Canadian Botanical Association 53rd Annual Meeting

L'association Botanique du Canada 53ème Réunion Annuelle






Canadian Botanical Association –
L'Association Botanique du Canada

ABSTRACTS - RÉSUMÉS

Laurier, Waterloo, ON, July 4-8, 2017

Tuesday, July 4th

Plenary Lecture

CBA-PL01

Evolution by association: symbiosis in a neo-Darwinian world

Sapp, J.

Department of Biology, York University, Toronto, Ontario, Canada

A profound change in our conception of life is emergent today. Organisms are increasingly understood to be symbiotic complexes - tightly intertwined communities of microbes functioning together with their hosts as a collective unit or "symbiome". In this presentation we shall see that such a symbiotic conception of life is not new, however. It first emerged from botanical studies 140 years ago, but developed close to the margins of biology in virtual conflict with some of biology's central doctrines- the neoDarwinian view of life as "red in tooth and claw" and of microbes as disease-causing "germs". In this context we will explore why it is that biologists have only recently begun to understand the importance of symbiosis in evolution.

Wednesday, July 5th

General Symposium
The Hidden World of Plants

CBA-GS01

Plants: they whisper, talk, and even move

Hangarter, R.

Department of Biology, Indiana University, Bloomington, Indiana, USA

As a group, plants are among the slowest forms of life. With their barely perceptible movements plants often go unnoticed by humans or are routinely treated as little more than ornamental objects. This presentation will use time-lapse imaging to demonstrate the remarkable dynamics of plant life. We will see how keenly sensitive plants are of their environment throughout their life as they navigate the space around them, respond to various stimuli they encounter, and communicate with other organisms. The sense of intrigue and mystery revealed by time-lapse imaging enhances our own awareness of plant life and provides insight into our relationship to plants and our environment.

CBA-GS02

Darwin's "abominable mystery" and the search for the first flowering plants

Friedman, N.

The Arnold Arboretum of Harvard University, Boston, Massachusetts, USA

Charles Darwin's "abominable mystery" has come to symbolize just about every question concerning the origin and early evolution of flowering plants. What did Darwin think was so abominably mysterious? This mystery will be explored through Darwin's correspondence with some of the most eminent evolutionists of his time who were also trying to understand where flowering plants came from and how they eventually came to dominate most of Earth's plant communities. Debates about the early evolution of angiosperms, in Darwin's and his correspondents' hands touched on everything from the completeness of the fossil record to the pace of evolutionary innovation (gradualism or punctualism). As will be seen, recent botanical discoveries associated with reproductive processes among the most ancient extant flowering plant lineages (*Amborella*, Nymphaeales, Austrobaileyales) are radically different from the static, if not dogmatic, views that dominated the twentieth century – and a far cry from anything that Darwin and successive generations of evolutionary biologists might have imagined.

CBA-GS03

Divergence patterns in the Neotropics: evidence from the palm family (Arecaceae)

Roncal, J.

Department of Biology, Memorial University of Newfoundland, St. John's, Newfoundland, Canada

The high species diversity of the Neotropics has attracted evolutionary biologists for centuries. Understanding the patterns and processes underlying the evolution of the high plant species richness requires multiple lines of evidence spatially, temporally and taxonomically. Here I present two case studies in the Arecaceae, a family considered to be a model to study tropical rain forest evolution. A dated molecular phylogenetic tree of the genus *Astrocaryum* (40 spp.), combined with an ancestral range evolution analysis, supported the constraining role of the aquatic Pebas system on colonization and *in situ* diversification in western Amazonia, and the role of the Guiana Shield as a source area from which species colonized adjacent regions in South America. Using a phylogeographic and ecological niche modelling approach we analyzed in more detail the evolution of a Western Amazonian clade (15 spp.) and found a phylogeographic break at ca. 5°S between two main clades growing in regions of contrasting geological and climatic characteristics. These results exemplify how geology and climate can shape divergence of Neotropical plants, but the underlying anatomical or morphological adaptations remain unknown.

We use the *Geonoma macrostachys* species complex as a second case study to capture different stages of speciation with gene flow in Amazonia. Using 29 variable traits we identified morphological entities and explored differentiation amongst them, including genetic variation, soil preference, and pollination biology. We found mixed patterns of population structure, niche breadth, and reproductive isolation within and amongst morphotypes of *G. macrostachys*, all of which are scale dependent. We conclude that differentiation occurs across our indices at varying scales, representing the complexity of the speciation process.

CBA-GS04

The twisted world of arbuscular mycorrhizal fungi

Stefani, F.

Agriculture et Agroalimentaire Canada / Agriculture and Agri-Food Canada, éd., Ottawa, Ontario, Canada

Arbuscular mycorrhiza fungi (AMF) are an ancient lineage of soil microorganisms belonging to the fungal kingdom and living in a mutualistic relation with most of the vascular plants. Mutualism based on AMF is so widespread that the benefits they provide expand far beyond the host plant and account at the ecosystem scale. The role of AMF at the ecosystem scale is still underestimated but their increasing use as biofertilizer raises the awareness of their ecological roles. Since the first description of AMF more than 200 years ago, our view on their diversity, taxonomy, genetics and ecological functions has undergone significant changes. The aim of this presentation is to tell the audience the past, present and future research about AMF. We will emphasize how the work of several generations of researchers that started on sporocarpic species of AMF is going to play a significant role in the development of a sustainable agriculture.

CBA-GS05

The mysteries of edge populations: the quintessential Canadian conservation question

Hargreaves, A.
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Up to 90% of Canadian plant species listed as 'at risk' have only the northern edge of their distribution in Canada. A century of theoretical interest in species distributions yields conflicting predictions about the true conservation importance of such edge populations. On one hand they are predicted to be small, isolated, unproductive, and of negligible importance to species overall survival. On the other, they are geographically poised to initiate range shifts under climate change, and may possess adaptations to edge environments that would facilitate such shifts. My research explores the conservation importance of edge populations now and in a warming world, through theory and experiment. Here I present some of our most recent findings, including evidence that edge populations can be simultaneously poor quality and locally adapted, that local adaptation gives edge individuals an advantage in habitat beyond the current range limit, but that edge populations can lose this 'edge' under climate warming.

Lionel-Cinq Mars talks

LCM01

Drivers of post-fire understory regeneration in the conifer dominated boreal forest of southern Northwest Territories

White, A.[1], Day, N. J.[1], Johnstone, J.[2], Cumming, S.[3], Mack, M.[4], Turetsky, M.[5], Walker, X.[4], and Baltzer, J.L.[1]
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In 2014, an unprecedented 3.4M ha of boreal forest burned in the Northwest Territories (NWT). The boreal forest is adapted to regular wildfire with fire regime playing a key role in plant community assembly post-fire. The frequency and severity of fire filters plant regeneration strategies, such as the ability to resprout from underground tissue. Understanding how variations in fire severity and other environmental variables impact the mechanisms of understory establishment may enable us to predict plant regeneration responses to changing fire regimes in the face of climate change. This research addresses whether the southern boreal forest of the NWT is experiencing changes in its successional trajectory, as seen in other western boreal locations, following the most severe fire year on record. Altering community composition can impact ecosystem functioning and wildlife habitat. In the first two growing seasons following the NWT fire, we established 224 vegetation plots across two ecoregions; a range of abiotic and biotic variables was measured, including depth of organic layer, fire severity and pre-fire stand composition throughout conifer-dominated stands. Species presence and modes of regeneration of vascular species were recorded. Based on previous work in the boreal forest, it was hypothesized that variations in fire severity would impact the relative success of plant regeneration strategies, influencing community composition post-fire. Results suggest that residual organic material and the seasonal timing of the burn may be key determinants in predicting the dominant mode of regeneration. The results of this research have implications for modeling wildlife habitat and managing forests in a changing climate.

LCM02

Root lifespan and overwintering strategies for two wetland species, *Sagittaria latifolia* and *Carex crinita*, in different climate zones

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Cold season hinders plant growth therefore plants respond either with tolerance or avoidance. In Northern Ontario with 150 days of growing season, roots of some perennial wetland species senesce in the autumn, while other species maintain their roots over the winter. Root senescence was observed to occur even if the roots are not exposed to soil freezing temperatures. Leaves of either strategy senesce. The distribution range of some of these wetland species can extend to warmer climates such as North Carolina with 208 days of growing season. This study aims to understand the effect of growing season length on root phenology of species across a climatic gradient of their natural distribution. We investigated two wetland monocot species with contrasting root strategies, *Sagittaria latifolia* with autumn-senescing roots and *Carex crinita* with overwintering roots. The plants were grown in a submerged mesocosms in Sudbury, Ontario and Charlotte, North Carolina. Four harvests were conducted throughout a year of plant growth in each location to assess the timing of spring root production and autumn root senescence. Vital staining with TTC (triphenyltetrazolium chloride) was used to assess root survival at each harvest event. As expected, *Carex crinita* maintained its roots alive throughout the winter in both sites, suggesting that their root system largely overwinters in both locations maintaining the same strategy regardless of the growing season length. Roots of *Sagittaria latifolia* senesced completely in the autumn at the northern location, however, preliminary data indicates that this species maintains alive some of its roots throughout the winter in the southern location. This might suggest that complete root senescence before the winter is a possible adaptation to long and unfavourable cold seasons. However, root senescence may be unnecessary when the cold season is short.

LCM03

Impacts of gold mining on plants and arbuscular mycorrhizal fungi in Northern Canada

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Gold mining continues to be an important part of economic development in Northern Canada. Since minerals and metals are non-renewable, it is important that mining development is carried out in a responsible and sustainable manner. A large portion of the gold that is found in the Northern territories is contained within arsenopyrite rock, therefore arsenic byproduct is of special concern. Currently, not much research has been done on the impacts of arsenic on plants and mycorrhizae in Northern Ecosystems. Previous research done in temperate regions has shown that the symbiosis formed between plants and arbuscular mycorrhiza can accelerate the remediation process in gold mines by supporting plant growth in poor soil conditions. The mine studied in this project is Tundra Mine, an inactive gold mine 240 km northeast of Yellowknife. Soil was collected from un-vegetated areas previously used as tailings ponds, but have since been treated to remove contaminants. Other sites were chosen at varying distances from the original tailings area to include a range of contamination levels and disturbances. Soil was analyzed for arsenic contamination as well as used to find mycorrhizal inoculum potential by quantifying spore density at each site. Several sites near the original tailings contained biologically relevant concentrations of arsenic in the soil up to 3.2mg/g. Mycorrhizal spores were found at all sites ranging from 800 spores/100mL to 15 spores/100mL of soil. Mycorrhizal plant species were also collected from each site in June and August 2016 for assessment of mycorrhizal colonization. Arbuscular Mycorrhizal colonization varied from site to site, but was found regardless of soil arsenic contamination. Arsenic analysis was done on plant species that were common to all sites, and it was found that samples exceeded the Canadian Food Inspection Agency in livestock feed of forage more than a hundredfold.

