversing extinction trends: new uses for (old) herbarium specimens to accelerate conservation of threatened species

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Although often not collected specifically for the purposes of conservation, herbarium specimens can offer sufficient information to reconstruct parameters needed to designate a species as ‘at-risk’ of extinction. In this seminar, I illustrate how historical records of rare species can, in conjunction with advances in species distribution modelling, help us effectively estimate the scope and severity of the threat of climate change in rare plant species of Canada. These estimates are especially relevant to rare species in northern ecosystems that have previously been assumed to experience reduced or no threats from human activities due to their remote habitats.

Herbarium specimens can also offer further information on the co- occurrence of cold-adapted species in southerly habitats, as well as their pollination and fruiting success. These pieces of information can offer valuable insight on how to halt the decline of these species by improving our ability to mitigate threats and execute successful species recovery. Collected specimens in Canada have largely been used to fill knowledge gaps in systematics, range extent, and past genetic diversity. This limited use represents untapped potential and I offer ways to increase our use of collected material to foster species recovery and reverse current extinction trends.

OP25

From genes to traits and ecosystems: reconstructing the evolution of extended phenotypes in *Sphagnum* (peat moss)

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Plants in the genus *Sphagnum* (peat moss) are the dominant biotic features of boreal peatlands that store roughly one-quarter of Earth's terrestrial carbon. Peat mosses are ecosystem engineers and create the peatlands that they inhabit through the accumulation of peat, or partially decayed biomass, and the functional traits underlying this extended phenotype. Interspecific trait variation promotes niche differentiation through the creation of ecological gradients along which species sort within communities. One prominent gradient relates to height-above-water-table wherein some species produce hummocks elevated above the water table, while others live in hollows at or near the water table. However, it is unclear how these traits evolved during *Sphagnum* diversification, to what extent natural selection produced functional trait variation, and which genes might contribute to such phenotypes.

I sought to better understand how genes can scale to ecosystems through plant functional traits using *Sphagnum* as a model system. Meta-analysis was used to demonstrate that variation in traits related to growth, decomposability, and litter biochemistry is phylogenetically conserved in *Sphagnum*, suggesting a genetic basis for these traits. Using field experiments, I found that selection favors different levels of decomposability corresponding to optimum niche. Genomic data were then used to show that genes involved in cell wall biosynthesis are related to decomposability and were among the targets of selection during the evolution of hummock and hollow lineages. These results demonstrate evolution of ecosystem engineering via selection on an extended phenotype, of a fundamental ecosystem process, and one of the Earth's largest soil carbon pools.

OP26

Genome evolution and sporophyte complexity in the moss family Funariaceae

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Whether evolutionary trajectories leading to a particular function or morphology are predictable is a fundamental question of evolutionary biology. Yet, there is little consensus on this issue and experimental evidence is contentious. The phenomenon of convergent evolution, the repeated evolution of traits in independent lineages, provides ideal replicates to test for constraints on the trajectory of the evolutionary processes. We investigate the genetic bases of parallel morphological evolution in a closely related group of moss species, the family Funariaceae. Fitting the classical example of parallel evolution, a reduced sporophyte phenotype has evolved multiple times independently in the funarioid mosses.

To understand the molecular mechanisms underlying their divergent sporophyte morphologies, we use the two species system *Funaria hygrometrica – Physcomitrium patens*. We carried out comparative transcriptomic analysis to identify genes with divergent expression dynamics throughout sporophyte development in the two species. In addition, we generated a chromosome-scale assembly of the *F. hygrometrica* genome to facilitate research on the role of structural variations of the genome in the evolution of sporophyte morphology.

Our data suggests that divergent sporophyte morphologies are mainly achieved by heterochronic expression of conserved developmental regulators. However, we also found that species-specific genes are significantly enriched among genes preferentially expressed during sporophyte development. Despite a shared history of ancient whole genome duplications and high collinearity, the genomes of *F. hygrometrica* and *P. patens* differ significantly in size and repetitive element content and composition, which raises the question to which extent genome structure is contributing to the differing sporophyte morphologies.

The genomic history of *P. patens*

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In 2008, *Physcomitrium patens* (previously *Physcomitrella patens*: Rensing et al. 2020) was the first fully sequenced non-seed plant model organism (Rensing et al. 2008) and within the first five sequenced plants. Exactly 10 years later the newest release was published. Over 2000 unordered scaffolds could be assembled into 27 chromosomes (Lang et al. 2018). Two rounds of whole genome duplication events and unusual distributions of transposable elements were found. Most of the analyses shown in these publications were performed on the *P. patens* ecotype Gransden. Recently we could show that Gransden lab-grown pedigrees accumulated hundreds of somatic mutations (Haas et al. 2020). We will report on the peculiarities of the genome structure and on natural and somatic mutations.

Haas, F.B., Fernandez-Pozo, N., Meyberg, R., Perroud, P.-F., Göttig, M., [..], Rensing, S.A. (2020) Single nucleotide polymorphism charting of P. patens reveals accumulation of somatic mutations during in vitro culture on the scale of natural variation by selfing. Front. Plant Sci. 11: 813.

Lang D, Ullrich KK, Murat F, Fuchs J, Jenkins J, Haas FB, [..], Rensing SA (2018) The Physcomitrella patens chromosome-scale assembly reveals moss genome structure and evolution. Plant J 93(3): 515–533.

Rensing SA, Goffinet B, Meyberg R, Wu SZ, Bezanilla M (2020) The Moss *Physcomitrium* (*Physcomitrella*) *patens*: a model organism for non-seed plants. Plant Cell 32: 1361–1376.

Rensing, S.A., Lang, D., Zimmer, A.D., Terry, A., Salamov, A., Shapiro, H., Nishiyama, T., [..], Quatrano, R.S. and Boore, J.L. (2008) The *Physcomitrella* Genome Reveals Evolutionary Insights into the Conquest of Land by Plants. Science 319: 64–69.

OP28

Whole genome duplication and reticulate evolution in the *Physcomitrium pyriforme* species complex

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Whole genome duplication (WGD) is a mechanism critical to evolutionary change and speciation across the plant tree of life. Changes to genomic structure resulting from WGD may be sufficient to produce reproductive isolation from progenitor populations. Both conspecific genome doubling (autopolyploidy) and WGD following hybridization (allopolyploidy) may result in morphologically distinct lineages. The moss *Physcomitrium pyriforme* is a widespread species complex found across North America and Europe that exhibits substantial morphological variation, evident in the recognition of 29 synonyms. We hypothesize that this species complex comprises numerous cytotypes resulting from repeated WGD events. We sampled over 200 populations of *P. pyriforme* across its North American and European distribution and use a target capture approach to sequence 648 genes to construct a phylogenetic tree establishing relationships among *P. pyriforme* populations, as well as identify allopolyploid populations by assessing heterozygosity across genes. We find evidence for four clades within *P. pyriforme* as well as the presence of at least eleven allopolyploid populations. Here we utilize the significant genetic resources generated by target capture sequencing, as well as a novel approach to subgenome allele phasing, to reconstruct the reticulate evolutionary history of allopolyploid lineages by identifying hybrid progenitors. WGD plays a substantial role in the evolution of the *P. pyriforme* complex and provides preliminary evidence for cryptic speciation via polyploidy.

OP29

Testing for Cryptic Species in *Physcomitrium pyriforme* using target capture sequencing of 800 nuclear genes

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Physcomitrium is a moss genus belonging to the family Funariaceae. This moss genus has a cosmopolitan distribution, and several known methods of speciation, current evidence supporting allopolyploidy and hybridization. *Physcomitrium pyriforme* is a moss species belonging to this genus, which range is located in Africa, Europe and North America. Prior evidence supports a rapid radiation within this species complex and suggested that *Physcomitrium pyriforme* may be non-monophyletic with substantial within-species phylogenetic structure. Cryptic species are also a concern among these mosses, which are difficult to distinguish via morphological characters that may be evolutionarily labile. Our results showed that samples of *Physcomitrium* sorted into three predicted areas of distribution: Africa, Europe and North America, with multiple clades within each geographic region suggesting the possibility of cryptic species.

We present new target capture sequencing results for over 200 new specimens collected with assistance from the PhyscoHunt iNaturalist citizen science project in North America and Europe. Using a combination of phylogenetic inference, principal coordinate analysis (PCA) and admixture analysis, we 1) test whether phylogenetic clustering in *P. pyriforme* is associated with a history of reproductive isolation, 2) characterize the extent of ongoing geneflow among clusters, and 3) identify biogeographic patterns within and among clusters.

OP30

Apospory-induced whole genome duplication triggers immediate shifts gene expression in the moss *Funaria hygrometrica*

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Autopolyploidy is widespread among plants, with 10–20% of extant species harboring polyploid populations. While such genome doubling likely serves as a significant speciation mechanism, the immediate consequences on genome architecture and gene expression are poorly explored in part due to the lack of a suitable model system. Here we characterize the transcriptomic profile of first generation autopolyploids, that is immediately following genome doubling via apospory. Our model is the moss *Funaria hygrometrica*, for which we generated diploid gametophytes from homozygous diploid sporophytes.

Comparisons of expression profiles of three replicates of isogenic wild haploid gametophytes, wild diploid sporophytes and F1 synthetic aposporous diploid gametophytes reveals that the transcriptomes of aposporous gametophytes differ consistently and thus predictably from their haploid counterparts. They express genes otherwise specific of sporophytes, and genes not (yet detected or) expressed on either wild generations, but also in the silencing of genes unique to the haploid gametophytes or expressed in both wild generations. Furthermore, the aposporous gametophytes differ in the degree of expression of genes, expressed in either the wild gametophyte or sporophyte or both. While these transcriptomic patterns of the aposporous gametophytes are in part shaped by inheritance of development pathways seemingly irreversibly initiated in the sporophytes other mechanisms must be sought to explain novel expressions and silencing.

These results highlight the potential of ploidy shifts in triggering innovation even in the first generation, and points to epigenetic mechanisms shaping gene expression in newly formed polyploids.

OP31

Effects of elevation and disturbances on the diversity of bryophytes in laurel forests of Madeira island

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The laurel forest of Madeira island is a bryophyte diversity hotspot. On Madeira, climate change scenarios predict a precipitation decrease of about 30% until 2100. Moreover, not only will the precipitation sum change, but it is likely that seasonal climatic conditions will also change in the future with longer drought periods or a decrease of fog and mist frequency in combination with increasing temperatures. These changes might have a strong negative impact on bryophyte diversity. Actually, many specialized species depend on the constantly humid conditions of the closed laurel forest at intermediate elevations or on light and moist conditions in the more open tree-heath forests at high elevations, for example many endemic bryophytes and other drought-sensitive species such as many liverworts.

In particular endemic bryophyte species might suffer from future climate change on Madeira, as suitable habitats might decrease by 62–87% depending on the species. According to the latest European Red List of bryophytes, all endemic species of Madeira were considered as threatened (three Critically Endangered, six Endangered, and one Vulnerable), and 80% of them occur in the laurel forest.

Our findings indicate the need for a strict protection status of the laurel forest on Madeira island to minimize human-related disturbances, for the development of management measures that could mitigate climate change effects by maximizing habitat suitability and for the implementation of species conservation programs to prevent future extinctions, in particular of endemic species.

OP32

Vegetation structure in boreal peatlands of North-western Québec

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Located in the Canadian boreal forest, the Eeyou Istchee James-Bay territory (EIJB) of North-western Québec is largely occupied by peatlands, up to 40% in some sectors. To date, only one extensive study of EIJB peatland vegetation exists, focusing mainly on tracheophytes. We seek to better understand today's distribution of bryophyte and tracheophyte species in EIJB peatlands and their interactions with environmental factors. Vegetation and environmental data were obtained from 36 peatlands in three sectors along a 1000 km transect. Vegetation communities were classified into groups by species composition and verified by randomisation.

Multivariate analyses established correlations between environmental data and identified vegetation groups. Results show that the poor fen group exhibits the greatest variation in species composition. While many species are common, woodland species such as *Blepharostoma trichophyllum, Calypogeia integristipula, Campylium stellatum, Clintonia borealis, Lepidozia reptans, Obtusifolium obtusum, Sphagnum squarrosum*, and *Syzygiella autumnalis* tend to be absent in poor fens while the more hydric environment of this group favours species such as *Carex* spp., *Drosera anglica, Eriophorum* spp., *Menyanthes trifoliata, Pallavicinia lyellii, Sphagnum riparium, S. tenellum,* and *S. venustum*. Our data also show that water table depth is the most important determining factor for peatland vegetation community composition, while water chemical composition is little correlated with community composition.

These results show how plant peatland communities and hydrology are intricately related in EIJB and that this interaction should be taken into consideration in developmental decisions, especially in the current situation of a changing environment, both climatic and socioeconomic.

OP33

Dispersal and taxonomy in disjunct oceanic-montane liverworts

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The globally rare mixed northern hepatic mat community is dominated by large, charismatic liverwort species, most of which have highly disjunct distributions consistent with the very scattered occurrence of the habitats in which they are found, such as oceanic-montane heath (OMH). These habitats are defined by conjunctions of topographic and climatic factors, including continually high levels of precipitation and a seasonally relatively stable temperature regime. Climate modeling suggests that they may shift northwards or be significantly modified, while populations of many species in Scotland have apparently lost the ability to reproduce sexually and may be at their distributional climatic limit. Understanding the origins, taxonomy and dispersal biology of OMH species is therefore key to their conservation.

Our ongoing research is examining genotypic diversity, taxonomic boundaries and biogeographical origins in a number of OMH species, including *Anastrophyllum alpinum*, *Plagiochila carringtonii* and *Adelanthus lindenbergianus*. Microsatellite markers were used to investigate genetic differences between six populations of *Anastophyllum alpinum* from Nepal and Scotland. A nested allele distribution of Scottish populations within Nepalese, and lower genetic diversity of Scottish populations, indicated that Scottish populations likely have their origins in the Sino-Himalaya, with disjunct populations certainly representing the same species.

Work is in progress using chloroplast and nuclear markers to investigate the taxonomic identity of Scottish populations of *Plagiochila carringtonii* and A*delanthus lindenbergianus* in relation to their disjuncts in the Sino-Himalaya, and in the Americas and South Africa respectively, with preliminary results pointing to a diversity of biogeographic and taxonomic patterns among different OMH species.

OP34

Can species distribution modelling improve climate threat assessments for bryophytes-at-risk in Canada?

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British Columbia is a hotspot for bryophyte biodiversity in Canada. Assessments of the impact of future climate change on bryophytes-at-risk based on widely used IUCN methodologies typically incorporate regional scale climate data and generalized qualitative predictions. *Bartramia halleriana* (Haller's Apple Moss) — assessed as Threatened in Canada — was chosen as a test species to develop a framework to quantitatively predict the impacts of future climate on species with low numbers of occurrences and/or occupying climatically heterogeneous environments such as the Rocky Mountains, where *B. halleriana* occurs. We used the ensemble of small models (ESM) species distribution modeling technique to predict differences between areas of climatically suitable habitat now and under the future climate change scenarios RCP 4.5 and 8.5 for 2085.

We hypothesized that climatically suitable habitat will shift upslope and northward in the future, and that range size will contract. Projected models support these hypotheses and indicate that the northward shift in suitable climate will also expand northeastward under both scenarios. Challenges to modelling the current distribution of *B. halleriana* include limited published microclimatic data, a paucity of information describing species-specific ecological requirements, and poor coverage of high-resolution environmental data. We intend to test the efficacy of the framework for other bryophytes-at-risk in Canada and will report on our progress during the symposium.

OP35

Bryophytes are predicted to lag behind future climate change despite their high dispersal capacities

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The extent to which species can balance out the loss of suitable habitats due to climate warming by shifting their ranges is an area of controversy. Here, we assess whether highly efficient wind-dispersed organisms like bryophytes can keep-up with projected shifts in their areas of suitable climate. Using a hybrid statistical-mechanistic approach accounting for spatial and temporal variations in both climatic and wind conditions, we simulate future migrations across Europe for 40 bryophyte species until 2050.

The median ratios between predicted range loss versus expansion by 2050 across species and climate change scenarios range from 1.6 to 3.3 when only shifts in climatic suitability were considered, but increase to 34.7–96.8 when species dispersal abilities are added to our models. This highlights the importance of accounting for dispersal restrictions when projecting future distribution ranges and suggests that even highly dispersive organisms like bryophytes are not equipped to fully track the rates of ongoing climate change in the course of the next decades.

OP36

Comparison of bryophyte cultivation in three different types of substrates

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Bryophytes are recognized to be difficult for cultivation and maintenance in glasshouse condition. This preliminary study aims to assess suitable growing substrates, cultivation method, and means for evaluating growth. Three acrocarpous mosses (*Hyophila involuta*, *Barbula consanguinea*, and *H. apiculata*) that commonly thrive on laterite soil (iron-rich soil) in the vicinity of Kanchanaburi Campus of Mahidol University were chosen to compare the growth without extra nutrient supply during two months. The three types of substrates were native soil where mosses were collected, commercial sand, and commercial peat moss. The growth was measured every second week using three indices i.e. growth area, the number of new plants, and wet weight.

Our results showed that the most suitable substrates for three mosses ranked by three indices were sand, native soil, and peat moss, respectively. Mosses can be successfully grown on sand and laterite soil if kept out of the direct light source and moist. Determining the number of new plants developed from propagules is the most reliable natural marker for growth in our mosses. Visual assessments of plant health showed that even spraying regularly with water did not prevent scorching and desiccation. The adverse impact of scorching and desiccation on plant growth is worst in peat moss. This study suggests that peat moss is not a suitable substrate for cultivating terricolous mosses because of its low pH condition. It would be feasible to use sand as media for growing, propagating, and maintaining mosses as experimental material in the future.

Intra- and interspecific interaction during early stages of moss development in vitro

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Interactions between moss species in their earliest growth stages have received little attention and it remains unclear if there is interspecific competition during spore germination and gametophyte development. Interspecific interaction between six common bryophyte species (*Atrichum undulatum, Byrum argenteum, Ceratodon purpureus, Funaria hygrometrica, Hypnum cupressiforme and Leptobryum pyriforme*) was assessed in in vitro conditions, where spores of these six species were sowed on agar plates and their germination and growth compared and evaluated.

Besides investigating whether spore germination and protonemal growth are affected by interspecific interaction, another aim was to check if there was a priority effect dependent on the first colonizer and if spore germination and gametophyte formation is density-dependent in the single-species. Spores from fully-grown sporophyte specimens collected in nature were sterilized and sown on agar plates in a nested design, in three treatments: (1) as single species cultures (controls); (2) as pairwise species cultures inoculated simultaneously); and (3) with a time lag of 20 days between the first and the second species. Data on the time needed for spore germination, germination rate, time needed for gametophyte differentiation, gametophores per germinated spore, and average diameter of colonies were collected.

Strong pairwise interactive effects when sowing spores of different species simultaneously or with the delay of 20 days were noticed, suggesting the presence of interspecific competition and priority effects. Resource competition and interference competition (allelopathy or chemical interference) can act simultaneously and analytical chemistry studies are currently undertaken in identifying potential bryophyte-released allelochemicals.

OP38

Predictors of epiphytic bryophyte and lichen biomass and hydrologic impact across a boreal- temperate ecotone

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Epiphytic bryophytes and lichens can be an important component of forest ecosystems. Although some estimates of the biomass and potential impacts of bryophytes and lichens exist, these have (quite understandably) often focused on ecosystems with visibly large epiphyte loads. While important, these estimate may not be representative of many other forest types.

We surveyed epiphyte communities at 82 sites across Minnesota (USA). This state covers the intersection of four North American biomes (Eastern Temperate Forest, Boreal Forest, Prairie and Aspen Parkland), providing a multi-regional perspective despite the limited geographic scope. We combine field estimates of trunk, canopy (inferred from twig litter) and ground cover with measurements of specific mass and water-holding capacity to calculate forest level epiphyte biomass and water-holding capacity (WHC). Site (e.g. forest type, dominant phorophyte, physiography, etc) and community characteristics (species richness) were used to identify the best predictors of epiphyte properties.

We found a very high variation in epiphyte mass, reaching ~1 ton/ha but often far less. Potential WHC was mostly much lower than reported in wetter forests (mostly 0.1–0.2 mm/ha) but occasionally quite significant. Forest type was a more important predictor than geographic location alone, reflecting the importance of phorophyte identity in determining epiphyte community properties. Lichens and bryophyte showed contrasting responses to latitude and climate. Identifying predictors of epiphyte biomass across forest types and biomes is important to modeling impacts of future changes in climate.

The importance of moss shoot and colony traits on their desiccation dynamics

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Mosses lack the ability to actively regulate their water content. Consequently, they depend on an intermittent water supply that conditions their metabolic activity. Moisture-keeping strategies are crucial for plant survival specially in the Mediterranean where plants are subject to long drought periods. However, we know little about the influence of shoot and colony traits on desiccation dynamics.

In our study we subjected the colonies of two Mediterranean mosses (*Syntrichia princeps* and *Pleurochaete squarrosa*) to a 60% density reduction in four gradual steps. In each step we measured desiccation rates, colony morphology (weight, height, density, number of shoot, shoot overlap), and shoot traits (length and number of leaves).

Our results show an acceleration of the desiccation rate related to density reduction that varies with the species and the morphological traits. These results highlight the importance of these traits, and especially colony density for the maintenance of moisture.

Are hornworts delicate plants? Contrasting effects of desiccation on gametophytes and sporophytes of hornworts

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Desiccation tolerance (DT) is the ability of an organism or structure to completely dry and subsequently survive from that air-dry state. DT may have played an important role during early land colonization by plants. Hornworts are excellent models along bryophyte lineages to examine desiccation effects as they have contrasting life histories (i.e. niches: epiphytes (e.g *Dendroceros*) and non-epiphytes; spores: green and non-green) that may be associated with DT. Here we show the main effects of DT on gametophytes and spores of four genera of hornworts (*Dendroceros*, *Nothoceros*, *Phaeoceros* and *Anthoceros*), exposed to different relative humidity, duration dry, and rate of rehydration treatments.

All DT treatments affected chlorophyll fluorescence (*Fv/Fm*) of the gametophytes, with species-specific responses: *Dendroceros crispatus* and *D. crispus* performed better than *Phaeoceros carolinianus* and *Nothoceros vincentianus,* including the fast recovery of *Fv/Fm* values after rehydration. Spore survival and sporeling size differed among the species examined (in general, with the highest survival in *P. carolinianus* and lowest in *D. crispatus*), with no effect of duration dry on survival. Our data evidenced that the gametophytes of epiphytic species (*D. crispatus* and *D. crispus*) were more efficient at withstanding drying effects under different conditions. Conversely, the capacity of non-green spores of *P. carolinianus*, *Anthoceros lamellatus,* and green spores of *D. crispus* to support DT. Desiccation tolerance responses, gametophyte and spore longevities highlight important trade-offs of spore dispersal and fast colonization (e.g. *Dendroceros*), and the spore banks of *Phaeoceros* and *Anthoceros* species.

The phenology of bryophytes — revisited after 150 years through eDNA

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Bryophyte spores are generally dispersed by wind, forming a spore cloud that differ in composition throughout the year due to the spore dispersal phenology of individual species. Spores have few traits that allow identification when air-borne, therefore sporulation phenology has thus far been carried out by observation of sporophyte maturation in situ – a topic largely untouched since the work of Arnell in the late 1800s.

In this project, we investigate the phenology of sporulation using eDNA (environmental DNA) originating from air filters collected by the FOI (Swedish Defence Research Agency) to monitor radioactive fallout. Filters were collected weekly since the 1960s at a weather station in Kiruna, northern Sweden. The project Swedish Biodiversity In Time and Space (SweBITS) sequenced a subset of these filters, seasonally restricted to periods with air temperature above 0°C, creating a large data base covering samples between 1974–2009. Reads match various kinds of organisms, including a high proportion of bryophyte spores.

Here we present preliminary data for a few chosen genera, for which we ask: (1) What are their main sporulation periods, and can we identify peaks of spore spread? (2) Can we see any changes in sporulation phenology during the time span? (3) Can we detect shifts in sporulation phenology between our modern dataset and the reports by Arnell in the 1800s? (4) Can we identify possible environmental and climatic causes for phenological shifts? We discuss methodological problems and their solutions, potentials and limitations of this kind of unusual datasets.

OP42

Biome evolution in subfamily Cercidoideae (Fabaceae)

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Studies show that some plant lineages have a tendency to remain within the same biome over time (biome conservatism), whereas others appear to have the ability to adapt more easily to new biomes (biome shifts). Subfamily Cercidoideae includes 13 genera and approximately 335 species that are found in many biomes around the world, particularly in the tropical regions of South America, Asia and Africa. The main objective of this project is to study biome shifts in a phylogenetic context, determining the extent to which there have been biome shifts or biome conservatism throughout the evolution of Cercidoideae lineages.

