

PLANT CANADA 2019

Time	Monday July 8 <sup>th</sup>	Tuesday July 9 <sup>th</sup>	Wednesday July 10 <sup>th</sup>
Place	Room: Rozanski 104	Room: Rozanski 104	Room: Rozanski 104
8-8:30	Coffee-break (concourse)	Coffee-break (concourse)	Coffee-break (concourse)
Session	Plant Biotechnology	Agronomy	Managing Plant Disease in Horticulture
Chairs	Dr. Rima Menassa & Dr. Abdelali Hannoufa	Dr. Helen Booker	Dr. Lone Buchwaldt & Dr. Valerie Gravel
8:30am	<b>Dr. Maureen Hanson</b> Cornell University, NY  <i>Improving photosynthesis in C3 plants</i>	<b>Dr. D. Brian Fowler</b> University of Saskatchewan, SK  <i>Winter wheat production in the high winter stress climate of western Canada – An experiment in crop adaptation</i>	<b>Dr. Mary Ruth McDonald</b> University of Guelph, ON  <i>Billions, trillions and quadrillions: The challenge of managing clubroot on canola and vegetables</i>
9:20am	<b>Dr. Bing Yang</b> University of Missouri, MO  <i>Genome editing enables disease resistance in rice</i>	<b>Dr. Clarence J Swanton</b> University of Guelph, ON  <i>Plant competition and the physiology of fear</i>	<b>Dr. Richard Bélanger</b> Université Laval, Québec, QC  <i>A unique interaction with a biocontrol agent alters the parasitic activity of powdery mildews on plants</i>
10:10am	<b>Dr. Leslie Sieburth</b> University of Utah, UT  <i>Beyond transcription factors: A degrading story of gene expression control</i>	<b>Dr. Jaswinder Singh</b> McGill University, QC CSPB C.D. Nelson Award Address: <i>New paradigms in the genetic regulation of pre- and post- harvest grain germination in cereals</i>	<b>Dr. Diane G.O. Saunders</b> John Innes Centre, UK  <i>The wheat-rust conflict: Shifty enemies and the long reach of genomics</i>
11:00am	Lunch at Creelman Hall	Lunch at Creelman Hall	Lunch at Creelman Hall
Session	<b>Schedule of Plenary Talks at Plant Canada 2019</b>		Root evolution, Development and Function
Chairs			Dr. Geoffrey Wasteneys
1:30 pm			<b>Dr. Liam Dolan</b> University of Oxford, UK  <i>Evolution and development of the earliest land plant rooting systems</i>
2:20 pm			<b>Dr. Siobhan Brady</b> U of California-Davis, CA  <i>Systems biology of root development</i>
3:10 pm			Coffee-break (concourse)
3:40 pm			<b>Dr. William Plaxton</b> Queen's University, Kingston, ON CSPB Gold Medal Address: <i>Feeding hungry plants: purple acid phosphatases play a pivotal role in phosphorous nutrition</i>
4:30 pm			CLOSING REMARKS

## PLENARY SPEAKERS FOR PLANT CANADA 2019

### ALL PLENARY TALKS WILL BE IN ROZANSKI HALL room 104

<a href="#"><u>Dr. Richard Bélanger</u></a> Université Laval, QC	<a href="#"><u>PS8</u></a>	A unique interaction with a biocontrol agent alters the parasitic activity of powdery mildews on plants
<a href="#"><u>Dr. Siobhan Brady</u></a> UC Davis, CA	<a href="#"><u>PS11</u></a>	Systems biology of root development
<a href="#"><u>Dr. Liam Dolan</u></a> University of Oxford, UK	<a href="#"><u>PS10</u></a>	Evolution and development of the earliest land plant rooting systems
<a href="#"><u>Dr. Brian Fowler</u></a> University of Saskatchewan, SK	<a href="#"><u>PS4</u></a>	Winter wheat production in the high winter stress climate of western Canada – An experiment in crop adaptation
<a href="#"><u>Dr. Maureen Hanson</u></a> Cornell University, NY	<a href="#"><u>PS1</u></a>	Improving photosynthesis in C3 plants
<a href="#"><u>Dr. Mary Ruth MacDonald</u></a> University of Guelph, ON	<a href="#"><u>PS7</u></a>	Billions, trillions and quadrillions: The challenge of managing clubroot on canola and vegetables
<a href="#"><u>Dr. William Plaxton</u></a> Queen's University, ON	<a href="#"><u>PS12</u></a>	CSPB Gold Medal Address-Feeding hungry plants: Purple acid phosphatases play a pivotal role in phosphorous nutrition
<a href="#"><u>Dr. Diane G.O. Saunders</u></a> Norwich Research Park, UK	<a href="#"><u>PS9</u></a>	The wheat-rust conflict: Shifty enemies and the long reach of genomics
<a href="#"><u>Dr. Leslie Sieburth</u></a> University of Utah, UT	<a href="#"><u>PS3</u></a>	Beyond transcription factors: A degrading story of gene expression control
<a href="#"><u>Dr. Jaswinder Singh</u></a> McGill University, QC	<a href="#"><u>PS6</u></a>	CSPB C.D. Nelson Award Address-New paradigms in the genetic regulation of pre- and post-harvest grain germination in cereals
<a href="#"><u>Dr. Clarence Swanton</u></a> University of Guelph, ON	<a href="#"><u>PS5</u></a>	Plant competition and the physiology of fear
<a href="#"><u>Dr. Bing Yang</u></a> University of Missouri, MO	<a href="#"><u>PS2</u></a>	Genome editing enables disease resistance in rice