LCM04

The influence of AM fungi on the relative magnitude of intra- and interspecific competition among plants

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Plant species vary in their growth response to arbuscular mycorrhizal (AM) fungi, with responses ranging from negative to positive. Differences in this response to AM fungi may affect competition between plant species, influencing their ability to coexist. We hypothesized that when species with different responses compete, AM fungi provide benefits such as pathogen protection and greater nutrient acquisition to more positively responsive species. However, these benefits may cause positively responsive individuals to compete more strongly with one another. Thus, we predicted that in the presence of AM fungi, positively responsive species would experience stronger intraspecific competition and weaker interspecific competition, and negatively responsive species would experience weaker intraspecific and stronger interspecific competition. To test these hypotheses, we grew *Plantago lanceolata*, which responds positively to AM fungi, and *Bromus inermis*, which responds negatively to AM fungi, in a competition experiment that varied both the total density and relative frequency of each species. Plants were grown in either sterile soil, soil that contained other soil microbes but no AM fungi, or soil containing AM fungi as well as other soil microbes. AM fungi increased the strength of intraspecific competition experienced by the positively responsive *P. lanceolata*, and decreased the strength of intraspecific competition experienced by the negatively responsive *B. inermis*. However, AM fungi had only weak effects on the strength of interspecific competition experienced by either species. In the absence of AM fungi, other soil microbes did not have a significant effect on the strength of competition experienced by either species. Our results show that the benefits of AM fungi for positively responsive species may be offset by increased intraspecific competition. In contrast, AM fungi may release negatively responsive species from self-limitation. Strong intraspecific competition among species that respond positively to AM fungi may prevent them from dominance, thus promoting coexistence.

LCM05

Interactive effects of temperature, light intensity and chemical treatment on aerobic methane emissions from canola

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Aerobic methane emissions make an important, albeit small, contribution to the global methane budget, and these emissions are influenced by environmental stresses. While different precursors, including biopolymers and the primary metabolite methionine, have been suggested for the aerobic methane emissions, the mechanism of its production remains unknown. Also, other primary metabolites have yet to be examined. We investigated the effects of temperature, light intensity, and promoters or inhibitors of endogenous ethylene on methane emissions, ethylene evolution, and amino acid content in canola

(*Brassica napus* L. cv. 6056 CR). Plants were grown under two temperature regimes (22/18°C or 28/24°C; 16 h light/8 h dark, respectively), at two light intensities (300 or 600 µmol m^{-2} s^{-1}) and exposed to three chemical treatments (no application as control); ethylene promoter (kinetin, 10^{-4} M); or ethylene inhibitor (silver nitrate, 10^{-4} M), for a total of 12 experimental conditions. Higher light intensity decreased both methane emissions and ethylene evolution, but higher temperature and chemical application had no effects on methane emission and ethylene evolution. Methionine was significantly decreased by higher light intensity, and effects of temperature and light were evident in all 13 measured amino acids, which were mostly increased by both higher temperatures and higher light intensity. Methane and ethylene were positively correlated only with the amino acid methionine; however, methane emission was negatively correlated with several methylated amino acids. These results have important implications for the mechanistic understanding of methane emissions from plants.

LCM06

Influence of moisture and nutrient availability on green alder function across topographic gradients on the low arctic tundra, NT

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Climate warming is driving the expansion of shrubs across the tundra biome with implications for energy balance and hydrology. Changes in tundra plant water use attributable to shrub expansion are predicted to increase evapotranspirative water loss which may amplify local warming and reduce runoff. However, little is known about the extent to which shrub expansion could enhance evapotranspirative water loss in tundra systems.

To make predictions about the consequences of shrub expansion, it is necessary to understand the abiotic factors that constrain shrub distribution. Shrubs are preferentially expanding in areas that have a higher potential of accumulating moisture, such as drainage channels. We predict shrub expansion is limited by the availability of water and nutrients across topographic gradients. Nevertheless, the associations between shrub expansion, tundra hydrology, and abiotic limitations remain understudied.

We address these knowledge gaps by characterizing green alder (*Alnus viridis*) water use on the low arctic tundra of the Northwest Territories and investigating the influence of moisture and nutrient availability on green alder sap flow across the tops, middles, bottoms, and channels of shrub patch slopes. We use functional traits to investigate potential differences in shrub attributes relating to resource use to provide insight into the downslope expansion trend. We demonstrate that differences in thaw depth are important drivers of shrub physiological function and seem to be linked with water limitations. We provide evidence of a functional trait spectrum that explains a gradient in fast to slow water and nutrient use strategies that corresponds with topography; channel shrubs reflect traits associated with higher resource environments and greater productivity and growth relative to the slow-return strategy of shrubs at the tops of patch slopes. Green alder is expanding rapidly across the low arctic tundra and understanding the drivers of its expansion is essential for predicting future tundra conditions.

LCM07

One grass, two grass, ice grass, new grass: A second taxon of *Phippsia* (Poaceae) in the Canadian Arctic based on molecular data

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Phippsia is a genus of two arctic-alpine grasses, *P. algida* (ice grass) and *P. concinna* (snow grass). Although the species were found to be distinct in northern Eurasia, the presence of *P. concinna* in North America is controversial. The objective of the present study is to resolve the taxonomy of *Phippsia* in the North American Arctic. Several DNA regions were sequenced for samples from across the Arctic. Maximum parsimony analysis of the ITS and ETS data revealed three clades: *P. algida* from all regions sampled, *P. concinna* from Russia and Norway, and a third distinct clade from High Arctic Canada and Greenland that is most closely related to *P. concinna*. Screening of 17 non-coding cpDNA regions revealed little to no variation. Preliminary morphological data also supports the recognition of three taxa within *Phippsia.* These results suggest that a second taxon, distinct from *P. concinna*, should be recognized in Canada. Additional morphological and molecular work is underway to determine whether this taxon is best recognized at the species or subspecies level, as well as its Canadian distribution.

LCM08

A functional assessment of the mycorrhizal community at Steeves Lake Shoreline, Colomac Mine NWT

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The mining industry has played a large role in Canada's economy since the beginning of the twentieth century and is expected to play a larger role in the future. As the industry grows so do the impacts; economic, social, and environmental. This study will focus on some of the environmental impacts of mining and potential techniques to mitigate them. Bioremediation, the use of living organisms to remediate pollutants, has been gaining attention as it is a less invasive method of remediation and has greater public acceptance than other methods. The living organisms that will be used in this study are northern plants and mycorrhizae collected from Colomac Mine, a study site in the Northwest Territories. The objectives of this study will be to: (1) evaluate the mycorrhizal and plant communities at the study site to assess whether there have been negative effects on them due to historic contamination, (2) quantify the effects of petroleum hydrocarbon contamination on northern plants and associated mycorrhiza and (3) assess the capacity of northern plants and associated mycorrhiza to remediate petroleum hydrocarbon impacted soils. The results of the field study combined with our controlled studies will increase our understanding of how these communities are affected by petroleum hydrocarbon contamination and provide new insight in the area of bioremediation.

LCM09

Caught in action: Fine-scale plastome evolution in *Cuscuta* sect. *Ceratophorae* (Convolvulaceae)

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Parasitic plants have reduced to completely absent reliance on photosynthesis, and are usually characterized by sweeping genomic changes in photosynthesis-related genes. The plastid genome (or plastome; highly conserved in autotrophic plants) houses many such genes and is thus a useful system for documenting the genomic effects of a loss of photosynthesis. The parasitic plant genus *Cuscuta* (dodders) represents one of 13 independent transitions to a heterotrophic lifestyle within angiosperms, and it contains more than 200 obligate hemi- and holoparasitic species. Plastomes in this genus have been reported to show a substantial degree of diversification in terms of length and gene composition, and present an opportunity for unprecedented fine-scale comparisons of plastid evolution between closely related species of heterotrophic plants. In particular, a complex containing eight species in *Cuscuta* sect. *Ceratophorae* was identified by a recently conducted slot-blot hybridization survey as being of special interest because it exhibited even more rapid evolution than the rest of the genus. This species complex was exhaustively sampled, and their total DNA sequenced via a high-throughput approach. Complete plastid genomes were assembled and annotated for each of eight species. They were found to be between 61-84 kbp in length, representing a 50-60% reduction relative to plastomes from photosynthetic Convolvulaceae. Three species have a more reduced plastome than the others due to the loss of the bulk of photosynthetic genes. The plastome variation observed in our fine-scale analysis of these eight very closely-related parasitic plant species suggests a phylogenetically progressive loss of plastid genes and offers an excellent opportunity to study the reduction of plastid genomes in parasitic plants 'caught in action'.