After establishing an updated and community-verified species list including all known synonyms and their accepted names, occurrence records were downloaded from the *Global Biodiversity Information Facility* (GBIF) and other herbarium databases. These records were then subject to an extensive data cleaning process in order to match the occurrences to their accepted names as well as to remove doubtful occurrences such as non- vouchered records, cultivated records and country centroids. Species distribution maps were produced in order to attribute individual species to biomes.

Based on previously generated phylogenies, we will be evaluating the number of biome shifts across the phylogeny. Preliminary analyses suggest multiple shifts, in particular between pairs of adjacent biomes such as the savanna and rainforest biomes, as well as the succulent and rainforest biomes. Ultimately, this approach will help better understand the evolutionary dynamics of plant species distribution through space and time.

OP43

Sphagnum traits and growth in a changing world

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Different *Sphagnum* species' growth responses to changes in the environment will affect the development of peatlands as sphagna maintain and engineer peatlands in the northern hemisphere. I will present results from a couple of different studies about *Sphagnum* production and traits, and discuss what is needed for continued *Sphagnum* and peat growth.

In one study with >45 scientists and 100 peatlands across the Holarctic, we analysed the importance of previously proposed abiotic and biotic drivers for *Sphagnum* growth (climate, N deposition, water table depth, and vascular plant cover). Precipitation and temperature were among the most important factors, but the species' (*S. magellanicum* s.l. and *S. fuscum*) responses differed. In another study - a lab experiment with manipulated water level, most hummock species had a relatively high water-loss resistance, and we argued that such species, e.g. *S. magellanicum*, are able to maintain a high water content at drawdown by storing large amounts of water when water availability is high.

The results from the Holarctic sampling effort showed that *S. magellanicum* s.l. – relatively large, loose and wet growing compared to *S. fuscum* – had a stronger response to climatic variation than *S. fuscum*. This implies faster length growth in *S. magellanicum* in a warming climate as long as precipitation is maintained. However, *S. magellanicum* with its high water-loss resistance, can also grow dry under a canopy, and I speculate it has an advantage in relation to other sphagna also in warmer and drier scenarios, as drier mires will result in more wooded peatlands.

Heterosis as a possible explanation of successful niche occupation in allodiploid Sphagnum species

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The genus of peatmosses (*Sphagnum*) is known for its comparably high number of diploid and triploid species within the class of Bryophyta. Most of these species seem to be of allopolyploid origins caused by hybridization. This study aims at the questions whether allodiploid Sphagna show better growth performance caused by heterosis effect and which ecological drivers might cause the successful establishment of those hybrids in their natural habitats. In total 13 species of 5 hybrid complexes (including the diploid *S. majus*, *S. jensenii*, *S. troendelagicum*, *S. russowii* and *S. skyense* plus the respective parental species) collected from at least three regions (Ireland, Scotland, Germany, Norway, Western and Eastern Siberia) have been included in a newly developed 'single head approach' growth experiment under controlled climate and nutrient conditions. Productivity has been used as a measure of competitional strength.

The results showed that the diploids *S. majus* and *S. jensenii* surpassed their respective parental species in terms of productivity and display clear effects of heterosis. The other diploid mosses showed intermediate to slightly improved productivities in comparison to their parental species. In addition, allodiploid sphagna tend to have an expected growth advantage under more nutrient-rich conditions, which corresponds to their naturally occupied habitats. This way diploid species are able to compete against or even outcompete the parental species in their natural habitat despite an often assumed reproductive disadvantage caused by the hybrid origin.

OP45

Nitrogen in bogs — it's complicated

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New insights into N cycling processes in bogs derives from research in bogs of northern Alberta, Canada, where background bulk N deposition is <2 kg/ha/yr. In these bogs, net N accumulation rates in peat exceed N deposition inputs. Biological N_2 fixation, mainly by methanotrophs associated with surface *Sphagnum*, is by far the major source of new N, and is sufficient to support annual net primary production (NPP) of *Sphagnum* and vascular plants combined. Net N mineralization rates in surface peat, are quite low, with net dissolved organic N production dominating over net NH^{4+}–N and NO^{3-}–N production. Field and laboratory N fertilization experiments have shown little evidence that *Sphagnum* (NPP) is N-limited, while shrub NPP (above and belowground) is stimulated by N addition.

Surface peat has a remarkable ability to retain atmospherically deposited N, even at high deposition rates. As experimental N addition increases, N_2 fixation is inhibited. N_2-fixation incorporates N into microbial biomass as organic N; for this N to become available for *Sphagnum* or vascular plants, it must be mineralized, with *Sphagnum* growth likely taking up most of this mineralized N. As N addition increases, the ratio of organic N inputs (products of N_2 fixation) to inorganic N inputs (from deposition) progressively decreases. Pulses of inorganic N inputs in sporadic rain events may deliver inorganic N into the rooting zone of vascular plants, stimulating shrub NPP. A major consequence of stimulated shrub NPP is an increase in shrub cover, which may lead to a decrease in *Sphagnum* cover resulting from shading.

OP46

Sphagnum peat moss thermotolerance is modulated by the microbiome

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Climate warming is expected to negatively impact carbon accumulation in peatlands and alter nutrient cycling, however peatland resilience to climate warming may depend, in part, on *Sphagnum*-microbiome associations. The ability of the microbiome to rapidly acclimatize to warming may aid *Sphagnum* exposed to elevated temperatures through host-microbiome acquired thermotolerance. Here we first examined the role of field warming in conditioning the *Sphagnum* microbiome and then the ability of the thermally conditioned microbiome to influence acclimation of *Sphagnum* growth to elevated temperatures. We first isolated microbiomes from *Sphagnum* within the Spruce and Peatland Responses Under Changing Environments (SPRUCE) warming experiment, inoculated germ-free *Sphagnum,* and then exposed the inoculated plants to temperature stress. Elevated temperature decreased growth of plants without added microbiomes while the addition of a microbiome from a thermal origin that matched experimental temperature resulted in similar growth to pre-warming growth rates. Metagenome and metatranscriptome analyses demonstrated warming changed microbiome structure and induced the plant heat shock response, suggesting that thermally conditioned microbiomes provided the host plant with thermal conditioning. We next repeated the experiment with microbiomes isolated from *Sphagnum* warming experiments in Iceland, Sweden, and France. Again, we found that *Sphagnum* growth rates were maximized when the experimental temperature treatment matched the inoculum origin temperature. Our findings show that *Sphagnum* temperature acclimation can be modulated by microbial interactions and may provide a valuable strategy for rapid response to environmental change.

OP47

Patterns of between species and within species gene flow and demographic history in *Sphagnum flexuosum* and *Sphagnum recurvum*

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Peatmosses (*Sphagnum* spp.) are spore producing plants capable of long-distance dispersal, which allows them to have wide geographic range and enables populations in different geographic regions to remain connected by gene flow. Also, several *Sphagnum* species can have between species gene flow through hybridization. The aim of this study is to investigate the role of geography in determining the patterns of within and between species gene flow in *Sphagnum*. A pair of sister species were studied: *S. recurvum* and *S. flexuosum*. Both species occur in eastern North America, and *S. flexuosum* have a separate population in Europe. The analysis of migration models was done using RAD-seq data and coalescent simulations of site frequency spectrum (SFS).

The results showed that within *S. flexuosum,* there is an asymmetric gene flow from eastern North America to Europe, suggesting that Europe might have been colonized by plants from eastern North America after the last glacial maximum. The rate of gene flow between *S. flexuosum* and *S. recurvum* is significantly lower than gene flow among *S. flexuosum* populations, suggesting some level of reproductive isolation between the species. The rate of between species gene flow is higher in sympatric populations than in allopatric populations, indicating that hybridization is more likely when both parents have overlapping distribution. Interestingly, there is a significant amount of gene flow from *S. recurvum* to the ancestor of both *S. flexuosum* populations, suggesting that the two species might have diverged while still partially connected (parapatry), by specializing in different ecological niches.

OP48

Genomic diversity of keystone peat bog moss *Sphagnum*

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Peat bogs represent important ecosystems in Northern habitats and play a crucial role in the global carbon cycle through sequestration of carbon as undecomposed peat. The dominant taxa within most bogs is *Sphagnum*, which engineers its environment through acidification and creation of anoxic conditions to suppress growth of competing plants and microbes. Sphagnum species live in sympatry, occupying various niche habitats in relation to the water table, with some species growing strictly in low valleys (hollows), high mounds (hummocks), or large lawns.

To understand the biology of this organism and how it dominates these ecosystems despite harsh conditions, we have generated two high-quality reference genomes for *S. angustifolium* (Hollow-lawn species; 395 Mb; Scaffold N50: 21 Mb) and *S. magellanicum* (Hummock species; 439 Mb; Scaffold N50: 17 Mb), accompanied by transcriptome data under various conditions (drought, dark, high/low pH and high/low temperature) and Illumina re-sequencing of 35 samples representing 15 taxa across the 5 major subsections of *Sphagnum*.

Our results show that *Sphagnum* is truly a unique organism, with strong genome collinearity among species that does not extend any other plant genome queried thus far. Analysis of transcription factor response to environmental conditions by *S. magellanicum* and *S. angustifolium* shows tight regulation of genes related to secondary metabolism, cell wall catabolism, ion exchange, and response to light, a result mirrored by signatures of selection among hummock and hollow taxonomic clades that diverged more than 5 million years ago. These high-quality genomes help shed light on the ways in which *Sphagnum* has become the dominant carbon sink in Northern peatlands.

OP49

Building a global consortium of bryophytes and lichens: keystones of cryptobiotic communities (GLOBAL)

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Digitization has greatly enhanced the use of herbarium data in scientific research, impacting diverse research areas, including biodiversity informatics, global change biology, analyses using next-generation sequencing technologies, and many others. Despite the entrance of herbaria into a new era with enhanced scientific, educational, and societal relevance, museum specimens remain underused; particularly in ecological studies, where the wealth of biodiversity hidden in each bryophyte/lichen specimen may reveal global patterns that are not observable from other data sources. We share a recently funded National Science Foundation project that aims to establish a novel cryptobiotic consortium integrating information about bryophytes and lichens with each other, and with their commensal organisms, including fungi, on a worldwide scale. We endeavor that this project will serve to connect members of the bryophyte and lichen communities together to answer global research questions centering on these biological communities. Our goals are to (1) establish a novel cryptobiotic consortium integrating 6 million records, (2) digitize label data and specimens for 1.2 million bryophytes/lichens focusing on non-North American specimens from 25 US herbaria, and (3) create a connected world through innovative automation, integration, image tagging, and machine learning. Digitization of specimen records and their associated data will provide unparalleled educational resources that can be tailored to diverse audiences. The diversity and expertise of collaborating institutions is leveraged and we discuss a multi-pronged approach to broader impacts that spans from K-12 to participatory citizen science initiatives.

OP50

Detecting the phylogenetic signal of glacial refugia in a bryodiversity hotspot outside the tropics

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Glacial refugia have likely been important in shaping diversity gradients outside the tropics. Many taxa that have high extra-tropical diversity in the present day, such as mosses, may have persisted in glacial refugia. However, the biogeographical histories of most species within refugia remains unclear. In this study, we reconstructed the regional phylogeny of the mosses of Haida Gwaii, a putative glacial refugium and 'hotspot' of moss diversity on the northwest coast of British Columbia, Canada, and used phylogenetic comparative methods to examine the macroecological imprint of glacial refugia on the geographic range structure and phylogenetic attributes of present-day moss assemblages.

We found that many mosses have widespread, but disjunct distributions, with few close relatives on the islands. We suggest that these features reflect the imprint of glacial history, whereby species within refugia represent isolated populations of previously more widespread species that may have diversified elsewhere. We also observed evidence for phylogenetic over-dispersion of species within high elevation habitats, which best match the climatic regime of the historical glacial refugium. Our results are consistent with the filtering of evolutionarily distinct glacial relicts within these habitats, which contrasts markedly with the patterns of phylogenetic clustering observed across other non-refugial habitat types. The islands of Haida Gwaii represent an extratropical hotspot of bryophyte diversity. Our study illustrates how phylogenetic methods can reveal the signal of glacial refugia, supporting paleoecological data, and illuminate the biogeographical histories of mosses to explain why some taxa are more diverse outside the tropics.

OP51

Small but visible: predicting the distribution and richness of rare bryophytes in boreal forests through remote sensing

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In Canadian boreal forests, bryophytes represent an essential component of biodiversity and play a significant role in ecosystem functioning. Despite their ecological importance and sensitivity to disturbances, bryophytes are overlooked in conservation strategies due to knowledge gaps on their distribution, posing a particular risk for their rare species. This study aims to develop predictive models of the presence of rare bryophyte species, as well as to identify their diversity hotspots in boreal forests using remote sensing (RS) data. The study area is located in western Quebec and covers 72,292 km^2. We selected 52 bryophyte species with <30 occurrences from a presence-only database (214 species, 389 plots in total). RS-derived variables at 30 m spatial resolution related to topography and vegetation were used as predictors. Models and predictive mapping were developed using the Ensemble of Small Models (ESMs) modeling framework from Maxent and Random Forest techniques. Subsequently, the patterns of rare bryophyte richness were mapped by aggregating their predictions.

The individual models showed a predictive value ranging from useful (better than random) to excellent for 73% of the species, despite their low number of occurrences. These models allowed to identify diversity hotspots of rare bryophytes, as well as to assess their spatial correspondence with those of overall bryophytes recently identified in a previous study. This study demonstrates the potential of RS for assessing and making predictions on inconspicuous and rare species across the landscape and lays the basis for the eventual inclusion of bryophytes into sustainable development planning.

The plight of plants in light of deforestation in the Amazon: insights from epiphyllous metacommunity dynamics

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Forest fragmentation continues to cause massive losses in biodiversity, particularly in the tropics. Anthropogenic activities have increased exponentially in the past half-century in these domains, and the survivability of plants from these megadiverse regions are difficult to elucidate since their generation times are generally much longer than the rates at which habitat destruction is presently happening. However, organisms that inhabit the phyllosphere (leaf surfaces) are ideal models for predicting the depth of such demographic consequences. We took advantage of phyllospheric bryophyte metacommunites, to evaluate the genetic structure associated with their temporal changes over 15 years at a landscape scale in central Amazonia. Specifically, two epiphyllous bryophyte species (*Radula flaccida* and *Cololejeunea surinamensis*) were studied using population abundance and genotyping by sequencing approach.

Our results showed that population size in small fragments (1 ha and 10 ha) was significantly reduced when compared with large reserves (100 ha and continuous forest). During the last decade, recovery in the abundance of these two species has been observed between the years 2000 and 2016. The population genetic structure in small fragments was considerably more different when compared to surrounding large reserves, suggesting that these populations are experiencing genetic drift. In conclusion, despite the increased population size in smaller fragments in the past year, both species are genetically vulnerable to the rapid loss of habitats in the Amazon forest.

OP53

Rebuilding the transatlantic bridge of *Orthotrichum consimile* group (Orthotrichaceae, Bryophyta) and predicting its geographical suitability in Europe

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Integrative taxonomy revealed, almost a decade ago, that the moss *Orthotrichum consimile* was actually a complex of four species. Whereas *O. consimile* s.s. was excluded from the European bryoflora, *O. columbicum* emerged as the only species in this complex present in both North America and Europe. However, we have recently discovered a locality in central Spain where these two species seem to cooccur. This was unexpected since the area exhibits a continental Mediterranean climate that seems to be unsuitable for these species. To shed light on this paradoxical situation, the identity of the specimens was confirmed by molecular data. Furthermore, we addressed the macroclimatic niche of both species and carried out ecological niche models (ENMs) to contrast the new locality with those recorded in America and Europe. We also projected the potential distribution of both species to evaluate suitable areas in Europe.

We report *Orthotrichum consimile* s.s. in Europe for the first time, which entails a new transatlantic disjunction within the complex. Our data also confirm the coexistence of *O. consimile* and *O. columbicum* in central Spain as it happens in many of their American localities. Regarding ENMs analyses, both species share a similar macroclimatic niche in America yet they show a climatic shift in Europe. Moreover, both species show suitable areas beyond their current recorded distributions. Western areas of the Iberian Peninsula and scattered localities in other Mediterranean peninsulas might be suitable for *O. comsimile*. Likewise, southern Europe (from Portugal to Turkey) might hold populations of *O. columbicum*.

OP54

The origins and conservation genetics of *Cirsium scariosum* in the Mingan Islands of Québec

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The Mingan Archipelago along the north shore of the Gulf of St. Lawrence is well known for the diversity and rarity of its vascular plants. This diversity is often explained by a combination of the islands' temperate maritime climate and its unusual regional geology where the islands are formed of calcareous sedimentary rock. Among the 80 species of rare plants on the islands, one in particular stands out, *Cirsium scariosum* (Meadow thistle), a species native to western North America, but with a disjunct population on the Mingan islands over 3500 km away. Initially recognized as a separate species, *Cirsium minganense*, when it was first discovered in 1924 by Marie-Victorin, recent authors believe these Mingan populations are either the result of eastern migration during the Pleistocene or a contemporary anthropogenic introduction. Nevertheless, the question of how these populations arrived on the islands or whether they should be treated as a separate species has not been resolved. The eastern populations of *Cirsium scariosum* are now endangered and conservation efforts have been made to save this emblematic plant.

To determine whether the Mingan populations might represent a separate species and to better understand the plants' breeding system and genetic diversity for conservation, a phylogeny of closely related species and a population genetic analysis using genotyping by sequencing (GBS) was conducted. Results suggest the Mingan island populations are not closely related to the western *Cirsium scariosum* and that outcrossing and dispersal between islands could be occurring.

OP55

From models to mummies: combating plant blindness through museum exhibits

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People go to natural history museums to learn more about wild species. Traditionally, ‘charismatic megafauna’, such as large predators, are the focus of many museum exhibits like dioramas, with plants merely providing an attractive background, if they are present at all. This practice both reflects, and may contribute to, societal ‘plant blindness’, a phenomenon where people underappreciate the importance of plants, and are less likely to support their conservation.

With funds raised from a capital campaign, the Manitoba Museum had an opportunity to build new exhibits for the Prairies Gallery. However, the retirement of the museum’s diorama artist meant that novel approaches to displaying botanical specimens would be necessary. Further complicating exhibit construction was the fact that most of the museum’s specimens were pressed flat, making them visually unexciting. As well, plants and fungi are perceived by the public as being passive and uninteresting, making their interpretation challenging.

We used a combination of models, three-dimensional dried and mummified plants and fungi, time-lapse videos, and computer animation to create new, visually attractive botanical exhibits. We chose three interesting themes to discuss: adaptation, reproduction, and endangerment. To increase empathy for plants and fungi, interpretive text and new museum programming describes them as creatures with agency that want the same things people do: water and food, a chance to reproduce, and to survive. Altering visitor perceptions will help combat plant and fungal blindness, and hopefully result in support of conservation efforts for these often ignored, and increasingly rare, prairie species.

OP57

Disturbance, growth, succession and nitrogen fixation in the boreal forest: a bryophyte perspective

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Bryophytes dominate the forest floor, regulate soil microclimate, and participate in the carbon (C) and nitrogen (N) cycles in coniferous boreal forests. The bryosphere represents the network of associations between microorganisms and invertebrates living on the leaves, stems, and decaying parts of bryophytes. Associations between mosses and diazotrophs (N-fixing microorganisms) are increasingly recognized as an important N source in northern and temperate ecosystems. In this presentation, I explore how canopy type (coniferous vs broadleaf deciduous), environmental conditions, and time since fire, affect moss succession, growth, and associated N_2 fixation in North American boreal forests.

Results support the hypothesis that leaf litter deposition exerts a strong control on moss assemblages, abundance, and growth rates in the boreal forest. In the absence of leaf litter mosses grow better and present higher rates of associated N fixation in coniferous than deciduous forests and experimental leaf additions negatively affect these processes in both forest types. The moss microbiome, N-fixation rates, and potential contributions to stand-level N cycling depend on the moss host species, forest type, and geographical location. Global changes in disturbance regimes, forest composition and climate can therefore have profound impacts on moss communities that may alter the structure and composition of the boreal forest.

OP58

The bryophyte friends of ecological restoration in northern climates

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Thirty years of research on the ecology of bryophytes in northern disturbed ecosystems has proven to be useful to improve the success of restoring degraded boreal ecosystems. We argue that the moss layer should be taken into account, not only vascular plants, in ecological restoration. First approaches on the use of bryophytes in ecological restoration, based on what was known on the ecology of mosses in the 1980s, started on the wrong footing. Through numerous experiments and observations at different scales (from petri dish to greenhouses experiments to extensive burnt or degraded ecosystems) several species of bryophytes have emerged as stars of ecological restoration.

A superstar in bog restoration is definitively *Polytrichum strictum*. Fens are more diverse in plant communities; consequently, several stars have been uncovered. *Ptychostomum pseudotriquetrum* and *Marchantia polymorpha* are good candidates as pioneer bryophytes to prepare the ground for later successional such as *Campylium stellatum* and *Tomenthypnum nitens*. *Sphagnum warnstorfii* should be included in the plant material for reintroduction if a rapid return of the carbon sequestration function is sought. When wetland rewetting is not optimal, *Aulacomnium palustre* is a good ally for restoring degraded ecosystems. In northern boreal roadside borrow pits, *Racomitrium canescens* and *Stereocaulon paschale* are the best species to reintroduce to restart soil formation processes. Data supporting the work of these stars in ecosystem restoration will be presented.

OP59

What do lichens tell us about landscapes?

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An essential part of ecological restoration is the ability to assess progress towards a desired state. Ideally, we can use benchmarks of ‘pristine’ conditions to assess the success of restoration actions. In the absence of historical data on a particular site, the presence of indicator species known to be sensitive to anthropogenic disturbances can be a useful tool. Scientists have long known that lichens are good indicators for air quality. Research in my landscape ecology lab has shown that they can also indicate the ecological condition of the wider landscape.

In this talk, I will highlight recent research from my lab group that merges expertise in landscape ecology and lichenology. We have used lichens to assess critical habitat for a species-at-risk, and developed strategic sampling techniques to assess nuances in habitat quality. These have included both micro-scale habitat (e.g., tree condition) and site level (stand condition) attributes as well as consideration of air quality and forest continuity. Our work has informed long-term monitoring in a national park, identified critical habitat for a species-at-risk, and helped to assess if lichens can be useful indicators for forested wetland classification.

Rich fens may be prone to retrogressive succession after in situ oil sands exploration disturbance without restoration measures

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Bryophytes have key roles in the formation of hummock-hollow topography in rich fens, and influence the development of vegetation with different elevation requirements relative to the water table. However, in the preparation of drilling pads for in situ oil sands exploration (OSE) in winter, peatland surfaces are reworked and flattened. When pads are abandoned after drilling, the depressed surface layers and reduced microtopography tends to leave most surface positions flooded after heavy summer rains.

In northeastern Alberta, Canada, we examined natural regeneration in rich fens 7 (2012) and 14 years (2019) after OSE with minimal restoration measures. Within each fen for both years, we examined bryophyte diversity and composition at the highest and lowest elevations relative to the water table, as well as tree regeneration and surface topography, on drilling pads and in adjacent reference habitat.

In 2019, tamarack seedling densities and bryophyte richness had decreased significantly on drilling pads and adjacent reference habitat compared to 2012. The frequency of most bryophytes was also lower than 2012, including some mosses that are seedbeds for tree establishment. We propose that heavy summer rains during the study caused surface flooding and a significant shift in bryophyte composition between years for sampled habitats.

Past research shows that development of artificial hummock topography on OSE drilling pads provides elevated habitat for flood-intolerant plants, including hummock-forming bryophytes. However, in the absence of restoration measures, OSE-disturbed rich fens with a water table near the surface may be susceptible to periodic surface flooding and successional retrogression.

OP61

Bryophyte and lichen responses to environmental changes resulting from seismic line disturbance in boreal ecosystems of northwestern Alberta

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Bryophytes and lichens often provide a growing medium for vascular plants, therefore, knowledge of how they respond to seismic line disturbances may improve understanding of succession, regeneration potential. We assessed environmental conditions and non-vascular species abundance and composition on seismic lines (used for oil and gas exploration), and in the adjacent ecosystem at two sites in Alberta: an upland boreal forest (near Swan Hills) and a boreal peatland (near Peace River). In the uplands, we studied less than a decade old low-impact seismic lines, and in the peatland, ~30–70-year-old conventional seismic lines.