**PS1. Monday, July 8, morning session at 8:30 am**

**Dr. Maureen Hanson and Myat T. Lin**  
Cornell University, NY

***Improving photosynthesis in C3 plants***

**Abstract:** Rubisco, which catalyzes the first step in carbon fixation, is a target for efforts to improve photosynthetic efficiency. Modifying the cellular environment surrounding Rubisco to enhance the CO<sub>2</sub> concentration, in order to prevent photorespiration, is one strategy underway in our lab. Another strategy is to alter the properties of Rubisco itself to increase its enzymatic efficiency and/or to increase its affinity for CO<sub>2</sub>. Manajit Hayer-Hartl's group recently demonstrated assembly of active Rubisco in *E. coli*, where the effects of mutagenesis can be quickly examined. Assembly of Rubisco requires multiple chaperones: Cpn60 $\alpha$ , Cpn60 $\beta$  and Cpn20, as well as RbcX, Raf1, Raf2 and BSD2, for assembly of large and small subunits into L<sub>8</sub>S<sub>8</sub> holoenzymes. We modified Hayer-Hartl's Arabidopsis vectors to express tobacco Rubisco by replacing the Arabidopsis assembly factor genes with tobacco ones. We used this system to survey the activity of enzymes comprised of individual members of the tobacco Rubisco small subunit family, by co-expressing each one with the single large subunit gene in *E. coli*. These novel *E. coli*-expressed Rubisco enzymes have carboxylation kinetics very similar to that of the native tobacco Rubisco. We also produced tobacco Rubisco with a recently discovered trichome small subunit in *E. coli* and found that it has a higher catalytic rate and a lower CO<sub>2</sub> affinity compared to the enzymes with other small subunits.

**Bio:**

Dr. Maureen Hanson is Liberty Hyde Bailey Professor in the Department of Molecular Biology and Genetics at Cornell University in Ithaca, NY. She previously was on the Biology faculty at the University of Virginia, Charlottesville. She holds a Ph.D. in Cell and Developmental Biology from Harvard University, where she subsequently held an NIH NRSA postdoctoral fellowship. She is a Fellow and recipient of the Lawrence Bogorad Award of the American Society of Plant Biologists and a Fellow of the American Association for the Advancement of Science. She received the SUNY Chancellor's Award for Faculty Service and the Cornell Award for Outstanding Accomplishments in Basic Research. Her lab is known for identifying the first single dominant fertility restorer (*Rf*) gene that suppresses the expression of a toxic mitochondrial gene encoding cytoplasmic male sterility, the rediscovery of stromules and the demonstration that molecules pass through them between chloroplasts, and identification of several gene families previously unknown to comprise plant organelle RNA editing machinery. Her group has ongoing projects concerning improving photosynthetic efficiency through synthesizing the cyanobacterial carbon-concentrating mechanism in chloroplasts or through engineering of the carbon-fixing enzyme Rubisco. <https://hansonlab.org/>



**PS2. Monday, July 8, morning session at 9:20 am**

**Dr. Bing Yang**  
**University of Missouri, USA**

***Genome editing enables disease resistance in rice***

**Abstract:** Engineered CRISPR (clustered regularly interspaced short palindromic repeats) systems have emerged as potent biotechnological tools for both basic and applied research. The most promising utilization of CRISPR/Cas9 is for targeted genome editing, leading to precise genetic alterations within any genome of interest, as demonstrated in a plethora of organisms including several important crop plants. Bacterial blight is an important disease of rice in Asia and Africa. The causal agent *Xanthomonas oryzae* pv. *oryzae* (Xoo) uses secreted TAL effectors (TALEs) to ectopically activate host SWEET sucrose transporter genes, enabling disease. Xoo uses a limited set of TALEs to target promoters of three SWEET (*SWEET11*, *13*, and *14*) genes in rice. Naturally occurring variant SWEET genes act as recessive resistance genes by interfering with TALE targeting. We used CRISPR/Cas9 to engineer rice lines that carry multiple mutations in three SWEET gene promoters. The SWEET promoter mutations were introduced into different rice varieties, and the disease evaluation showed that editing SWEET promoters generated robust, broad-spectrum BB resistance. We also created rice lines that carry knockout mutations individually or in combination in three SWEET (*SWEET11*, *13*, and *14*) genes. The knockout lines are useful diagnostic tools to determine SWEET-inducing TALEs in field Xoo isolates and guide the deployment of resistance genes derived from the naturally occurring or genome edited SWEET promoter mutations.