LCM10

Exploring the impact of a carbonatite rock deposit on a Northern Ontario forest ecosystem

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Geological resources, like carbonatite rocks, have often been suggested as low-cost alternatives to inorganic fertilizers. Thus, research into carbonatites has only considered them as nutrient sources for plants, and because of this focus, information regarding their effects on soils and soil microorganisms is lacking. This study aims to provide insight into how a carbonatite rock deposit near the Spanish River (Ontario, Canada) has affected the soils, vegetation, and soil microorganisms in the area. The Spanish River Carbonatite (SRC) deposit is divided into 3 mineralogically-distinct zones: the inner core, the transition zone, and the outer core. Within each of these zones, as well as outside the deposit and at the quarry where SRC is mined, two sampling sites were selected. At each site, a modified-Whittaker plot was used to collect information regarding the plant communities as well as samples for soil nutrient chemistry and soil microbial community determination. It was found that the depth from the soil surface to the deposit has a dominant role in determining SRC influence. When this depth was 90m or less, the primary soil changes were an increase in soil pH from 4.8 to 5.8, an increase in Ca content from 188 to 2184 ppm, and a decrease in Al content from 1990 to 1197 ppm. Soil chemistry changes drove plant community composition and explained 25.9% of community variation as indicated by redundancy analysis. With the exception of one OTU in the Micrococcaceae family which was more abundant in SRC-affected soils than non-SRC affected soils, the soil bacterial communities did not appear to be strongly affected by SRC. Overall, this study demonstrates that geological resources such as carbonatites have impacts across soil-plant-microorganism systems. Because the components of these systems interact to affect plant growth, an understanding of these impacts will help guide their use in agriculture.

LCM11

Effects of wildfires on tree establishment in conifer-dominated boreal forests in southern Northwest Territories

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Natural wildfire is the primary driver of boreal forest dynamics. *Pinus banksiana* and *Picea mariana* are dominant conifers in the boreal and regenerate almost exclusively after fire due to cone serotiny. Historically, fire return intervals in western Canada are 50-200 years; when forests burn, *Pinus banksiana* and *Picea mariana* have matured and produced seeds that are available for dispersal. Climate warming is altering the fire regime in the boreal by increasing the frequency and severity of fire years. The fate of the Northwest Territories' (NWT) boreal forests under an altered fire regime is unclear; they may be resilient and experience typical successional patterns of stand replacement or they may shift to a new stable state dominated by a different set of species, as has been observed in Alaska. 2014 was an historically unprecedented fire season in the NWT. In response, in 2015 we established 224 vegetation plots across a 400km latitudinal gradient in conifer-dominated stands that burned in 2014. Results suggest that the degree of canopy consumption is the major driver of *Picea mariana* seed rain post-fire. Establishment of deciduous seedlings (*Populus tremuloides* and *Betula neolaskana*) was determined by seedbed characteristics following fire. Date of burn was important in determining which species of conifer established; early season fires led to the recruitment of *Picea mariana* while *Pinus banksiana* establishment responded positively to late season fires. This work provides insight into the impacts of a changing fire regime in the NWT and unparalleled data for post-fire forest succession in the NWT.

LCM12

Sumatroscirpus: taxonomic revision and the discovery of a new monotypic Southeast Asian sedge tribe (Cariceae-Dulichieae-Scirpeae Clade, Cyperaceae)

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The Cariceae-Dulichieae-Scirpeae Clade (~2,050 species, Cyperaceae) represents one of the most diversified lineage of flowering plants in the temperate and boreal zones of the Northern Hemisphere. Our knowledge of phylogenetic relationships within CDS (Cariceae-Dulichieae-Scirpeae Clade, Cyperaceae) has grown dramatically in recent years due to increased efforts to identify the sister-group to *Carex* (~1,996 species) and to clarify the taxonomy of the paraphyletic tribe Scirpeae. Approximately half of all CDS species have now been included in phylogenetic studies, but a single genus has escaped attention due to its extreme rarity: the putatively monotypic *Sumatroscirpus*, which is believed to be endemic to remote mountains in North and West Sumatra. As part of ongoing tribal- and generic-level revisionary work on CDS, we have reexamined the taxonomy and phylogenetic position of this genus. Its current placement in tribe Dulichieae appears at odds with several unique characteristics such as sheathing spikelet prophylls and inflated tubercles on fruits. Molecular phylogenetic analyses support these observations in showing its isolated position within CDS, and justify the recognition of *Sumatroscirpus* as the sole member of a new Cyperaceae tribe. In addition, field studies combined with the examination of all extant herbarium material indicate that the taxonomic diversity of *Sumatroscirpus* has been dramatically underestimated, with a total of four morphologically-distinct species now recognized, and with important new records extending its range into continental Southeast Asia.

LCM13

Understanding multitrophic interactions in vineyards exposed to different diversification and alternative ecological systems

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How can our understanding of community ecology help us implement sustainable management strategies in agriculture? Heavy reliance on agrochemicals and other intensive agricultural practices have led to changes in soil quality and ecosystem interactions. Alternative agroecosystem techniques should attempt to model naturally occurring ecosystems where maintaining a diverse array of plants, beneficial invertebrates and microorganisms support ecosystem functions and services. The use of non-synthetic soil amendments (e.g. cover cropping, mineral inputs, etc.) has become an increasingly studied approach to restore naturally occurring services in heavily managed agricultural systems. However, there is a need to better understand how such techniques may affect multitrophic interactions within the system as well as yield. This research aims to examine how vineyards respond to different ecological alternatives that aim to enhance soil health and promote pest and weed control. The targeted strategies include the addition of cover crops, Spanish River Carbonatite (SRC) as an agromineral (which can help enhance soil fertility), and beneficial soil microorganisms. More specifically my objectives are: 1) to investigate how combinations of cover crops, SRC, and microbes influence the functional diversity and production within this agroecosystem, 2) demonstrate the influence of these amendments on above and below ground invertebrate assemblages, and 3) provide a theoretical framework of ecosystem interactions that encompass these multi-trophic levels and elucidate how they can benefit this agroecosystem. In this presentation, I describe the model that is being used to define these interactions and deliver preliminary results from some of the plants that may also affect results through allelopathy.

POSTERS

Ecology

E-P01

Legacy effects of forest establishment on prairie plant and seedbank communities in a northern rough fescue prairie

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Forest encroachment resulting from fire suppression, modified grazing, and climate change poses a threat to northern prairie ecosystems. Encroaching trees alter the composition and function of plant and soil communities and can compromise the restoration of affected prairies. To evaluate the hypothesis that legacies of forest encroachment persist over time in restored communities, we examined the composition of plant and seedbank communities along a chronological sequence of prairie restoration

following tree removal. Study sites were located within two historic white spruce (*Picea glauca*) plantations established between 1930 and 1940 on rough fescue prairies in Riding Mountain National Park, MB. Within each site, we compared plant cover and seedbank composition between areas of native prairie, remaining plantation stands, and three tree removal treatments (1997, 2012, 2015). Our observations indicate that tree removal increased the abundance of weedy species and that these communities declined in diversity over time. Principal component analysis of the plant community indicated that in addition to forest legacy, the time since tree removal and the presence of invasive species were key factors in explaining the variability in restored communities. Our results indicate that tree removal is insufficient for prairie restoration and that persistence of low-diversity plant communities, consisting of invasive grasses, constitutes an important legacy of forest encroachment and an important barrier to prairie restoration. Ongoing research will explore changes in soil communities following tree removal to provide a functional perspective to the restoration of encroached prairies.

E-P02

New solutions or more problems: response of vegetation to wood ash application in interior British Columbia

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Increased demand for renewable energy has resulted in the rise of bioenergy systems and consequently, associated waste residuals. Wood ash application as fertilizer in forest ecosystems may provide a sustainable option for bioenergy waste products while concomitantly alleviating nutrient loss, ameliorating soil acidity, and increasing tree growth. This study examined the response of understory vegetation to the application of wood ash plus nitrogen (N) on spruce stands growing on fine-textured soils in Interior British Columbia. Two hybrid spruce (*Picea glauca* X *engelmannii*) stands in the Aleza Lake Research Forest were treated in May 2015 with two types of bioenergy-produced wood ash: Canfor ash (29.7% total C), UNBC ash (7.3% total C) and a control, with or without urea fertilizer, in a factorial design. Ash and urea treatments were applied at a rate of 5000 kg loose ash (dry basis)/ha and 100 kg N/ha of urea in pellet form to plots with an 8.0 m radius. Percent cover of ground vegetation was measured using a 1 m^2 quadrat square. There was a significant ($p<0.05$) effect of urea, and wood ash plus urea application on the relative abundance of species groups: bryophytes, lichens, forbs, grasses, shrubs, and trees. UNBC ash and urea application decreased the cover of forbs, grasses and tree seedlings, and increased the cover of shrubs. Canfor ash and urea application increased the cover of bryophytes. Lichens did not respond to ash or urea application. Our results indicate that the application of ash and urea to conifer stands in the interior of British Columbia can induce a shift in understory vegetation in the short-term, but that ash application had no negative impact on total ground cover one year post-treatment. With long-term monitoring practices encouraged, ash can be applied to landscapes as a fertilizer without damaging effects on ground vegetation.

E-P03

Influence of understory plant effect traits on post-disturbance forest productivity

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Despite the growing consensus on the importance of predicting ecosystem services using a functional trait approach, previous studies which supported the idea that functional diversity might affect short-term ecosystem resource dynamics were more theoretical than empirical. The general objective of the present study is to detect the effects of understory effect traits on forest productivity following different silviculture treatments. Data were collated from five different studies conducted in the Clay Belt region. In these forests, different silviculture treatments were applied: careful logging, clear cut, pre-commercial and commercial thinning, agricultural plantations and forest plantations. To identify the key traits affecting forest productivity, we selected 15 plant traits representing plant morphology, regeneration strategy and resource utilization. We will model (generalized linear mixed model) the responses of forest productivity (measured as tree annual increment) to variables that are related to functional diversity (FRic, FEve and FDiv), the richness and abundance of each trait group (33 trait groups in total), silviculture treatments and forest attributes (e.g. forest type, time since last fire). The lmer function from the lme4 R package will be used for generalized linear models, and two random effects of "site" and "plot" will be incorporated on the intercept into all models. We hypothesize that there is strong relationship between functional diversity and tree growth, and the silviculture treaments have impact on the relationship between functional diversity (or key traits) and tree growth.

E-P04

Using spatial genetic patterns to evaluate dispersal limitations of *Crossocalyx hellerianus* (Nees ex Lindenb.) Meyl.