Soil moisture and light were higher on the lines at both sites. Soil at 2–25 m from the line edge was also drier than interior peatland 75 m away, indicating edge effects. Soil temperature was higher on the seismic lines at the upland, but not the peatland site. At the upland site, bryophytes and lichens were less abundant on the lines than in the forest when sampled in 2014, but five years later, they have shown a remarkable recovery on the lines. At the peatland site, lichens were less abundant 2–25 m from the line edge, compared to 75 m away. On the lines, *Sphagnum* constituted a nearly 100% cover, while other bryophytes and lichens were almost absent. However, *Sphagnum* and feathermoss were equally and highly abundant in the adjacent peatland. Environmental conditions and vascular and non-vascular species composition did not differ among the lines of different ages in the peatland, indicating arrested succession, and a need for active restoration.

OP62

The role of bryophytes in carbon exchange in disturbed and restored peatlands in Canada

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Resource development across Canada has resulted in a network of disturbances, including peat extraction areas, mines, well-pads, transportation corridors and seismic lines, many of which intersect with peatland ecosystems. While structural and hydrological changes resulting from these disturbances are usually readily apparent, how they affect carbon storage and greenhouse gas exchange remain understudied. Nevertheless, restoration treatments have been designed and are now being applied, with evidence suggesting they can restore carbon sink function in many cases. Bryophytes play a critical role in peatland carbon storage in undisturbed ecosystem, but vascular plants have been shown to dominate carbon uptake in many disturbed and restored sites. Using a series of case studies, the role of bryophytes in carbon and greenhouse gas exchange in disturbed and restored peatlands will be explored.

Hornwort biology and a new era of possibilities

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Although the least specious and diverse of flagellated plant groups, the hornworts present shared and unparalleled adaptations to life on land. Plants are thalloid, lack organized appendages such as hairs and leaves, and contain abundant mucilage in specialized cells and internal canals. Chloroplasts are often solitary and typically have pyrenoids, a localized site of RuBisCO for carbon concentration shared with algal streptophytes. Cell division is strictly monoplastidic and plastids serve as the focal points for the mitotic and meiotic spindles. The cyanobacterial symbiosis is universal in all hornwort taxa and involves the development of internal elongated or globose *Nostoc* colonies.

Gametangia are sequestered in chambers or embedded directly in thallus tissue. Male gametes are biflagellated and demonstrate little variability across hornwort diversity. The sporophyte is a single sporangium that elongates from its base and continually produces sporogenous tissue upward. Stomata are present in most taxa but have been lost in two lineages.

The advent of molecular applications and genetic transformation of hornworts opens the way for fundamental and unique biological questions to be addressed based on the intriguing biology of the group.

OP63

Cell biology of hornworts

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The peculiarity of hornworts in land plants also extends to their characteristics at the cellular level. One of the exceptional characters is that the cells of hornworts usually contain only one chloroplast, and the chloroplast often contains pyrenoids composed of aggregated RuBisCo, the CO_2 fixing enzyme. During cell division, the chloroplast divides and migrates prior to the division of the nucleus, and nuclear division follows the division axis of chloroplasts. The microtubule system extends from the chloroplast surface is involved in the reliable allotment of chloroplast to daughter cells and the determination of the cell division axis. Such cell division system is different from liverworts, in which the mitotic spindle develops from a centrosome-like structure, and mosses, in which the mitotic spindle develops without a scaffold organelle. In mature cells of hornworts, the outer shape of the chloroplast is not smooth, and many elongated protrusions are often formed. Currently, hornworts have been shown to occupy the most basal position of the bryophyte phylogeny. Therefore, hornwort cells may provide an interesting model for studying the evolution of cellular systems in land plants. I summarize the cell biology of hornworts with particular attention to chloroplasts and a view to future research.

Closing the gaps: hornwort evolutionary developmental biology

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Extant land plants consist of two deeply divergent monophyletic lineages, vascular plants and bryophytes, which shared a common ancestor some 500 million years ago. Land plants have evolved body plans in a way that overall complexity remained low in the bryophytes but reached greater overall complexity in the vascular plants. Comparative evolutionary developmental biology of complex and less complex lineages can help to understand how complexity evolved via the reorganization of gene regulatory networks.

While information about vascular plants and two of the three lineages of bryophytes, the mosses and liverworts, is accumulating, research on the developmental biology of hornworts have been widely neglected. Yet, as the sister group to liverworts and mosses, hornworts are critical in understanding the evolution of key land plant traits. More specifically, inference about the complexity of the common ancestor of land plants is ambiguous. This is, in part, due to the deep divergence of the three groups of bryophytes, as well as bryophytes and vascular plants, that provided ample time for independent gains/losses of genes to occur. Comparison of the developmental, physiological and molecular features of hornworts with those of mosses and liverworts will provide a more accurate picture of the nature of the common ancestor of bryophytes and that of all land plants. It will also help to understand the diversity and molecular basis of evolution and development across bryophytes and vascular plants.

To this end, I will introduce the major developmental biological features of the emerging hornwort model system *Anthoceros agrestis* providing critical information on the evolution of key land plant traits. Furthermore, I will present results starting to resolve some questions concerning the evolution of these traits in land plants.

The lab life of the model hornwort *Anthoceros agrestis*, from spores to transformation

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Hornworts are one of the most fascinating land plant groups. Despite their key phylogenetic position and their unique biology, hornworts have been widely overlooked. Until recently there was no hornwort model species amenable to systematic experimental investigation. *Anthoceros agrestis* has been proposed as a model species to study hornwort biology. I will introduce the emerging hornwort model system *A. agrestis* with a special focus on the newly developed nuclear transformation technique.

OP67

Expanding the genomic and genetic toolkits for hornwort research

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Hornworts have an array of unique features that can help illuminate not only the early evolution of land plants, but also the alternative paths for nitrogen and carbon assimilation (respectively via cyanobacterial symbiosis and a carbon-concentrating mechanism). Despite this, hornworts are also one of the few plant lineages having only limited genomic and genetic resources available. To address this issue, we have assembled eight new high-quality genomes from across the hornwort phylogeny, covering all the families and most of the genera. Importantly, these genomes represent a diverse trait combination—including presence/absence of pyrenoids, stomata, and sex chromosomes—and will form the basis for future comparative studies. Furthermore, a biolistic-mediated transformation has been developed that can effectively introduce genetic elements into the model hornwort *Anthoceros agrestis*, as well as a few other species. Building upon these new resources and tools, we are investigating the genetics of hornworts' carbon-concentrating mechanism, and our preliminary findings will be presented here. We anticipate that enabling genetic research in hornworts will not only complement the other two bryophyte models (the moss *Physcomitrium patens* and the liverwort *Marchantia polymorpha*), but will also bring unprecedented opportunities to study a distinct plant with unparalleled biological properties.

OP68

Differential gene expression in the hornwort *Anthoceros punctatus* during establishment of its nitrogen-fixing symbiosis with the cyanobacterium *Nostoc punctiforme*

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Endosymbiotic associations between hornworts and nitrogen-fixing cyanobacteria form when the plant partner is limited for combined nitrogen. We examined the patterns of differential gene expression by RNA- Seq during culture of *Anthoceros punctatus* in the absence of combined nitrogen and absence and presence of the model symbiotic cyanobacterium *Nostoc punctiforme* in a 6-point time-course.

The raw sequencing reads were analyzed via the MaSigPro algorithm yielding 1448 genes that were significantly differentially expressed at a $P < 0.05$. This data set was subjected to cluster analysis with a nine-cluster output. In five of the clusters, transcripts from *A. punctatus* nitrogen-starved in the absence of *N. punctiforme* increased in expression within two days of incubation, relative to the time zero control, and either remained elevated (two cases) or declined at different rates; in the remaining four clusters, transcription declined. Co-culture with *N. punctiforme* resulted in either increased (three cases) or decreased (two cases) transcription by *A. punctatus* in a reciprocal manner, relative to the absence of *N. punctiforme*. Conversely, the presence of *N. punctiforme* had no substantial effect on the patterns of transcription in four of the clusters, relative to its absence. Functional assignments of the protein products of differentially expressed genes have been compiled and will be discussed.

We conclude that a major adaptation to nitrogen starvation in *A. punctatus* is to decrease photosynthetic light harvesting capacity in order to minimize production of reductant and this transcriptional response can be ameliorated by dinitrogen-derived ammonium supplied endophytically by *N. punctiforme.*

OP69

Centres of bryophyte endemism in southern Africa

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Endemic and rare species are more prone to extinction than common species because they are habitat-specific and most of them present specific life strategies. In recent years the efforts to preserve rare organisms and seek out and protect areas of high endemism have acquired increased urgency in the light of the accelerating natural habitat and biodiversity losses through impacts of human action and climate change among others.

In recent checklists of the mosses and liverworts of southern Africa (FSA region), 190 species, 23 genera and 14 families were identified as endemic to the region. The Cape fold mountains and the Drakensberg Mountains along the Great Escarpment of South Africa have recently been determined as centres of moss diversity in southern Africa. The Cape Floristic, Succulent Karoo and Maputaland-Pondoland Regions are recognized as the three regions of vascular plant diversity and endemism for South Africa.

The aim of this study is to describe the centres of bryophyte endemism according to the number of endemic species per ½° grid square. The cells will then be grouped according to intervals, 0, 1 – 5, 6 – 10, 11 – 15, 16 – 20, 21–25, 26–30, 31–35, 36–40, 41–45 species per grid. These groups will be mapped to determine the centres of bryophyte endemism. The centres will then be compared with rainfall, altitude, phytogeographic regions, centres of moss diversity and ecoregions in southern Africa. The centres of bryophyte endemism will also be compared with centres of vascular plant endemism in southern Africa.

OP70

Continental drift originated the E African – S Indian disjunction of *Lewinskya firma* (Orthotrichaceae, Bryopsida): fact or fiction?

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Disjunct distributions at specific level are common among bryophytes. When studied from a phylogeographic point of view, long-distance dispersal seems to be the most plausible mechanism for explaining most of such disjunctions. Even though, in some particular situations the contribution of other processes, such as continental drift or stepping-stone migration, cannot be ruled out. On the other hand, current taxonomical studies often show that apparently disjunct distribution patterns of bryophyte species actually correspond to complexes of cryptic species with much narrower distribution ranges and which not necessarily are closely related species.

We analyse the apparently disjunct distribution of *Lewinskya firma*, a widespread species in the Afromontane forests of East Africa. Only one population of this species is known outside Africa, located in the Nilgiri Mountains in southeast India. Since this distribution is consistent with the drift of the Indian subcontinent since the Late Cretaceous, it is suggestive that this disjunction could in fact correspond to a process of vicariance. To verify this, an integrative taxonomy study has been undertaken, combining morphological and molecular analyses.

The results of the morphological study support the existence of three well-defined morphotypes within the current *Lewinskya firma* concept. Two of them are mosses spread in Africa, while the third one corresponds to the population from the Indian subcontinent. The distinction of the two African morphotypes is also supported on the basis of the molecular data and could date from the Oligocene. Surprisingly, the Indian morphotype is molecularly closely related to one of the African morphotypes, pointing to a recent diversification. Further analysis including additional molecular data are needed in order to fully understand the evolutionary history within *Lewinskya*.

Targeted sequencing supports morphology and embryo features in resolving the classification of Cyperaceae tribe Fuireneae s.l.

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Molecular phylogenetic studies based on Sanger sequences have shown that Cyperaceae tribe Fuireneae s.l. is paraphyletic. However, taxonomic sampling in these studies has been poor, topologies have been inconsistent, and support for the backbone of trees has been weak. Moreover, uncertainty still surrounds the morphological limits of *Schoenoplectiella*, a genus of mainly small, amphicarpic annuals that was recently segregated from *Schoenoplectus*. Consequently, despite ample evidence from molecular analyses that Fuireneae s.l. might consist of two to four tribal lineages, no taxonomic changes have yet been made. Here, we use the Angiosperms353 enrichment panel for targeted sequencing in order to (1) clarify the relationships of Fuireneae s.l. with the related tribes Abildgaardieae, Eleocharideae and Cypereae; (2) define the limits of Fuireneae s.s., and (3) test the monophyly of Fuireneae s.l. genera with emphasis on *Schoenoplectus* and *Schoenoplectiella*.

Using more than a third of Fuireneae s.l. diversity, our phylogenomic analyses strongly support six genera and four major Fuireneae s.l. clades that we recognise as tribes: Bolboschoeneae stat.nov., Fuireneae s.s., Schoenoplecteae, and Pseudoschoeneae tr.nov. These results are consistent with morphological, micromorphological (nutlet epidermal cell shape), and embryo differences detected for each tribe. At the generic level, most sub-Saharan African perennials currently treated in *Schoenoplectus* are transferred to *Schoenoplectiella*. Our targeted sequencing results show that these species are nested in *Schoenoplectiella*, and their treatment here is consistent with micromorphological and embryo characters shared by all *Schoenoplectiella* species.

Integrative taxonomic study disclosed a hidden diversity in hygrophilous species of the genus *Pseudohygrohypnum*

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Molecular and morphological study of the hygrophilous species of *Pseudohygrohypnum, P. eugyrium* and *P. subeugyrium*, revealed their severe heterogeneity. Plants referred hiterto to *P. eugyrium* comprise three allopatric species occurring in Europe, North America and East Asia, and those of *P. subeugyrium* belong to five species. Distributions of the latter lineages are partly overlapped. *Pseudohygrohypnum subeugyrium* s.str. is a North Atlantic species, while East Asian populations are referred to *P. purpurascens,* that is thus resurrected. In addition, three exclusively or predominantly North Asian lineages from harsh continental climates were revealed. Results of Maxent distribution modeling and niche identity and similarity tests indicate remarkable divergence of niches of all lineages excepting East Asian '*P. eugyrium*' and *P. purpurascens*, which actually are not related. Considerable nucleotide distances and results of the ASAP test suggest a need to split two hygrophilous *Pseudohygrohypnum* species into eight.

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Spatial phylogenetics of the North American moss flora

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Spatial phylogenetics is a relatively new and important approach that adds an evolutionary dimension to traditional measures of biodiversity based on species richness and endemism, using measures such as Phylogenetic Diversity (PD — the phylogenetic relatedness of lineages within areas), Relative Phylogenetic Diversity (RPD — the distribution of phylogenetic branch lengths across a landscape), and CANAPE (Categorical Analysis of Neo-and Paleo-Endemism).

In this study we aimed to identify the important regions within North America north of Mexico for PD, RPD, and CANAPE and to examine climatic patterns that may help explain these measures. The dataset included occurrence data and a phylogeny for 971 mosses (70.1% of the flora). PD peaks in the Pacific Northwest, and is bimodally distributed between the east and west coasts of the continent. PD and RPD are both significantly higher than expected (based on a spatial randomization test) in the eastern US, indicating phylogenetic overdispersion and a significantly high concentration of long phylogenetic branches. Significant centers of phylogenetic endemism discovered by CANAPE include California, Florida and the Gulf Coast, and isolated areas throughout the mountainous west. These patterns can be explained in part by the magnitude and seasonality of current precipitation, however historical factors including glaciation migration patterns and refugia from more ancient climate regimes also appear to play an important role in explaining the current distribution of lineages across the region.

OP74

Hornwort (Anthocerotophyta) diversity in Mexico

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Hornworts (Anthocerotophyta) are classified within the non-vascular embryophytes, characterized by a laminar gametophyte and a protruding horn-like sporophyte; the most recent diversity estimation recognizes 12 genera and 205 species worldwide within the division. Hornwort diversity concentrates near the tropics; crossed almost to the middle by the Tropic of Cancer, Mexico harbors unique scenarios were Neartic and Neotropical taxa distribute. Nevertheless, Mexican hornwort floristic studies are scarce. In 1863, Gottsche enlisted seven hornwort species for the country; since then, Mexican hornwort flora was partially included in North American studies; however, a complete and updated documentation is lacking. In 2012, Delgadillo-Moya and Juárez-Martínez estimated Mexican hornwort diversity to nine species and four genera, recognizing three endemic species.

The aim of this study is to document and update Mexican hornwort species diversity, contributing to the biogeographical knowledge of this group, and to facilitate their identification. Herbarium and literature revisions were carried out alongside field collections. Seven genera and 26 species of Anthocerotophyta are recognized for Mexico in the present study; two new records for America and four new records for the country are documented. Mexican hornwort flora, dominated by *Anthoceros* species, presents a mixture of Nearctic, Neotropical, endemic and cosmopolitan taxa. The fact that a few collecting expeditions resulted in several new records highlight the needs of increasing sampling efforts, and of implementing molecular resources to test the monophyly of geographically disjunct or ill-defined taxa.

OP75

Systematics of the *Sphagnum magellanicum* complex: genomics, phylogeny, ecology, and taxonomy

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Sphagnum magellanicum has been interpreted as a global species that is an important component of peatland communities around the Northern Hemisphere as well as throughout South America. Recent molecular work has shown that *S. magellanicum* s. str. is limited to South America whereas two other related species occur in western Europe and North America: *S. medium* and *S. divinum*. We undertook a systematic analysis of this species complex through a global sampling of plants. Molecular approaches included whole genome sequencing and RADseq, complemented by morphological, biogeographical, and ecological comparisons.

Our results indicate that the complex includes at least seven clades. South American plants comprise a Fuegan clade and a northern clade found in the Andes Mountains northward to Central America. In North America, we resolved four clades including *S. divinum* and *S. medium*, plus two clades that represent undescribed species. Of the four taxa in eastern North America, only *S. divinum* occurs in western North America. That species is also confirmed from Russia, and from northern Japan (Hokkaido). An additional clade was identified from China and Taiwan. Some but not all of the species occupy ecologically distinct microhabitats, even where they occur at the same site. The taxa differ weakly in morphological traits, but are largely reproductively isolated. This research takes on particular importance because '*S. magellanicum*' is the focus of intensive genomic and ecological research; the reference genome generated by the U.S. Department of Energy's Joint Genome Institute (JGI) is shown to belong to the segregate species, *S. divinum*.

OP76

Some unlikely extrapolations from the improbable architecture of *Herzogianthus vaginatus* (Herzogianthaceae)

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Underleaves are one of the characteristic features of leafy liverworts. Two shoot architectures are known in leafy liverworts, having ratios of leaves to underleaves of 1:1 or 2:1, and pendulous or helical segmentation sequences by the apical meristematic cell, respectively. *Herzogianthus* fits neither of these two modes and further exhibits architectural flexibility, and hierarchical structure, both unprecedented features among leafy liverworts. Although much remains unknown about *Herzogianthus* and its shoot architecture, including the precise mechanism by which the unusual architectures are achieved, this ought not prevent us from exploring the broader ramifications of some of these mechanisms, if realised, for the evolution of structural diversity and organisation across liverworts. *Herzogianthus* also presents a timely reminder of the need for us all to be prepared for, and receptive to, surprising observational data.

Genomes of *Syntrichia*: insights into traits, populations, ecology, and evolution

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Syntrichia is a diverse genus of mosses occurring worldwide in dryland habitats and demonstrating an unusual amount of ecological variation. Within the 3D Moss collaboration we took a genomic approach to generate hypotheses about drivers of desiccation tolerance, speciation, population genetic structure, physiological plasticity and habitat selection. The cornerstone of this approach was the establishment of genomic resources anchored by high-quality chromosomal level genome assemblies for two key species: *S. caninervis* and *S. ruralis*.

The assembled genomes are similar in size and gene content but differ in chromosome number, with *S. caninervis* at 331.83 Mb as 13 chromosomes and *S. ruralis* at 381.24 Mb as 12 chromosomes. Both genomes contain a large chromosome that has low gene and high repeat content and represent female sex chromosomes. Transcriptomic resources for both species have been constructed and we have identified transcriptome signatures for desiccation, rehydration, moderate heat, heat-shock, and cold for both species. Mapping of these signatures to the genomes and their structural features allowed to identify novel genes that we hypothesize to be important in the evolution of desiccation tolerance. Comparative genomics analyses revealed evidence for a whole genome duplication event and suggests chromosomal or segmental losses in the evolutionary history of *S. caninervis*. A similar analysis is underway for the *S. ruralis* genome; and there are plans to sequence two more species, *S. princeps*, and *S. norvegica*. Genomic tools have also been developed to assist in the population genetics, phylogenetic, and ecological aspects of the 3D Moss collaboration.

Population genetic structure in *Syntrichia caninervis*

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Syntrichia caninervis is globally distributed in deserts and drylands, and is a dominant member of soil communities in both the Mojave and Colorado Deserts of the western North America. Within its western North American range, this species occurs across diverse dryland habitats, from creosote scrubland to piñon juniper woodland, suggesting either broad ecological tolerance or physiological specialization within *S. caninervis*. In this study, we sampled *S. caninervis* populations along elevation gradients (low / mid / high) in both the Mojave Desert (Nevada, US) and the Colorado Plateau (Utah, US) to capture two series of geographically proximate yet environmentally distinct habitats. Samples from the six populations were genotyped using double-digest restriction enzyme associated sequencing and analyzed for genetic structure. Our results indicate minimal influence of isolation by distance in shaping patterns of genetic differentiation in our study populations, and instead highlight the possible role of local climate (chiefly, mean annual precipitation, MAP) in driving observed diversity patterns. Loci with the strongest contribution to discriminant analysis of *S. caninervis* genetic clusters and those whose alleles significantly covary with MAP are described with reference to transcriptome signatures generated by the 3D moss project.

A global phylogeny of the dryland moss genus *Syntrichia*

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Though its approximately 90 named species occur in varied habitats worldwide, the moss genus *Syntrichia* is known for its dryland specialists, demonstrating a remarkable amount of variation in life history and ecology. The goal of this study was to understand the higher-level relationships of the genus. We addressed the following questions (1) Is *Syntrichia,* as currently defined, a monophyletic group? (2) What are the closest relatives of *Syntrichia*? (3) What are the major clades within this group? and (4) What can we tell about its biogeographic history?

Our research group is undertaking phylogenetic analyses of *Syntrichia* at several scales; here we report results based on data from a genome skimming approach. We sequenced 608 samples chosen to represent the full biogeographic, morphological, and taxonomic variation in the group. From *de novo* genome assemblies for each sample and from mining NCBI Genbank, we selected a small set of loci: chloroplast *rbc*l, *rps*4, and trnL-trnF; mitochondrial *nad*5; nuclear rDNA (including ITS regions), and 9 single-copy nuclear loci. Phylogenetic analysis proceeded in two steps using an ML approach (1) analyzing each locus separately to compare gene tree topologies; (2) concatenating all loci into a single matrix to infer the backbone phylogeny.

Results include a well-supported *Syntrichia* clade and the discovery of a diverse, primarily Northern Hemisphere clade that includes the *S. ruralis* complex and *S. caninervis* complex and may represent a recent and extensive radiation in ecology and morphology. We also find evidence of a Southern Hemisphere origin with multiple northward transitions.

OP80

Phylogenetic systematics of *Syntrichia*: a tale of two Codes

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Syntrichia is a diverse clade of mosses that occurs worldwide and is abundant in habitats ranging from late-successional desert biocrusts, to tree trunks and boulders in mid-elevation forests, to mesic alpine meadows. *Syntrichia* demonstrates an unusual amount of variation in ecology, physiology, and reproductive biology among closely related lineages.

The goal of this portion of the overall 3D Moss collaboration was to clarify the higher-level classification of this clade in a phylogenetic context (for which see the preceding talk by Ekwealor et al.). We addressed the following questions: (1) What exactly is *Syntrichia*? (2) What are its closest relatives? (3) What are the major clades that should be named within *Syntrichia*? (4) What advantages/disadvantages are there to using the traditional *International Code of Botanical Nomenclature* versus the newly published *PhyloCode*? To address the latter we propose two parallel classifications and compare them.

Based on our backbone phylogeny we apply the name *Syntrichia* (as a genus under the ICBN) to a large, well-supported clade whose closest relatives are currently placed in the genera *Hennediella, Chenia, and Tortula*. Some smaller, currently accepted genera proved to be nested in *Syntrichia* and will need to be transferred. There are several major clades within *Syntrichia* to which we apply sectional names (under the ICBN), including a diverse Northern Hemisphere radiation that contains both the *S. ruralis* and *S. caninervis* complexes. Species-level classification remains uncertain in many parts of the tree, and will be addressed later, following finer-scale phylogenetic analyses now underway.

OP81

Physiological responses to rainfall in the desiccation-tolerant moss *Syntrichia caninervis:* the role of acclimation and local adaptation

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Anthropogenic change is causing shifts in precipitation patterns across the globe, and bryophytes in dryland systems are likely to be faced with increasingly dry conditions and less predictable wet periods when growth can occur. The magnitude of carbon uptake during periods of hydration varies widely across species of the desiccation tolerant moss genus *Syntrichia*, suggesting taxonomic variation in physiological traits related to differential survival. Such variation may also exist within species with large geographical ranges, where traits associated with carbon uptake may be driven by environmental factors (plasticity) or local adaptation.