**Bio:**

Dr. Bing Yang is professor in the Division of Plant Sciences at the University of Missouri – Columbia and member at Donald Danforth Plant Science Center. He received PhD degree in plant pathology at Kansas State University in 2000, joined Iowa State University as an assistant professor in 2007, and moved to the University of Missouri – Columbia and Danforth Plant Science Center in 2018.

Yang works on development and application of TALEN- and CRISPR-based genome editing technologies in crops such as rice, maize, wheat, sorghum and soybean. His research also focuses on basic understanding of host susceptibility/resistance to bacterial infection and using genome editing tools to engineer disease resistance in crop plants.

<https://cafnr.missouri.edu/person/bing-yang/>

<https://www.danforthcenter.org/scientists-research/principal-investigators/bing-yang>



**PS3. Monday, July 8, morning session at 10:10 am**

**Dr. Leslie Sieburth**  
**University of Utah, USA**

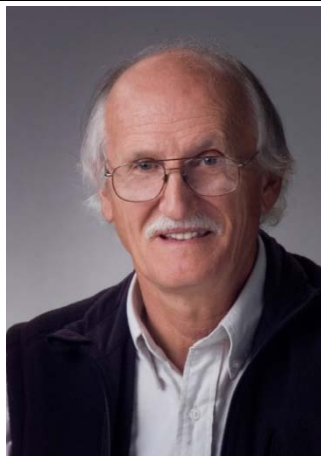
***Beyond transcription factors: A degrading story of gene expression control***

**Abstract:** Gene expression is a common component of many studies, and typically is quantified as mRNA abundance. mRNA abundances, however, are controlled by both rates of synthesis (transcription) and rates of decay, and yet roles of mRNA decay in regulating RNA abundances are largely unknown. To address this problem, my lab uses genetic and genomic approaches to identify mRNA substrates of the decay pathways in Arabidopsis. Mutants are used to link mRNA substrates with decay pathways, and our work focuses on *varicose* (*vcs*), which is required for the mRNA decapping step that initiates 5'→3' decay, and *suppressor of varicose* (*sov*), which encodes a 3'→5' exoribonuclease. The *vcs* mutant was initially identified because its phenotype includes thick and misshapen veins, especially in cotyledons and leaves. By contrast, the *sov* mutant has no obvious developmental defects. Genome-wide measurements of mRNA decay revealed that mRNA decapping carries out a majority of the fast-decaying mRNAs, and the fast-decaying mRNAs include those encoding transcription factors, components of signal transduction pathways, and genes annotated as responding to stress or developmental signals. Analysis of mRNA substrates of *sov*, by contrast, led to identification of an mRNA decay feedback pathway. In *sov* mutants, an over-compensating feedback mechanism reorganizes patterns of mRNA decay, decay rates, and also affects transcription. The profoundly altered gene expression dynamics in *sov* mutants maintains mRNA abundance at near wild-type levels. The implications of mRNA decay rates and feedback pathways for regulation of gene expression will be discussed.

### **Bio:**

Dr. Leslie Sieburth is a Professor and the Associate Director of the School of Biological Sciences at the University of Utah. Dr. Sieburth's research uses genetic, genomic, and cell biological approaches to dissect fundamental processes in plants. A major project focuses on gene expression, and regulatory roles of mRNA decay in controlling mRNA abundance. Her lab was the first to identify VARICOSE (VCS), a scaffold protein that is essential for functional assembly of the mRNA decapping complex, and also discovered SUPPRESSOR OF VARICOSE (SOV), another cytoplasmic mRNA decay pathway. Recent studies using genome-wide approaches identified the mRNA substrates of mRNA decapping and SOV, which also revealed overcompensating feedback pathways in mRNA decay mutants. A second project examines root-to-shoot signaling, and identified the *BYPASS1* gene as encoding a negative regulator of a root-derived signaling molecule that causes strong physiological and developmental responses in the shoot. This pathway appears to coordinate shoot physiology with perception of rhizosphere conditions, and because *BYPASS1*-like genes are present in genomes of all land plants, this work suggests that inter-organ communication mediated by BPS1 was vital as plants colonized land. Leslie began her independent academic career in the Biology Department at McGill University.