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Dispersal limitations affect the genetic variability of a species, and may possibility lead to extinction of local populations and/or ultimately speciation. Most bryophytes are only a few bryophyte species are assumed to use long distance dispersal, consequently most bryophyte propagules would demonstrate distance dependent dispersal. Although some studies confirm this limited dispersal capacity, other studies report long distance dispersal in bryophytes that is independent of distance from the source population. Using genetic tools with sophisticated molecular markers is an easy approach to fill in the gaps in our knowledge of bryophyte species dispersal. *C. hellerianus* is a minute dioecious epixylic liverwort with a circumboreal sub-continental distribution, which primarily reproduces through asexual gemmae. Although it is a rare and patchily distributed in Europe, it is a relatively common species in boreal Quebec and Canada. We are going to study *C. hellerianus* dispersal at the population, metapopulation and bioregional scales using genetics tools. We test the hypotheses: *H1:* dominant asexual reproduction results in low dispersal capacity, and therefore low levels of genetic variation within and among the metapopulations and populations in Quebec. *H2:* colonies present in Quebec and the other regions of Canada, show high levels of genetic spatial structuring with samples and spatial information of the species will be collected from different in Quebec, other provinces in Canada and from other countries as possible. Extracted DNA will be analyzed using Inter simple-sequence repeats (ISSR markers) and will be analyzed to find haplotype relationships, population parameters, calculation of geographic distances and genetic relationships within populations, and among populations. These results will help to understand factors influencing dispersal and will contribute to the proper management of genetic diversity of threatened and rare species.

E-P05

Microbial abundance and diversity as impacted by the agromineral Spanish River Carbonatite

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Phosphorus (P) and Nitrogen (N) are plant growth-limiting nutrients deficient in most agricultural soils, and current soil management strategies rely heavily on chemical fertilizers, the overuse of which poses adverse threats to the ecosystem. P fertilizers are mined from a finite phosphate rock while N fertilizers require energy-intensive processes which have additional negative environmental impacts. Therefore, there is an urgent need for a sustainable alternative to chemical fertilizers capable of sustaining plant growth while having little to no adverse effect on the ecosystem. We are proposing a long-term strategy which involves the use of beneficial soil microorganisms, cover crops, and agromineral. The short-term study presented here was designed to assess the effects of two legumes and an agromineral on the diversity and abundance of soil bacteria. Under greenhouse conditions, we planted alfalfa and red clover separately in pots. Soil samples were collected before and after growing the legumes for seven weeks in soil amended with or without the agromineral SRC (for Spanish River Carbonatite). The numbers of colony-forming unites (CFU) per gram of soil as well as the colony morphology on three different selective media were used to assess microbial abundance, diversity, and gross function. We are interested in generalist microbes, phosphate-solubilizing and nitrogen fixing micro-organism. From preliminary data with nodulated plants, we expect to count more CFUs in soils where legumes have grown; because of the root exudates which provide carbon to the micro-organisms. Furthermore, we expect to see an increase in the abundance of symbiotic rhizobia in soil samples which have been amended with SRC compared to those without SRC. The results from this study will offer insight into the benefits of an integrated management strategy on microbial abundance and diversity, providing a sustainable alternative for plant nutrients.

E-P06

Factors influencing the regeneration of 4 species of fen true mosses in a fen restoration context

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The Peatland Ecology Research Group (PERG; Canada) have developed a technique which enables the revegetation of post extracted peatland into bogs, but, this technique isn't adapted to the revegetation of fens. The first large scale mechanical restoration of fen in eastern Canada couldn't bring back the typical fen true mosses on the site, underlining the lack of knowledge of what factors can influence the regeneration of fen true mosses.

This study looks at many factors that could influence the regeneration of 4 species of fen true mosses: *Aulacomnium palustre, Campylium stellatum, Scorpidium cossonii* and *Tomenthypnum nitens*. We tested the reaction to (1) fragment size (1 mm, 1 cm, whole) (2) the capacity to regenerate with increasing distance under the apex (3) phosphate fertilization (5, 10, 15, 20, 25, 40 g/m^2) (4) liming (pH 4.5 and 6.6). Those experiments were made in petri dish, the regeneration was evaluated after 8 to 10 weeks by counting the amount of innovation per petri.

All species reacted the same way: (1) the more fragmented the moss was, the more innovation it produced (2) the first 3 cm of the mosses produced the most innovations (3) phosphate fertilizing increased regeneration (4) liming had no effect on regeneration except for *Campylium stellatum*. For those experiments, the treatments were applied in ideal condition regarding humidity. Harsher meteorological condition, as often seen on the field, could negatively influence these results. The combination of treatments allowing for the best result was tested on the field. The result of this field experiment will also be discussed.

E-P07

Using historic grazing intensity to predict the plant-trait composition of northern fescue prairies

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Rough fescue prairies are one of the most degraded ecosystems in western Canada and continue to face challenges from development, fire suppression, and exotic plants invasions. Despite these pressures, remnant grasslands remain important for biodiversity conservation and as habitats for species at risk. Since 1973, Riding Mountain National Park, MB has been monitoring the restoration of rough fescue prairies, seasonally grazed by cattle inside the park, prior to 1969. In this project we examine the recovery of historically grazed prairies and test the hypothesis that the functional trait composition, but not the species composition of disturbed prairies, recovers following the removal of grazing. In 2015, we revisited 33 permanent transects, established in 1973 to monitor the effects of cattle on rough fescue prairies inside the park. Each of the 33 transects was classified using historic grazing intensities and used to record the composition and abundance of vascular plants. In addition, we assembled functional trait data for the ten most abundant species using a global trait database (TRY). Based on preliminary analyses, 82 native and 10 exotic species were identified along the 33 transects. Historic grazing intensity remained significantly correlated with species richness and effective richness. Since 1973, two exotic grasses, Kentucky bluegrass (*Poa pratensis*) and smooth brome (*Bromus inermis*), have become dominant across all transects, while the native plains rough fescue (*Festuca hallii*) only appeared on lightly and moderately grazed transects. Our results illustrate that exotic species pose a risk to the structure and function of restored fescue prairies. Ongoing analyses combine the functional traits of dominant plants to examine whether the long-term recovery of disturbed prairies is confounded by a small number of persistent, grazing-tolerant invaders and contrast the ecological function of invaded versus native plant communities.

E-P08

Development of field deployable assays to monitor and quantify the effects of waterborne contaminants on wetland plants and associated soil fungi

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The field deployable assay (FDA), created by Wilfrid Laurier University's Dr. Kevin Stevens, is an early alert system for toxicological assessment. It facilitates long term exposure in both a contained and controlled environment. The device was designed as an alternative to current monitoring systems, with increased control over environmental variables. The FDA is covered in the upper portion by the germination cassette while its main body is comprised of 100-300 um slits which allow for water entry while excluding soil particles. Through capillary action seedlings can draw water up and the scientist can monitor numerous same aged plants within the chosen environment. The validity for the FDA's orientation was confirmed with both vertically and horizontally grown seedlings. For both *Lactuca* *sativa* and *Phalaris arundinacea* vertically grown seedlings grew significantly longer roots suggesting impeded growth occurred in horizontal systems. This result was replicated 8 times with 10 seeds in each petri dish. When exposing said replicates to arsenic, a hormetic dose response was exclusively revealed in vertically grown roots. Another study was completed in Baker Creek, Yellowknife, North West Territories. This study aimed to prove the sensitivity of the FDA within the field. The site where the study had taken place is undergoing arsenic remediation. Arsenic negatively effects growth of both plants and seedlings. Those grown in the FDA's showed significant differences between sites for the germination rates. The implications of these results elude to the functionality it possesses. It picks up sensitive responses in the field, grows mycorrhiza and is a paramount tool equated to other current toxicological screening approaches.

Plant Development

PD-P01

Interactive effects of key climate change variables on growth and development of *Arabidopsis thaliana*

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Higher temperature and elevated carbon dioxide (CO2) concentration are expected to cause changes in global precipitation patterns and thus increased water stress events in soils. Few studies have reported the interaction between plants and the main components of climate change. In the present study, the abscisic acid (ABA)-insensitive mutant (abi1-1) and its associated wild- type (WT) of *Arabidopsis thaliana* were used to determine the effects of these three factors on growth and development. After sowing the seeds on normal Murashige and Skoog medium, the eight-day-old *A. thaliana* seedlings were grown for 10 days under two temperature regimes (22/18°C and 28/24°C, 16 h light/8 h dark), two CO_2 concentrations (400 and 700 μmol mol^{-1}), and two watering regimes (well-watered – watering to field capacity; and water-stressed – watering at wilting point). Then, plant morphological (e.g., total biomass), hormonal (e.g., ethylene, ABA and cytokinins (CK's)) and anatomical parameters were measured. The negative effects of the higher temperature and water stress on biomass were partially diminished by elevated CO2 in both cultivars, and to a higher extent in the WT cultivar. The levels of hormones increased in the water-stressed plants for both cultivars. The most critical factors affecting hormone balance in the abi mutant were water and temperature, but in the WT cultivar, they were temperature and CO2. CK response to the three tested factors was significantly higher in the abi mutant than in the WT cultivar. Abi1-1 had a higher stomatal density than the WT. Higher temperatures and elevated CO2 increased the cell size, but decreased the stomatal number and cell density in both cultivars. Findings from this study should provide us with a better understanding of plant responses to the combined effects of the three key components of climate change.

PD-P02

Cytokinin stimulates mycorrhizal colonization in pea

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Through altering gene expression, phytohormones are involved in all aspects of plant growth and development, including symbiotic relationships with arbuscular mycorrhizal fungi (AMF). One of these hormones, cytokinin (CK), promotes cell division and differentiation and in doing so increases the sink strength of areas where CK accumulates. As obligate biotrophs, AMF are strong carbon (C) sinks because they require C from their plant hosts, which they receive while providing phosphorus to them. This nutrient transfer occurs in structures known as mycorrhizae. CK ability to direct the movement of C by increasing sink strength suggests a potential link between CK and mycorrhizae. Here, we hypothesize that CK promotes the mycorrhizal colonization of pea (*Pisum sativum L.)*. To test this hypothesis, E151 (*sym15*), a pleiotropic pea mutant, was compared with the wild-type (WT) because E151 possesses a hyper-mycorrhizal phenotype and its roots accumulate high CK levels. These were manipulated in AMF-inoculated WT and E151 plants by applying exogenously chemicals known to either increase CK levels or inhibit its effect. Mycorrhizal colonization was determined in 35-day-old plants via the gridline intersect technique. Increasing CK levels by reducing the rate of CK degradation (INCYDE) or applying synthetic CK (BAP) increased mycorrhizal colonization in WT and E151. Conversely, inhibiting CK activity (PI-55) by blocking CK receptors resulted in decreased colonization. Statistical significance was tested between specific comparisons using Student's t-tests. While treatment with 1μM INCYDE yielded significant results, no other treatment was found to be statistically significant. However, trends could be seen in our results that strongly suggest a link between CK and increased number of mycorrhizae. Further investigation into this relationship is needed as this research holds much agricultural significance, because of the growing evidence that plant CK levels are affected by environmental factors, which could subsequently influence mycorrhizal activity.