In this study we used infrared gas analysis to examine environmental versus genetic contributions to post-hydration carbon balance in *Syntrichia caninervis* collected from three field sites spanning a 1200 m elevation and 130 mm precipitation gradient in Nevada, USA, paired with cultured samples of the same populations in a laboratory common garden environment. We also quantified 12 photosynthetic traits and 5 leaf-level morphological traits in all field-grown and lab-grown samples. Mosses from the highest precipitation/elevation site remained hydrated longer than samples from the lower elevation/precipitation sites, and also displayed the highest carbon balances. Importantly, carbon balances remained high in the mosses from the high elevation/precipitation site in the common garden experiment, indicating at least partial genetic control on physiological traits associated with carbon uptake. Mosses from the highest precipitation/elevation site also had leaves with the highest photosynthetic area and longest awns, suggesting these are critical morphological traits related to water uptake and retention during periods of growth.

Rehydration in dryland mosses: environmentally driven influences including prehydration

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Dryland mosses, renowned for their ability to survive life without water, are highly attuned to changing environmental conditions. The rate of rehydration, or the time it takes to transition from a desiccated state to full turgor, has been largely overlooked in studies of desiccation tolerance. Yet depending on the level of cellular damage during desiccation, rapid rates of rehydration can result in a loss of intra-cellular compounds, requiring cellular repair and decreasing the time available for growth. In nature, ambient humidity levels increase prior to rain events which should provide an opportunity for mosses to absorb water vapor directly from the air and ease their transition to a rehydrated state. Mosses are also thought to coordinate a diverse suite of functional traits at the leaf and cellular level to improve water retention and uptake and minimize rehydration damage.

Using two species from the dryland moss genus *Syntrichia*, we compared the recovery of prehydrated and control shoots following rehydration. We also evaluated rates of rehydration for seven species of *Syntrichia*, and related differences to variation in internal versus external water uptake and holding capacity, and morphological traits known to influence moss water content.

Prehydration mitigated the effects of rapid and/or prolonged desiccation for both species. The seven species of *Syntrichia* varied in their rates of rehydration. We discuss these results in relation to differences in internal and external water uptake and key leaf and cell traits.

OP83

Moss-dominated biocrusts show successional reversal and compositional resistance after persistent rainfall reduction

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The increasing probability and severity of droughts is one expression of climate change likely to have a meaningful impact on dryland ecosystem functions linked to and supported by its biodiversity. We studied the effects of long-term induced drought on the composition and structure of moss-dominated biological soil crust communities (biocrusts) in central Colorado Plateau. We surveyed an array of 25 rainfall reduction shelters, each paired with a control, after eight years of 35% precipitation reduction. We hypothesized that precipitation reduction would induce a successional reversal in the community structure, which would be indicated by a decline in moss and lichen cover and increase in cyanobacterial cover; and higher initial diversity would confer greater resistance of species composition.

We found a significant effect of long-term drought on the cover of biocrust functional groups (bryophytes, lichens and cyanobacterial cover). The percentage of bare soil increased by 13.1% ($p = 0.062$) and light cyanobacterial cover by 17.6% ($p = 0.031$). In contrast, moss cover decreased by 31.6% ($p = 0.017$) and we found no effect in lichen cover or in dark cyanobacterial cover. We found species composition to be broadly similar between drought and control communities, however dissimilarities among communities had a weak positive correlation with diversity ($R2 = 0.072$, $p = 0.110$). We found no structural resistance given the biocrust successional reversal, and a broad resistance of species composition, but richer communities seem to be more susceptible to experiencing a greater change in their composition.

OP84

An examination of pattern–process relationships at a model krummholz-island treeline in Newfoundland, Canada

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Alpine treelines — ecotones in which forests transition to alpine ecosystems — display a variety of spatial patterns ranging from abrupt lines to diffuse zones of increasingly small, deformed, and/or clustered trees. These spatial patterns may have direct and/or indirect implications to tree species' responsiveness to climate warming. Recent studies have reported a link between spatial pattern and treeline responsiveness, with some spatial patterns rarely observed to advance (e.g., krummholz-island treelines). An increased understanding of mechanisms driving different spatial patterns may increase our ability to explain variability in treeline response. Krummholz-island treelines are characterized by stunted, deformed individuals that are clustered into islands surrounded by dissimilar vegetation. The formation of this spatial pattern is hypothesized to be driven by two mechanisms: (1) establishment is limited by the availability of safe sites, which are thought to be positively associated with tree islands, and (2) dieback of established individuals constrains tree stature. To examine the generality of these mechanisms, we paired a seedling transplant experiment with an observational study examining tree stature at a krummholz-island treeline in central Newfoundland.

Despite observing changes in microclimatic conditions with distance from tree islands, there were no trends in seedling survival. Seedling survival was high, regardless of transplant position, suggesting that establishment at this treeline is not limited by the number of safe sites. Moreover, we observed no trends in tree height suggesting that dieback is not constraining tree stature. Our results suggest that the hypothesized mechanisms driving krummholz-island spatial patterns are not limiting a response to climate warming at this alpine treeline.

OP85

Diversity and composition of arboreal bryophytes and lichens along a temperate to boreal elevation gradient at Mont Mégantic National Park, Québec

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Understanding the processes of community assembly along environmental gradients has important implications for predicting future ecological responses to environmental change. Here we report patterns of alpha diversity and composition of arboreal macrolichens and bryophytes along an elevational gradient and lateral gradients (around a tree bole influenced by inclination or aspect) of sugar maple and balsam fir trees at Parc National du Mont Mégantic. For lichens on firs, alpha diversity increased and composition varied as elevation increased. In contrast, for bryophytes on maples, alpha diversity and composition were more responsive to the lateral gradient, with greater diversity on the upper surfaces of inclined tree boles. Finally, the alpha diversity of lichens on maples showed a weaker, negative relationship with inclination. Our results indicate that the important predictors of arboreal cryptogam diversity vary more among tree species (maple vs. fir) than focal taxa (lichens versus bryophytes). Patterns are likely due to different effects of water, temperature, and competition among bryophytes and lichens.

Comprendre la dynamique de la biodiversité le long de gradients environnementaux est crucial pour prédire les réponses écologiques dans un contexte de changements globaux. Dans cette étude, nous avons examiné les patrons de diversité alpha ainsi que la composition des communautés arboricoles de macrolichens et de bryophytes le long d'un gradient d'altitude et de gradients circulaires (autour du tronc d'un arbre, influencé par l'inclinaison ou l'aspect) des érables et des sapins au parc national du Mont Mégantic. Pour les lichens sur les sapins, la diversité alpha a augmenté et la composition a varié en fonction de l'altitude. Par contre, pour les bryophytes sur les érables, la diversité alpha et la composition étaient plus sensibles en fonction des gradients circulaires, et la diversité était plus élevée sur les surfaces supérieures des troncs fortement inclinés. Finalement, pour les lichens sur les érables, le rapport entre la diversité alpha et les gradients circulaires était faible, et montre une relation négative en fonction de l'inclinaison du tronc. Nos résultats indiquent que les prédicteurs significatifs de la diversité des communautés cryptogames varient davantage parmi les arbres hôtes (érable ou sapin) que les taxons (bryophyte ou lichen). Nous spéculons que ces patrons sont affectés par un effet différent de l'eau, de la température et de la concurrence entre les bryophytes et les lichens.

OP86

Bryophyte communities in *Quercus garryana* ecosystems on South East Vancouver Island: preliminary mesohabitat assessment

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Quercus garryana ecosystems are threatened Mediterranean-like sites that occur in a limited range on the west coast of North America. This ecosystem has higher plant diversity and rarity than any other in British Columbia, and the less than 10% remaining are relicts due to habitat loss, fragmentation, and degradation. The bryophyte component remains understudied, and identification of habitat associated communities could provide a more accurate picture of ecosystem health at remaining sites. We used floristic habitat sampling and multivariate analyses to determine bryophyte diversity and community composition among three prominent mesohabitats (meadows, outcrops, *Quercus garryana* epiphytes) in five intact sites.

We found that total species richness was highest in meadows (67), high in outcrops (63), and lowest on *Quercus garryana* (40) and included 11 provincially rare species. Alpha diversity and mean transformed abundance classes were significantly lower in the *Quercus garryana* mesohabitat versus meadows and outcrops. Multi-response permutation procedure indicated the *Quercus garryana* epiphytic community as statistically unique, whereas there was no significant difference between meadow and outcrop mesohabitat communities. Several species were identified as indicators for each mesohabitat type. Observations were compiled with micrographic images as a special project using the citizen science application iNaturalist. This study of *Quercus garryana* ecosystems from southeastern Vancouver Island, B.C., provides a preliminary mesohabitat assessment for bryophytes in this rare and threatened heterogeneous ecosystem. These baseline results can help identify priority sites for restoration based on habitats associated with bryophyte species diversity.

OP87

Habitat fragmentation and its role on bryophyte diversity: a study in the boreal forest

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The habitat fragmentation (HF) process is one of the principal drivers of biodiversity loss all over the world. A consequence of HF is a change in the landscape configuration, with effects on biodiversity that could be different from the habitat loss. The boreal forest in Quebec has experienced fragmentation by anthropogenic and natural disturbances that may put at risk its stability and resilience. Bryophytes (liverworts and mosses) are one of the principal biological components of this forest occupying a wide variety of microhabitats. Due to their susceptibility to environmental changes, they are an ideal study group to evaluate HF. The objectives of this study are (1) to assess HF effect on bryophyte diversity (α and β) and their community composition, and (2) to know what the landscape configuration and composition features influence the diversity patterns and community assembly. Around 100 landscapes with a gradient of conditions (e.g., trees species composition, age, and size of forest stands) were analyzed.

Preliminary results show a variation in the alpha and beta diversity of forest stands from the landscapes studied. This variation in the diversity of bryophytes could be explained by differences in the quantity of habitats, the quality of the stands, and their spatial arrangement in the landscapes. This study will improve HF knowledge considering an integral vision of the landscape configuration of the boreal forest. This research will provide information about how landscape configuration could help to keep the biodiversity and quality of the forest in a sustainable forest management context.

OP88

Heathland vegetation ecology relies on specific symbiotic fungi

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Background: Heathlands are protected habitats supporting numerous endangered plants and animals. Heathland soils are acidic, nutrient-poor, mainly sand and peat, and fluctuate between extreme dry and wet conditions. To access soil nutrients, vascular plant roots and liverwort rhizoids form mutualistic symbioses with fungi exchanging nutrients for photosynthates between the mycobionts and their hosts. As such, symbiotic fungal communities contribute to heathland plant survival, nutrient cycling and carbon sequestration.

Objectives: To investigate diversity and function of heathland plants' fungal symbionts to understand heathland below-ground ecology and thus improve habitat restoration and conservation strategies for the delivery of ecosystem services.

Methods: Through multidisciplinary approaches combining molecular identification, cytology, isotope tracing and cultivation experiments, we examined root and rhizoid fungal colonisation and identified the fungi of both common and rare heathland plants, including: the heathers *Calluna vulgaris* and *Erica tetralix*, the dominant grass *Molinia caerulea*, the rare lycophyte *Lycopodiella inundata*, and the liverwort *Cephalozia bicuspidata*, plus the encroaching trees, *Pinus sylvestris* and *Betula* spp. We also conducted isotope tracing experiments to assess mutualistic status between partners and tested the liverworts as carriers of fungal inoculum for heather establishment.

Results: Heathland plants maintain specific mycorrhizal or mycorrhizal-like associations with different fungal clades despite the proximity of other symbiotic fungi in adjacent vegetation. Using liverworts as bio-fertilisers for Ericaceae sharing mycorrhizal fungi offers a practical source of fungal inoculum for restoring heathlands.

Conclusion: Understanding the mutual preferences between heathland plants and their fungal symbionts is critical for protecting and managing this rare and endangered habitat.

OP89

Vegetation classification and ecology of barrens and heathlands in Nova Scotia

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Nova Scotia’s barrens are culturally iconic and ecologically important, with distinct vegetation and associated environmental drivers. Following Canadian vegetation classification standards, we describe a recently released plant community classification for these ecosystems. We sampled 331 relevé plots from 173 barren sites across their geographical range in Nova Scotia. Plot data included: vascular plant, bryophyte and lichen species abundances, plant community structure, humus form and depth, mineral soil structure and chemistry, and 19 other environmental variables. We used multivariate ordination and clustering statistics to determine key environmental drivers and to classify Nova Scotia barrens vegetation.

Our study inventoried 595 species of vascular plants, bryophytes and lichens. The classification describes 22 distinct community types, of which most are low shrublands with dominant species from the Ericaceae. Moisture regime, wind and salt spray exposure are among the most important factors explaining variations in the species composition, structure and distribution of plant communities on barrens in Nova Scotia. The factors that maintain open barrens vegetation in this largely forested region include climatic limits to soil development and tree growth, wildfire, and past land use. The classification allows estimation of a species pool for each community, and combined with aerial imagery, can help resolve the spatial context for barrens vegetation dynamics. Similar information can be used to help assess the vulnerability of barrens communities to anthropogenic impacts, including climate change. Sampling barrens stratified by classified communities also improves understanding of the relationships between plant traits and species persistence in these environments.

OP90

Moss diversity in plant communities associated with a penguin rookery on Deception Island, Maritime Antarctica

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In order to determine the influence of a penguin rookery on the diversity of vegetation on Deception Island, we studied the composition of bryophytes of a transect of approximately 2 km between Irízar Lake and the penguin rookery (*Pygoscelis antarcticus*) of La Descubierta point. A total of 39 new vegetation carpets formed mainly by bryophytes were detected, distributed in three main sectors, next to Irízar Lake, in Vapour Col and at La Descubierta point. The bryophytes correspond to 15 moss species and only 2 liverworts, with 11 moss families represented.

Two mosses, *Sanionia uncinata* (31) and *Polytrichastrum alpinum* (9), were found to dominate the moss carpets, being also the most frequent species. In addition, we found a new site on the island where the moss *Bryum orbiculatifolium* is present, which grows directly associated with the penguin rookery. In addition, we also observed that there are 5 species of mosses common to the three sectors, with five other species growing only in the penguin area that are significantly different than the other two sectors. Soil analysis show elevated contents of soil nitrogen in the penguin rookery compared to the surrounding area. Vascular plants were not detected in the entire study site. We argue that these sites are in states of early colonization where biota is marked by the presence of pioneer mosses that grow around penguin colonies, influenced likely by nutrient input through deposited guano as well as climate warming affecting the Antarctic Peninsula.

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OP91

Off with their head: a tale of decapitation and auxin

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Branching patterns are a primary determinant of plant architecture and strongly impact on productivity by regulating light harvesting potential and resource allocation. Plants colonized land over 450 million years ago, and underwent architectural diversification in the haploid (gametophyte) and diploid (sporophyte) genetic stages of the life cycle independently. Although similar branching mechanisms evolved in both genetic stages, our functional understanding of branching is limited to diploid flowering plant models such as *Arabidopsis*.

To test whether the same molecular cues regulate similar lateral branching mechanisms that have evolved independently, we previously undertook a computational and genetic analysis of branching patterns in the haploid leafy shoot of a moss, *Physcomitrium patens*, and showed that a simple model co-ordinating the activity of shoot tips across the plant can account for the branch distribution, and that three known hormonal regulators of branching in flowering plants generate the pattern. To explore further the underpinning genetic mechanism, we analysed the transcriptome of decapitated leafy shoots, in which branch initiation is activated. We identified new roles for auxin signaling and metabolism, which I will discuss.

Evolution of sexual systems in the brown algae

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Over the last few years, the brown algae have emerged as a highly valuable group to study the evolution of sex chromosomes and reproductive systems because they exhibit a remarkable diversity of sexual traits and because there have been multiple transitions between sexual systems over a relatively short evolutionary time period. The maintenance of a high level of diversity of life cycle and sexual features in a single, evolutionarily young group is outstanding among the eukaryotes, and points to a complex evolutionary history of the underlying regulatory systems. I will describe how we are using the brown algae to gain novel insights into the mechanisms and evolutionary trajectories of sex determination systems and to reveal the functional and evolutionary interactions between the sex chromosomes and key reproductive and life cycle traits.

OP93

A conserved genetic switch determines volvocine algal sex and mating-types

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Volvocine green algae have well-studied haplontic sexual cycles that are typical for chlorophytes. In heterothallic volvocines the *MID* (minus dominance) gene governs sexual differentiation and is found exclusively in the *MT*-haplotype or male sex-determining region. In isogamous unicellular *Chlamydomonas reinhardtii* (Chlamydomonas) and oogamous multicellular *Volvox carteri* (Volvox) the expression of *MID* is necessary and sufficient to induce *minus* or male gametogenesis, respectively, while in its absence *plus* or female differentiation occurs as a default program. However, it has remained unknown how the default programs of female or *plus* are specified and are modified by expression of MID protein.

Using a comparative transcriptomics approach, we identified a conserved gene, *VSR1*, whose expression correlates with gametogenesis in both Volvox and Chlamydomonas. Using genome editing we generated a *Volvox VSR1* null mutant whose novel phenotype was blockage of spermatogenesis and the conversion of sperm cell precursors to vegetative stem cells. Female *VSR1* mutants made sterile egg-like cells that also reverted to vegetative stem cells. Similarly, a Chlamydomonas *VSR1* null mutant was sterile in both mating types. We tested and validated a simple model for mating type or sexual differentiation where *VSR1* is required for female or *plus* gametogenesis when expressed on its own, but becomes a male or *minus* differentiation factor when co-expressed with Mid. Our data fill a major gap in understanding green algal sex determination and provide a paradigm for understanding the evolution of sexual differentiation in other green lineage systems through interactions between conserved transcription factors.

Ancient, gene-rich sex chromosomes in *Ceratodon* harbor conserved regulators of sexual development

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Non-recombining sex chromosomes, like the mammalian Y, often lose genes and accumulate transposable elements, a process termed degeneration. The correlation between suppressed recombination and degeneration is clear in animal XY systems, but the absence of recombination is confounded with other asymmetries between the X and Y. In contrast, UV sex chromosomes, like those found in bryophytes, experience symmetrical population genetic conditions. Here we generate and use nearly gapless female and male chromosome-scale reference genomes of the moss *Ceratodon purpureus* to test for degeneration in the bryophyte UV sex chromosome system. We show the moss sex chromosomes evolved over 300 million years ago and expanded via two chromosomal fusions. Although the sex chromosomes show signs of weaker purifying selection than autosomes, we find suppressed recombination alone is insufficient to drive gene loss on sex-specific chromosomes. Instead, the U and V sex chromosomes harbor thousands of broadly expressed genes, including numerous key regulators of sexual development across land plants.

OP95

Sex determination system in the liverwort *Marchantia polymorpha*

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Sexual reproduction is a key process to increase genetic diversity. Land plants have a life cycle with alternation of generations and show sexual differentiation in either (or both) gametophyte (*n*) and sporophyte (*2n*) generations. The regulation of sex-specific differentiation has been studied extensively on sporophyte organ development in flowering plants, but our knowledge on sex determination and sex-dependent differentiation in the gametophyte generation is limited. The liverwort *Marchantia polymorpha* is a haploid dioicous species with sex chromosomes, U for female or V for male. Amongst bryophytes, the liverwort, *M. polymorpha* is a model liverwort for which genome sequences and molecular genetic tools are available (Yamato et al. 2007; Bowman et al. 2017; Montgomery et al. 2020; Ishizaki et al. 2016), and provides unique opportunities for research on fundamental aspects of reproduction.

Spontaneous *M. polymorpha* segregants having both male and female sex chromosomes develop the female morphology, suggesting that *M. polymorpha* has a dominant sex-determining ‘feminizer’ gene on the U (Haupt 1932), but its identity was not known. Previously we reported that a molecular toggle switch for sexual differentiation in *M. polymorpha* is composed of FEMALE GAMETOPHYTE MYB (MpFGMYB), a transcriptional regulator for female differentiation, and SUPPRESSOR OF FEMINIZATION (MpSUF), an antisense long non-coding RNA, at a single autosomal locus (Hisanaga et al., 2019). The alternative expression of MpFGMYB or MpSUF is dependent on the presence or absence of the U chromosome, respectively. In this symposium, we would like to report current progress in the identification of the feminizing factor encoded by the U chromosome in the liverwort *M. polymorpha*, and genetic relationship between ‘feminizer’ lined to U-chromosome and autosomal Mp*FGMYB-MpSUF*.

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OP96

Whither the sex chromosome during the evolution of monoicy from ancestral dioicy

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Liverworts comprise one of the six primary lineages of land plants, with the predicted origin of the extant diversity of liverworts dating to the Silurian. The ancestral condition of liverworts is dioicy, with monoicy evolving multiple times independently. In cases where it has been investigated, in dioicious liverworts sex is determined chromosomally, with the female possessing a U chromosome and males having a V chromosome, with the discovery of plant sex chromosomes being made by Charles Allen in *Sphaerocarpos donnellii* more than a century ago. Subsequently, chromosomes presumed to be sex chromosomes have been described in members of all three lineages of extant liverworts, suggesting that the ancestral dioicious liverwort also harboured sex chromosomes. We have been investigating the fate of the sex chromosomes during the evolution of monoicy from dioicy, and we will present data primarily based on our analysis of the *Ricciocarpos natans* genome.

OP97

Clade III TGACG-motif binding basic leucine zipper transcription factors mediate *BLADE-ON-PETIOLE* dependent regulation of plant development

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Plant growth and development relies on meristems. Lateral organs formed by the shoot apical meristem (SAM) are separated from surrounding stem cells by regions of low growth called boundaries. Impairment of boundaries can lead to SAM termination and/or structural defects at the base of organs. Specific aspects of plant architecture controlled by boundaries include leaf shape, branching complexity, and abscission. In the model plant species *Arabidopsis thaliana*, *BLADE-ON-PETIOLE 1 AND 2* (*BOP1*/2) represent a class of genes important for boundary patterning in land plants. Members of this family lack a DNA binding domain and interact with TGACG-motif binding (TGA) basic leucine zipper (bZIP) transcription factors for recruitment to DNA.

Here, we show that clade III TGA transcription factors, *TGA3* and *TGA7*, previously associated with plant defense, are important partners of *BOP1/2* in regulation of plant development. *TGA3* and *TGA7* are expressed at organ boundaries and function in the same genetic pathway as *BOP1* and *BOP2* required for SAM maintenance, flowering, and inflorescence architecture. Further, BOP1 and BOP2 require *TGA3* and *TGA7* for the deposition of lignin in vascular tissues of the stem. Yeast two-hybrid assays show that TGA3 and TGA7 proteins form a complex with BOP1 and BOP2, possibly involved in the co-activation of genes required for boundary establishment or lignin biosynthesis. These studies identify a dual role for clade III TGA factors in development and defense.

OP98

Discerning biological function of the cytosine methyltransferase *DNMT2* in the moss *Physcomitrium patens*

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DNA Methyltransferase2/tRNA Methyltransferase1 (DNMT2/TRDMT1) is an m^{5}C RNA methyltransferase that methylates cytosine-38 in the anticodon stem loop of Aspartic acid, Valine and Glycine tRNAs. This modification is crucial for stability of tRNAs and for translation of poly Asp containing proteins under stress. DNMT2 is highly conserved in eukaryotes. Unlike animal systems where its role in cellular response to heat, oxidative and arsenite stress is well established, its biological function in land plants has remained enigmatic. In this study, we describe the role of *DNMT2* in the moss *Physcomitrium patens*.

On the basis of reverse genetics, biochemical, genome-wide transcriptomic and quantitative proteomic studies we show that *PpDNMT2* plays a crucial role in oxidative stress management, ion homeostasis, chromatin and epigenetic gene regulation in moss protonemata. *PpDNMT2*-deficient plants are indistinguishable from wild type plants under standard laboratory conditions. However, under salt and osmotic stress the mutants are unable to maintain stable tRNA^{Asp}, transcript levels and biochemical activities of antioxidant enzymes, levels of apoptosis associated protein encoding genes, levels of genes encoding Ubiquitin-26S proteasome components and genome stability. Our work also reveals that PpDNMT2 exists in complex with CuZn-SOD *in vivo* and in yeast nuclei. On the basis of biochemical, quantitative gene expression and protein deletion studies we further show that PpDNMT2 function possibly affects activity of other tRNA modifying enzymes, as levels of genes encoding tRNA-Guanine-N-7-methyltransferases (Trm8) that catalyze formation of m^{7}G46 in many tRNAs are differentially expressed in *PpDNMT2*. Further, PpDNMT2 also physically interacts with Trm8, Trm8L1 and Trm8L2 *in vivo*.