[https://faculty.utah.edu/u0143322-LESLIE\\_E\\_SIEBURTH/research/index.html](https://faculty.utah.edu/u0143322-LESLIE_E_SIEBURTH/research/index.html)



**PS4. Tuesday, July 9, morning session at 8:30 am**

**Dr. Brian Fowler**

**University of Saskatchewan, Saskatoon, SK**

***Winter wheat production in the high winter stress climate of western Canada – An experiment in crop adaptation.***

**Abstract:** The winter wheat production area on the North American Great Plains only extended as far north as southern Alberta in the 1970's. At that time, a research and development program was initiated with the objective of expanding production north and east into higher winter stress areas of the Canadian prairies. Winter survival was considered the main limitation in this region while market access, diseases and agronomic problems also restricted its acceptance as a viable cropping option. Intensive plant breeding efforts to increase cultivar winter hardiness were unsuccessful. However, research and development work started in the 1970's demonstrated that no-till seeding into standing stubble for snow trapping could successfully overwinter winter wheat if available cold hardy cultivars were grown using recommended management practices. Subsequent plant breeding improvements increased yield potential, straw strength, and rust resistance and winter wheat became one of the most environmentally sustainable cropping options. Commercial grain yield ranged from 125 to 149% of spring wheat and production increased to a high of 1.2 million ha in 2007 in Saskatchewan and Manitoba. In light of recent environmental concerns, changing weather patterns, diminishing world wheat reserves, and an ever increasing global population to feed, one would assume that winter wheat production in western Canada would continue to expand. However, marketing obstacles and difficulties inserting winter wheat into spring crop rotations, both of which have a direct influence on farmers' net returns, remain to be overcome before the full potential of this cropping option will be realized.

**Bio:**

Brian Fowler is a Professor in the Department of Plant Sciences at the University of Saskatchewan where his primary responsibilities have been in the areas of winter wheat plant breeding, genetics, drought, and mineral stresses, with special emphasis on cold hardiness and conservation farming systems. He has been a leader in winter cereal variety development and no-till research in the Great Plains region of North America. These efforts involved close co-operation with farmer and environmental groups that has been recognized by awards from the Manitoba-North Dakota Zero Tillage Farmers Association, the Saskatchewan Soil Conservation Association, the Alberta and Saskatchewan Winter Wheat Commissions and Winter Cereals Manitoba. In 2011, he was presented a Ducks Unlimited North American Recognition Award "for his passion of preserving the natural landscape across Canada". He was made a Fellow of both the Canadian and American Societies of Agronomy in recognition of his "significant contributions to the development of winter cereal production and conservation farming systems on the Canadian Prairies and the Northern Great Plains". In 2018, he was inducted into the Saskatchewan Agriculture Hall of Fame.

[https://www.researchgate.net/profile/David\\_Fowler6;](https://www.researchgate.net/profile/David_Fowler6)

<https://www.wheatworkers.ca/wcsm.php>



**PS5. Tuesday, July 9, morning session at 9:20 am**

**Dr. Clarence J. Swanton, N. Berardi and S. Amirsadeghi  
University of Guelph, ON**

***Plant Competition and the Physiology of Fear***

**Abstract:** Plant competition is recognised as one of the most important biological interactions that influences plant community structure and individual plant fitness. The competitive interactions for limited resources of light, water and nutrients are thought to be the primary mechanisms by which plants are harmed. This presentation will explore an alternative view, a view that suggests that the primary mechanism of plant competition is the creation of a cellular imbalance. Experimental evidence will be presented to show that under resource independent competition, far red enriched light reflected from neighbouring weedy plants can alter the balance between the production of reactive oxygen species and the plant's ability to detoxify through antioxidant defence mechanisms. Specifically, the determination of singlet oxygen involvement in early responses of crop plants to neighbouring weeds changes everything that we know about plant competition. It also provides a unique opportunity to compare physiological responses of mammals and plants to competition, hence the "physiology of fear".