PD-P03

Production of a recombinant form of the putative β-helix motif of the Toc159 M-domain

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The majority of nuclear-encoded chloroplast proteins rely on translocons at the outer and inner envelope membrane of chloroplasts (TOC and TIC complexes, respectively) for import. The TOC complex is composed of two GTPases (Toc159 and Toc 34) and one β-barrel protein channel (Toc75). Toc159 is a receptor involved in preprotein recognition and regulation of import at the surface of chloroplasts, and is composed of three distinct domains: the N-terminal acidic (A-) domain, the central GTPase (G-) domain, and the C-terminal membrane (M-) domain. The M-domain of Toc159 anchors the protein within the outer membrane; however, the domain does not contain a canonical membrane-anchor, and the nature of its association with the outer membrane is not understood. Previous work on the Toc159 homolog from *Bienertia sinuspersici*, revealed that it possesses a β-strand-rich region in the M-domain, which has been called the M2 sub-domain. Based on homology modelling it has been suggested that this region adopts a β-helix conformation, and is potentially involved in the association of Toc159 with the chloroplast outer membrane. The present study aims to confirm the structure of the putative β-helix motif of Toc159 from the model plant, *Arabidopsis thaliana*, produced as a recombinant protein in *E. coli*. The cloning, expression and purification of the recombinant protein will be described as a step toward the characterization of the structure of the M-domain and its function in membrane association and TOC complex assembly.

PD-P04

Characterization of protein targeting pathways into the outer-envelope membrane of chloroplasts

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There are 117 known Outer Envelope Proteins (OEPs) that reside in the chloroplast outer membrane. Of these 117 OEPs, only a few have been extensively studied regarding their targeting. With the exception of Toc75 which uses the general pathway involving an N-terminal cleavable transit peptide (TP) for targeting, the OEPs that have been studied so far either use the signal-anchored, tail-anchored, or beta-barrel pathway for targeting. However, previous studies showed that a key component of the translocon at the outer envelope of chloroplasts (Toc complex), Toc159, possesses a novel TP-like sorting signal and an unconventional membrane anchor within the C-terminus for its own targeting and insertion into the outer membrane. Moreover, recent studies using bioinformatics tools predicted that eight additional OEPs also contain transit peptide-like sequences at their C-termini. Transient expression assays in Arabidopsis mesophyll protoplasts demonstrated that two candidates, OEP18 and a putative GTPase, appear to be targeted to the chloroplast outer membrane using such a signal. My research focuses on determining the precise subcellular locations of OEP18 and the putative GTPase using protoplast transient expression assays, chloroplast fractionation and Western blot analysis. An additional objective is to perform secondary structure and membrane topology prediction analyses for all 117 OEPs so that they can be grouped according to their targeting pathways. These findings will allow for a better understanding of protein targeting to the outer membrane of chloroplasts.

PD-P05

BLADE-ON-PETIOLE 1 and 2 are required for innate immunity against pathogens in *Arabidopsis thaliana*

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Plants employ both innate and induced immune systems to detect and fight pathogens. BLADE-ON-PETIOLE (BOP) genes encode an evolutionarily conserved subclade of BTB-ankyrin proteins that control development within the NON-EXPRESSOR OF PATHOGENESIS-RELATED GENES1 (NPR1) family of plant defense regulators. NPR1 and its closest homologs are master regulators of an immune response known as systemic acquired resistance. BOP genes on the other hand have no known role in plant defense. We show here that Arabidopsis BOP1/2 are required in innate immunity, the first and most ancient layer of plant defense based on the recognition of conserved pathogen-associated molecular patterns (PAMPs) by plant pattern recognition receptors in the plasma membrane. We used a microarray approach to investigate the transcriptome of BOP1 overexpressing plants. Gene Ontology (GO) analysis of these data revealed that 35% of upregulated genes are associated with plant defense, in particular innate or PAMPs-triggered immunity (PTI). Among these genes were Clade I TGA factors that interact with BOPs to control development and have a previously characterized role in PTI. Direct pathogen testing confirmed that bop1 bop2 and tga1 tga4 mutants have similar defects in innate resistance to Pseudomonas syringae possibly functioning in the same genetic pathway to regulate key responses including callose deposition. Conversely, plants overexpressing BOP1 show increased innate resistance to this pathogen, a stronger oxidative burst, and abundant callose deposition. Collectively, these data reveal that Arabidopsis BOP1/2 have dual functions in development and defense. This work provides insight into the evolution of plant immune systems.

PD-P06

Antioxidants and ROS in the regulation of lace plant programmed cell death

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The lace plant *Aponogeton madagascariensis* is an aquatic monocot that has a perforated leaf morphology created by programmed cell death (PCD) as part of its normal development. This plant has emerged as a model for studying developmental PCD in plants due to the high degree of predictability of the process, combined with nearly transparent leaves that facilitate live cell imaging, and the availability of axenic cultures that allow for efficient propagation and pharmacological experimentation. Although the dynamics and time-course for lace plant PCD have been elucidated, the regulatory mechanisms are not well understood. The first visible sign that cells will undergo PCD during the window stage of leaf development is the disappearance of anthocyanins, which are known to be potent antioxidants. Therefore, the current study investigated the roles of antioxidants and reactive oxygen species (ROS) in lace plant PCD during the formation of perforations. The techniques employed included pharmacological experiments, histochemical staining for ROS, a novel long-term live cell imaging assay, spectrophotometric assays to determine anthocyanin and antioxidant levels, as well as western-blot analyses for superoxide dismutase 1 (SOD1) and catalase (CAT) antioxidant enzymes. Data indicate that the relative balance between antioxidants and ROS plays a significant role in lace plant PCD signaling and that cells with greater antioxidant scavenging capabilities compared to ROS production are resistant to PCD induction and persist beyond the formation of perforations.

Systematics

S-P01

On the evolutionary advantage of fruit indehiscence in *Cuscuta* subg. *Grammica* (Convolvulaceae)

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Cuscuta (dodder) is a genus of about 200 species of obligate stem parasites with subcosmopolitan distribution. The fruit, generally regarded as a capsule has a thin pericarp containing one to four seeds and opening at the base (circumscissile dehiscence; DE), or remaining closed (indehiscent; IN). IN has evolved multiple times in *Cuscuta* from DE, and is most common in the North American clades of subgenus *Grammica*. In addition, some species produce irregularly dehiscent fruits, either structurally (IrA) via thinning of the endocarp towards the base, or functionally (IrB) via other fruit traits and/or external factors. In this study, we explored the putative evolutionary advantage(s) of fruit indehiscence by examining the distribution of *Grammica* species based on their fruit type(s). We also compared the floatability and germination between seeds and capsules of *C. gronovii*, a species with indehiscent and functionally irregularly dehiscent (IN+IrB) capsules. The infructescence architecture in subg. *Grammica* was analysed to determine if a relationship exists with dehiscence modes. Within N America, IN+IrB fruit species have a larger geographical range size and more northern distribution than DE fruit species. IN+IrB fruit species also have more compact infructescences than DE or IN species, which contributes to their irregular dehiscence (since IN and IrB capsules are structurally identical). Seeds of *C. gronovii* are capable of floating for up to two days until imbibition occurs, whereas their capsules may continue to float for over nine days, which is probably a sufficient time to potentially allow long distance dispersal by water. These results suggest that IN species, particularly those that also break irregularly, have an enhanced dispersal capability compared to species with strictly DE fruits. Seeds of *C. gronovii* exhibit a delayed germination when not removed from their IN fruits; a strategy known as bet-hedging.

S-P02

Chromosome number and genome size variation among species of *Cuscuta* (Convolvulaceae)

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Cuscuta (dodder) is one of the most diverse groups of obligate parasitic plants *comprising* about 200 species. Systematics of the genus is challenging because of the lack of morphological characters, hybridization and polyploidy. Dodders exhibit significant karyotype variation, with reported chromosome numbers varying from $2n = 8$ to $2n = 60$. In addition, the genus is diverse in its chromosome size, symmetrical or asymmetrical karyotypes, monocentric or holokinetic chromosomes, and a high variation in nuclear DNA content. The aim of this study is to preliminarily explore the karyotype diversity in *Cuscuta* as a step towards understanding the chromosome evolution and polyploidy in the genus. Twenty five species were analyzed using iron hematoxylin and DAPI staining. Quantification of genome size in 15 of these species was also performed using flow cytometry. Most species examined presented $2n = 30$ with the exception of some tetraploids, such as *C. racemosa*, *C. gronovii*, *C. veatchii*, and an unknown *Cuscuta* sp. The latter two species displayed $2n = 60$ and $2n = 90$, respectively. Among the species with asymmetrical karyotypes, *C. angulata* and *C. africana* (subgenus *Pachystigma*), stood out through their strongly bimodal karyotypes. Some polyploids, mainly *C. veatchii* and *Cuscuta* sp. had about 30 chromosomes larger than the others, suggesting allopoliplody. The largest chromosomes were found in *C. monogyna* (subgenus *Monogynela*) and *C. indecora* (subgenus *Grammica*). With regard to the nuclear DNA content, *C. denticulata* and *C. monogyna*, had the lowest and the highest genome size, respectively, with $2C = 2.23$ pg and $2C = 66.08$ pg. These results indicate that the karyotype diversity in this genus is much more extensive than previously thought and suggest that hybrid speciation and polyploidy have played a major role in *Cuscuta* diversification.

Weresub Lecture

Some common fungi we thought we knew

Thorn, G.