OP99

Extensive N4 cytosine methylation is essential for *Marchantia* sperm function

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4-methylcytosine (4mC) is an important DNA modification in prokaryotes, but its relevance, and even presence in eukaryotes have been mysterious. Here we show that spermatogenesis in the liverwort *Marchantia polymorpha* involves two waves of extensive DNA methylation reprogramming. First, 5-methylcytosine (5mC), a well-known eukaryotic DNA modification, expands from transposons to the entire genome. Notably, the second wave installs 4mC throughout genic regions, covering over 50% of CG sites in sperm. 4mC is catalyzed by two novel methyltransferases (MpDN4MT1a and MpDN4MT1b) specifically expressed during late spermiogenesis. Deletion of MpDN4MT1s eliminates 4mC, alters the sperm transcriptome, and produces sperm with swimming defects. Our results reveal extensive 4mC in a eukaryote and define a new family of eukaryotic methyltransferases, thereby expanding the repertoire of functional eukaryotic DNA modifications.

OP100

Novel *de novo* DNA methylation by CMT and DNMT3 orthologs in *Physcomitrella patens* and their role in genome regulation

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Cytosine methylation, a key process in regulating genome function, is established and maintained by DNA methyltransferases (DNMTs). DNMT3 known to establish methylation in mammals. In plants, altered DNMT3 homologs, *DOMAINS REARRANGED METHYLTRANSFERASE*s (DRMs), were shown to establish methylation via the RNA directed DNA methylation (RdDM) pathway, yet the role of true plant DNMT3 orthologs remained elusive.

To elucidate the role of plant DNMTs, we profiled both genomic and *de novo* methylation in the basal moss plant, *Physcomitrella patens*, mutated in each of its *PpDNMTs*.

To evaluate *P. patens* DNMTs role in *de novo* methylation, we introduced the repetitive DNA sequence (RPS) from *Petunia hybrida*, uncommon to *P. patens*. Methylation analysis of RPS at the first transgenic generation (T1), using bisulfite sequencing, reveal that RPS is methylated in WT cells in all three methylation contexts, CG, CHG, and CHH, implying on its ability to be *de novo* methylated in *P. patens*.

Methylation status of *Ppdnmt* mutants reveals that PpDNMT3b mediates CG and CHH *de novo* methylation, independently of PpDRMs. Complementary *de novo* CHG methylation is specifically mediated by the *CHROMOMETHYLASE*, PpCMT. Intragenomically, PpDNMT3b functions preferentially within heterochromatin and is affected by PpCMT. In comparison, PpDRMs target active-euchromatic transposons.

Our data resolve how DNA methylation in plants can be established in heterochromatin independently of RdDM pathway; suggesting that DRMs have emerged to target euchromatin; and link DNMT3 loss in angiosperms to the initiation of heterochromatic CHH methylation by CMT2. The role of CG and non-CG methylation in regulating transcription will be discussed.

OP101

Riccia fluitans, an informative amphibious liverwort to study plant terrestrialization

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The colonization of land by streptophyte algae, ancestors of embryophyte plants, was a fundamental event in the history of life on earth. Bryophytes are evolutionary informative as they enable to investigate adaptation mechanisms from freshwater to terrestrial ecosystems. The amphibious liverwort *Riccia fluitans*, a member of the most species-rich genus in complex liverworts, can thrive in aquatic and terrestrial habitats by undergoing morphological transitions resulting in distinctive water and land form features. The *R. fluitans* water form develops slender, elongated thalli that branch occasionally and lack air pores and rhizoids. Thallus of the *R. fluitans* land form is wider, frequently branched and forms air pores and rhizoids. This morphological plasticity realized by one genotype makes *R. fluitans* ideal to study the adaptive molecular mechanisms enabling the colonialization of land by aquatic plants.

To make *R. fluitans* amenable for genetic analyses, we established a transformation protocol using *R. fluitans* callus tissue and generated the first transgenic *R. fluitans* lines. Furthermore, for comprehensive studies spanning all *R. fluitans* life stages, the switch from vegetative to reproductive development can be induced by flooding or starvation of land form thalli. These new transformation and sexual induction protocols will make *R. fluitans* accessible in the future for investigating adaptations to a terrestrial plant life style.

Althoff, F., Zachgo, S. 2020. Transformation of *Riccia fluitans*, an amphibious liverwort dynamically responding to environmental changes. International Journal of Molecular Sciences 21 (15): 5410.

OP102

Role of phytochelatin synthase in heavy metal detoxification in the early land plant *Marchantia polymorpha*

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Marchantia polymorpha has an active Phytochelatin synthase (PCS), but its actual contribution to heavy metal tolerance *in vivo* remains an open question.

The aim of the present work was to elucidate functionally the role of *MpPCS* in the detoxification of different heavy metals and to characterize the effects that its knockout has on the plant transcriptome.

We obtained by CRISPR/Cas9 genome editing two independent mutant alleles of *PCS*, *Mppcs*^{ge}*_1* and *Mppcs*^{ge}*_2* and tested them for susceptibility to different metal(loid)s. We further compared the WT and *Mppcs*^{ge}*_1* transcriptomes by Illumina RNA-Seq analysis of differentially expressed genes followed by pathway analysis.

Thiol-peptide quantification demonstrated the complete lack of phytochelatins in the mutants, which showed no visible phenotype in normal growth conditions. However, they resulted extremely sensitive to treatment with cadmium, but tolerant to zinc. Noteworthy, mutant plants were highly tolerant to the metalloid arsenic. Whole transcriptome analysis of WT and one of the mutant lines identified a range of differentially expressed genes in different metabolic pathways that clearly distinguish the mutant even in the absence of heavy metal stress and of a visible phenotype.

These results demonstrate that the phyochelatin-mediated detoxification of heavy metals is an ancestral trait in land plants. Despite *PCS* playing a major role in the detoxification of divalent, non-essential heavy metals, the results further suggest that phytochelatin synthase may contribute to metal homeostasis in normal conditions. The mutant genotypes obtained further represent highly sensitive bioindicators of cadmium contamination, and as such they could find application in biomonitoring.

Finetuning the *in vitro* growth of the model hornwort *Anthoceros agrestis*

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Hornworts are an understudied lineage of bryophytes with unique sets of evolutionarily and agriculturally relevant genes. As part of a concerted effort to develop effective functional genetic tools in hornworts, we evaluated the contribution of several culture medium addenda on the gametophytic growth of the model hornwort *Anthoceros agrestis* (Oxford strain). Tissue development was rapidly quantified using time-lapse imaging spanning four weeks of culture of homogenized tissue grown on modifications of Hatcher's solidified medium. Equal amounts of starting tissue material were added to each medium at four petri dishes (replicates). Aside from microscopic observations, whole petri dish images were captured and analyzed through trainable image segmentation to obtain two-dimensional area of total green tissue (thalli) per dish.

Incremental addition of exogenous activated charcoal, ammonium nitrate, sucrose, MES buffering, Gamborg vitamins and growth regulators (6-benzylaminopurine, 2,4-dichlorophenoxyacetic acid and thidiazuron) were evaluated, resulting in a gradient of phenotypic effects that include changes in gametophyte tissue survival, tissue color, patterns and speed of thalli growth, as well as frequency of rhizoid formation. Based on these findings, an improved medium composition and growth regimen for *A. agrestis* gametophyte tissue was formulated, which maintained tissue vitality while increasing the average area of thalli by more than five times following three weeks of culture. Importantly, this amount of thalli growth was more than double the amount after four weeks of culture on various baseline hornwort solidified media (Hatcher's, BCD and KNOP). These results provide critical groundwork towards establishing effective tools for studying gene function in hornworts.

OP104

Climate change and a new dominant seaweed on the Atlantic coast of Nova Scotia

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Fucus serratus was introduced into Nova Scotia in the 19th century from western Europe and has become a dominant component of the subtidal flora in the southern Gulf of St. Lawrence and the shores surrounding Cape Breton Island. Here, we report a major change in geographic distribution of *F. serratus* on the Atlantic coast of Nova Scotia from its previously documented occurrences near the southwestern tip of the province (from the 1950s), near Lunenburg (from the early 1990s), and Tor Bay (from the mid 2000s), an overall distance of approximately 500 km.

In 2020 and 2021 we found attached *F. serratus* intertidally and subtidally at many sites along the Atlantic coastline, especially on the South Shore of Nova Scotia, and thalli in the wrack at many locations. In addition, we describe a new pattern of seaweed zonation for the northwestern Atlantic Ocean in which *F. serratus* has become a canopy-forming dominant species in large portions of the low to mid intertidal zone, where it can occupy from 20% to 40% of shore area, and dense populations extend to about 4 m below chart datum. This coastline of Nova Scotia has been identified as a regional hotspot for ocean warming, and adjacent annual air temperatures have risen over 1 °C since the 1990s. We attribute the change in distribution and ecology of *F. serratus* to regional climate warming previously associated with major reductions in populations of kelp and sea urchins.

Evaluating salt marsh rhizosphere carbon stocks and arbuscular mycorrhizal colonization across a chronosequence in the Bay of Fundy, Nova Scotia

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Salt marshes are essential ecosystems that stabilize coastlines while providing habitat and nursery for many invertebrates, juvenile fishes, and birds. Unfortunately, due to the development of agriculture, commercial land, and embanking/dyking, salt marshes are declining worldwide. Salt marshes can accumulate and store large amounts of carbon as 'blue carbon'. Carbon is trapped from the atmosphere and rhizosphere by the salt marsh, which allows it to be utilized by salt marsh vegetation and their fungal associates. Recent studies have found that beneficial fungi form associations with salt marsh plant roots. Arbuscular mycorrhizal fungi (AMF) form these associations with approximately 80% of all land plants. AMF receive fixed carbon from their host plant, and in return, provide the plant with mineral nutrients and an increased surface area, which leads to greater carbon storage.

We are investigating the role of AMF in helping salt marshes sequester carbon. We are examining the correlation between the amount of carbon and AMF colonization present in salt marsh plants. Additionally, we are analyzing the quantity of nitrogen, phosphorus, and salt present in the rhizosphere and exploring its effect on AMF colonization. Furthermore, we are evaluating how rhizosphere carbon stocks vary with vegetation types across a chronosequence of salt marshes in comparison with dykeland habitats fringing the Bay of Fundy, Canada. We have found high AMF colonization rates in *Spartina pectinata* roots with varying organic carbon rates. A further understanding of carbon stocks and mycorrhizal associations will increase our knowledge of their contributions to salt marsh restoration methods.

OP106

Implications of warming for conservation of endangered plants: a Nova Scotian case study

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Nova Scotia has warmed by about a degree centigrade between the two climate normal phases over the last 60 years. Taking these climate normal brackets as summaries of 30 years of weather data, the average annual air temperature increased by 0.8 °C in 30 years. Period summaries and yearly averages of a whole region mask regional changes. The rate of change in some areas has been more rapid, e.g., a 2 °C shift in temperature occurred on Brier Island from its cool normal for 1961–1990 to a 'new normal' beginning in 2006. The impact of sudden warming on the endangered Arctic-alpine, Eastern Mountain Avens was not anticipated; 'planning for and mitigating impacts of climate change on Eastern Mountain Avens' was ranked of low priority in the Action Plan (Environment Canada 2018) although the Recovery Strategy (2010) stated that threats (e.g., nutrient enrichment, interspecific competition, low water table, shrub growth) could be compounded by climate change.

We discuss the challenges of adaptive management of this endangered plant on a changing landscape and consider the tolerance limits of its physiology. Conservation concerns of imminent and active warming of a cold-origin, endangered species, however, are different from those that apply to warm origin, Atlantic Coastal Plain Flora. We contrast the cases of the Arctic–alpine Avens with the coastal plain Plymouth Gentian and Rockrose and look at the timing of impacts on key ecosystem processes (water tables, decomposition, ice scour, mineralization, transpiration, fire) and the vulnerabilities of growth and reproductive processes to climate change.

OP107

Experimental warming and drying reveals high stress resistance in jack pine versus reduced carbon uptake and growth in black and white spruce

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In boreal forest ecosystems, the projected increase in temperature and water stress is expected to modify many ecophysiological processes in trees, with amplified effects on seedlings. Moreover, tree species show different responses to climate change which suggests that acclimatation capabilities are species-specific.

During our study, we subjected three boreal seedling species (*Picea mariana, Picea glauca* and *Pinus banksiana*) to four drought intensities (control, moderate, severe and low frequency respectively) nested in two temperature treatments (ambient versus projected temperature (+4 °C)). Throughout the season, we observed and recorded their phenological and physiological responses.

Our results show that drought treatments did not impact the physiological processes, growth, and phenology of jack pine. On the contrary, both spruces reduced their photosynthesis as well as their biomass production. In response to water stress, jack pine displays an anisohydric strategy while the spruces exhibit an isohydric strategy.

Warming increased jack pine photosynthesis (19.5 ± 0.18%), while it remained unchanged in both spruces. Temperature increases had contrasting effects on seedlings growth rate. Warming led to a higher growth rate for jack pine, while it remained unchanged for black spruce. White spruce growth rate decreased with warming. Also, both spruces grew earlier in the season with increasing temperature (13.3 ± 0.14 days for white spruce and 15.5 ± 0.13 days for black spruce). However, under ambient and elevated temperatures, jack pine is the faster growing species.

Our results suggest that jack pine could be more tolerant to warming and drought stresses compared to black and white spruce.

Exploring phytobiomes and bulk soils across biogeoclimatic zones in the coast, interior, and northern British Columbia

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Climate change will cause plants to migrate. Plant-associated organisms, including in soil food webs (e.g., fungi, bacteria, soil fauna), may move at different speeds creating novel phytobiomes. A phytobiome encompasses a plant, its associated micro- and macro-organisms, and the environment. Soil nematodes aid soil food web nutrient cycling and are bioindicators sensitive to different soils and abiotic conditions.

We set out to compare the effects of planting interior Douglas-fir (*Pseudotsuga menziesii* var. *glauca* (Mayr) Franco) from two seedlots (southern adapted and northern adapted) on phytobiomes in replicate clear-cut sites ($N = 3$ per zone) located in coastal, interior, and northern British Columbia. After a year of growth, seedlings were randomly sampled for root and shoot biomass, rhizosphere organisms (i.e., nematode abundance, and DNA sequencing for ecological communities of prokaryotes and eukaryotes), and soil properties ($N = 54$ per seedlot). Bulk soils into which seedlings were not planted were also collected ($N = 54$).

Plant biomass (shoot, root) was significantly lower at northern sites ($P < 0.001$). Overall, shoot biomass of northern adapted seedlings was greater than southern adapted ($P = 0.026$), but there were no significant differences within sites. Planted seedlings increased nematode densities relative to bulk soil ($P = 0.004$), with no seedlot effect. In conclusion, the addition of Douglas-fir seedlings increased the local abundance of soil nematodes on clear-cuts, regardless of the seed source. Forthcoming sequencing data will explore whether there are accompanying effects on nematode community composition and fungal and bacterial components of the phytobiome.

OP109

The question remains: are bryophytes tolerant to ultraviolet-B radiation?

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Although being a minor component (around 0.25%) of solar radiation, the UV-B band (280-315 nm) is an important regulatory factor of plant physiology. However, in excess, UV-B can be harmful due to diverse types of damage. Almost 70 bryophytes (one hornwort, 16 liverworts, and 50 mosses) have been tested for UV-B tolerance in more than 100 studies, but the enormous diversity of conditions used for experimentation makes it difficult to generalize the results obtained. Thus, the question remains: are bryophytes tolerant to UV-B radiation?

Aiming to help answer this question, we applied the same UV-B treatment to 64 bryophytes (two hornworts, 23 liverworts, and 39 mosses) collected in diverse mid-latitude environments, in the most extensive study to date on the subject. Using UV-B LEDs and cut-off filters, we applied 9 W m^{-2} UV-B (around 5-fold the peak irradiance received in a sunny day at mid-latitudes) to the samples for one hour under controlled conditions. UV-B tolerance was assessed using chlorophyll fluorescence variables. We confirmed that UV-B tolerance of bryophytes depends on the species considered, and is greatly influenced by the taxonomic group.

Overall, mosses were more UV-B-tolerant than liverworts and hornworts, although a certain overlap between mosses and liverworts occurred. For example, *Hookeria lucens*, *Mnium hornum*, and *Fontinalis squamosa* were sensitive mosses, while *Frullania tamarisci* and *Porella arboris-vitae* were tolerant liverworts. UV-B tolerance was significantly correlated with the content of potentially protective UV-absorbing compounds, such as flavonoids, and with the sclerophylly of the shoots. Structural, physiological, and ecological aspects are discussed.

OP110

Mosses as biomonitor: atmospheric metal load of pre and post pandemic periods

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The steadily increasing trend of atmospheric metals requires continuous monitoring of the environment, their dispersion pattern, possible sources and their influence on ecosystems. For this mosses are preferred as ideal monitoring tools due to their wide-spread and potentials to survive in extreme harsh conditions. Instrumental monitoring is expensive as it is associated with deployment of instruments at a number of sampling sites and manpower to run these. Bryophytes, on the other hand, are wide in distribution and need no care for growth. Lack of root and conducting tissue rules out absorption of metals from the substratum. Additionally, the absence of cuticles make their cell walls easy to assess for metals and allows metal absorption over the entire surface. Mosses have mechanisms to cope with the elevated concentrations of metals and this could be due to induction of metal-binding protein (Zulema et al 2018). These mechanisms resulted in the ability of many bryophytes to survive and colonize in metal-rich areas.

The results of the analysis of moss transplant samples from the past 15 years till 2015 (pre-pandemic period) have shown an increasing trend of atmospheric metals. However, studies conducted during pandemic periods i.e. last week of March 2020, when a nationwide lockdown was declared by the Government of India due to the pandemic, exhibited an alarming decrease in atmospheric metal load in moss samples harvested and analyzed for metals. A diminution in metal accumulation in moss samples measured during the lockdown period could be owing to minimal or no vehicular movement and halted operations of the factories and construction sites.

Zulema Varela, Sofía Debén, Dinesh K. Saxena, J.R. Aboal, J.A. Férnandez . 2018. Levels of Antioxidant compound glutathione in moss from industrial areas. Atmosphere 9, 284, doi 10.3390.2-8.

New insights into the liverwort and moss backbone phylogeny using the GoFlag probe kit

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Phylogenomic inferences from large suites of loci are anticipated to resolve the suprafamilial relationships within the three bryophyte lineages, whose diversification spans at least 400 million years. The newly designed GoFlag probe kit for target enrichment provides a universal tool for generating large nuclear datasets to resolve phylogenetic relationships among flagellate land plants. We present ongoing phylogenomic analyses of 444 nuclear loci (exons) from assembling a genus wide molecular phylogeny of mosses and liverworts, with hornworts serving as the outgroup. We inferred relationships among the over 500 bryophyte specimens using Maximum Likelihood (RAxML) and a species tree analysis using ASTRAL. The RAxML and ASTRAL analyses yielded largely congruent results with a highly supported backbone phylogeny for mosses and liverworts. We evaluate the targeted loci and their phylogenetic usefulness and propose a selection of loci that work best for mosses and liverworts including their various subgroups such as rapidly evolving families.

OP112

Applying an 802-gene probe set to moss phylogenetics, with an emphasis on the pleurocarp lineage

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Reconstructing relationships within and among major lineages of pleurocarpous mosses remains a significant challenge in plant systematics. The pleurocarp lineage split from their most recent common ancestor shared with acrocarpous (or putatively ‘proto-pleurocarpous’) mosses well over 100 million years ago and was accompanied by rapid bouts of diversification. Ultimately, this rapid diversification led to over 5200 extant species that are distributed worldwide, comprising 40–50% of all moss species. Unsurprisingly, current molecular phylogenetic analyses suggest that families and genera within Hypnanae are abundantly polyphyletic. Without an accurate circumscription of major lineages in Hypnanae, taxon sampling for phylogenetic analysis, for example within families, may artificially exclude close relatives or include distantly related taxa. To address this challenge, we designed a set of probes representing 802 nuclear genes to be used for target enrichment. Here, we present a phylogenomic approach that uses 802 nuclear genes of 368 species representing all major clades within Hypnanae, as well as a broader discussion of the utility and efficiency of this probe set.

OP113

Exploring systematic relationships and morphological evolution in the moss genus *Fissidens* using data generated from herbarium specimens

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Fissidens is a charismatic and morphologically distinct genus of mosses containing over 400 named species that have a distichous leaf arrangement and a leaf lamina that is split into a ‘V’, pocketing the leaf above into the one below. We are using a molecular phylogenetic approach to examine the relationships and test the monophyly of two classification systems for Fissidentaceae Subgenera and Sections proposed by Pursell and Bruggeman-Nannenga in 2004 and Suzuki, Inoue, and Tsubota in 2018. We have assembled two complementary datasets using material sampled from herbarium specimens to examine these relationships. First, in collaboration with the National Science Foundation funded GoFlag project, we have assembled a dataset including over 400 loci for approximately 40 *Fissidens* species and secondly we have assembled a three loci (*trnL-F*, *trnA-nad7*, ITS2) dataset for over 100 samples representing approximately 50 *Fissidens* species. Preliminary analyses of these data indicate that Subgenus *Aloma* and Subgenus

Pachyfissidens are each monophyletic and that subgenus *Octodiceras* is nested within subgenus *Fissidens*. Our ongoing studies will use ancestral character state reconstructions and correlation analyses to explore the evolution of and relationships between morphological characters of Fissidentaceae species, focusing on the axillary hyaline nodules, limbidia, costa anatomy, peristome teeth, and sexual systems. The results of this study will help to deepen our understanding of morphological evolution in this diverse lineage of mosses.

OP114

A 400-gene phylogeny of the hornworts unveils new relationships and new insights on character evolution and diversification

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Recent plant phylogenomic studies strongly support bryophytes (hornworts, mosses and liverworts) as a clade. Hornworts are the least species-rich bryophyte group (~220 spp.) and they are sister to setaphytes (liverworts plus mosses). A renewed interest in hornworts has been fueled by nuclear genomic analyses of their unique traits such as endophytic cyanobacterial symbiosis and the atavistic presence of pyrenoids, a physical carbon concentrating site found otherwise in algae. In previous analyses based on five organellar loci, hornwort relationships seemed to be stable with *Leiosporoceros* (Leiosporocerotales) reconstructed as sister to all other species. This solid topology has been the base of multiple ancestral character reconstruction, divergence times and diversification studies. For example, pyrenoids were reconstructed as a derived condition in hornworts simply because *Leiosporoceros* lacks this trait.

We present ongoing phylogenomic analyses of 427 genes from 79 species (ca. 35% of hornwort diversity) encompassing all five orders and eleven hornwort genera. Maximum likelihood and ASTRAL were used to estimate gene and species trees. Our phylogenomic analyses recover two hornwort clades: *Leiosporoceros* + *Anthoceros sensu lato* and the rest of the hornwort genera. The position of *Leiosporoceros* as sister to genus *Anthoceros* and within the order Anthocerotales is supported by 87% of the quartet trees inferred by ASTRAL. The unexpected relationship is justified by gametophytic morphological characters related to antheridia. This topology requires a reinterpretation of the evolution of the previously considered plesiomorphic features of *Leiosporoceros* that include *Nostoc* strands, chloroplast ultrastructure and spore morphology. We will present divergence times and ancestral character reconstructions and propose new scenarios of character evolution, including the pyrenoid.

Trait Evolution and Biogeography of *Syntrichia* Brid.

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Syntrichia is one of the most diverse genera of the family Pottiaceae. It contains around 90 named species distributed in almost all terrestrial ecosystems. It is a dominant group of mosses in habitats ranging from temperate to desert biocrusts across western North America. Yet many taxa occur in the Neotropics, most of which are concentrated in the Andes or polar climates from the southernmost regions of South America.

Only a few phylogenetic analyses have been performed in *Syntrichia*; and these have only focused on a particular subclade or geographic area using a restricted number of molecular markers. The backbone relationships within the genus are still challenging and require careful integration of morphological and molecular analyses.

Our research group is undertaking phylogenetic analysis at several scales; here we report results based on target enrichment sequencing data (GoFlag project) that yielded about 450 nuclear loci for most named species of *Syntrichia* worldwide plus additional outgroups (98 OTUs) to understand (1) the evolutionary history of the group, (2) trait evolution, and (3) global biogeography. We use a newly developed morphological character matrix (42 characters) to distinguish major clades for integration with molecular data in total-evidence phylogenetic analyses.

Our results suggested that *Syntrichia* is a monophyletic group that likely originated in South America. We identified major clades based on morphology and/or geographic range, including a large Northern Hemisphere clade that originated from South America. Functional traits involved in water relations evolved multiple times in the group and are correlated with habitat preference.