**Bio:**

Dr. Swanton obtained his BSc in Botany from the University of Toronto, His MSc in Agrometerology from the University of Guelph, and a PhD in Plant Ecology from the University of Western Ontario. During the years between earning his MSc and his PhD, he was employed as a field agronomist with the Campbell Soup Company of Canada and later as a weed biologist with the Ontario Ministry of Agriculture and Food. In 1985 he joined the University of Guelph as a faculty member in the Department of Crop Science. In 1996 he was promoted to full professor. From 1998 to 2004, Clarence served as the first Chair of the Department of Plant Agriculture which included the Departments of Crop Science, Horticulture and the Horticulture Research Institute of Ontario. From 2007 to 2008 he served as President of the Canadian Weed Science Society. He has won numerous awards for his research. In 2013 he received the Outstanding Canadian Award in the area of Crop Protection from Bayer CropScience for exceptional contributions to science and innovation. His research is focused on weed ecology and the development of integrated weed management systems for field and horticultural crops. <https://www.plant.uoguelph.ca/cswanton>



**PS6. Tuesday, July 9, morning session at 10:10 am**

**Dr. Jaswinder Singh**  
**McGill University, Montreal, QC**

***CSPB C.D. Nelson Award Address:***

***New paradigms in the genetic regulation of pre- and post-harvest grain germination in cereals***

**Abstract:** In small grain cereals, it is an important goal to breed for the right balance of resistance to pre-harvest sprouting on one hand and reduced seed dormancy for rapid and uniform germination on the other, especially in many post-harvest processes. The antagonistic action of gibberellin and abscisic acid has been intensively investigated in recent years leading to an improved understanding of mechanisms underlying seed dormancy/germination. There is also emerging evidence for role of epigenetic mechanisms in seed dormancy which could be an alternate hormone independent genetic mechanism for seed dormancy. A key gene of RdDM pathway, *ARGONAUTE4\_9* has been found to be associated with pre-harvest sprouting in barley and wheat. Significant variation in the expression of *AGO4\_9* class genes in dormant and non-dormant barley and wheat genotypes was observed. Post-harvest seed germination commences after imbibition of dry seed activating many metabolic activities involving different carbohydrate reserves. During this process, we identified a specific Thaumatin- Like Protein, TLP8 which regulates the amount of  $\beta$ -glucan in germinating barley grains.  $\beta$ -glucan is one of the major bioactive components of endosperm cell walls for dietary fibers, excessive amount of which causes major hindrance during the malting process. Currently, we are employing CRISPR-based gene editing approaches to understand novel biological network during pre- and post-germination in barley. Overall, our efforts shed new light on the genetics of pre-harvest sprouting and on the protein-carbohydrate interaction during post-harvest germination, which could be potentially valuable for the development of future generation of healthy, and productive cereals.

### **Bio:**

Dr. Jaswinder Singh is currently an Associate Professor in the Department of Plant Science, McGill University, Canada. After completing his PhD from CSIRO Plant Industry, Canberra Australia, he did his postdoctoral studies at the University of California Berkeley. His research focuses on the enhancement of quality traits, and stress tolerance in crop plants using functional genomics tools. His laboratory is actively researching precocious germination from a unique perspective. His group has recently discovered a novel barley gene, which regulates the  $\beta$ -glucan activity during germination. His findings have shown for the first time the reversal of epigenetic silencing in plants. He has published over 50 research articles and delivered over 50 invited talks in international meetings and renowned academic institutes. He served in various executive positions in different plant science societies, notably as Eastern Director of Canadian Society of Agronomy (2010-12), International Committee member of the American Society of Plant Biologists (2012-15), is the current President of the Canadian Society of Agronomy and a Board Member, Plant Canada. The Canadian Society of Plant Biologists recognized his research with prestigious C. D. Nelson award in 2018 for his outstanding contribution to plant science. <https://www.mcgill.ca/plant/faculty/singh>





**PS7. Wednesday, July 10, morning session at 8:30 am**

**Dr. Mary Ruth McDonald and Bruce D. Gossen**  
**University of Guelph, ON; AAFC-Saskatoon**

***Billions, trillions and quadrillions: The challenge of managing clubroot on canola and Brassica vegetables***

**Abstract:** Clubroot, caused by *Plasmodiophora brassicae* Wor., is a problem wherever brassica crops are grown. The pathogen produces enormous numbers of long-lived resting spores, so keeping resting spore numbers low is key to effective clubroot management. One infected canola plant can produce 5 to 23 billion resting spores, and concentrations of  $10^6$  to  $10^9$  resting spores per gram of soil are common. Host resistance is often effective but not durable because intense selection for virulent pathotypes occurs on quadrillions of spores in each heavily infested field. As a result, there is renewed interest in physical and cultural controls to reduce disease pressure and protect genetic resistance. This has led to some unexpected findings. For example, a 2-year break from canola reduced spore numbers in soil by 99%, but this still left enough spores to cause 100% disease in a susceptible host. Also, spore survival was consistent with a Type III survival curve; spores that survive the initial two years can live a very long time. Other studies showed that no symptoms developed in infected plants at temperatures below 12 °C, so planting time can play a role in disease avoidance, especially for vegetable crops. Increasing soil pH to 7.2 or above can reduce severity, but is not fool-proof when temperature and soil moisture are optimum. Application of lime, calcium cyanamide, boron, solarisation or even fumigation can suppress clubroot. One or more of these soil treatments can be combined with grass cover crops to manage small patches of clubroot in canola fields.