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Mushrooms – the macroscopic fruiting bodies of certain fungi – abound in myriad forms and colours. Some of these are well known as wild-harvested edibles, having been first described in Europe in the 18th or 19th centuries and then reported from multiple habitats around the world. But how ubiquitous and well known are they? The honey mushroom, *Armillaria mellea*, was perhaps the first such widespread and ecologically ubiquitous mushroom to have been studied by a combination of microscopy, mating studies, and eventually molecular phylogeny. Canadian mycologists James B. Anderson and Jean Bérubé featured prominently in dissecting *Armillaria* to eventually reveal ten species in North America, each with distinctive ecology and distribution. Despite this early lesson, field guides to North American mushrooms remain filled the names of species first described in Europe. Iconic and delicious edible mushrooms such as *Boletus edulis, Cantharellus cibarius, Lactarius deliciosus*, and *Auricularia auricula* are all restricted to Eurasia, whereas their North American counterparts deserve separate – and sometimes multiple – species names. This work is ongoing, and gradually improving our knowledge of the North American mycota.

Thursday, July 6th

Ecology Section Symposium
Examining Plant Ecology through the Lens of Functional Traits

E-SY01

Exploring functional space along gradients of species richness

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If we measure n functional traits then this defines an n-dimensional "functional space". The values of these traits for a given individual defines its position in this space. A "functional niche" is the volume of this functional space occupied by the individuals of a given species. As we look at plant communities containing more and more species, how do these coexisting species occupy this functional space? Do new species tend to occupy previously unoccupied or previously occupied areas? Do species in species-rich communities tend to be more functionally specialized (smaller functional niches)? We explore these questions using two different and complimentary data sets: First, we combine data sets around the world from boreal to tropical communities. Second, we present data from an experimental study involving orthogonal gradients of soil fertility and disturbance rates.

E-SY02

Examining response and effect traits on bryophytes and lichens: towards a national network for Canada

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Bryophytes and lichens share a variety of characteristics, such as their poikilohydric nature, small reproductive propagules, and taxa often associated with specific habitat and microenvironment conditions, and have historically been grouped together as "cryptogams". While cryptogams are sensitive to different types of disturbance and are therefore frequently used as a "response" group, they also influence ecosystem functions in temperate, boreal and arctic systems where they represent significant proportions of biomass. Cryptogams contain a significant amount of intraspecific and interspecific variation with different life forms, reproductive structures, chemistry, and hydration mechanisms, lending themselves well to the study of functional traits and how they influence ecosystem processes. Furthermore bryophyte and lichens are among the least documented groups in terms of distribution and ecology in Canada. Considering the importance of cryptogams in Canadian ecosystems, we propose here a project to develop response (to habitat/disturbance) and effect (on ecosystems) functional traits for these colonial, morphologically diverse groups in Canada. Internationally there has been some work on the "moss" or "lichen" effect on ecosystem functions, and preliminary frameworks have been proposed for both response and effect traits for bryophytes and lichens, we will build on this baseline, and in conjunction with the TOPIC database, will propose a framework for future work in Canada.

E-SY03

The TOPIC network: collaborative science to make trait data available to Canadian scientists

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An important challenge in trait based ecology is the integration of large quantities of ecological knowledge from various sources into a structured, common format that facilitates analysis. The objective of this presentation is to present the collaborative science approach used by the TOPIC (Traits of Plants in Canada) network to meet logistical and data needs of trait-based ecology. TOPIC is a network of scientists from academia and government as well as practitioners that stimulates, promotes and facilitates research in plant ecology and community ecology. The network is principally centred on a structured eco-informatic platform that stimulates the documentation and storage of data on traits on Canadian species, as well as facilitates data sharing among scientists. The network also fosters the application of the trait approach by encouraging the creation of working groups focused on specific ecological issues for which knowledge gaps exist. TOPIC has also increased the availability of trait data in Canada by organizing collaborative trait gathering campaigns targeted at specific data needs to adequately address knowledge gaps at the appropriate scale. Such grassroot networks can serve as a critical link between individual labs and global scale consortia (e.g. TRY) by facilitating groups of researchers with closer geographical ties all while pushing disciplinary boundaries and embracing new data management approaches.

Ecology Section - Contributed Papers

E-CP01

Nutrient uptake in wetland plants during leaf senescence

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Root phenology is known to differ from leaf phenology, but the importance of nutrient uptake during above-ground senescence in herbaceous plants is not well known. This study investigated nitrogen uptake late in the growing season for two wetland monocots with contrasting senescence patterns: *Carex lasiocarpa* (Cyperaceae) with late leaf senescence and roots that survive the winter, and *Sparganium emersum* (Typhaceae) with early-senescing leaves and roots that completely senesce before the winter. The plants were grown outdoors in pots in Sudbury, Ontario. A solution of $^{15}NH_4{}^{15}NO_3$ was administered on either August 25 or on September 20. The plants were harvested on November 13 after leaves of both species had fully senesced. The content of ^{15}N was analysed in all overwintering parts, which for *S. emersum* was rhizome only, and for *C. lasiocarpa* roots, shoot winter bud and rhizome. The enrichment led to higher concentrations of ^{15}N in both species at both application times. The highest $\delta^{15}N$ was found in *S. emersum* rhizomes and in *C. lasiocarpa* winter buds. The amount of administered $\delta^{15}N$ taken up and found in the overwintering parts of *C. lasiocarpa* was 26% and 31% of the applied amounts, while in *S. emersum* these values were 9% and 14%. The proportion of ^{15}N of the total N in the overwintering plants was higher in *S. emersum* than in *C. lasiocarpa*. We conclude that despite the well-progressed leaf senescence and imminent root senescence of *S. emersum* in September, roots of this species were still able to take up the marker. This late-season N uptake was proportionally more important for the N content of the overwintering plants in *S. emersum* than in *C. lasiocarpa*. The larger absolute amount of the marker taken up by *C. lasiocarpa* could be explained by the larger size of that species.

E-CP02

Aerobic methane emissions from plants: an overview

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It has been more than a decade since the discovery of aerobic methane emissions from plants. At the beginning, this discovery received with skepticism, and since then there has been debate on the origin, emission rates, the method of estimation, and the atmospheric contribution of this new source of methane. Although there is still uncertainty about the source and biochemical pathway of methane in plants, and its impacts on global methane budget, there are now sufficient published documents in support of the non-microbial methane emissions from plants. Methane is the second important greenhouse gas after carbon dioxide, but its global warming potential is much higher than carbon dioxide. Therefore, many scientists from different institutions around the world have interested in knowing the factors that affect aerobic methane production as well as its origin in plants. Abiotic stress factors, including high temperature, enhanced ultraviolet-B radiation, water stress, and low light or blue light can increase methane emissions from plants. Physical injury has also been reported to increase aerobic methane emissions. However, elevated carbon dioxide concentrations have been shown to reduce the adverse effects of environmental stress factors on plants and, in turn, decrease methane emissions from plants. It has also been shown that methane emissions vary with species and cultivars, plant organs, and developmental stages of plants. Methane emissions were higher from stem than leaf, and from upper shoot than lower shoot, and it decreased as plant aged. Initially methoxyl groups of pectin were suggested as precursor of aerobic methane in plants. Later, other chemicals, including cellulose and lignin, leaf surface wax, and methionine, were suggested as origin of methane in plants. Further studies should provide more information about the origin and global contribution of aerobic methane emissions from plants.

E-CP03

Wild Species 2015: the general status of species in Canada

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Canadian Wildlife Service, Environment and Climate Change Canada, Government of Canada

The first step in preventing the loss of species is to know which species we have in Canada, where they occur and what their status is. The mandate of the program on the General Status of Species in Canada (www.wildspecies.ca) is to provide this overview. The main product of the program is the report series *Wild Species: The General Status of Species in Canada*. In the latest report, *Wild Species* 2015, the conservation status of about 30,000 species was assessed. All known species in Canada of vascular plants, bryophytes, macrolichens, and selected macrofungi were included, as well as several animal species. Results indicated that the majority of species in Canada are secure. However, vascular plants represented the taxonomic group that had the most endemic species ranked as presumed extirpated, possibly extirpated, critically imperiled, and imperiled at the national level in Canada. Results also underlined the presence of a large number of exotic species in Canada, especially for vascular plants. In fact, 25% of all species of vascular plants in Canada are exotic. Furthermore, several species were unrankable or unranked at the national level because of a lack of knowledge. In the future, the *Wild Species* series will continue to consolidate our knowledge of species in Canada.

E-CP04

Clonal growth yields enhanced siring success with no effect on selfing rates in a population of *Sagittaria latifolia* Willd. (Alismataceae)

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Most herbaceous plants are capable of some form of clonal reproduction but its consequences for sexual fitness are not well understood. Recent theory and experimentation have shown, contrary to the prevailing view of the past 30 years, that vegetative expansion of plants via clonal growth can enhance siring success with limited effects on selfing rates. This theoretical result depends on the degree of clonal intermingling and the distance over which pollen is dispersed and it has not been tested in natural populations. To study the consequences of clonal growth on sexual fitness we mapped and genotyped all flowering ramets in an isolated population of *Sagittaria latifolia* using 7 SSR loci to identify the size (number of ramets) and spatial extent of genets. We then genotyped one seed per flower to measure selfing rates at the ramet and genet levels and to examine patterns of siring success at the genet level. As predicted for populations with intermingled genets we found (1) no association between clone size and selfing rates and (2) a significant positive association between genet size and siring success. Our results support recent theoretical work on the consequences of clonal expansion for sexual fitness.

E-CP05

Habitat heterogeneity stimulates the regeneration of bryophytes and vascular plants on highly degraded minerotrophic peatlands

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Large areas of minerotrophic peatland in northern Alberta are degraded by in situ oil sands exploration. These operations require winter exploration of deeply buried bitumen deposits along a dense network of temporary drilling pads. This eliminates the hummock topography that is characteristic of wooded fens when pads are abandoned in spring, and creates flooded surface conditions during a portion of the growing season. Recovery of the many specialized bryophytes and vascular plants in these modified ecosystems is thought to depend on the recovery of hummock topography.