OP116

Phylogeny of Orthotricheae (Orthotrichaceae, Bryophyta) under the light of the GoFlag data

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Over the last two decades, the increase in the knowledge of the moss subfamily Orthotrichoideae has driven important taxonomic changes, including a rearrangement at the generic level. Accordingly, our understanding of the phylogenetic relationships of the main taxa within the subfamily recently have been revised based on molecular data generated by Sanger sequencing. However, in some cases, analyses based on only a few loci can be misleading due to different genetic phenomena such as reticulation and incomplete lineage sorting. We here present a molecular phylogenomic reconstruction of 68 taxa of the tribe Orthotricheae based on approximately 400 nuclear loci generated by target enrichment using the GoFlag 408 probe set.

Our preliminary results overall agree with the current phylogenetic proposal. Orthotricheae is divided into two main clades that correspond to the subtribes Orthotrichinae and Lewinskyinae. Orthotrichinae includes the diverse genus *Orthotrichum*, whereas Lewinskyinae comprises both *Lewinskya* and *Ulota* together with some smaller genera including *Plenogemma*, *Pulvigera*, and *Atlantichella*. The genus *Atlantichella* has been recently segregated from *Ulota* and now is validated by the target enrichment data. In addition, we provide evidence for the segregation of a new monotypic genus currently included within *Ulota*. Finally, our results suggest that *Nyholmiella* should no longer be considered as a member of Orthotrichinae. Further studies are needed to determine whether this genus should be treated as a member of Lewinskyinae or segregated as an additional subtribe.

OP117

Epiphytic bryophyte diversity in *Juglans neotropica* plantations of Ecuador

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Tropical montane forests are considered biodiversity hotspots, where epiphytic bryophytes are an important component of diversity and functioning of these forests. We evaluated the diversity of bryophytes in secondary forests and plantations of *Juglans neotropica*. The presence and cover of epiphytic bryophytes was registered in 100 trees. We analyzed the effects of microclimatic factors on bryophyte richness using a generalized linear model (GLM), and the changes in species composition using multivariate analysis. Fifty-five bryophyte species were recorded, of which 42 species in secondary forest and 41 in mixed plantations. At tree level, richness was higher in the mixed plantation of *J. neotropica* compared to the secondary forests, due to the presence of species adapted to high light conditions, however species composition were negatively affected by the more open canopy in the mixed plantation of *J. neotropica*. We conclude that shade bryophytes are threatened by deforestation, and *J. neotropica* plantations do not act as refuge for these species.

Tree-forest composition drives bacterial associations with feather-mosses

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Bryophytes host a variety of bacterial linages in their phyllosphere (leaf surfaces), including N_2-fixing cyanobacteria that play a key role in the nitrogen cycle (fixing up to 7 kgN $ha^{-1}yr^{-1}$) in nitrogen-limited boreal forests. Despite the high abundance of bryophytes in boreal coniferous ecosystems, few studies have explored the complete bacterial diversity associated with bryophytes and the factors driving these associations. While moss species identity seems to be the main driver of moss-phyllosphere composition, it has been suggested that certain environmental conditions may also play a role. In order to determine the relative importance of moss-species identity and environmental conditions defined by tree-canopy dominance in determining moss-phyllosphere composition, we quantified changes in microbial communities as a function of moss-species identity (*Pleurozium schreberi* and *Ptilium crista-castrensis*) and forest type (black spruce versus trembling aspen) in boreal forests of northwest Quebec.

Results indicate that forest type was the most important driver of moss-associated bacterial community composition. Also, *Cyanobacteria* drove this pattern as they were highly abundant in trembling aspen stands and less prevalent in black spruce stands. While the intrinsic physicochemistry of leaves can explain host identity as a driver of moss-phyllosphere associations, moss chemical composition also changes with environmental conditions and individual requirements. The heterogeneous and nutrient-rich aspen understory might influence the moss phyllosphere via abiotic effects, competition and facilitation processes. Considering that boreal forests are increasingly dominated by deciduous trees, due to natural fires, human land uses and climate change, effects on bryophyte phyllosphere could result in changes in ecosystem services.

OP119

Off-site impacts of mines on understory plants and moss phyllosphere bacteria in boreal ecosystems: integrating mine stages and habitats

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Mining is one of the main anthropogenic disturbances on boreal biodiversity and ecological services in Canada. The off-site ecological impacts of mines are a growing concern with increasing global mining activities over the last decade. This study examined and evaluated the off-site impacts of mines on understory plants and phyllosphere bacterial communities (PBCs) of feather moss (*Pleurozium schreberi*) with six mines at two stages (operating and non-operating) in Quebec. Six to eight transects were established perpendicularly to each mine's periphery through different types of ecosystems (forest types and peatlands). Plant and phyllosphere samples were collected inside plots spread along each transect at different distances from each mine's periphery.

We found that: (1) the diversity of plants and PBCs present a significant association with the distance from the edge of mines; (2) Mine stages and ecosystem types present a significant association with the magnitude of off-site impacts of mines. For instance, the relative abundance of Bacteroidetes and Chloroflexi was higher near mines in peatland plots, while no significant impacts were found in non-peatland plots. Non-native plant species were more abundant near operating mines than that of non-operating mines.

In conclusion, our results supported the presence of off-site impacts of mines on the diversity and structure of understory plants and phyllosphere bacteria. Furthermore, mine stage and ecosystem type can influence the off-site impacts of mines. These results provide a baseline reference and evidence to guide ecological risk assessments for mining projects considering off-site impacts involved in boreal areas.

Revegetation of disturbed lands: establishing native plant communities on borrow pits in northern Manitoba

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The historic occurrence of hydroelectric development in northern Manitoba has resulted in disturbed areas without vegetative cover on ancestral First Nation's land within the boreal forest. These disturbed areas remain with compacted soil lacking in nutrients, organic matter and possess low water-holding capacities. Northern climate conditions and short growing seasons further inhibit recovery potential. The study objective was to develop a strategy for encouraging self-sustaining native plant communities on borrow pits in northern Manitoba. Using fertilizer and mycorrhizal inoculations, seeding, transplants and cuttings were carried out using locally sourced plant species. Soil nitrogen, phosphorus, organic matter content, pH and electrical conductivity were analyzed for differences among treatments and the surrounding undisturbed forest to determine impacts of material extraction on the land. Plant number, height, leaf-area and chlorophyll fluorescence as a proxy for stress were monitored to assess differences among treatments.

Preliminary results of the study show transplantation as the most effective planting method due to extremely low germination rates of seeds and survival of cuttings. Soil nutrients were significantly higher in fertilized treatment plots, although no significant differences were identified in number, size or stress of plants between treatments. This research provides vital information for cost effective site preparation and amendments required for revegetation efforts that can be widely implemented across borrow areas in northern ecosystems. By encouraging a full working ecosystem to develop using local plant species for sustenance and medicinal practices the land will provide more value to the local communities and wildlife populations.

The impacts of rock climbing on lichen and bryophyte cliff communities in northwestern North America

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Cliff-dwelling biodiversity is threatened by the increasingly popular sport of rock climbing. In cliff ecosystems lichens and bryophytes are often the most abundant and diverse organisms. Here we report how the popularity, difficulty, and age of rock climbing routes impacts bryophytes and lichens at two different climbing areas in Spokane County, Washington, USA (McLellan Rocks and Rocks of Sharon). We compared 16 rock climbing routes with adjacent unclimbed cliff face for abundance and diversity of lichens and bryophytes from 254 plots, each 0.5 m^2. To control for variation among paired transects across sites we collected slope and rock heterogeneity for each plot, and aspect, and canopy cover per transect. For climbed transects we recorded route age, difficulty, popularity, and approach distance. Linear mixed effect models were used to test how rock climbing impacts lichens and bryophytes.

Lichen and bryophyte cover was higher overall in unclimbed transects compared to climbed transects. Route age and plot height explained most of the variation in lichen and bryophyte cover. Older routes had higher lichen but lower bryophyte cover than newer routes. Lichen abundance was directly related to bryophytes at both sites; the lower the bryophyte cover, the higher the lichen cover. New county records and rare species were found across both groups, including the lichens *Henrica americana* and *Umbilicaria vellea* and the liverwort *Frullania californica*. Our results highlight the importance of including route age, climbing intensity, a paired transect study design, and detailed lichen and bryophyte diversity when creating data-driven management plans for rock climbing areas.

OP122

Native plant and insect communities along perimeter plantings and interiors of vineyards

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Niagara Region is home to many vineyards. As monocultures, the way these vineyards are structured and managed can make a big difference to the local biodiversity. In this study, plant and insect species in both organic and conventional vineyards were surveyed within their perimeters and vineyard interiors. Native and invasive plant species were identified, as were beneficial and pest species of insects. Beneficial insects included in the study were some predatory beetles and parasitoid wasps, while pests were aphids, thrips, and leafhoppers.

The results showed that more native plants and invasive plants were found in the perimeters of vineyards. Organic vineyards had greater insect abundance overall, but plant species diversity didn’t significantly differ. Native plants and beneficial insects were positively correlated, and there was a slight correlation with native plants and pest insects, as well as overall insect abundance. Other non-native non-invasive plant species were negatively correlated with beneficial insects and insect abundance in general. Invasive plants did not show significant correlation with either groups of insects, though was correlated to insects that were not pests or beneficials. Biological insect control is just one of the ecosystem services that landscapes rich in native plants can provide. These results contribute to a better understanding of how vineyard management, structure, and diversity can impact beneficial insect populations, which can inform sustainable practices within viticulture.

OP123

How does larch influence the composition of herbaceous and bryophyte species in the understory?

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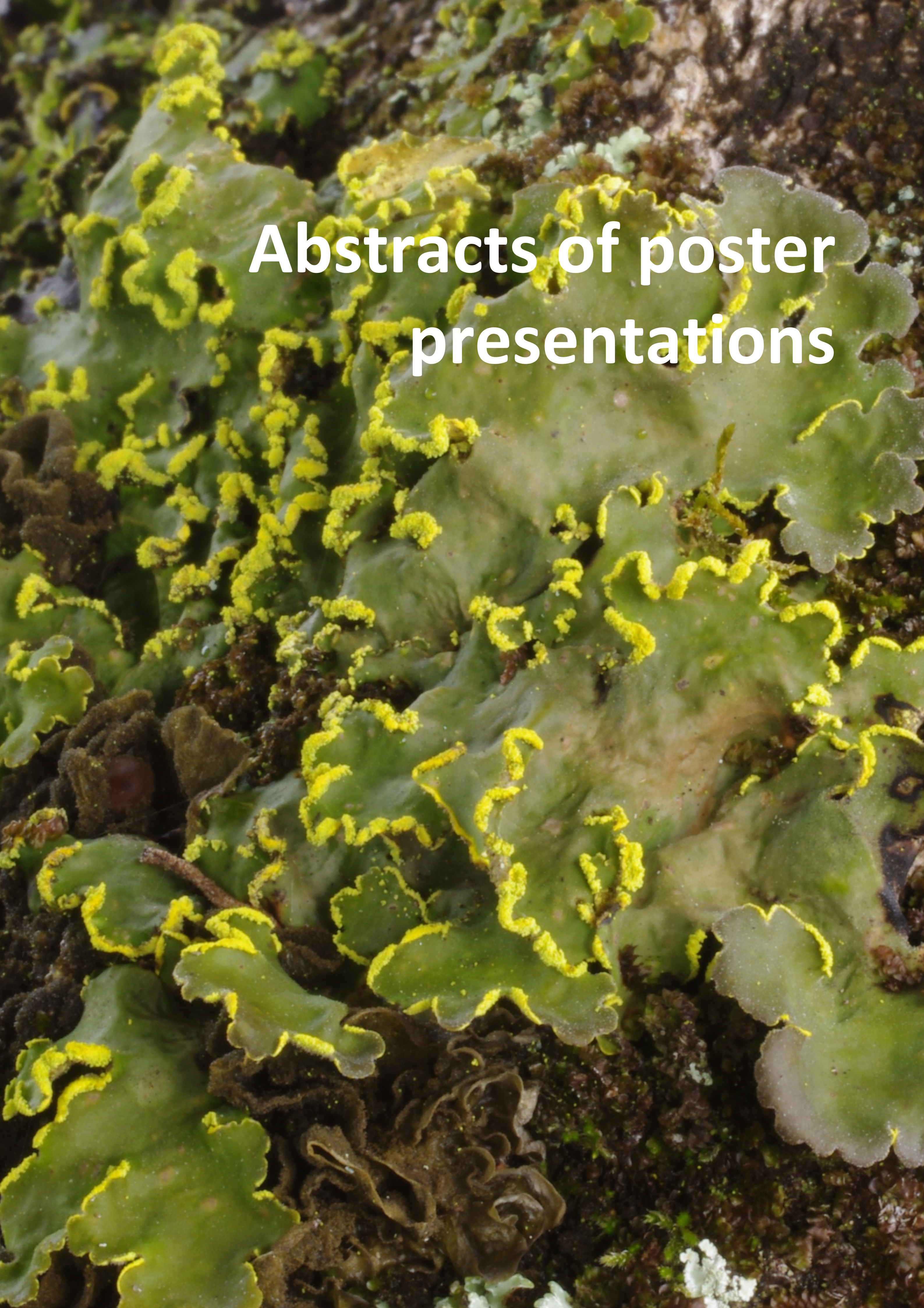
High quality litter deposition and low light interception by trees in hardwood stands results in rapid nutrient cycling compared to evergreen conifer stands. This rapid cycling favors the establishment of vascular plants and bryophytes adapted to rich, light environments in the understory. Does tamarack (*Larix laricina* (Du Roi) K. Koch), a deciduous conifer, have the same impact on understory floristic communities? The objective of this study is to understand the influence of tamarack on the composition of understory vascular plant and bryophyte communities in the boreal forest. Therefore, we studied soil hydrogeochemical characteristics, canopy closure, and the composition and functional traits of understory vascular and bryophyte communities in 19 sites selected to cover a tamarack gradient in Northern Quebec. A total of 10 inventory quadrats were sampled in each site.

Our results illustrate a gradient in the composition of understory plants and bryophytes associated with the proportion of tamarack in the canopy. For sites without tamarack, some associated herbaceous species are *Drosera* spp., *Rhododendron groenlandicum*, *Kalmia angustifolia*, *Smilacina trifolia*, *Kalmia polifolia*, *Rubus chamaemorus*, and *Chamaedaphne calyculat*a. For sites with a majority of tamarack (more than 75%), some associated species are *Dryopteris disjuncta*, *Symphyotrichum* cf. *ciliolatum*, *Mitella nuda*, *Aster radula*, *Anemone quinquefolia*, *Pyrola elliptica* and *Alnus rugosa*. We observe that the herbaceous species associated with stands with a lot of tamarack are species of rich and luminous environments compared to the species associated with black spruce stands. In conclusion, tamarack stands have a more rapid cycling of nutrients comparable to hardwood stands.

Abstracts of poster presentations



PP1

Evolutionary and functional analysis of SQUAMOSA-PROMOTER BINDING PROTEIN-LIKE (*SPL*) gene family in *Marchantia polymorpha*, an emerging model plant system

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Marchantia polymorpha is a dioecious liverwort that emerged as a model plant because of its haploid dominant life cycle and low-level redundancy in the regulatory genes compared to genomes of other land plants. The SQUAMOSA-PROMOTER BINDING PROTEIN-LIKE (SPL) family of transcription factors is functionally diverse in controlling a number of fundamental aspects of plant growth and development. Each *SPL* gene encodes a protein with highly conserved DNA binding domain, known as the SBP domain. In *Marchantia*, four *SPL* family members have been identified (*MpSPL1 – MpSPL4*). However, the evolutionary patterns and driving forces of SPL genes in this liverwort are still not well-characterized.

Our phylogenetic analysis classified MpSPL4 protein in group 1, with the rest of *Marchantia* SPL proteins in group 2, according to Zhang's classification. The motif analysis revealed that the conserved SBP domains of Marchantia SPL proteins mostly resemble that of land plants than the green algae. To investigate the role of *MpSPL3* and *MpSPL4* genes, we have generated CRISPR/Cas9 genome-edited lines for both these genes and the phenotype analysis is currently underway. To monitor the transcriptional activity of *MpSPL3* and *MpSPL4* genes in plants, we have prepared GUS and Citrine reporter lines under native promoter regions of both genes. Additionally, we have prepared over-expression lines of both genes to investigate the impact of overaccumulation of MpSPL3 and MpSPL4 proteins in Marchantia during its life cycle. Our studies on *Marchantia SPL* genes will foster substantial insights into the genetic basis for variation in plant life history.

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Growth inhibition effects of some mosses on the phytopathogenic fungus '*Bipolaris sorokiniana*''

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Mosses have proved to have anti-fungal properties due to their specific chemical compounds. In this study, the different extracts of some mosses collected from Iran were tested on a phytopathogenic fungus i.e. *Bipolaris sorokiniana*, an important pathogens of crops, especially wheat and compared to the commercial fungicides Benomyl, Difnoconazole and Tetraconazole. For this purpose, the dried moss samples were extracted by ethanol, methanol and acetone. The antifungal activity was tested by disc-diffusion method on plates of Potato Dextrose Agar. 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 then transferred into pots containing a 1 : 10 mixture of soil and soil contaminated with *B. sorokiniana*. After 35 days, the root and crown of wheat plants were examined based on Wallwork scale. The experiment was conducted as a completely randomized design with three replications. The results showed that, ethanolic extracts of *Oxystegus tenuirostris*, *Cinclidotus riparius*, *Palustriella commutata* and *Eucladium verticillatum* produced similar inhibitory effects as Difnoconazole and Tetraconazole while acetonic and methanolic extracts had limited effects. *In vivo* observations had also indicated that, ethanolic extract of *E. verticillatum* can prevent the growth of mycelium and in some cases, had similar effects as Benomyl.

Observations and experiments on lichen grazing in Atlantic Canada

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In this study, the grazing of epiphytic lichens is documented for the first time in the province of Newfoundland and Labrador, using a combination of a night survey, time-lapse camera photos and a laboratory experiment. Both time-lapse cameras and the night survey captured the feeding of gastropods and sowbugs/woodlice on lichens of the genus *Lobaria*. The laboratory experiment involved a multiple-choice feeding design. Three lichen species were sewn onto mesh and attached to red maple sticks inside a

terrarium where four, *Cepaea nemoralis,* snails were included. The level of grazing and choices by the snails surprised us. Herbivory was high for all lichen species but was highest for *Platismatia glauca* for which 70% of thalli were consumed after only 24 hours. Our results show that gastropods and other invertebrates are most likely affecting the distribution and abundance of epiphytic lichens in the forests of Atlantic Canada.

Contribution to the study of the lichen diversity in the Remchi region (Tlemcen western Algeria)

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The study we have conducted aims to inventory and identify the lichen flora of the Remchi region.

The taxonomic identification of lichens has been carried out with the help of available floras and guides: *Les Lichens: Étude biologique et Flore illustrée* (Ozenda and Clauzade 1970); *Guide des Lichens de France: Lichens des Arbres* (Van Haluwyn et al. 2013), Tela Botanica's lichen booklet (2019), and *A Key to Common Lichens on Trees in England* (Nimis 2019). Based on more than one hundred surveys carried out by the partial sampling method 38 species of lichens were identified, they are distributed in 22 genera whose dominant ones are *Physcia*, *Lecanora*, *Zanthoria*, and 11 families whose most dominant ones are respectively Parmeliaceae, Physciaceae, Lecanoraceae and Teloschistaceae.

The taxa recorded are divided into three types of thallus: 84 leafy, 27 crustose and 1 complex.

PP5

Systematic revision of *Cuscuta* L. section *Indecorae*: a combined ecological, morphometric, and phylogenetic approach

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Cuscuta section *Indecorae* contains both pests that pose significant threats to agricultural crop production, and others that are of conservation concern. Past taxonomic revisions of section *Indecorae* used solely morphology, reproductive biology and host preference to separate taxa. However, preliminary phylogenetic analyses using molecular data inferred species and infraspecific level polyphyly of *C. indecora*, strongly suggesting that species limits and infraspecific variation must be reconsidered.

The objective of this study is to use new phylogenetic data in combination with morphometric and ecological studies to resolve this systematic issue of apparent polyphyly in section *Indecorae*.

Herbarium specimens from across the geographic range of all section *Indecorae* taxa will be examined. Specimens will be sampled for DNA isolation, amplification, sequencing, and alignment. Phylogenetic trees will be generated using plastid DNA (*trnLF* region) and nuclear ribosomal DNA (*ITS* region) data. Photographs and measurements for morphometric and micromorphological analysis will be captured using light and scanning electron microscopy. Measurements will be aggregated and the extent of morphological variation among taxa will be analyzed using clustering and ordination algorithms. Ecological information including geographical range, host range, and habitat will be obtained by examining herbarium specimens and labels. Specimens that include host species will also be used to generate a host frequency index (HFI) for each taxon and analyzed as a bipartite network.

Systematic classification at species and interspecific level is significant as it is critical for the management of both endangered and invasive taxa.

PP6

Protected areas become increasingly important for lichen conservation with a changing climate in Nova Scotia, Canada

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Many lichens are very sensitive to climate change and cyanolichens are particularly so. Nova Scotia, Canada is expected to experience an increase in mean annual temperature of 2.4 °C and increase in mean annual precipitation of 6% by 2080. Nova Scotia recently increased the area of parks and protected areas to 13% of the province which included 8800 ha for the purpose of protecting rare lichen habitat. It is unknown how well these areas protect the available habitat or how well these permanent protected areas will conserve lichens in the future with a changing climate. Four species of at risk lichens: *Erioderma pedicellatum, Erioderma mollissium, Pannaria lurida* and *Pectenia plumbea* were modeled using BIOCLIM machine learning software to determine their current climate niche envelope. This was overlaid with protected areas on a geographical information system (GIS) to determine how much of the existing climate envelope is within protected areas for each species.

The climate envelope for each species was then forecast to the year 2080 with climate change projections. Currently, protected areas in Nova Scotia protect 7, 11, 11 and 7% of the climate envelope for each of *Erioderma pedicellatum, Erioderma mollissium, Pannaria lurida* and *Pectenia plumbea* respectively. Future climate forecast to 2080 indicates the area of suitable climate will decrease by 99, 99, 89 and 100% for each species respectively. The area of remaining suitable climate within protected areas will increase to 100%, 100% and 93% of the total for the province for *Erioderma pedicellatum, Erioderma mollissium* and *Pannaria lurida* respectively. The forecast suggests there will be no suitable climate for *Pectenia plumbea* by 2080 in Nova Scotia. The results of this study indicate that protected areas will be increasingly important for the conservation of some lichen species with a changing climate. However, GIS mapping indicates suitable climate of each species will shift northwards in the province. It is uncertain whether lichens will be able to migrate as rapidly as the migration of suitable climate.

Floristics and barcoding of low Arctic bryophytes

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The Arctic tundra represents a heterogeneous landscape with diverse habitats where bryophytes are a dominant component. Victoria Island, the second largest island (217,291 km^2) in the Canadian Arctic Archipelago, lacks a checklist of bryophyte species and collections are few. Floristic habitat (FHS) and non-random quantitative sampling were performed in 2018 and 2019 in the vicinity of Cambridge Bay and Wellington Bay to assess bryophyte diversity. Based on 728 specimens, 97 bryophyte taxa (85 Bryophyta and 12 Marchantiophyta) were enumerated to date, of which 60 are new records for the island. Barcoding techniques utilizing genetic sequence data from 285 specimens, based on nrDNA (internal transcribed spacer region *ITS2*) and cpDNA (*rbcLa* and *trnL-F*) regions were generated in collaboration with the Centre for Biodiversity Genomics (BRPOL, Barcode of Life Database, University of Guelph).

The results from Victoria Island, based on complementary morphological and sequence data, establishes a robust checklist and discernment of bryophyte assemblages in the Cambridge Bay vicinity. This study also forms a baseline to explore the genetic and floristic diversity for a comprehensive arctic bryophyte flora program (Bryophyte Flora of the Canadian Arctic Archipelago (BRYCAA), La Farge Lab.)

Chromosomal-scale assembly of *Marchantia paleacea*

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Many current problems faced in the establishment of high accuracy genome assembly are related to obtaining high-molecular-weight DNA and the presence of repetitive DNA significantly impacting genome assembly quality. Here we present a de-novo assembly of *Marchantia paleacea, a* dioecious liverwort species with an estimated genome size of ~280 Mbp, using ONT sequencing. We generated an assembly of 277 contigs, with a total length of 263 Mbp (N50 = 2.3 Mbp) with 0.00% of genome gaps. We built a Hi-C library and retained 117 scaffolds, with all fragment lengths > 1 kb and the first nine large scaffolds representing the eight autosomes and one sex chromosome.