### **Bio:**

Mary Ruth McDonald is a professor in the Department of Plant Agriculture, University of Guelph and she is also a Research Program Director at the university. Her research focuses on plant diseases, pathogen biology and integrated pest management for vegetable crops and canola, and also some aspects of sustainable vegetable production and adaptation to climate change. Mary Ruth teaches portions of undergraduate agriculture course and a graduate course on plant disease epidemiology. Prof. McDonald has published over 70 peer reviewed papers and has been an invited keynote speaker at regional, national and international conferences, including recent presentations in the U.K., Sweden and Mexico. She is the recipient of local, national and international awards for excellence in research, extension education, and integrated pest management. <https://www.plant.uoguelph.ca/mrmcdona>



**PS8. Wednesday, July 10, morning session at 9:20 am**

**Dr. Richard R. Bélanger**  
**Université Laval, Québec, QC**

***A unique interaction with a biocontrol agent alters the parasitic activity of powdery mildews on plants***

**Abstract:** The phyllosphere harbors a diverse microbial community in which fungi occupy a predominant space. In the course of evolution, all leaf surface fungi have acquired specific properties that enable them to compete and survive in this restricted ecological niche in spite of the apparent limited resources on the leaf. While we, as scientists, have been trying to ascribe a certain hierarchy among the fungi inhabiting the phylloplane, it is nonetheless important to remember that in a balanced environment, each of these fungi manages successfully to acquire the resources necessary for its establishment and reproduction on the leaf surface. For instance, recent observations have highlighted that closely related organisms co-habit in this environment with albeit quite different lifestyles. Among them, the Ustilaginaceae, including the genera *Ustilago* and *Pseudozyma*, comprise members that can be plant pathogens, biocontrol agents, or simple epiphytes. Comparative genomic analyses among different members of the Ustilaginaceae have revealed that these opposite lifestyles in similar environments are seemingly associated with the presence/absence of a very limited number of genes coding mostly for effector proteins. In the same manner, the members lacking the effector proteins to be a plant pathogen, for example, seem to have acquired specific features, including their own unique set of effectors, to adopt a different lifestyle. These complex and subtle evolutive processes appear to play key roles in the adaptation of fungi occupying specific ecological niches, and in their ability to extract resources necessary for their survival in a given environment.

### **Bio:**

Dr. Richard Bélanger is full professor in plant pathology and holder of a Canada Research Chair in plant protection at Laval University. His research endeavors concentrate on the development of biological and non-chemical approaches to control plant diseases. Along those lines, sustained efforts have been devoted toward biological control of powdery mildews with natural antagonists. Belanger's lab has pioneered the exploitation of the fungus *Pseudozyma flocculosa* and its unique properties to attack powdery mildews. This research has led the way to the development of a commercial product and to the elucidation of an unusual tritrophic interaction where the plant, the pathogen and the biocontrol fungus each contributes coordinated factors leading to the collapse of the pathogen.

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**PS9. Wednesday, July 10, morning session at 10:10 am**

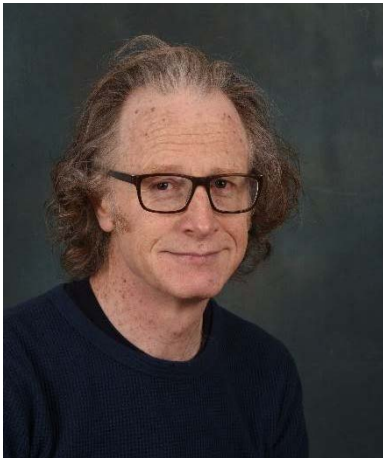
**Dr. Diane G. O. Saunders**  
**John Innes Centre, Norwich Research Park, UK**

***The wheat-rust conflict:  
 Shifty enemies and the long reach of genomics***

**Abstract:** Wheat rusts have been associated with crop failures and famine throughout history. Recent outbreaks of yellow (stripe) and stem rust in Europe have been linked to expansions in pathogen geographic distribution, exotic incursions and increased virulence. Our rapid “field pathogenomics” strategy, that uses transcriptome sequencing of infected wheat leaves taken directly from the field, has enabled us to gain insight into the population structure of the yellow rust pathogen over successive seasons and track the recent re-emergence of wheat stem rust in western Europe. Whilst effectively capturing pathogen diversity, transcriptome sequencing of infected host tissue can also be leveraged to assess the genotype and expression profiles of the host in its natural environment. Through analysis from the host side of the interaction we also identified changes in the expression of primary metabolic pathways including photosynthesis through comparative differential gene expression analysis of wheat varieties with differing levels of susceptibility. Analysis of independent wheat mutants for several of these genes has shown that they play a key function in enabling disease progression, with mutants displaying a severe reduction in disease symptoms. Developing and applying a genomics-driven approach to pathogen surveillance, we have generated valuable new knowledge on both the pathogen and host sides of the interaction that could be extremely useful for disease management.