Within an extensive peatland complex in late winter, we extracted large blocks of frozen peat from the flattened surface of drilling pads and placed them next to their excavated hollows. The drilling pads were revisited four years later to assess the effectiveness of mounding on the natural development of peatland vegetation.

Bryophyte composition differed substantially between the mounded and unmounded areas on drilling pads. Mounds supported numerous species not adapted to the characteristically saturated growing conditions in the adjacent flattened areas. Trends for vascular plants were less pronounced. Bryophytes (true mosses, *Sphagnum*, and liverworts), and trees, shrubs, and forbs, had significantly higher species numbers on mounds as compared to flattened areas. In contrast, graminoids (mostly Cyperaceae, Poaceae, and Juncaceae families) had significantly more species within the unmounded areas. The increased habitat heterogeneity derived from mounding was a major contributor to total species numbers across the study area.

Developing a large volume of elevated peat substrate following exploratory drilling operations may be required for restoration of minerotrophic peatland vegetation. However, this substrate will need to persist long enough to allow for natural hummock-forming mosses to establish, which ultimately will be required for the recovery of a wide range of bryophyte and vascular plant species. A number of factors affecting mound formation and persistence require further study.

E-CP06

Restoration of Big Meadow Bog: Steps towards the recovery of the globally endangered *Geum peckii* (Eastern Mountain Avens)

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At Big Meadow Bog on Brier Island, Nova Scotia, agricultural ditching in 1958 lowered the water table. Nesting Herring Gulls colonized the bog twenty years after ditching, and resulted in extensive death of the primary Canadian populations of Eastern Mountain Avens (*Geum peckii*). Thousands of colonial Herring Gulls annihilated the bog vegetation via trampling and nutrient enrichment that resulted in zones of exotic weeds and raspberry canes. Gull colonization of bog areas, their abandonment and subsequent recovery was investigated using historic aerial photographs, plant survey and seed bank analysis. Vegetation and seed bank made radical adjustments that included: dominance of above and below ground by introduced weeds, replacement of weeds by *Rubus idaeus*, an early recovery mixture of canes/biotically-dispersed shrub and clonal herbs, and the establishment of a diverse, native wetland. A massive (18 thousand seeds.m-2) weed seed bank in the gull grass phase declined to zero after 26 years (half-life = 4.16 years). Seed bank dynamics of similar magnitude ensued for native non-bog species. Biotic dispersal of seed, and not seed bank, dominated the early recovery stage. The recovered community meets basic restoration targets for moss, native herbs and shrubs but not *G. peckii*. Full restoration of the original hydrological regime is required to achieve ombrotrophy and a high water table lagg to complete the Recovery Plan of the endangered *Geum peckii*. Blockage of the drainage ditches began in 2016 and will be completed in August 2017.

E-CP07

The hydrological niches of tallgrass prairies

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Differences in water use between plant species is emerging and an important factor allowing for coexistence. However, most studies on differential water use only examine a small number of the common species present in a community. Most plant communities have a few dominant and a large number of uncommon (rare) species. The role of these rare species and the factors controlling their distribution has received little attention. Wet, tallgrass prairie communities have mostly disappeared from the grasslands of North America. They can have a remarkably large number of uncommon species. Typically, these communities experience spring flooding followed by mid-summer drying. I measured soil surface drying and the depth of the anaerobic soil layer caused by flooding in three tallgrass communities, and used these data to define the hydrological niche of all the plant species in the communities. Although the three sites formed a continuum of drying conditions, the majority of the species were found on all three sites, suggesting site to site differences in hydrology have little effect on community composition. Indicator species analysis suggested the communities could best be divided into two subgroups. Species in these subgroups showed a clear separation along the soil hydrology gradient. A comparison of the hydrological niches of each species pair, using kernel density estimation, showed that less than 10% of the species pairs showed significant differences in their hydrological niche. This suggests that competitive exclusion would likely occur the absence of disturbance in these communities. The uncommon species were found rare hydrological conditions rather than hydrological conditions of a particular value. This suggests rare species may benefit from environment variability in tallgrass prairies.

Friday, July 7th

Plant Development Section Symposium
Organelle Dynamics

PD-SY01

Function and mechanism of light-dependent chloroplast movements in leaf cells

Hangarter, R.
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Light-dependent chloroplast movements function to optimize light absorption in photosynthetic cells. Under high light intensity leaf cells locate chloroplasts along their sides and in low light the chloroplasts are relocated to the upper and lower sides of cells. This repositioning of chloroplasts is stimulated by the plasma membrane-associated phototropin photoreceptors and appear to be driven by actin re-organization at the plasma membrane. I will discuss how chloroplast movements dynamically affect the optical properties of leaves to fine-tune photosynthesis. In addition, results will be presented

showing that the plasma membrane-associated protein, Thrumin1, is required for normal chloroplast movement and functions in reorganization of the cortical actin cytoskeleton during light-dependent chloroplast movements.

PD-SY02

Dynamic inter-organelle co-operation and networking in plant cells

Mathur, J.
Laboratory of Plant Development & Interactions, Department of Molecular & Cellular Biology, University of Guelph, Guelph, Ontario, Canada

While animals tend to move away as they perceive changes in their surroundings plants readily start adjusting to the environmental alterations. The subtle, subcellular adjustments made in plant cells eventually account for their long-term survival as well as successful colonization of seemingly harsh habitats. My lab uses fluorescent protein aided live-imaging to understand the rapid but often transient subcellular responses that occur in plant cells. Our recent work has focused on the behavior of chloroplasts, mitochondria, peroxisomes and the ER. The resultant picture of the co-operation amongst biochemically and functionally unique compartments, that is involved in maintaining cellular homeostasis in living plant cells will be presented.

PD-SY03

Myosin-driven organelle movements in tip-growing cells

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Cytoplasmic streaming is a prominent feature that is easily observable in most plant cells. These rapid movements of organelles within the cytoplasm are driven by myosin XI motors that move actively along actin filaments. Reverse genetic approaches in the model species *Arabidopsis thaliana* have established that myosin motors are required for normal cell expansion. This connection between intracellular movements and cell growth is most evident in root hairs and pollen tubes that require targeted delivery of secretory vesicles to their tip where all growth takes place. For example, we have found reduced organelle motility in myosin mutants that also showed reduced root hair tip growth. Curiously, accumulation of putative secretory vesicles at the root hair tip in one of these mutants was not affected. We also found similar results in pollen tubes where a double mutant of highly similar myosin paralogs resulted in dramatically reduced organelle movements but normal vesicle accumulation at the tip. Interestingly, loss of myosin motors was accompanied by reduced dynamics of actin filaments and, in the case of the pollen double mutant, by changes in the overall organization of the actin cytoskeleton. These double mutant pollen tubes also elongated significantly more slowly than wild-type pollen which resulted in reduced seed set compared to wild-type, demonstrating a role of myosin motors not only in cytoplasmic streaming and actin organization, but also in cell growth, and ultimately in fertilization.

PD-SY04

Novel players in plant clathrin-mediated endocytosis

Stefano, G., Renna, L., Wormsbaecher, C., Gamble, J., Zienkiewicz, K., and Brandizzi, F.
MSU-DOE Plant Research Lab and Plant Biology Department Michigan State University, East Lansing, Michigan, USA

Eukaryotic cells, through the endocytic process, internalize an equivalent of one to five times per hour their cell surface. In order to support this massive mechanism the endocytic recycling pathway must be precisely and finely regulated to maintain a perfect homeostasis at the plasma membrane. To date it is still unknown, where and how exactly endocytic clathrin-mediated events starts at plasma membrane level. It is well known that clathrin-coated vesicles (CCV) are necessary to start the endocytic process. However, in plant cells little is known about all the molecular mechanisms and accessory proteins involved in this process.

Here, I will present the role of two novel proteins in clathrin-mediated endocytosis and propose a new model that describes the establishment of specific areas of the PM where endocytosis events start.

Contributed Papers

Systematics & Phytogeography Section

SP-CP01

Phylogenetic relationships and hybridization in asters of the *Doellingeria-Eucephalus* clade (Astereae, Asteraceae)

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In North America, asters of the tribe Astereae mostly belong to a single large monophyletic group including at least 77 genera and 770 species. Within this clade, the earliest-diverging lineage consists of the two genera *Doellingeria* (3 species in eastern North America) and *Eucephalus* (10 species in western North America). Nuclear (ITS-ETS) sequences from all species of the *Doellingeria-Eucephalus* clade support the monophyly of this early lineage. Morphological features of the two genera are also consistent with a single origin of the group. However, plastid sequences from these species do not form a monophyletic gene tree. Instead they fall into two divergent subgroups, one consisting of *Doellingeria* + *Eucephalus elegans*, and the other comprising all remaining species of *Eucephalus*. Plastid sequences of the former group closely resemble those of the bog aster *Oclemena nemoralis,* and form a clade with *Oclemena* and several other genera including *Herrickia, Machaeranthera, Eurybia* and *Oreostemma*. These results suggest apparent chloroplast capture resulting from an ancient hybridization event involving *Doellingeria-Eucephalus* ancestors and the genus *Oclemena* or one of its close relatives. Our phylogenetic analyses also shed light on the relationship between *Doellingeria* and *Eucephalus*. Although the two genera have long been treated as separate on the basis of qualitative morphological differences and their non-overlapping geographic distributions, our results suggest that *Eucephalus* is paraphyletic rather than monophyletic. We therefore propose that the two genera should be combined under the older of their two names, *Doellingeria*.

SP-CP02

A new phylogenetic classification of Poeae subtribes Poinae, Coleanthineae, and Miliinae (Poaceae)

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Subtribes Poinae, the largest subtribe in the grass family with over 700 species in 29 genera, Miliinae (1 genus, 5 spp.), and Coleanthineae (10 genera, 163 spp.) together form one of three clades in tribe Poeae, the largest tribe in Poaceae. Here we present a revised classification of this clade based on molecular phylogenetic data (ITS, ETS, trnT-trnL-trnF, MatK, and rpoB-trnC). Our analysis includes 39 of the 40 genera, with broad sampling within all of the large genera and all or most of the species in the small genera (>800 samples.). We compare our classification with previous classifications based on morphology and/or molecular data, and discuss the evolution of several morphological characters. Subtribes Miliinae and Coleanthineae resolved as monophyletic with strong support; however, Poinae (sensu Soreng et al. 2015) is paraphyletic because Miliinae is embedded within it. The genus Poa is more closely related to Milium, and possibly Phleum, than it is to other genera traditionally placed within Poinae s.s. Here we redefine subtribe Poinae to include only the genus Poa, recognize both Miliinae and Phleinae as monogeneric subtribes, and subdivide the remaining 26 genera of Poinae s.l. into several well-defined subtribes, some of which are reticulate in origin. Morphological and habit characters traditionally used in the classification of the group, such as annual versus perennial, one-flowered versus multi-flowered spikelets, glume length relative to floret length, spike-like panicles, and awn development and insertion, were determined to be highly homoplasious among and within the subtribes.