New insights on post-fire bryophyte succession

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Background: *Funaria hygrometrica*, *Ceratodon purpureus* and *Marchantia* spp. are well documented as the bryophytes most characteristic of burnt sites 1–2 years after heathland and forest fires. However, little is known about the earlier post-fire successional stages alongside the provenance of the recolonizing species and their reproductive biology.

Objectives: We investigated these features of bryophyte biology following a major fire on a heathland in southern England in May 2020 formerly dominated by *Polytrichum* spp. and *Campylopus introflexus* following a previous fire in 2006.

Results: The first bryophytes appearing 50 days after the fire were *Campylopus pyriformis* and *Funaria hygrometrica* followed by *Marchantia polymorpha* subspecies *ruderalis*, *Ceratodon purpureus* and *Polytrichum* spp. after 100 days. Whereas *Funaria* and *Marchantia* derived from spores, followed by further spreading via gemmae, the *Polytrichum* spp. arose from subterranean rhizomes and *Campylopus pyriformis* most likely from long-lived rhizoidal tubers plus caducous leaves. Normal life cycles are profoundly disrupted by fires and in *Funaria* and *Marchantia* are far more protracted than in culture. Initially appearing as lawns of gemmiferous protonema, after 100 days Funaria produced inflorescences and after 140 days, young sporophytes. Sporophytes were much rarer in *Ceratodon* and were not seen in *Polytrichum juniperinum* until spring 2021. Fire interrupts the life cycle in *P. juniperinum* and *P. formosum* by 1 year, and by 2 years in *P. commune*. Carpocephala were first seen on *Marchantia* after 186 days and the vast majority were antheridiophores. There was no sign of regeneration of *Campylopus introflexus* on the burnt areas.

PP10

Green pigmented cell clusters induced by Fipexide on *Sphagnum capilliforium*

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Fipexide (FPX) is a chemical agent which has auxin like activities. We found FPX promoted the production of green-pigmented cell clusters on *Sphagnum capillifolium*. Rhizoid-like filamentous structures were extended from the cluster surface.

S. capillifolium was aseptically cultured using agar or liquid Y medium (Simola 1969) containing FPX, IAA, NAA or 2,4-D under continuous illumination at 23 °C.

Green pigmented cell clusters were induced on the cultured stem and auxins promoted the induction. The cell cluster may be equivalent to the callus reported on *S. imbricatum* (Kajita et al. 1987), however the cluster had rhizoid-like filamentous structures extended from the surface. No thalloid protonema was observed among the filamentous structures. The clusters were induced from several areas of the stem, indicating that cells having higher potential of division are not uniformly distributed on the stem, whereas there were not any visible differences on the initial materials between the cluster induced and non-induced regions. Gametophores were directly induced on the cluster during prolonged culture. Formation of the rhizoid-like filamentous structures was clearly stimulated by FPX application. The FPX-induced clusters were successfully maintained and proliferated also in liquid static culture but the filamentous structures were vigorously elongated than those on the agar medium.

We think FPX-induced cell clusters would be useful materials for research of the organogenesis as well as mass propagation of the moss.

Diversity and Evolution of Inflorescence in *Cuscuta*

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Cuscuta or dodder includes approximately 200 species of plant obligate stem parasites and has a nearly cosmopolitan distribution. Around 15–20 *Cuscuta* species have detrimental economical impact and cause yield losses in numerous agricultural crops. Due to their parasitic nature, *Cuscuta* species lack the vegetative characters seen in green plants, which are often used for identification. Therefore, their flowers, inflorescences, and fruits must be relied on for species separation. Although several studies have considered the flowers and fruits, there are currently no studies that have evaluated the evolution and diversity of inflorescences in *Cuscuta*. The inflorescence is the specific arrangement of branches that bear flowers. These develop according to distinct patterns and play important roles in pollination and plant reproduction.

The objective of this study is to document the diversity of inflorescences within the genus *Cuscuta* to better understand the form-function relationships, and their evolution. This will be done by rehydrating herbarium specimens for approximately 120 dodder species and documenting their inflorescence architecture under a stereo microscope. Additionally, living plants will be grown to study their inflorescence development within the major infrageneric groups in *Cuscuta*. From these studies, possible relationships between inflorescence forms and their function will be explored to better understand sexual reproductive traits in *Cuscuta*, including breeding systems. This information will be useful for regional floras and biodiversity programs to distinguish the *Cuscuta* species that are invasive agricultural pests from native ones, as well as to better understand the evolutionary relationships among species within the genus *Cuscuta*.

On *Paraphymatoceros* sp. (Anthocerotophyta) from Mexico

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The genus *Paraphymatoceros* was postulated by Gabriela Hässel de Menéndez in 2006 within the Notothyladaceae family (Anthocerotophyta). This genus is characterized by narrow and solid thalli that might develop marginal tubers, one chloroplast per cell without pyrenoid in gametophyte surface, erect and stomatifer capsule with a central columella, and yellow to brownish spores with a gibbous distal surface. The type species, *P. diadematus*, was described from Chile, while the remaining three species (*P. hallii*, *P. pearsonii* and *P. proskaueri*) have been reported from USA, displaying a highly disjunct distribution.

A population of *Paraphymatoceros* was collected in central Mexico from 2011 to 2014. Morphological and anatomical characters of gametophyte and sporophyte were documented using light microscopy. Scanning electron microscopy was used to illustrate spore morphology. A CTAB modified protocol was followed for DNA extraction, *rbcL* and *nad5* regions were amplified, and a molecular phylogenetic analysis was carried out adding GenBank sequences to complete ingroup and outgroup taxa.

Mexican plants morphologically resemble more to *P. pearsonii* than to any other species in the genus; nevertheless, a few morphological traits and some spore characters, which are considered diagnostic traits in most hornwort genera, differ from *P. pearsonii*. Even more, molecular phylogenetic analysis does not resolve Mexican plants as sister to *P. pearsonii*, but as sister to the USA *Paraphymatoceros* clade (*P. hallii*, *P. peasonii* and *P. proskaueri*), reflecting a geographic pattern and probable speciation of Mexican plants.

A review of the current situation of three *Sphagnum* spp. in Québec, Canada: *S. divinum* Flatberg & Hassel, *Sphagnum medium* Limpr., and *S. venustum* Flatberg

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Recent molecular, genetic, and morphological studies have proven the existence of three species in Québec from the *Sphagnum* genus: *Sphagnum divinum*, *S. medium*, and *S. venustum*. Information obtained from recent field observations is presented in order to improve current understanding of the distribution and ecology for these three species. The discovery *S. venustum* dates to 2007 in Labrador. Its presence has since been established in Norway, and Northern Québec, specifically the territories of Nunavut and Eeyou Istchee James-Bay. Observations occur mainly in soligenous poor fens, as in the holotype description, but also in a few ombrotrophic peatlands or muskegs with stands of *Picea mariana* [Mill.] BSP. The recent separation of *S. magellanicum* into three species now constitutes the 'magellanicum complex'. Two are currently found in the Northern hemisphere, *S. divinum* and *S. medium*, with the latter having been reinstated as a separate species based on its epitype. The third, *S. magellanicum*, is currently restricted to the southern part of South American. Numerous previous observations of the former *S. magellanicum* suggest that the first two species of the complex should be common, but their individual distributions remain unknown. Currently, *S. medium* has only been observed on a few rare occasions in open bogs while *S. divinum* has been observed across various peatland types stretching from the James/Hudson Bay to southern Québec. Distribution maps and ecological niches of these three species are presented here in order to promote the sharing of new knowledge on the status of these Québec *Sphagnum* species.

Des découvertes moléculaires, génétiques et morphologiques ont récemment démontré l'existence de trois espèces du genre *Sphagnum* au Québec : *Sphagnum divinum*, *S. medium* et *S. venustum*. Nous présentons l'état des connaissances actuelles sur leurs répartitions et écologies en s'appuyant sur des travaux de terrain récents. La découverte de *S. venustum* remonte à 2007 au Labrador avant qu'elle ne soit observée en Norvège et au Québec dans les territoires septentrionaux du Nunavut et de l'Eeyou Istchee Baie-James. L'holotype et la majorité des observations postérieures ont eu lieu dans des tourbières faiblement minérotrophes et soligènes, puis plus rarement dans des tourbières plus ombrotrophes et boisées avec du *Picea mariana* [Mill.] BSP. En 2018 *S. magellanicum* s'est vue divisée en trois espèces, formant le «complexe magellanicum». Deux se trouvent actuellement dans l'hémisphère Nord, *S. divinum* et *S. medium*, cette dernière ayant été rétablie en tant qu'espèce sur la base de son épitype ; la troisième, *S. magellanicum*, n'étant présente qu'en Amérique du Sud méridionale. Les nombreuses observations de l'ancien *S. magellanicum* suggèrent que les deux premières espèces seraient très présentes au Québec, mais que leurs répartitions restent inconnues. *S. medium* n'a été confirmée qu'à quelques reprises dans des tourbières ombrotrophes ouvertes, tandis que *S. divinum* a été observée dans des habitats divers entre la Baie-James et le sud du Québec. Les cartes de répartition et les descriptions écologiques de ces espèces sont présentées ici dans le but promouvoir le partage des nouvelles connaissances sur le statut de ces sphaignes québécoises.

Hymenostyliella llanosii (Pottiaceae) new to Myanmar and its phylogenetic position

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Hymenostyliella Bartram is a rare genus of the moss family Pottiaceae, characterized by strongly involute leaf margins, adaxially bulging-mammillose and trigonous upper laminal cells, and sporophytes born laterally on short branches (Zander 1993). Three species are recognized: *H. calcarea* (Dixon) Z.Iwats. and *H. llanosii* (Müll.Hal.) H.Rob. from Southeast Asia, and *H. alata* (Herzog) H.Rob. from South America. During floristic research in Myanmar in June 2019, the first author collected a pottiaceous moss from a karst in Kayah State. Subsequently, we concluded that the plants were identical to *H. llanosii*, representing the first record of the genus in the country.

The populations in Myanmar were from limestone cliffs in partial shade at an elevation of around 1400 m. Based on examination of type material, no significant differences were found between *H. calcarea* and *H. llanosii*, and they should be treated as conspecific, with *H. llanosii* (Basionym: *Barbula llanosii* Müll.Hal., 1900) taking precedence. *Hymenostyliella alata* is sharply distinguished from *H. llanosii* by an abaxial costal epidermis winged with two lamellae, and a cucullate leaf apex. The bulging patterns of laminal cells are also different between these two species, i.e. adaxially bulging cell walls in *H. llanosii*, but adaxially bulging lumen in *H. alata*. The phylogenetic position of *H. llanosii* was first inferred based on chloroplast and nuclear DNA sequences. The species was resolved in the clade corresponding to the tribe Pleuroweisieae in which several genera also have characteristic trigonous areolation or long-lanceolate leaves with distantly dentate margins.

A contribution to the bryophyte flora of Pakistan: some recent developments in Bryology

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Pakistan is one of the unexplored regions of South Asia in the field of bryology. The Northern part of Pakistan, including the Western Himalayas, is an ideal place for the bryophytes and it hosts one of the richest and diverse ecosystems in this region. Unfortunately, the Pakistani bryophyte flora is poorly known and very few and scattered studies are available which are mainly done by the foreign bryologists e.g. Japanese bryologists. The Bryophyte flora of Pakistan consists of around 388 species, and according to the number of species, Pottiaceae is the largest family followed by Bryaceae.

The current initiative is planned to update the moss flora of Pakistan, which has not been done in the last several years. The study is aimed to taxonomically revise the dominant families, the addition of new records and ultimately present an updated checklist of the bryophytes of Pakistan. Recent field surveys have been conducted throughout the country to collect fresh specimens. The herbarium collection of the Japanese bryologists, collected during their expedition in the 1990s, were also consulted. Some new records have been found and a few families have been morphologically described. For the study of the bryophytes of Pakistan, research collaborations have been made with different bryologists, to study different families and genera including Pottiaceae, Polytrichaceae, Bryaceae, Brachytheciaceae, Amblystegiaceae, Hypnaceae, Orthotrichaceae, *Plagiothecium*, *Frullania* etc. This present study of bryophytes will help to contribute to the Bryology of Pakistan especially in relation to South Asia and Western Himalayas.

PP16

Discovery of a simple thalloid liverwort *Metzgeriites kujiensis* from Late Cretaceous Japanese amber

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Kuji amber is the largest amber deposit in Japan. It is one of the most important sources for the reconstruction of terrestrial ecosystems in the Late Cretaceous East Asia continental margin, especially for revealing fauna and flora for microscopic species such as insects and bryophytes.

In the present study we describe a new species of fossil liverwort preserved in the Late Cretaceous Kuji amber (Santonian; approximately 85 Ma), the first evidence of a fossilized liverwort shoot found in Kuji amber and only the second record of a bryophyte from the Late Cretaceous bryoflora in Japan.

An extinct liverwort species, *Metzgeriites kujiensis* T.Katag., is characterized by thalloid plants with a distinct midrib and lamina, narrow thalli of 0.6–0.8 mm wide, regularly 1-pinnate ramification pattern, and presence of discoid branches. The new species represents the first record of the liverwort family Metzgeriaceae (Metzgeriales, Marchantiophyta) from the Late Cretaceous from East Asia. The present study sheds light on the Late Cretaceous diversification of simple thalloid liverworts, especially of Metzgeriaceae, and also contributes to the further age calibration of the diversification of simple thalloid lineages.

PP17

The North American moss, *Physcomitrium immersum*, is a hybrid species of yet unresolved progenitors

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While interspecific hybridization has long been recognized as a significant mechanism of speciation in vascular plants, it was regarded as insignificant in mosses. Recent evidence suggests, however, that hybridization is widespread and hence possibly significant in the diversification of mosses. Here we report on the hybrid origin of *Physcomitrium immersum,* a short-lived annual species endemic to North America.

We initially sampled gametophytes via target capture of 700 nuclear loci, which revealed extensive heterozygosity within *P. immersum*. This suggested the species is likely an allodiploid, and after phasing the alleles for select loci, we resolved the alternate alleles in two distinct lineages of the *Physcomitrium* complex. To confirm the hybrid origin of the species, we then screened herbarium samples at a single locus to test if heterozygosity was fixed among specimens.

All eleven samples screened from four North American states and provinces share the same heterozygous sites, with polymorphisms matching the two phased alleles. The demonstration of consistent fixed heterozygosity among samples suggests a single origin. Although repeated hybridization between the same two parental species is possible, inference from plastid loci suggests a single maternal species and hence also supports a single hybrid origin of *P. immersum.*

This study serves as the first molecular confirmation of *Physcomitrium immersum* as a hybrid moss species and, by identifying hybrid origins in a well-known and common moss species endemic to North America, indicates the potential of molecular methods in identifying cryptic speciation and hybridization in morphologically simple moss species.

PP18

Effects of copper-polluted soil on the moss *Tortella squarrosa* in culture: damages observed in moss tissues and amelioration by two soil amendments

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Tortella squarrosa (Brid.) Limpr. (= *Pleurochaete squarrosa* (Brid.) Lindb.) has been suggested as an alternative moss species for biomonitoring studies in the Mediterranean Basin. However, little is known about its responses to different pollutants. Here we present a study on the effects of copper-polluted soil on *T. squarrosa*, the efficacy of two amendment treatments, and an exploration on the resistance mechanisms possibly involved.

Adult shoots of *T. squarrosa* were grown indoors using an acidic sandy soil, with very low organic matter content. Four doses of copper sulfate (0–2000 mg Cu/kg) were artificially supplied. We also tested two soil amendments, $CaCO_3$ (90 g/kg), and peat + $CaCO_3$ (40 + 96 g/kg). After six weeks, we assessed the damages observed in the plants, we tested for copper in their tissues (rubeanic acid test and SEM-EDX), and also checked pH and bioavailable copper (Mehlich-3 method) in the soils.

In unamended soils, medium and high doses have pronounced effects on the plants. Both amendment treatments prevent these damages, and were effective in reducing copper bioavailability. However, bioavailable copper levels of 880.2 mg/kg in the peat + $CaCO_3$-amended soil caused little effect in the plants, whereas in unamended soil only 90 mg/kg resulted in evident damages, pointing at an interaction of copper and soil acidification as the main toxicity factor.

Histochemical tests and SEM-EDX results suggest an exclusion mechanism allowing resistance to copper pollution in this species, with more efficiency in soils with near neutral pH. This questions the usefulness of this moss in biomonitoring environmental metal pollution.

PP19

Effects of lead-polluted soils on the establishment of vegetative moss propagules

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Bryophytes have been frequently used in lead pollution biomonitoring. Most studies focus on adult populations, and little is known about lead effects on the initial stages of development. This work intends to evaluate the response to lead of vegetative propagules of three species of mosses common in Europe: *Homalothecium aureum*, *Syntrichia ruralis* and *Tortella squarrosa.*

We sowed vegetative propagules (0.125 mg/cm^2) on soil-filled pots. We selected a soil with low organic matter content and applied experimentally four doses of a soluble lead salt ($Pb(NO_3)_2$): 0,75 mg/kg, 270 mg/kg and 2700 mg/kg (representing the thresholds of lead pollution for different soil usages in the local legislation). The experiment was kept in greenhouse conditions and regularly watered to maintain soil at full capacity for three months. At the end of the experiment, we measured coverage of new shoots and observed damages in tissues. Additionally, we explored the presence of lead in the tissues using histochemistry and SEM-EDX.

The results show successful establishment of the propagules at low and intermediate doses. Considering the high bioavailability of lead in the soils, our results confirm the high resistance to lead of these species even in their early stages of development. There are some interspecific differences (*H. aureum* is the most resistant species). The histochemical and SEM-EDX results suggest the existence of an exclusion mechanism probably involved in the resistance to metal pollution in these mosses. If such exclusion mechanisms are widespread in mosses, the value of these organisms in direct biomonitoring would be compromised.

Les bryophytes ont été fréquemment utilisés dans la biosurveillance de la pollution par le plomb. La plupart des études se concentrent sur les populations adultes, et on connaît peu les effets du plomb sur les premiers stades du développement. Ce travail vise à évaluer la réponse au plomb des propagules végétatives de trois espèces de mousses communes en Europe: *Homalothecium aureum*, *Syntrichia ruralis* et *Tortella squarrosa*.

Nous avons semé des propagules végétatives (0,125 mg/cm^2) sur des pots remplis de terre. Nous avons choisi un sol à faible teneur en matière organique et appliqué expérimentalement quatre doses d'un sel de plomb soluble ($Pb(NO_3)_2$) : 0,75 mg/kg, 270 mg/kg et 2700 mg/kg (représentant les seuils de pollution au plomb pour différents usages du sol dans la législation locale). L'expérience a été maintenue dans des conditions de serre et arrosée régulièrement pour maintenir le sol à pleine capacité pendant trois mois. A la fin de l'expérience, nous avons mesuré la couverture des nouvelles pousses et observé les dommages dans les tissus. De plus, nous avons exploré la présence de plomb dans les tissus en utilisant l'histochimie et le SEM-EDX.

Les résultats montrent un établissement favorable des propagules à des doses faibles et intermédiaires. Considérant la forte biodisponibilité du plomb dans les sols, nos résultats confirment la haute résistance au plomb de ces espèces même dans leurs premiers stades de développement. Il existe quelques différences interspécifiques (*H. aureum* est l'espèce la plus résistante). Les résultats histochimiques et SEM-EDX suggèrent l'existence d'un mécanisme d'exclusion probablement impliqué dans la résistance à la pollution métallique chez ces mousses. Si ces mécanismes d'exclusion sont répandus chez les mousses, la valeur de ces organismes dans la biosurveillance directe sera compromise.

Challenging the morphological characters that determine a species. The case of *Aloina obliquifolia* (Müll. Hal.) Broth.

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The current classification of the genus *Aloina* Kindb. (Pottiaceae) is only based in a morphological approach due to the lack of molecular data. Presently, two species with mucronate apex are recognized: *Aloina cornifolia* Delgad. and *A. obliquifolia* (Müll. Hal.) Broth. The distribution of the first one is limited to China while *A. obliquifolia* has been reported also in Europe and South America. The phylogenetic relationships between them and its closest species, *A. rigida* (Hedw.) Limpr., are not clear.

In the framework of a molecular study of the genus *Aloina*, we have studied numerous specimens of *A. obliquifolia* to determine if the characters used as diagnostic in this species, including the mucronate apex, are valid and clarify the phylogenetic relationships between these species. To this purpose a morphological study and a molecular analysis were carried out. The last one includes both rDNA I*TS 1–2* region and the chloroplastic regions *trnL–trnF*, *atpB–rbcL*, and *trnG*. The results suggest that the specimens of *A. obliquifolia* could belong to different phylogenetic lineages, and that characters as the mucronate apex should not be used as a diagnostic character for this species. In conclusion, this study shows the necessity of a revision of the diagnostic characters for the genus *Aloina*, in which the morphological limits between the species are unclear.

Abscission in plants: Structural, chemical and transcriptomic analysis of protective surface layers

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Plants undergo a self-pruning mechanism called abscission to detach organs. Efforts to understand this process have been led by studies in a model plant species, *Arabidopsis thaliana*, in which the outer parts of the flower (sepals, petals, stamens) are shed to make way for the developing fruit. Abscission involves specialized cell layers called the abscission zone where separation takes place. When organs detach, newly exposed cells on the plant surface become sealed against water loss and pathogen entry through the formation of a protective layer. Plants in which the protective layer develops slowly or weakly are often susceptible to disease, making the study of this layer of importance to agriculture. The protective layer in *Arabidopsis* plants is suggested to be a lipid-based, cell wall-associated polymer such as cutin or suberin.

To determine the identity of this polymer in *Arabidopsis*, abscission zones were harvested and subjected to chemical analysis using gas chromatography with flame ionization and mass spectroscopy methods of detection. This analysis indicates that a form of cutin is the primary component of the *Arabidopsis* protective layer. Light and electron microscopy will be used to examine the structure and deposition of this layer. Transcriptomic analysis will be carried out to test for the expression of key biosynthetic enzyme genes. Mutations in these genes will used to assess the impact of surface layer composition on the abscission process. These studies will shed light on the synthesis of protective surface layers in abscission zones.

PP22

A custom-made system for real-time monitoring of cryptogam physiological activity during desiccation-rehydration cycles

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Gas-exchange systems employing infra-red gas analyzers have been widely used to assess CO_2 and water vapor exchange in plants, being an important tool for the determination of physiological characteristics and associated responses to environmental changes. Future climatic disturbances are expected to influence vascular plants in many ways, but how these changes will impact the cryptogamic flora is not clear. Poikilohydric lifestyle of lichens and bryophytes provides major ecophysiological advantages in habitats with highly fluctuating environmental conditions, and thus, cryptogams fill niche gaps in ecosystems inhabitable by most vascular plants. They are particularly important components of the carbon sequestration and significant contributors to biodiversity in northern ecosystems where the effects of climate warming are predicted to be most pronounced.

We propose to assess the physiological responses of lichens and bryophytes and their stress tolerance under future climatic scenarios using real-time monitoring of gas exchange characteristics with a custom-made chamber which allows the rehydration of the samples immediately after desiccation through a built-in spraying setup, while maintaining the chamber closed and avoiding the interruption of the measurement. This enables simultaneous real-time measurement of volatile organic compounds (VOCs) using online trace-gas analyzers to evaluate plant stress response. We identify different interspecific levels of stress resistance under simulated cycles of desiccation-rehydration. Our data improves the current knowledge of climate warming repercussions in the cryptogamic vegetation where future shifts are likely to occur under the ongoing global change.

PP23

Patterns in the diversity and specificity between the lichenized fungus *Niebla* and its green algal symbiont *Trebouxia*

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Lichens are a dominant terrestrial mutualism comprised of an alga or cyanobacterium (photobiont) and a fungus (mycobiont). We know a great deal about the evolution, distribution, and diversity of the mycobionts, but much less is known about the photobiont or the specificity of the interactions between them. This uneven characterization and multiple origins of lichenization in both symbionts obscure our understanding of the unique mechanisms governing symbiont specificity and the evolution of this symbiosis.

Lichens containing cyanobacterial photobionts (e.g., *Peltigera*) are among the best investigated for symbiont specificity; however, lichens containing green algal photobionts (~90%) escape comparable scrutiny. The high dispersal potential of cryptogams inherently complicates their study, as taxonomic sampling for widespread genera is challenging and endemic lineages are rarely speciose. Our study profiles the association of *Niebla* s. lat. and *Trebouxia*, endemic to the Pacific Coast of the Americas, and the symbionts' diversity. While all associations rely on coastal fog, they are distributed along broad climatic and ecological gradients. We seek to delimit the taxonomic diversity of fungal and algal symbionts to develop a foundation for understanding the evolution of their mutual specificity.