### **Bio:**

Dr. Diane Saunders is a Project Leader at the John Innes Centre, Norwich Research Park, Norwich, UK. Dr. Saunders received her BSc from Exeter University where she continued her PhD in the laboratory of Prof. Nick Talbot studying the genetic mechanisms that regulate plant pathogen development. After receiving her PhD in 2009, she joined Prof. Sophien Kamoun’s group at The Sainsbury laboratory to continue to study the molecular mechanisms that underpin plant-pathogen interactions. In 2014, Diane became a computational biology fellow at the JIC and Earlham Institute, and moved to a Project Leader in 2017. Diane’s research focuses on (re-)emerging plant pathogens that pose a significant threat to agriculture, and particularly wheat rust pathogens that are known as the “polio of agriculture”. She uses an array of approaches to improve our understanding of how plant pathogens cause disease. To gain insight into the population dynamics of the wheat rust pathogens, Diane pioneered a revolutionary genomics-based pathogen surveillance technique called “field pathogenomics” to generate high-resolution data directly from infected field samples. This information is essential to help breeders to develop wheat varieties that are resistant to the wider range of yellow rust isolates that they now find in the field. <https://www.jic.ac.uk/people/diane-saunders/>



**PS10. Wednesday, July 10, afternoon session at 1:30 pm**

**Dr. Liam Dolan**  
**University of Oxford, UK**

***Evolution and development of the earliest land plant rooting systems***

**Abstract:** The evolution of the first rooting systems some time before 400 million years was a key innovation that occurred when the first complex multicellular eukaryotic photosynthetic organisms – plants – colonized the land. The rooting systems of the earliest diverging group of extant land plants comprised unicellular tip-growing filaments called rhizoids and are morphologically similar to cells that develop at the interface between the plant and the soil in vascular plants – root hairs. Subsequently specialized axes – multicellular structures that develop from self-renewing populations of cells called meristems – with evolved that carry out rooting function. A major aim of our research is to use fossils and genes to understand key events in the evolution of land plant rooting systems. Fossils demonstrate the variety of forms that existed and how these forms developed. We have identified the oldest rooting structures with meristems. Genetics has allowed us to define the regulatory mechanisms that controlled the development of the first land plant root system and demonstrate how these mechanisms changed during the course of evolution. This positive regulatory mechanism is preserved in most land extant plant lineages. By contrast, negative regulatory components of the mechanism evolved independently in different lineages and some are more than 300 million years old. By combining evidence from paleontology, genetics and development we can construct a picture for the evolution of rooting systems in the 100 million years after plants colonized the land and radiated across the continental surfaces.

**Bio:**

Liam Dolan graduated with a degree in Botany at University College, Dublin. He carried out PhD research on plant developmental genetics in cotton and Arabidopsis at the University of Pennsylvania with Scott Poethig and a post doc with Keith Roberts at the John Innes Centre in Norwich. After 13 years running his own research group at the John Innes Centre, he moved to the University of Oxford as the Sherardian Professor of Botany in 2009. He was Head of the Department of Plant Sciences between 2012 and 2017.

His research uses fossils and genes to understand how roots develop and evolved in the 470-500 million years since plants colonized the land. Fossils reveal the structure of ancient rooting systems. Genetics identifies developmental mechanisms controlling cellular development of rooting structures. Comparative developmental genetics illustrates how these mechanisms evolved in the course of plant evolution. A major discovery was the demonstration that the same genetic mechanism controlled the development of the simple rooting structures on the first land plants and the development of root hairs on the surface of extant vascular plant roots.

<https://www.plants.ox.ac.uk/people/liam-dolan>



**PS11. Wednesday, July 10, afternoon session at 2:20 pm**

**Dr. Siobhan Brady**  
**University of California-Davis, USA**

***Systems biology of root development***

**Abstract:** The plant vascular system supports the transport of water and nutrients throughout the plant body. Xylem cells contained within this tissue allow for long distance transport from the plant root to the shoot. Although the majority of plant cells are totipotent, xylem cells are unusual in that they undergo terminal differentiation. While the genes regulating this process are well characterized, much less is known regarding the dynamic behavior underlying the transition to xylem cell differentiation.

I will highlight the use of high-throughput yeast one hybrid network mapping, automated phenotyping, mining of publically available gene expression data and single cell sequencing approaches. Collectively, these approaches have led to the identification of double the number of transcription factors and novel modes of regulation involved in nitrogen metabolic regulation, and a bistable switch that underlies xylem cell differentiation.