SP-CP03

Pantropical biogeography and allometric associations with seed size evolution in *Plukenetia* (Euphorbiaceae)

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Plukenetia is a pantropical genus of twining lianas and vines with notable seed size variation. Several species are traditionally cultivated in South America and Africa and are emerging as popular economic crops due to their high polyunsaturated fatty acid (omega-6, omega-3) and protein content. The genus is a promising system to study oil biosynthesis and accumulation, as well as drivers of seed size evolution and pantropical disjunct distributions. Here, use five nuclear and two plastid molecular markers to resolve the backbone relationships of *Plukenetia*. We find support for the monophyly of two morphological divisions and three major lineages, the pinnately-veined clade (New world species group "2") and the palmately-veined clade (Sect. *Plukenetia* + Old World *Plukenetia*). Molecular dating and biogeographical analyses revealed *Plukenetia* originated in the Atlantic forest of South America during the Oligocene and then migrated/dispersed repeatedly into the Amazon and then Central America and Mexico prior to the formation of the Isthmus of Panama. The pantropical distribution of *Plukenetia* is best explained by multiple trans-oceanic long-distance dispersals, first to Africa and from there independently to Madagascar and SE Asia. Within the genus, seed size evolution is dynamic and best associated with growth form and habitat. The ancestor of *Plukenetia* was likely a large-seeded high climbing robust liana and its decedents experienced four transitions to slender liana growth forms that are putatively correlated with seed size reductions. We suggest allometry could be a process that seed size variance develops among closely related organisms.

SP-CP04

Phylogeny and biogeography of the Cariceae-Dulichieae-Scirpeae Clade (Cyperaceae): new tribes, genera and species based on morphology, embryology and phylogenomics

Starr, J.R.[1,2], Léveillé-Bourret, É.[1,2], Ford, B.A.[3], Gilmour, C.N.[1,2], Naczi, R.F.C.[4], Donadío, S.[5], Nguyễn, T.K.T.[6], Vũ, A.T.[7], Chen, B.[8], Spalink, D.[9], Sytsma, K.[10], Lemmon, E.M.[11], and Lemmon, A.[12]
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With approximately 40% of all sedge species (>2050), the Cariceae-Dulichieae-Scirpeae (CDS) clade is a cosmopolitan lineage that is found in habitats ranging from deserts to tropical rain forests. Although comprised of three tribes, the CDS clade is dominated by Cariceae, a monotypic tribe for *Carex*, one of the world's largest plant genera (ca. 2000 spp.). The genus' diverse biogeography, intriguing cytology, and morphological singularity have made it a promising model for studying speciation, ecology and biogeography, but its relationships within the CDS clade remain unclear. This has important consequences for the conclusions drawn in all *Carex* studies since outgroups have a significant impact on homology assessment, character polarisation and biogeographical analyses.

Over the past decade, we have focused our research on the relationships of Cariceae to the approximately 86 species and infraspecific taxa that make up the remaining members of the CDS clade. Using representatives for all 18 CDS genera currently recognised and approximately two thirds of Scirpeae and Dulichieae species, our five marker DNA sequence dataset (*matK*, *ndhF*, *rps16*, ETS 1f, ITS), in conjunction with morphological, anatomical and embryological data, suggest there are seven well supported major lineages within the CDS clade with Dulichieae and *Khaosokia* as successive sisters to all other lineages. Although our previous trees had weak or unresolved backbones due to a rapid radiation among CDS lineages (10 million years), we have since employed universal angiosperm enrichment probes to generate a 461 nuclear gene matrix using next generation sequencing technology. These phylogenomic analyses are fully congruent with our Sanger-sequence datasets and morphology, but backbone nodes are fully supported (100% BS). Consequently, we can now propose a new tribal and generic classification for the CDS clade that includes four new tribes and a new subtribe, in addition to the discovery of several new genera and species.

Plant Development Section – Contributed Papers

PD-CP01

Carrie Derick – Botanist and Canada's first woman professor

Dickinson, T. A.[1,2]
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Carrie Matilda Derick (1862—1941) served as Professor of Comparative Botany at McGill University from 1912 until she retired in 1929. Her education, appointment, and career all exemplified the difficulties and frustrations encountered by women in Canada who sought higher education and endeavoured to have academic careers in their own right and on a par with men. Unfortunately, despite the pioneering efforts of Derick and other women at McGill and elsewhere, during the first half of the 20th century, the sexist barriers to women's participation in Canadian science generally, and in Canadian botany in particular, were not broken down until the Second World War and the dramatic social changes that followed it. Even today achieving equity is a work in progress that is even more complex since it involves breaking down barriers of class, color, and culture as well. This presentation is intended to remind Canadian botanists of an important academic foremother, to review some of the challenges that remain, and to take note of some of the efforts being made to address these challenges.

PD-CP02

Selection of herbicide tolerant common bean via genome editing

Nowak, J., Marsolais, F., and Tian, L.
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Herbicide tolerance is a key trait for crop management. For *Phaseolus vulgaris* (common bean) the herbicide Pursuit is generally utilized pre-emergence or preplant incorporated to control broadleaf weeds. Although common beans have good tolerance to this herbicide, a major disadvantage is a narrow margin of crop safety which can result in crop injury and reduced yield. Pursuit is part of the imidazolinone or group 2 herbicides which act as inhibitors of acetolactate synthase (ALS). Other crop species with resistance to this herbicide have been developed and marketed in parts of Canada. These cultivars integrate variants of the ALS enzyme incorporating mutations rendering the enzyme insensitive to the imidazolinone inhibitor acting as the herbicide. We have determined the locations of the putative mutation that would be required to induce tolerance to Pursuit in common bean ALS genes. Using our successful regeneration methods, we are in the progress of developing a transformation system in AAC Burdett Pinto bean variety. In parallel, we are working to build a CRISPR/Cas9 platform that will allow us to use that technology to specifically target the area of interest in the ALS gene via homology-directed repair mechanism. Downstream goals of this project are to apply efficient tissue culture techniques in common bean to developing herbicide resistant cultivars for Canadian agriculture in combination with genome editing.

PD-CP03

Parasitic chalcid wasps are able to manipulate gene expression of Douglas-fir ovules to benefit developing larvae

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In Douglas-fir (*Pseudotsuga menziesii*), megagametophyte development occurs even in the absence of pollination. A receptive megagametophyte containing receptive eggs will, once fertilized, develop substantial storage reserves to feed its developing embryo. Should pollination or fertilization fail, then storage reserves will not accumulate and the megagametophyte aborts. Abortion also occurs if an embryo dies prematurely in the megagametophyte. The chaclid wasp *Megastigmus spermotrophus* has found a way to bypass abortion of Douglas-fir megagametophytes. Female wasps oviposit their eggs into unpollinated, unfertilized megagametophytes, which accumulate storage reserves *as if they had their own embryo to feed.* Instead, it is the parasitic insect larvae that are well fed. Our RNA sequencing study shows that megagametophyte development is manipulated by the insect. We studied ovules in four conditions: 1. pollinated and uninfested, 2. pollinated and infested, 3. unpollinated and uninfested, and 4. unpollinated and infested. A de novo reference transcriptome was assembled in Trinity. Expression values were estimated based on the alignment of the original reads back onto the reference transciptome using RSEM. Transcripts were annotated based on sequence similarity to genes of *Pinus taeda*, *Arabidopsis thaliana*, *Nasonia vitripennis*, and the UniProt database. Differential gene expression in Douglas-fir suggests that *M. spermotrophus* is capable of manipulating its host. Infested ovules, whether pollinated or unpollinated, have more transcripts related to seed storage, cell division/growth, solute transport, programmed cell death and hormone signaling than do unpollinated, uninfested ovules. Furthermore, gene expression profiles of infested ovules are quite similar to those of pollinated, uninfested ovules. Although larval feeding triggers some genes involved in wounding, defense genes against herbivory are not up-regulated, meaning the insect achieves an uncontested access to the ovule's eventual storage reserves.

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Cultivars of *Vicia faba* (Fabaceae) differ in the size, shape, ratio of trichome types, and nectar production of the extrafloral nectaries on their stipules

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Extrafloral nectaries occur on the vegetative plant body and often lead to interesting insect-plant relationships, thus attracting wide research attention in the ecological realm. Many studies have demonstrated that the presence of aggressive, nectar-seeking insects (especially ants) reduces herbivory by phytophagous insect species, resulting in a net benefit to the nectar-yielding plant. Much less studied are the structural features of extrafloral nectaries in connection to their nectar-production capacity, a shortcoming addressed in this investigation. Four cultivars of broad bean (*Vicia faba* L.) possessing an extrafloral nectary on the abaxial surface of each stipule were studied in small field plots and in growth chambers. Each stipular nectary consisted of multicellular secretory trichomes (4-8 head cells above a stalk and basal cell) surrounding elongate, non-secretory trichomes usually extending beyond the former. Nectaries varied significantly in their average area, as well as in their shape owing to irregularities at their boundaries. Moreover, within a nectary, the ratio of secretory to non-secretory trichomes always exceeded unity but was highly variable among cultivars; some nectaries lacked the non-secretory hairs entirely. Similarly, average volumes and carbohydrate quantities of extrafloral nectar per stipule varied significantly among cultivars. Relatively few species of agronomic importance possess extrafloral nectaries, and the results of this study suggest that the ecological role played by stipular nectaries in agricultural settings of *V. faba* is likely cultivar-dependent.