We have uncovered a diversity of *Trebouxia* lineages, including several putatively novel taxa, within the larger so-called clade A. In addition to phylogenetic specificity between *Trebouxia* and *Niebla*, the diversity of both symbionts seems strongly correlated to substrate (e.g., wood or rock). Existing analyses are based on limited select loci, but pending phylogenomic analyses will likely provide new and deeper insights into symbiont specificity.

PP24

Conservation of bryophytes of Western Ghats of India: a look into the problems and prospects in the context of *Riccia sahyadrica* and *Micromitrium vazhanicum*

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Background: Located in the tropics and with elaborated geological history, the Western Ghats of Southern India is a centre of rich biodiversity and evolution. The knowledge base of its bryophyte assemblages has increased considerably over the recent past. However, awareness about this group has not improved much. The major stakeholders of conservation or habitat management are least bothered about this group. The situation is quite different from the other parts of the world.

Objectives: An attempt is made to examine the status of conservation of Bryophytes in the Western Ghats of Southern India.

Methods: Detailed survey was done for documents on aspects of conservation, policy or guidelines on management of habitats, utilization, etc of bryophytes of the Western Ghats. It was also assessed in the light of new findings of taxa such as *Riccia sahyadrica* Manju & Cargill (2019) and *Micromitrium vazhanicum* Manju et al. (2019).

Results and conclusion: No policy documents or guidelines are available for the proper management or utilisation of bryophytes of the Western Ghats, or India at large. The recent findings of some curious taxa such as *Riccia sahyadrica* and *Micromitrium vazhanicum* from highly neglected habitats prompts an urgent need of paradigm shift. It will be a tough task ahead to convey the significance of these unique species, and their least valued seasonal habitats in the present scenario.

Bryophyte diversity of Anamudi Shola National Park, a Sky Island in the Western Ghats of Southern India

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Background: The tropical montane forests or cloud forests, called *sholas* in Southern India, are the summits of unique assemblages of biodiversity. The documentation of the bryophyte diversity of *sholas,* however, is far from complete. The Anamudi Shola National Park (ASNP), located at an altitude of 1600–2440 m in the Western Ghats of Kerala in Southern India is explored for its bryophytes for the first time.

Objectives: We aim to document the bryophyte diversity of ASNP.

Methods: Intensive exploration was conducted during 2015 to 2020 to document the bryophyte diversity of different microhabitats in the mosaic of macrohabitats (evergreen forest, *Shola* forest, grassland, and plantations), composed of three *sholas*, *viz.*, Mannavan, Pullaradi and Idivara totalling 7.50 km^2. Voucher specimens are deposited in the Zamorin's Guruvayurappan College (ZGC).

Results and conclusion: A total of 153 taxa of liverworts (57 species, 35 genera, 23 families, 6 orders), hornworts (2 species, 2 genera, 2 families, 2 orders) and mosses (94 species, 70 genera, 33 families, 12 orders) were recorded. Species diversity varied in the *shola* patches, *viz*. Mannavan (125 species in 5.18 km^2), Pullaradi (48 species in 1.62 km^2) and Idivara (23 species in 0.61 km^2) according to the size and habitat types. A total of 41 species were new distribution records for areas such as India (1 liverwort, 5 mosses), Peninsular India (1 liverwort, 6 mosses), Western Ghats (1 moss), South India (1 liverwort, 1 moss) and Kerala State (11 liverworts, 1 hornwort, 13 mosses).

PP26

Diverse outcomes of interactions between pairs of fungal endophytes in the liverwort *Marchantia polymorpha*

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Marchantia polymorpha (*sensu lato*) is a widespread liverwort globally and the model organism for liverworts. This taxon is unusual among its liverwort relatives in not forming mycorrhiza-like fungal symbioses. However, it still harbors a diverse community of fungal endophytes that can have a wide range of effects. Experimental gnotobiotic systems using *M. polymorpha* can serve as conveniently compact models of plant microbiota dynamics. In this study, *M. polymorpha* and seven Ascomycete endophyte strains were used to investigate how the presence of multiple endophytes changes the outcome for a host. A wide variety of interactions were observed, with variation in direction (beneficial or harmful), magnitude, and variability of impact on the host. The various endophyte strains displayed different susceptibilities to having their effects overridden by a co-inoculated strain.

Rate of outer layer bark loss is predicted by species of tree

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We quantified the rate of outer-layer bark loss on seven common North American tree species in Minnesota forests to determine if differences in these rates among species were significant. Bark loss rates are an often-cited factor for lichen community development on trees, but few sources have attempted to quantify the actual rate of loss on different tree species. In summer 2019, we applied vinyl paint to the outer bark surface of bark in 1 cm × 5 cm swatches and returned in the summer of 2020 to measure paint loss using a count on a fixed grid. Beta-binomial regression was used to analyze bark loss rates because the loss rates were substantially variable from tree to tree within a given species.

Loss rates ranged from 11% (bur oak, *Quercus macrocarpa*) to 4% (paper birch, *Betula papyrifera*). Differences in average bark loss rates among tree species were significant ($p < 0.001$). Significant differences were also found in the proportion of trees without bark loss compared with those that lost bark ($X^2 = 26.612$, df = 6, $p = 0.0001711$). Species with the highest bark loss were bur oak (*Quercus macrocarpa*), pines (*Pinus resinosa* and *Pinus strobus*) and maple (*Acer saccharinum*). Lowest rates of bark loss were observed on birch (*Betula papyrifera*), basswood (*Tilia americana*), and aspen (*Populus tremuloides*). Results of the study suggest that rates of bark loss cited as an influence on lichen community development should be studied and further quantified with special consideration to host tree species.

PP28

Development of genomic tools for *Bryum argenteum*: genome assembly and annotation using long and short reads

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Background: *Bryum argenteum*, also known as silvery-threaded moss (STM), is a moss with high desiccation and heavy metal tolerance belonging to family Bryaceae. STM is a cosmopolitan moss and its adaptive characteristics have allowed it to thrive in urban environments such as roadsides, cracks in sidewalks, asphalt, industrial areas, etc. Recently, the moss has been able to invade golf courses around America, competing with turf grass for nutrients and space. STM populations in putting greens are phenotypically different from native gametophytes. with fast-growing filamentous colonies consisting only of female gametophytes. Assembling a genome of STM will provide a platform for understanding how adaptation and plasticity impact the rise of STM as an invasive species.

Objectives: We present a draft genome of STM assembled using long (Nanopore PromethION) and short (Illumina NovaSeq) reads. We explore several assembly and quality control methods and annotate the genome using RNAseq data from one female and one male genotype. Our draft genome will help identify genes responsible for high desiccation and heavy metal tolerance and if those genes are homologous to those found in resurrection plants and metallophytes, respectively. Future applications of the genome assembly include: (1) why the putting green STMs are different than its native strains, (2) why there is an absence of males from the putting greens and (3) how to control or get rid of invasive STMs from golf courses.

PP30

Short-term metabolic response of *Polytrichum strictum* to UV-B radiation in a subantarctic peatland

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Bryophytes have a well-known capability to respond to poly-extreme environmental conditions by modulating their metabolism. In southern South America, bryophytes are exposed to high latitude climate conditions, in addition to extreme increasing UV-B radiation during the Antarctic ozone hole in spring. Moreover, climate change has boosted the probability of extreme atmospheric events, augmenting the sub- Antarctic region's climatic instability and constantly pushing these sessile organisms' acclimation process. The cosmopolitan *Polytrichum strictum* (Polytrichaceae) is an acrocarpic moss, usually found in open sub-Antarctic habitats ranging from high Andean tundra to Sphagnum moss peatlands, revealing a high tolerance to a wide range of environmental conditions.

This work aimed to analyze bryophyte phenotypic plasticity in response to natural short-term variations of sunlight radiation. We analyzed the metabolic response of *P. strictum* to mid-day sunlight exposition in a sub-Antarctic peatland ecosystem in Navarino island, Chile. Our results showed different primary and secondary metabolite accumulation patterns in response to short-term sunlight exposure. This observation suggests that *P. strictum* respond to short-term sunlight exposure changes in part by shifting their phenylpropanoid derivatives accumulation. Primary metabolites were observed shortly after resuming sunlight exposure, suggesting a fast recovery of cellular Carbon cycle processes. We propose the cosmopolitan moss *P. strictum* as a model bryophyte to study metabolic plasticity and the acclimation process of characteristic subpolar vegetation facing future extreme climatic events due to global warming.

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PP31

Undergraduate research experience in upper-level Plant Physiology laboratory courses during the COVID-19 pandemic

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Research-intensive undergraduate laboratory courses appear to provide an enriched educational experience for biology students. A number of inquiry-driven, student-centered, open-ended research projects have been developed and introduced in two upper-level plant physiology and plant development laboratory courses in 2020–2021 session during the COVID-19 pandemic. Students worked in groups to develop their research proposal and design their research projects in the areas of plant physiology, ecophysiology, and plant development. Since undergraduate students were not permitted to work in the laboratory, the laboratory staff and teaching assistants conducted the proposed lab experiments. The project data was made available to the students. Students presented their research findings in the form of written journal-style research reports, and short 'Three-Minute Thesis (3MT)' oral presentations. The significance of these undergraduate research experiences and assessment strategies will be discussed.

PP32

Bryophyte species composition reflects management treatment in oligotrophic grasslands: results from a 10-year manipulative experiment in central Slovakia (Western Carpathians)

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Bryophytes are important components of semi-natural grasslands, yet many hypotheses about their community structure remain untested. Here, we assessed change in species composition of bryophytes in an experimental grassland extensively grazed by cattle and sheep and irregularly cleaned from colonizing trees and shrubs, located in the Poľana Mts (central Slovakia) over a period of 10 years.

The experiment consisted of 24 plots in four replicates of six treatments. Three of the treatments were fenced to avoid grazing: mulching in autumn (MUAU), mulching in spring (MUSP) and plots without any management (NM), whereas the other three treatments were placed outside the fence: grazing (GR, control), mulching in autumn combined with grazing (MUGR) and mowing in spring combined with grazing (MOGR). Plants were sampled in 4 m^2 plots and in sixteen 0.01 m^2 subplots in the corners of each plot. The analyses were based on 32 bryophyte taxa. PCA ordination using Monte Carlo permutation test was performed to illustrate shifts in species composition within the treatments in time.

Significant influence on bryophyte assembly within 10 year period was confirmed in MUAU, MOGR and NM treatments. Decreasing frequency and cover was found especially in *Abietinella abietina*, *Thuidium assimile* and *Climatium dendroides* in case of NM and MUAU, while *Plagiomnium affine* and *P. cuspidatum* increased in time on the same plots. Our results suggest that for an effective maintenance of particular bryophyte communities removal of vascular plant biomass through grazing and mowing is required.

Assembly of the first allopolyploid moss genome based on *Physcomitrium* sp. from North America

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Polyploidy is the state of having entire multiples of a haploid set of chromosomes. Whole-genome duplications occur throughout the diversification of plants and are considered major drivers of innovation and speciation. Allopolyploids present unique challenges to genome sequencing and assembling because they combine the genomes of two parental lineages following hybridization. Mosses are well suited for the allopolyploid genome sequencing because of the haploid nature of their vegetative body. Here we present the assembly of a population of *Physcomitrium* species from the *P. pyriforme* complex. High levels of heterozygosity reveal that this population is of hybrid origin. We generated long-read sequence data for the initial assembly and are complementing these with Illumina data for final annotation. After quality checks and removing potential contaminants, we assembled the genome with Flye, and this has resulted in a polyploid genome of 2 Gbp. This is the first confirmation based on genomic data of a hybrid species in the *Physcomitrium* complex which comprises the model taxon *P. patens*, and also the first assembled allopolyploid genome of a bryophyte. This sample may serve as a model to assess patterns of expression of genes inherited from distinct parental species of bryophytes.

Mapping unprotected phylogenetic diversity of bryophytes

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By combining information on modeled bryophyte habitat ranges with phylogenetic diversity and protected regions, we have created a map of unprotected phylogenetically diverse hotspots for bryophytes within the USA. This work provides an initial survey of potential target locations for bryophyte conservation. These regions would conserve several species simultaneously, with special emphasis on bryophyte genetic diversity and species of particular evolutionary distinctiveness. We also intend to release a version allowing the easy modification of relative weighting of these different conservation objectives to help identify and inform conservation priorities. By combining occurrence data from 1500+ bryophytes species from the Consortium of North American Bryophyte Herbaria location data, and modeling in maxent using WorldClim climate data we produced species distribution models. By factoring in the percentage of projected habitat which is already in protected lands from the PADUS dataset, we apply scaled weighting to species that exist disproportionately outside protected lands, thereby highlighting regions with high biodiversity of unprotected bryophytes species. Then, by incorporating phylogenetic data on a subset of 800 bryophyte species we created a map combining species richness of highly evolutionary distinct bryophytes with the least protection.

Behavior of apical cells in gemmarling and early bifurcation of *Marchantia polymorpha*

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The thalli of *Marchantia polymorpha* can reproduce asexually by producing multicellular gemmae in gemma cups. In order to clarify the behavior of apical cell(s) through the dorsiventral differentiation and initial bi-furcation in geminating gemma (gemmaling), we observed serial sections of the apical notches and visualized cell division frequencies using EdU assay. In the apical notch of mature dormant gemma, there were four potential apical cells with wedge-shaped and they were adjacent in squarely to each other.

When a gemma was placed on a damp filter paper and cultivated under white light, the four potential apical cells initiate regular division associated with dorsoventral differentiation. However, two of the four apical cells, located on the future dorsal side gradually stopped dividing and mitotic activity of the surrounding cells was also decreased. Meanwhile, the two apical cells on the side facing the future ventral side continue to divide. The dorsoventral differentiation originated from the position of the two apical cells, and the two apical cells also contributed to the initiation of the first bi-furcating branching. Although the apical notch of mature thallus of Marchantia usually has a single apical cell, the apical notch of gemma seems to have a special property. The squarely arranged four potential apical cells in the apical notch of the gemma may allow any two apical cells to touch the moist ground side when the flat gemma falls to the ground with either side up, and also allow initiate immediate bi-furcating branching from the two apical cells arranged in parallel.

PP36

Riccardia virea (Aneuraceae, Marchantiophyta), a liverwort species new to Canada and North America

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Riccardia vitrea Furuki is a simple thalloid liverwort species in the family Aneuraceae which was first recorded in Japan (Honshu, Shikoku, Kyushu). Its known range was subsequently slightly expanded to China and Russia and it became an East Asian species from an endemic to Japan. To date *R. vitrea* has not been reported outside of East Asia. However, a new population in boreal forest was observed in a recent fieldwork in north-west Quebec, Canada. A maximum likelihood tree was constructed based on *rbcL* gene for associated species.

Combining morphological and molecular phylogenetic analysis, this new record is an addition to the bryophyte flora of Canada and North America. There are four species recorded in the genus of *Riccardia* in Canada*, R. chamedryfolia, R. latifrons, R. palmate* and *R. multifida*. *R. vitrea* is easily distinguished from them by (1) numerous small oil bodies in both surface and inner cells, and (2) prostrate, wide and poorly developed ultimate pinnules. This species could be widely overlooked due to the fact that dry specimens without oil bodies are often used in identification, and it is probably more widespread than currently known in boreal forests of Canada.

PP37

How hornworts attract their cyanobacterial symbionts: searching for the hormogonium inducing factor

Yuling Yue, Anna Neubauer, Peter Szövényi

Plant-microbial symbiosis are major drivers of plant evolution. Although plant–mycorrhizal symbiosis is actively studied, very little is known about genetic regulation of plant–cyanobacteria symbiosis. The initiation process of symbiosis is shared by all cyanobacteria–plant symbioses. It starts with plants' secretion of chemoattractants and a hormogonium-inducing factor (HIF). HIF will attract cyanobacteria to enter the plant host, however, its exact chemical identity remains to be determined.

We use the tractable system of hornwort, *Anthoceros agrestis* and the cyanobiont, *Nostoc punctiforme*, to better understand how plant hosts attract cyanobiont. Hornworts only secret HIF when starved of combined nitrogen. Therefore, we carried out a nitrogen-starvation experiment and generated a time-series RNA-seq data to identify genes with significant expression change. We found that genes of flavonoid and strigolactone biosynthesis pathways were significantly upregulated. Flavonoids are efficient inducers of expression of heterocyst-related genes in cyanobacteria and important in attracting nodule-forming bacteria. Strigolactones are plant hormones acting as stimulating signals in both mycorrhiza- and nodule-forming symbiosis. In addition, we found that the ortholog of *RAM1*, kinase *CCaMK* and its target transcription factor *Cyclops*, showed a continuous increase in expression during starvation.

These results suggest that various molecules known to be involved in initiating plant–mycorrhiza and nodule-forming bacteria symbioses are produced under nitrogen starvation and are potentially involved as HIF in hornwort-cyanobacteria symbiosis. Altogether, we propose that molecular signals involved in the initiation of hornwort-cyanobacteria symbiosis may be shared with plant-mycorrhiza and nodule-forming bacteria symbioses and could have evolved from a general starvation response.

Floristic characteristics of bryophytes and their biomonitoring of heavy metal pollution from carbonate-type manganese ores in the southern China

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Carbonate-type manganese ores covered about 73% of all types of Chinese manganese ores. For studying the floristic characteristics of bryophytes and their monitoring for metal pollution of carbonate-type manganese ores in southern China, supported by the grants of NSFC-31960044 and the DSTFGC-2019, a series of bryological surveys were carried out from 2019 to 2021.

The following are some results: (1) About 450 samples and specimens of bryophytes were collected from 15 mines in southern China; (2) The bryoflora consists of 217 taxa belong to 69 genera and 27 families. Twelve taxa are liverworts belonging to 11 genera of 8 families, 205 taxa are mosses belonging to 69 genera of 27 families and no hornworts. (3) There were five life-forms of bryophytes in carbonate-type manganese ores mines. They are short turfs, wefts, mats, tall turfs and pendants. The turfs accounts for 78.56% of the species whereas the pendants are only 2.65%. (4) There were 12 phytogeogrphical elements in research areas. Among them, East Asia elements (20.68%) is the most, and East Asian and North American disjuncted elements (0.98%) are the least. (5) By means of applying ICP, AAS and AFS, the metal content of Mn, Fe, Cr, Cu, Zn, As, Cd, Hg, Pb, Ba, Co and Ni of bryophytes and their substrates were analyzed. Relationship between distribution of bryophytes and heavy metal pollution were assessed. It was concluded that the bryophytes can be used as indicator species in carbonate-type manganese ores.

PP39

Aquatic bryophyte communities as biomonitoring indicators for heavy metal pollution from 'Manganese Ores Mining Triangle Area' in rivers in China

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The 'Manganese Ores Mining Triangle Area' refers to the three neighboring counties including Songtao, Huayuan and Huayuan Counties in southern China, where the carbonate-type manganese industry is developing rapidly with heavy metal pollution. To study the ecology of aquatic bryophytes and their monitoring for heavy metal pollution in the river environment, supported by the NSFC-31960044 and the DSTFGC-2019, two bryological fieldworks were carried out in September 2019 and August 2021.

The following are some results: (1) About 235 samples and specimens of bryophytes were collected from three rivers with heavy metal pollution in this area; (2) Fifty-one aquatic bryophyte communities were found in the river and surrounding wet environment, which consists of 110 taxa belonging to 58 genera and 29 families. The main dominant families are Bryaceae, Bartramiaceae, Amblystegiaceae and Brachytheciaceae; (3) Using the method of the CCA, we studied the relationship between heavy metal pollution sources and ecological distribution of aquatic bryophytes; (4) By means of applying ICP and AAS, the metal content of Cr, Mn, Co, Zn, Hg, Ni and Sr of five aquatic bryophytes and their substrates were analyzed. Among them, *Gymnostomum aurantiacum*, *Hyophila nymaniana* and *Trichostomum zanderi* have a significant correlation between the Mn content in aquatic mosses and the river, while the Zn content in the Hyophila nymaniana is correlated with the Zn content of river and wet soil, indicating that they have good biological monitoring value. We concluded that aquatic moss communities can be used as biomonitors for heavy metal pollution in these rivers.

PP40

Recent taxonomic progress on genus *Marchantia* L. in Japan

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The genus *Marchantia* L. is one of the most familiar genera of bryophyte. Unlike its extensive use as a model plant in emerging field, the taxonomic study on this group has not made much progress in Asia. Here, I conducted the first comprehensive revision on *Marchantia* in Japan by morphological examination of specimens and phylogenetic analysis. The following progress has been made so far:

(1) Morphology of gemmae was newly proved to be taxonomically informative. Gemma of Japanese *Marchantia* taxa can be divided into two morphological groups based on character such as shape, presence or absence of mucilage hair, etc., which was also supported by molecular phylogenetic analysis.

(2) Previously, four Japanese species, *M. tosana* Steph., *M. cuneiloba* Steph., *M. radiata* Horik. and *M. tosayamensis* Steph. were considered conspecific with *M. emarginata* subsp. *tosana*. Our study newly proved the synonymy of *M. tosana* and *M. tosayamensis* under *M. papillata* subsp. *grossibarba* and the proposal of *M. emarginata* subsp. *cuneiloba* to replace former group of subsp. *tosana*. Several taxonomic and morphologic incongruences was also found in sect. *Papillatae* Bischl., which indicated that classification of the section needs to be further revised.

(3) We try to verify the subspecific treatment of *M. paleacea* Bertol. from morphologic, phytogeographic and reproductive perspective. Two subspecies can be easily distinguished from each other by ventral scale appendage and unfertilized archegoniophore. They also possess complementary geographical distribution in Japan. A putative hybrid plant was also discovered. Artificial cross-breeding experiment is in progress.

PP41

An experimental study on the hygroscopic movement with the Arthrodontae peristome of *Ulota crispa* (Orthotrichaceae, Bryophyta)

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The hygroscopic movement of the Arthrodontae peristome has a significant effect on the spore discharge in mosses. This experiment controls the water and humidity environment, and explores the conditions, methods and processes of hygroscopic movement with peristome of *Ulota crispa* Hedw., aiming to provide a reference for the study of moss spore reproduction characteristics.

Research results: (1) The hygroscopic movement of the peristome changes with the environmental humidity, and water droplets have a stimulating effect on the hygroscopic movement. Capsule opens at a humidity of 51–63%, opens fully at a humidity of 97.3%, and cycles as the environmental humidity changes. (2) According to the characteristics of peristome movement, a hygroscopic movement period can be divided into three different continuous stages: opening stage, spore release stage and closing stage. In each stage, the capsular characteristics change significantly, the shrinkage or expansion of 0.86 times with the change of humidity, the distortion of the capsules and capsule stalks were twisted. (3) The peristome rotates to open and close, along with capsule twisting to assist the peristome in sporulation.The hygroscopic movement of the *U. crispa* peristome and the synchronous rotation movement of the capsule increase the probability of spore release and provide more opportunities for spore reproduction.

Notes on the hygroscopic movement of Nematodontae peristome: *Polytrichum commune* Hedw. var. *commune* (Polytrichaceae, Musci)

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The hygroscopic movement of the Nematodontae peristome was little known. In order to reveal the structure and function of the peristome hygroscopic movement on nematodontae spore release, *Polytrichum commune* Hedw. was selected as the research subject under the change of humidity condition.

Research results: (1) When the humidity increased, the size of the peristome structure and epiphragm increased significantly, then recovered when the humidity dried again. The space between the peristome increased significantly from 8.33 μm to 11.53 μm, and the area of the epiphragm increased by 20%. (2) In the experiment of continuous wind blowing, the quantity of spores released during the initial period of the hygroscopic movement increased significantly, then decreased with the recovery of the peristome structure, and eventually stayed at a very low quantity. As the humidity increases, so does the percentage of cluster spores in the released spores, and increased with the decrease of the released spores, and reached a significant difference when the peristome structure recovered. (3) The wind experiments were carried out at the dry stage, the initial stage of the hygroscopic movement and the peristome structure in the recovery stage respectively. It was found that the quantity of spores released at the initial stage of the hygroscopic movement was significantly higher than that at the dry and re-recovery stages of the peristome structure. Therefore, the structure of the peristome changed during the hygroscopic movement, and this was of positive significance to spore release and spread of this species.

The International Association of Bryologists was established in 1969 to promote international cooperation and communication among all persons interested in the biology of bryophytes. This is achieved through sponsorship and arrangement of meetings and symposia that relate to the various aspects of bryology, and by IAB-sponsored publications including *The Bryological Times* and *Bryophyte Diversity and Evolution*. The Association also supports the publication of reviews, lists, software, and compendia.

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