Nitrogen is essential for plant growth. Insufficient nitrogen leads to decreased agricultural yield while nitrogen application from fertilizers results in increased plant productivity but can have a negative impact on the environment. Changes in nitrogen availability are perceived by dual function nitrate transporters in the root resulting in a signaling cascade and subsequent changes in gene expression. Despite the importance of transcriptional regulation in this adaptive response, a minimal number of nitrogen metabolic transcriptional regulators have been identified.

### **Bio:**

Siobhan Brady received her PhD at the University of Toronto in 2005, and she was a Natural Sciences and Engineering Research Council of Canada Postdoctoral Fellow at Duke University from 2005 – 2008. In 2009 she began an Assistant Professor Position and became an Associate Professor in 2015 at the University of California, Davis in the Department of Plant Biology and in the Genome Center. In 2016, she was named as a Howard Hughes Medical Institute Faculty Research Scholar. Research in the Brady lab focuses on the global regulation of gene expression and its contribution to root morphology and development in *Arabidopsis thaliana*, *Solanum* species, *Sorghum bicolor* and maize.

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## PS12. Wednesday, July 10, afternoon session at 3:40 pm

Dr. William Plaxton

Queen's University, Kingston, ON

### ***CSPB Gold Medal Address:***

### ***Feeding hungry plants: Purple acid phosphatases play a pivotal role in phosphorous nutrition***

**Abstract:** Phosphorus is an environmentally-limiting macronutrient that roots can only assimilate from soil as soluble inorganic phosphate (Pi,  $H_2PO_4^-$ ). The most abundant P fraction of many soils exists as organic Pi-monoesters (derived from decomposing biomaterial) unavailable for root uptake until hydrolyzed by secretory purple acid phosphatases (PAPs). Plant PAPs belong to a relatively large multigene family whose specific functions in P-metabolism are poorly understood. Purification, characterization, and identification via LC-MS/MS (peptide sequencing) of intracellular (vacuolar) and secreted (cell wall) PAP isozymes upregulated by Pi-starved suspension cell cultures of the model plant *Arabidopsis thaliana* have been complemented by studies of the corresponding loss-of-function mutants. This has allowed us to pinpoint the predominant Pi-starvation-inducible PAP isozymes (*i.e.*, AtPAP12, AtPAP17, AtPAP25, and AtPAP26) that facilitate *Arabidopsis* P-acquisition efficiency. AtPAP26 is of particular interest since it is: (i) the predominant PAP isozyme upregulated by Pi-deprived *Arabidopsis*, and (ii) also markedly upregulated during leaf senescence to remobilize Pi to developing seeds. Kinetic studies with purified vacuolar and secreted AtPAP26 glycoforms demonstrated that it effectively hydrolyzes Pi from a wide range of substrates with high catalytic efficiency. Furthermore, a Pi starvation- and senescence-inducible, tyrosine-phosphorylated and dual-targeted (*i.e.*, cell wall & vacuole) GNA-apple domain lectin (AtGAL1) interacts with, stabilizes, and activates a high-mannose glycoform of AtPAP26. AtPAP26 is emerging as a promising candidate for enhancing the P-acquisition and P-use efficiency of engineered crop plants. Achieving this goal is urgently required to reduce the massive overuse of non-renewable, inefficient, and polluting Pi-containing fertilizers in agricultural production.

### **Bio:**

William Plaxton received BSc (in 1980) and PhD (in 1984) degrees in Biochemistry from Carleton University (Ottawa). His PhD dissertation was under the supervision of Ken Storey and focussed on the metabolic adaptations of intertidal marine molluscs to anoxia stress. Plaxton was awarded an NSERC Post-doctoral Fellowship to conduct research on plant starch metabolism with Jack Preiss at the Dept. of Biochemistry, Michigan State University. In 1986 he was appointed to the faculty in the Dept. of Biology at Queen's University (Kingston). Plaxton's research program has been funded by NSERC and the Queen's Research Chair Program to conduct studies of the organization and control of plant (especially oilseed) glycolysis and respiratory metabolism, and the metabolic adaptations of phosphorus-starved plants. This research has integrated various biochemical, proteomic, genetic, and cell biology tools to characterize the molecular and functional properties of key enzyme proteins (with a particular interest in the crucial post-translational enzyme modifications such as phosphorylation and glycosylation). He has served as the President of the CSPB, and he is the recipient of both the CSPB C.D. Nelson Award and The Society Medal. Plaxton also enjoys Canada's magnificent outdoors and natural beauty, keeping fit, and playing upright and electric bass.

<https://biology.queensu.ca/people/department/professors/plaxton/>